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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-30368. The polypeptides sequences are designated SEQ ID NO: 30369-60736. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-30368 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-30368. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-30368 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-30368.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-30368; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-30368. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 30369-60736); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-30368; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention.

Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ

ID NO: 1-30368.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-30368. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55).

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-30368; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 30369-60736; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 30369-60736. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-30368; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 30369-60736. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

5 The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

10 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that
15 corresponds to any of the polynucleotides of SEQ ID NO: 1-30368 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-30368 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-30368 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

20 The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

25 The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at
30 least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-30368, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most
35 preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-30368, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-30368 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-30368 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altshul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-30368, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-30368, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 30369-60736 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-30368 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-30368), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxycarboxymethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -nucleic acid molecule. An α -nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-30368). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-30368 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaire *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 30369-60736 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-30368 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.

Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 30369-60736.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 30369-60736.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.

The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTTLL2, TF-1, Mo7e, CMK,

- 5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in

- Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

10 Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

15 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

20 **4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY**

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (*e.g.*, a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J.

Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:

Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Finc et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates
15 and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

20 **4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY**

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events
25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

35 **4.10.11 CANCER DIAGNOSIS AND THERAPY**

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguanzone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cell lines are available, *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, e.g.,

choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motor Sensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, *et al.*, 1983, *Science*, 219:56, or by B. Waksman *et al.*, 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

5 manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present
10 invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid
15 form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to
20 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally
25 acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection,
30 Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's
35 solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred.

The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 30369), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention that is located on the

surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, **133**:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, **107**:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)²} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab)/2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain F_v (scFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimide HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminopentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-30368 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-30368 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

- 5 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, 10 T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the 15 present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a 20 sample which is compatible with the system utilized.

- In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present 25 invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

- In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to 30 another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which 35 contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-30368, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kasieczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-30368. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-30368 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include *in situ* hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent *in situ* hybridization of chromosome spreads has been described, among other places, in Verma *et al* (1988) *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of *Science* (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) *J. Clin. Microbiol.* 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) *Mol. Cell Probes* 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-Melm₇), is then added to a final concentration of 10 mM 1-Melm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-Melm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) *Nucleic Acids Res.*

20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

- 5 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid

Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-30368 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-30368) of the present invention are incorporated in the attached Sequence Listing. A subset the predicted polypeptide sequences contain an unknown amino acid, a stop codon, a possible nucleotide deletion or a possible nucleotide insertion. These sequences have been shown in their entirety with the special characters in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-30368. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by

reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-30368 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 121 and Geneseq release 200103 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-30368. The nearest neighbor results for SEQ ID NO: 1-30368 are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provides the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by PFAM analysis for each peptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-30368. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/540,217

Table 1

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	39-41 192 197-200 315-316 540-542 576-580 608-622 635 1004 1185-1187 1273-1279 1431 1474 1721-1722 2036 2136-2137 2457 2471-2474 2513 2599-2603 2988- 2989 3105-3106 3212 3276-3277 3306-3308 3352 3365 3374-3376 3433 3448-3450 3555-3558 3693 3949-3953 4067-4072 4160-4162 4558-4560 4581-4582 4612-4614 4837-4840 5483-5484 5603-5606 5700 5802 5980-5984 6135-6136 6403-6404 6452-6453 7209-7212 7447-7449 7452-7460 7536-7541 7554-7555 7622-7623 7630-7636 7660-7665 7701-7703 7771 7778-7783 7798-7801 7921- 7923 7994 8010-8012 8025-8026 8145-8151 8227-8229 8415 8497-8499 8936-8938 8986-8991 9002-9004 9013- 9017 9337-9338 9366-9368 9375-9376 9391-9392 9395- 9396 9431-9436 9443 9475-9476 9517-9518 9522-9525 9586-9589 9603-9604 9851-9852 9854-9855 9874-9895 9905-9908 9947-9952 9969-9980 9986-9992 10025- 10026 10033-10037 10167-10172 10277 10480-10482 10488-10489 10498-10503 10520-10522 10537-10538 10592-10594 10628-10630 11226-11227 11339-11344 11406-11407 11431-11432 11731-11734 12150-12151 12239 12241-12244 12555-12559 12615-12618 12785- 12787 12978-12981 12984-12985 12997-12999 13567- 13568 13592-13595 13606-13608 13873-13875 13999- 14004 14360-14369 14650-14651 14684-14685 15013- 15018 15096 15174-15181 15209-15210 15250-15251 15257 15323-15324 15548-15552 15568-15572 15576- 15577 15588-15589 15699-15700 15881-15883 16438- 16439 16473-16478 16496-16497 16609-16611 16686- 16693 16700-16701 16727-16729 16836-16842 16934- 16937 16949-16953 17455-17456 17857-17861 17958- 17963 18029-18030 18136-18138 18423-18425 18516- 18518 18535-18537 18624-18626 18668-18672 18719- 18722 18750-18756 18790-18793 18802-18804 18836- 18838 18899-18903 18919-18921 18943-18945 18947- 18950 18964-18969 18989-18990 19013-19017 19045- 19048 19057-19065 19142-19147 19154-19155 19224 19316-19317 19345-19349 19355-19360 19362 19370 19385-19389 19415-19417 19422-19431 19442-19444 19503 19560-19562 19566 19604-19607 19693 19709- 19710 19727-19732 19736-19742 19772 19804-19808 19921-19929 19933-19938 19943-19946 19969-19981 20015-20017 20029-20043 20087-20094 20099-20102 20111-20112 20122-20127 20161-20164 20167-20171 20180-20181 20189-20194 20198-20199 20215-20218 20281-20282 20289 20321-20324 20349-20354 20361 20393-20400 20415-20417 20437-20440 20524-20535 20542-20545 20554-20558 20607-20612 20614-20615 20646-20652 20698-20707 20718-20725 20727-20732 20789-20791 20806-20812 20844-20849 20888-20889 20926 20938-20942 20999-21004 21027-21031 21062- 21066 21072-21075 21137-21140 21145-21148 21153-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			21154 21272-21274 21277-21283 21410-21414 21434- 21439 21485-21491 21495-21500 21647-21655 21729- 21733 21929-21935 21958-21961 21973-21974 21978 22000-22006 22026-22029 22040-22041 22087-22088 22101-22107 22141-22143 22160 22250-22252 22284- 22289 22309 22314-22317 22336-22342 22347-22348 22358-22359 22372 22405-22408 22495 22534-22539 22634-22643 22653-22654 22661-22662 22665-22667 22671-22674 22700-22701 22794-22796 22805-22809 22887-22891 22899-22900 22948-22950 22952-22953 22982-22986 22991-22994 23059-23060 23071 23141 23249 23251 23329-23337 23412-23414 23489-23490 23492-23493 23508-23509 23543-23544 23704 23834- 23835 23890-23892 23959 24014-24018 25289-25290 25319-25321 25374-25375 25966-25968 26205-26206 26258-26259 26303 26316-26321 26327 26337 26373- 26374 26596-26601 26788-26789 26843 26850-26852 26897 27067-27070 27100-27102 27150-27151 27247- 27251 27304-27305 27439-27440 27493-27495 27636- 27639 27750-27754 27814-27818 27861-27864 27890- 27892 27989-27990 28099-28100 28311-28313 28424 28426-28428 29278-29283 29409-29416 29444 29718- 29721 30141-30142
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC002	4007 4037-4042 4177-4190 4193-4199 4905-4907 5030 5036-5046 5326-5330 7036-7037 7043-7055 7089-7091 7094-7099 7175-7177 7374 7392-7395 7407-7414 7421-7442 7444-7446 8466-8476 8710-8715 8802-8806 8839-8841 8855-8859 8866-8868 9150-9151 9182-9193 9201-9208 9213-9229 9231-9234 9258-9259 9277-9286 9291-9296 9300 9312-9313 10324-10325 10330-10331 10349-10350 10443-10444 10704-10718 10723-10724 10726-10750 10755-10769 10773-10777 10835-10839 10842-10867 10879-10880 11890-11891 13176 13184-13188 13324-13325 13701 13706-13736 13751 13815-13818 13823 13825-13831 13854-13860 14962 14981-14983 15110-15114 15718-15725 15838-15841 15847-15854 15910-15911 15939-15943 15951-15960 15964-15982 15991-16000 16016-16018 16024-16027 17275-17277 17409-17430 17637-17641 17688-17696 17699-17700 17748-17751 17771-17776 17783-17786 17805-17806 17813-17817 17819-17824 17828-17829 17837-17841 17843-17847 17871-17873 17876-17879 17888-17890

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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bone marrow	Clontech	BMD007	373-374 4174 4362-4365 8320-8322 9531 15908-15909 16044-16046 16652 17160-17167 18771-18772 19749-19751 19814-19815 20698-20707 22310-22311 23070 25370-25372 26266 27702-27706
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Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL016	373-374 847-848 4581-4582 7465-7466 7745-7746 9267-9268 13638-13641 14344-14345 15277-15278 15356-15357 18825-18828 19049-19053 19306-19307 19370 19706-19708 20263-20264 20345-20348 20425-20426

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short arm of chromosome 8	Genetic Research		6796-6800 7019 7026 7028-7029 7031-7035 7041-7055 7058-7091 7094-7099 7173 7175-7177 7371-7372 7374 7392-7395 7407-7414 7421-7425 7444-7445 7469-7472 7475 8466-8476 8710-8715 8800-8813 8820-8841 8850- 8853 8855-8859 8862-8868 8877-8902 9047-9048 9081- 9085 9088-9099 9145-9149 9152-9181 9193 9205-9208 9213-9229 9231-9234 9239-9259 9269-9276 9291-9299 9314-9315 9962-9964 10320-10325 10329-10331 10334- 10342 10443-10444 10679-10683 10723-10724 10726- 10741 10748-10750 10755-10757 10759-10765 10775- 10777 10822-10830 10834-10867 10879-10880 11058- 11062 11416-11418 11890-11891 12218-12220 13000- 13004 13127-13128 13130-13136 13142-13174 13176- 13190 13307-13311 13316-13318 13324-13337 13425- 13495 13677 13681-13682 13695-13698 13706-13707 13712-13721 13723-13727 13730-13751 13815-13821 13823 13831 13854-13860 14876-14877 14962-14977 15120-15123 15593-15599 15705-15708 15710 15718- 15741 15773-15774 15780-15788 15815-15817 15826 15828-15831 15836-15837 15842-15845 15915-15916 15939-15943 15946-15956 15964-15976 15978-15980 15991-15996 16001-16018 16047-16052 16258-16268 17232 17366-17368 17579 17593-17598 17602-17609 17637-17667 17673-17684 17688-17700 17703-17707 17722-17724 17734-17789 17791-17799 17805-17806 17818-17824 17828-17829 17836-17849 17857-17861 17864-17868 17871-17873 17876-17879 17881-17885 17888-17894 17902-17904 17909-17916 18008-18012 18024-18028 18066-18068 18075-18089 18139-18151 18155-18156 18161-18162 18166-18168 18186-18187 18197-18203 18207-18214 18216-18218 18226 18230- 18239 18242-18245 18247-18253 18255-18263 18275- 18277 18286-18288 18291-18294 18308-18329 18335- 18349 18353-18359 18365-18370 18380-18392 18398 21304-21325 21501-21515 21534-21553 21557-21563 21568-21646 21656-21711 21718-21724 21728 21738- 21743 21748-21751 21788-21799 21863-21876 22523- 22533 22582-22588 22596-22602 22605-22606 22610- 22617 22658-22660 22817-22818 23029-23045 23532- 23539 23993-23998 24183-24196 24199-24225 24227- 24268 24274-24312 24319-24324 24333-24387 24397- 24470 24473-24490 24607-24631 24646-24665 24681- 24702 24722-24770 24775-24816 24820-24862 24869- 24923 24925-24951 24964-24977 24985-25060 25093- 25111 25114-25146 25158-25170 25178-25212 25220- 25224 25228-25246 25249-25253 25359-25363 25366- 25367 25450-25470 25475-25494 25506-25514 25539- 25561 25572-25593 25598-25603 25633-25656 25660- 25679 25690-25800 25807-25847 25853-25875 25878- 25880 25883-25896 25906-25951 25957-25965 25969- 26018 26050-26053 26077-26086 26090-26120 26127- 26129 26133-26143 26157-26184 26189-26194 26219- 26220 26237-26239 26629-26655 26691-26694 27677- 27688 27714-27717 27809-27811 28352-28357 28489- 28510 28514-28548 28556-28572 28579-28627 28635-

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Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	1604-1607 4008-4036 4049-4051 4180-4190 4923-4928 5242 5326-5330 7067-7087 7093 7175-7177 7426-7442 7475 8807-8813 8822-8835 8839-8846 8850-8853 8855- 8858 8862 8870-8873 8876 8892-8898 9088-9099 9152- 9181 9205-9208 9226-9229 9239-9257 9259 9294-9296 9301-9304 10343 10347-10350 10443-10444 10726- 10727 10759-10764 10775-10777 10842-10867 13000- 13004 13307-13308 13341 13422-13423 13425-13495 13730-13735 13737-13750 13823 14981-14983 15110- 15111 15120-15123 15718-15725 15815-15817 15827- 15833 15939-15943 15966-15968 15991-15996 16016- 16018 17606-17608 17701 17836 17857-17874 17876- 17887 17891-17894 18097-18134 18145-18151 18155- 18156 18184 18255-18263 18291-18292 18335-18340 18354 21549-21553 21573-21586 21660-21711 21728 21788-21799 21863-21876 22525-22530 22596-22598 22605-22606 22658-22660 24187-24193 24227 24358- 24369 24436-24438 24473-24480 24607-24609 24722- 24726 24749-24771 24795-24816 24869-24870 24908- 24923 24963 25017-25048 25052-25060 25078-25084 25091-25100 25114-25139 25147-25170 25187-25192 25247-25248 25359-25363 25461-25470 25489-25494 25515-25521 25539-25550 25572-25593 25623 25633- 25650 25676-25679 25728-25732 25741-25782 25883- 25889 25901-25902 25906-25911 25957-25959 25969- 26016 26059-26067 26136-26138 26150-26152 26157- 26164 26629-26653 27943-27947 28522-28524 28533- 28539 28571 28607-28614 28646-28650 28709-28719 28748 28754-28760 28768-28781 28809-28814 28822- 28824 28882-28887 28914-28916 28933-28935 29012- 29031-29038 29071-29082 29087-29095 29104-29107 29116-29141 29154-29158 29327 29446-29450 29492- 29494 29590-29605 29614-29620 29630 29645-29654 29663-29678 29686-29703 29741-29742 29763-29836 29842-29869 29879 29902-29911 29964-29968 30002- 30003 30048-30052 30084-30093 30118-30134 30145- 30149 30167-30177 30179-30182 30201-30204 30236- 30239 30254-30255 30275-30281 30343-30347
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal brain	Clontech	FBR001	202-203 847-848 1097-1098 1259-1262 1721-1722 2404-2406 2951-2955 5276-5278 5802 7902-7903 8377-8379 9196-9200 9443 9828 9969-9980 10273-10274 10326-10328 10876 10976-10978 11024-11025 11476-11478 11731-11734 11803-11804 12127-12128 12150-12151 13107-13117 13581-13583 14604 17366-17368 17455-17456 18627-18628 18964-18969 19018 19211-19212 19362 19387-19389 19401-19402 20328-20330 20345-20348 20554-20557 21256-21266 21377-21397 21434-21439 21978 22141-22143 22200-22203 22637-22643 22899-22900 23222 23709 23893-23902 25416-25417 26307-26309 26329 26831 27113 27245-27246 27386-27389 27976-27982 28186 30141-30142
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fetal brain	Clontech	FBR006	3-4 168 192 197-200 240-250 324-325 329-330 362 373- 374 464-465 532-535 553-554 576-578 613-614 713-715 847-848 912 927 934-935 949-950 1044-1045 1071 1097- 1098 1203-1204 1235-1237 1273-1279 1304 1411-1413 1488-1489 1569-1570 1591-1592 1678-1687 1705-1714 1923-1924 1977 2023-2029 2145 2228 2231-2253 2259- 2264 2356 2375 2396-2400 2404-2406 2431 2437-2439 2475 2525-2528 2599-2603 2656-2658 2663-2665 2707- 2716 2720-2732 2734-2745 2770-2772 2808-2811 2871- 2873 2889-2891 2931-2935 2951-2955 3001 3039 3080- 3081 3105-3106 3205-3207 3213 3261-3263 3377 3477- 3478 3507 3512-3514 3555-3558 3596 3671-3673 3683 3687-3691 3693 3708 3711-3712 3729-3730 3781-3784 3809 3939-3941 3949-3953 4055-4061 4065 4091-4100 4122-4126 4137-4139 4209-4210 4542 4562-4568 4574- 4576 4667 4673 4683-4684 4720-4725 4765-4773 4795- 4809 4845-4851 4854-4856 4870-4871 4948 4964-4965 4970 5136-5137 5139 5246 5251-5252 5291-5294 5392 5532-5533 5557-5560 5567-5568 5594-5602 5744-5747 6011-6021 6137 6155-6161 6209-6211 6217-6222 6378- 6388 6393-6395 6406-6410 6452-6453 6488-6490 6513- 6515 6542-6543 6669-6670 6674-6675 6775-6778 7194- 7197 7220-7227 7236-7237 7264-7266 7350-7352 7364- 7365 7426-7442 7452-7460 7482-7517 7557-7559 7580- 7597 7604-7605 7630-7636 7657-7659 7695-7696 7745- 7746 7778-7783 7787-7788 7898-7900 7946 7957 7986- 7987 7993 8013-8016 8079 8137-8141 8152-8156 8162- 8173 8187-8200 8204-8205 8211-8213 8230-8233 8247- 8249 8263-8265 8301-8310 8313-8314 8320-8322 8335- 8336 8347-8348 8351-8360 8371-8374 8383-8389 8420- 8421 8426-8428 8457-8458 8461-8465 8497-8499 8506 8512-8513 8588-8597 8607-8609 8688 8733-8735 8758- 8759 8762-8766 8919-8933 8936-8945 8974-8977 8982- 8983 8998-9004 9029-9030 9043-9045 9068 9306-9311 9380-9381 9510-9518 9529-9531 9585 9603-9604 9729- 9731 9763-9767 9799-9800 9808-9812 9829-9832 9929- 9935 9958-9959 9969-9980 9989-9992 9997-10009 10015-10016 10033-10037 10449-10453 10477-10478 10483 10513-10518 10523-10530 10537-10538 10603- 10608 10638-10639 10780-10782 10901-10902 10931- 10933 10965 11026 11081 11123-11124 11317 11345- 11350 11465-11472 11476-11478 11577 11672 11711- 11712 11731-11734 11739-11740 11803-11804 11934 12102-12110 12117-12118 12131-12132 12202-12208 12215-12217 12226-12228 12333-12334 12374-12377

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal brain	Clontech	FBRs03	2724-2726 4581-4582 7681-7687 11081 11937-11938 12150-12151 12258 14004 16168-16171 17070-17071 18919-18921 19526-19529 19709-19710 20927-20928 21877-21880 22115-22116 22160 22277-22283 22343- 22346 22973 23543-23544 23793-23797 27114-27120 27814-27815 27989-27990 30135-30140
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fetal kidney	Clontech	FKD001	30 177-178 279-280 329-330 373-374 508 524-525 656 726 785-786 1006-1007 1012-1017 1021-1025 1028 1047 1092-1094 1235-1237 1269-1272 1290 1302-1303 1309 1314 1431 1499 1678-1680 1705-1714 1887-1889 2063-2065 2306 2550-2552 2649-2650 2874-2876 2926 2988-2989 3105-3106 3461-3463 3531-3534 3705-3706 3737 4255 4438-4443 5141-5145 5311-5325 5335-5336 5827-5828 5919-5921 6348-6349 6405-6410 7536-7541 7561-7562 7640-7642 7728 7745-7746 7757-7759 7778-7783 8043-8044 8277-8295 8466-8476 9018-9020 9038-9039 9306-9311 9339 9456-9458 9460 9531-9534 9617-9626 9664-9665 9826 9829-9832 9993-9996 10012 10273-10274 10277 10306 10488-10489 10494 10592-10594 10615-10623 10638-10639 10873-10875 11431-11432 11435-11436 11476-11478 11549-11550 11761-11763 11803-11804 11842 12150-12151 12202-12205 12361 12483-12485 12519-12540 12543-12544 12637 12723 12796-12798 12978-12981 13077-13079 13592-13595 13603-13605 13888-13895 13931-13933 13939-13953 14004 14090-14093 14261-14263 14784 15124-15125 15151-15157 15221 15290-15291 15576-15577 15588-15590 15623-15626 15686-15687 15878 16044-16046 16284-16289 16371-16372 16636-16637 16652 16828-16831 17330-17332 17455-17456 17958-17962 18015-18016 18527 18625-18626 18644-18650 18738-18744 18761 18778-18780 18796 18802-18807 18857-18880 18899-18903 18919-18921 18934-18935 18960-18963 18975 18989-18990 19062-19065 19074-19083 19224 19257 19351-19354 19370 19405-19411 19415-19417 19422-19431 19445 19461 19503 19522-19524 19526-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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induced neuron cells	Stratagene	NTD001	188-191 289-291 576-578 617-618 716-717 1030 1034 1097-1098 1646 2540-2541 2599-2603 2675-2678 2724-2726 2871-2873 2973 3326-3331 3374-3376 3649-3653 3908-3910 3930 3949-3953 4165-4170 4486-4487 4515-4516 4581-4582 4984-4985 5053-5054 5272-5275 5335-5336 5777-5778 5802 5919-5921 5980-5984 6403-6404 6787-6790 6795-6800 7170-7172 7258-7263 7325-7343 7363 7368-7369 7557-7559 7688-7689 7693-7694 7701-7703 7745-7746 7778-7783 7906-7912 7990-7992 8187-8200 8250 8497-8499 8689-8690 8758-8759 8998-9001 9029-9030 9040-9042 9047-9048 9087 9321-9323 9559-9560 9829-9832 9909-9912 9947-9952 9993-9996 10477-10478 10494 10531-10532 10592-10594 10615-10623 10842-10867 10980-10985 11045 11228-11229 11314-11315 11405 11431-11432 11541-11543 11546 11609 11700-11707 11739-11740 11803-11808 11886-11891 11941-11944 12131-12132 12241-12244 12258-12262 12898-12899 12902-12905 12997-12999 13592-13595 13609-13612 13652-13659 14304-14305 15182-15183 15190-15191 15290-15291 15588-15589 15969-15974 16028-16029 16180-16181 16545 16619-16621 16642 17292-17296 17401-17432 17435 17455-17456 18029-18030 18097-18134 18300-18307 18400-18402 18412-18418 18691-18692 18771-18772 18796-18801 18839-18841 18846-18853 18899-18903 18989-18990 19001-19004 19012 19074-19080 19106-19118 19207-19208 19256-19257 19266-19267 19306-19307 19316-19317 19343 19355-19360 19387-19389 19447-19448 19458-19460 19488-19493 19566 19598-19601 19617-19619 19659-19661 19736-19742 19804-19808 19813 19939 19972-19980 20029-20043 20099-20102 20106-20110 20114-20119 20122-20127 20182-20188 20208-20218 20485-20490 20521-20523 20607-20612 20681 20698-20707 20827-20835 20853-20854 20871 21105-21111 21248-21271 21275-21280 21284-21294 21463-21465 21495-21500 21587-21646 21929-21935 22020-22025 22045-22046 22070-22073 22141-22143 22160 22187-22192 22195-22198 22243-22245 22358-22359 22365-22371 22381-22388 22433 22653-22654 22671-22674 22690 22916-22922 22977 23201-23202 23251 23358-23360 23420-23421 23700-23701 23798-23799 23806-23809 23890-23892 24749-24754 24928-24938 24985-24988 25029-25040 25279-25288 25376-25379 26024-26028 26205-26206 26209-26213 26266 26280 26310-26314 26327 26361-26365 26678-26680 27091 27100-27102 27269-27270 27446-27449 27522-27539 27544-27545 27729-27739 27861-27864 27896-27927 27989-27990 28315-28316 28361-28364 29117-29123 29328-29337 29343-29345 29418-29419 29426-29431 29885-29891 30167-30177 30352 30361-30368

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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neuronal cells	Stratagene	NTU001	240-250 373-374 425-427 576-578 847-848 1388-1401 1432-1435 1470 1499 1778-1779 2306 2599-2603 2944 3040-3076 3107-3108 3326-3331 3421-3422 3477-3478 3483-3484 3789-3794 3912-3915 4055-4058 4171-4172 4206-4208 4515-4516 4562-4568 4581-4582 4785-4789 5186-5189 5253-5266 5272-5275 5279-5283 5525-5526 5943-5945 6135-6136 6403-6404 7264-7266 7346-7352 7784-7786 7815-7818 8203 8227-8229 8465 8497-8499 8716-8718 8998-9004 9007-9008 9038-9039 9049-9068 9472-9474 9479-9481 9535-9537 9594-9602 9735-9738 9929-9935 9969-9980 10161-10163 10167-10196 10516-10518 10615-10623 10873-10875 10915-10918 11308-11310 11334-11335 11775-11776 11840 12150-12151 12258 12590-12592 12653-12654 12716-12719 12997-12999 13552-13555 13638-13641 13847-13849 14038-14041 14044-14045 14137-14138 14277-14280 14640-14642 14814-14815 15025-15069 15100-15109 15277-15278 15408-15411 15530-15531 15563-15564 15576-15577 15588-15589 15863-15870 16141-16143 16174-16176 16182-16189 16545 16642 16652 16836-16842 16851-16853 17284-17285 17435-17440 17451-17454 17958-17962 18029-18030 18043 18097-18134 18500-18501 18562-18576 18671-18672 18796-18801 18825-18828 18857-18880 18925-18933 18975 18993-18995 19049-19053 19153 19298-19300 19306-19307 19316-19317 19351-19354 19370 19375-19379 19395-19400 19415-19417 19432-19434 19511 19515-19521 19526-19529 19564-19566 19625 19659-19661 19683-19687 19813-19815 19855-19856 19938 19940-19942 19965-19967 19972-19980 20026-20027 20099-20102 20106-20110 20161-20164 20200-20207 20241 20289 20336-20338 20406-20407 20437-20440 20485-20490 20521-20523 20537-20541 20602-20612 20631-20634 20639-20640 20646-20648 20666-20671 20792-20797 20827-20843 20871 20897-20900 20924-20925 20927-20928 20938-20942 20957-20962 21032-21045 21208-21210 21241-21247 21256-21262 21272-21283 21295-21296 21554-21556 21587-21655 21899-21904 21936-21938 21951-21954 21958-21966 22007-22015 22040-22041 22047-22049 22070-22073 22152-22156 22165-22168 22171-22175 22218-22224 22243-22245 22253-22255 22292-22299 22312-22313 22343-22346 22372-22373

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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pituitary gland	Clontech	PIT004	307-308 395 845-846 1440-1447 1451 1453-1454 2272-2274 2362-2363 3105-3106 3322-3323 3433 4080-4082 4612-4614 4714-4719 4971-4974 5284 5335-5336 5572-5573 6140-6143 6405 6488-6489 7216-7219 7611-7612 7988 8343-8344 8917-8918 9007-9008 9029-9030 9444 9759-9762 10451-10453 10640-10644 10873-10875 11649-11650 11660-11661 11731-11734 11803-11804 11835-11836 12361 12637 13077-13079 13592-13595 14261-14263 14723-14724 15093-15095 15190-15191 15392-15396 16141-16143 16422-16429 16636-16637 16642 16894-16896 18691-18692 18836-18838 18899-18903 18975 19074-19080 19260-19262 19362 19415-19417 19458-19460 19921-19923 20161-20164 20452-20455 20548-20553 20575-20578 20629-20630 20666-20671 21072-21075 21149-21151 21256-21262 21881-21885 21955-21957 22160 22187-22192 22199 22358-22359 22375-22376 22383-22388 22644-22651 22768-22770 22805-22809 22852-22853 22991-22994 23080-23083 23242-23244 23704 23720-23721 23761 26196-26199 26327 26361-26365 26431 26755-26756 27067-27070 27254-27260 27755-27756 27825-27826 27861-27864 28311-28313 29332-29337 29360-29362 29370 30085-30087 30141-30142 30150-30156
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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rectum	Invitroge n	REC001	180-181 534-535 540-542 1681-1687 1705-1714 1721- 1722 1745-1746 2272-2274 2675-2678 2695-2698 2813- 2846 3326-3331 3555-3558 3687-3691 3717-3720 3834- 3835 3949-3953 4692-4695 4857-4861 5246 5337-5341 5572-5573 5802-5804 5919-5921 6209-6211 6400-6404 6406-6410 7209-7212 7426-7442 7609 7747-7751 7757- 7759 7778-7783 8074-8078 8323-8325 8329-8334 8453- 8454 8741-8750 8986-8991 9029-9030 9043-9045 9305 9375-9376 9391-9392 9456-9458 9531 9585 9828 9921- 9922 9986-9988 10263-10264 10277 10306 10480-10482

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salivary gland	Clontech	SAL001	260 307-308 331 551-552 832-836 969-971 981-985 1312-1313 1721-1722 1810-1811 2072 2303 2306-2307 2599-2603 2847 2850-2860 3151-3154 3657 3723-3728 3737 3840-3852 3949-3953 4515-4516 4531-4533 4555- 4556 4581-4582 4857-4861 4971-4974 5269-5271 5525- 5526 5652-5653 5658 5700 6337-6338 6411-6412 6442- 6449 6762-6764 7452-7460 7678-7687 7701-7703 7745- 7746 7778-7783 7805 7988 8145-8151 8187-8200 8337- 8342 8383-8389 8554-8555 8986-8991 9018-9020 9038- 9039 9427-9428 9531 9535-9537 9782-9783 9828 9899- 9901 9923-9924 9997-10009 10306 10531-10532 10607- 10611 10876 11009 11123-11124 11609 11644-11648 11669-11671 11731-11734 11835-11836 12040-12041 12175-12176 12202-12205 12229-12230 12362 12434 12468-12469 12474 12565-12568 12573-12574 12642-

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Salivary gland	Clontech	SALs03	981-985 8698-8700 11538-11540 14546-14549 20316 27814-27815 27989-27990 28424
skin fibroblast	ATCC	SFB001	1307 3374-3376 6285-6288 6791-6794 10306 12258 17026-17028 18029-18030 19011 19939 19972-19980 20182-20188 22141-22143 22160 22495 23415-23418 28424 30150-30156
skin fibroblast	ATCC	SFB002	2926 5805-5807 6166-6168 10306 12258 17026-17028 17038-17041 17455-17456 18029-18030 19011 19548- 19553 19813 21060-21061 22141-22143 22160 22373- 22495 22531-22533 26879 27636-27639 28424 30150- 30156
skin fibroblast	ATCC	SFB003	5803-5804 6166-6168 12258 17335-17339 18029-18030 18778-18780 19062-19065 19548-19553 20182-20188 22007-22015 23051-23052 23419 25340-25341 27269- 27270 27814-27815 28424 30150-30156
small intestine	Clontech	SIN001	83 87-94 195-200 307-308 332 373-374 557-559 674-675 783-784 852-855 901-904 1071 1240-1241 1470 1678- 1680 1755-1762 1764-1766 1769-1772 2030 2048 2089-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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			27600-27601 27814-27815 27819-27820 28142-28145 28233 29367 30141-30142
uterus	Clontech	UTR001	124-125 188-191 227-230 251-252 301 329-331 738-740 919-922 1028 1047 1453-1454 1562-1564 1705-1714 1893-1901 1912-1913 2366 2374-2377 2926 2988-2989 3001 3205-3207 4557-4560 4712-4713 4971-4974 5903-5906 5919-5921 6114-6136 6235-6237 6403-6404 6533-6535 6625-6626 6932-6938 7678-7680 7728 7771 7798-7801 7921-7923 7946 8010-8012 8084-8085 8090-8093 8137-8141 8313-8314 8368-8370 8415 8420-8421 8689-8690 9072-9074 9264-9265 9517-9521 9535-9537 9577-9578 9828-9832 9848-9850 9929-9935 9953 10033-10037 10268-10272 10508-10512 10537-10538 10980-10985 11071-11075 11135 11505-11506 11546 11609 11731-11734 11803-11804 12023-12026 12046-12049 12190-12191 12378-12397 12432-12433 12894-12897 13107-13117 13592-13597 13888-13895 13954-13956 14058-14059 14261-14263 14445-14447 14604 14650-14651 14988-14992 15182-15183 15187-15189 15290-15291 15390 15576-15577 15699-15700 15855-15857 16145-16146 16174-16176 16600 16643-16648 16716-16723 16851-16853 17330-17332 17454 17958-17962 18015-18016 18527 18655-18658 18673-18677 18761 18789 18825-18834 18894-18896 18899-18903 18936-18939 19036-19039 19074-19083 19362 19370 19375-19379 19387-19389 19442-19444 19560-19562 19609-19615 19693 19727-19732 19764-19767 19816-19818 19926-19929 19933-19937 19950 19981 20029-20043 20120 20122-20127 20146-20148 20151-20154 20289-20296 20298 20328-20330 20366-20368 20401-20405 20427-20431 20469-20471 20491-20494 20554-20557 20602-20606 20629-20630 20649-20652 20689-20692 20753 20758-20767 20801-20805 20858-20862 20864 20938-20942 21005-21008 21072-21075 21213-21215 21281-21294 21377-21397 21911-21912 21955-21957 21978-21982 22019-22025 22050-22055 22090-22091 22187-22192 22218-22224 22251-22252 22261-22264 22358-22359 22362-22364 22373 22405-22408 22571-22581 22622-22624 22644-22651 22663-22664 22887-22891 22955-22957 22969-22970 23047-23050 23094-23097 23141 23425-23427 23439-23447 23543-23544 24029-24033 24130-24144 25085-25090 25340-25341 25374-25375 25416-25417 26221-26223 26270-26272 26285-26290 26327 26607-26609 26676-26677 26755-26756 26853-26854 26860-26862 27173-27174 27294 27348-27353 27493-27496 27602-27606 27636-27639 27649-27654 27729-27739 27861-27864 27896-27927 28105-28121 28133-28137 28311-28313 28424 28426-28428 29339-29340 29378-29379 29962-29963 30150-30156

*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen),

- 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
1	30369	C	1	23	76	
2	30370	B	2	1	735	
3	30371	B	3	1	783	
4	30372	B	4	104	266	
5	30373	B	5	1	1113	
6	30374	C	6	3	164	
7	30375	B	7	112	279	
8	30376	B	8	198	405	
9	30377	B	9	1	687	
10	30378	C	10	346	598	
11	30379	B	11	1	960	
12	30380	B	12	44	350	
13	30381	B	13	264	465	
14	30382	B	14	483	1556	
15	30383	B	15	140	838	
16	30384	B	16	1	372	
17	30385	B	17	1	1404	
18	30386	B	18	25	2013	
19	30387	C	19	1	381	
20	30388	C	20	605	755	
21	30389	B	21	1	912	
22	30390	C	22	124	315	
23	30391	C	23	44	310	
24	30392	B	24	1	330	
25	30393	B	25	1	411	
26	30394	B	26	147	257	
27	30395	B	27	1	597	
28	30396	B	28	201	862	
29	30397	C	29	249	515	
30	30398	B	30	41	816	
31	30399	C	31	26	142	
32	30400	B	32	259	2528	
33	30401	B	33	1	759	
34	30402	B	34	964	2121	
35	30403	C	35	298	449	
36	30404	C	36	115	396	
37	30405	C	37	148	318	
38	30406	C	38	383	483	
39	30407	B	39	1	1125	
40	30408	B	40	1	831	
41	30409	C	41	363	602	
42	30410	B	42	1	324	
43	30411	B	43	64	199	
44	30412	B	44	1	1007	
45	30413	C	45	380	583	
46	30414	B	46	1	432	
47	30415	C	47	1	249	
48	30416	B	48	1	798	
49	30417	B	49	14	1070	
50	30418	C	50	1	225	
51	30419	B	51	1	2673	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
52	30420	B	52	1	258	
53	30421	B	54	1	624	
54	30422	C	55	166	333	
55	30423	B	56	298	380	
56	30424	C	57	139	379	
57	30425	B	58	1	157	
58	30426	B	59	1	447	
59	30427	B	60	1	579	
60	30428	B	61	1	1059	
61	30429	B	62	1	816	
62	30430	B	63	1	558	
63	30431	B	64	1	540	
64	30432	B	65	1	555	
65	30433	B	66	1	648	
66	30434	B	67	1	798	
67	30435	B	68	1	1455	
68	30436	B	69	1	1278	
69	30437	B	70	88	3012	
70	30438	B	71	1	1092	
71	30439	B	72	575	1033	
72	30440	B	73	644	926	
73	30441	B	74	1	1239	
74	30442	B	75	1	1074	
75	30443	B	76	81	467	
76	30444	C	77	44	286	
77	30445	B	78	1	297	
78	30446	B	79	1	978	
79	30447	B	80	72	715	
80	30448	B	81	1	1296	
81	30449	B	82	63	162	
82	30450	C	83	22	420	
83	30451	C	84	201	733	
84	30452	C	85	417	575	
85	30453	B	86	1	267	
86	30454	B	87	112	738	
87	30455	C	88	260	379	
88	30456	B	89	77	399	
89	30457	B	90	158	420	
90	30458	B	91	1	1437	
91	30459	C	92	22	321	
92	30460	B	93	1	843	
93	30461	B	94	142	2798	
94	30462	B	95	887	8434	
95	30463	B	96	1	1014	
96	30464	B	97	1	1197	
97	30465	B	98	16	555	
98	30466	B	99	1	423	
99	30467	B	100	1	651	
100	30468	B	101	233	556	
101	30469	B	102	192	883	
102	30470	C	103	65	274	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
103	30471	C	104	328	546	
104	30472	B	105	80	3900	
105	30473	B	106	1	951	
106	30474	C	107	1	279	
107	30475	C	108	246	368	
108	30476	B	109	1	819	
109	30477	B	110	1	634	
110	30478	B	111	1	379	
111	30479	B	112	80	2747	
112	30480	C	113	139	414	
113	30481	C	114	1	330	
114	30482	B	115	53	618	
115	30483	B	116	1	426	
116	30484	C	117	135	296	
117	30485	C	118	239	432	
118	30486	C	119	381	776	
119	30487	B	120	1	381	
120	30488	C	121	42	175	
121	30489	C	122	1	399	
122	30490	B	123	1	792	
123	30491	B	124	1	894	
124	30492	B	125	1	3498	
125	30493	B	126	8	874	
126	30494	B	127	1	2160	
127	30495	B	128	1	1776	
128	30496	B	129	1	567	
129	30497	B	130	195	728	
130	30498	B	131	1	615	
131	30499	B	132	1	420	
132	30500	B	133	661	2711	
133	30501	B	134	1	621	
134	30502	C	136	1	465	
135	30503	C	137	113	502	
136	30504	C	139	78	269	
137	30505	C	140	98	472	
138	30506	B	141	403	533	
139	30507	C	142	64	315	
140	30508	B	143	1	591	
141	30509	C	144	528	1151	
142	30510	C	145	1	414	
143	30511	B	146	1	936	
144	30512	C	147	91	195	
145	30513	C	148	562	705	
146	30514	C	149	122	313	
147	30515	B	150	566	1535	
148	30516	C	151	75	248	
149	30517	C	152	1	624	
150	30518	C	153	551	655	
151	30519	C	154	315	497	
152	30520	C	155	262	554	
153	30521	C	156	1	282	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
154	30522	B	157	1	508	
155	30523	C	158	243	545	
156	30524	B	159	8	395	
157	30525	C	160	33	194	
158	30526	B	161	50	355	
159	30527	B	162	128	1230	
160	30528	B	163	243	710	
161	30529	B	164	121	742	
162	30530	B	165	152	227	
163	30531	C	166	156	503	
164	30532	B	167	67	1280	
165	30533	B	168	1	444	
166	30534	B	169	161	206	
167	30535	B	170	189	1207	
168	30536	B	171	1	613	
169	30537	B	172	1	70	
170	30538	C	173	611	751	
171	30539	B	174	398	2472	
172	30540	B	175	87	646	
173	30541	B	176	1	1455	
174	30542	C	177	1	339	
175	30543	B	178	1	1458	
176	30544	B	179	278	766	
177	30545	B	181	85	749	
178	30546	B	182	50	498	
179	30547	C	183	1	522	
180	30548	B	184	90	482	
181	30549	B	185	86	442	
182	30550	C	187	129	308	
183	30551	C	188	1	414	
184	30552	B	190	1	378	
185	30553	C	192	252	308	
186	30554	B	193	1	576	
187	30555	C	194	1093	1311	
188	30556	B	195	45	324	
189	30557	B	196	1	249	
190	30558	C	197	309	443	
191	30559	C	198	615	866	
192	30560	B	199	86	1332	
193	30561	B	200	49	334	
194	30562	B	201	64	638	
195	30563	C	202	195	338	
196	30564	C	203	1	357	
197	30565	B	204	1	693	
198	30566	C	205	121	291	
199	30567	C	206	156	380	
200	30568	C	207	1211	1456	
201	30569	B	208	62	328	
202	30570	C	209	105	179	
203	30571	B	210	229	1483	
204	30572	B	211	1	749	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
205	30573	B	212	1	190	
206	30574	C	213	121	367	
207	30575	B	214	121	456	
208	30576	B	215	1	2631	
209	30577	B	216	63	419	
210	30578	B	217	114	485	
211	30579	B	218	628	1447	
212	30580	C	219	252	377	
213	30581	B	220	1	847	
214	30582	B	221	68	343	
215	30583	B	222	138	911	
216	30584	B	223	44	882	
217	30585	B	224	1	429	
218	30586	B	225	87	312	
219	30587	C	226	44	343	
220	30588	C	227	41	286	
221	30589	C	228	1145	1372	
222	30590	B	229	1	720	
223	30591	C	230	1	430	
224	30592	C	231	58	297	
225	30593	B	232	613	683	
226	30594	B	233	613	683	
227	30595	C	234	238	455	
228	30596	B	235	319	615	
229	30597	C	236	255	494	
230	30598	B	237	106	600	
231	30599	B	238	1	654	
232	30600	B	239	1	654	
233	30601	B	240	243	356	
234	30602	B	241	1	932	
235	30603	C	242	36	215	
236	30604	B	243	1	288	
237	30605	C	244	25	186	
238	30606	B	245	1	574	
239	30607	B	246	1	1257	
240	30608	B	247	162	263	
241	30609	C	248	79	207	
242	30610	B	249	194	276	
243	30611	B	250	1	1671	
244	30612	C	251	118	311	
245	30613	B	252	88	1485	
246	30614	B	253	339	443	
247	30615	B	254	667	1165	
248	30616	B	255	1	981	
249	30617	B	256	450	3131	
250	30618	B	257	900	1199	
251	30619	C	258	5	271	
252	30620	B	259	65	689	
253	30621	C	260	1	321	
254	30622	B	261	1	137	
255	30623	B	262	34	282	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
256	30624	B	263	46	856	
257	30625	C	264	157	468	
258	30626	B	265	148	403	
259	30627	C	266	248	481	
260	30628	B	267	171	393	
261	30629	B	268	1	1078	
262	30630	B	269	1	550	
263	30631	B	270	1	1455	
264	30632	B	271	171	602	
265	30633	B	272	1	1056	
266	30634	B	273	1	1101	
267	30635	B	274	1	2335	
268	30636	B	275	303	419	
269	30637	B	276	1	615	
270	30638	B	277	1	543	
271	30639	B	278	1	1602	
272	30640	C	279	585	1001	
273	30641	C	280	260	379	
274	30642	B	281	1	1437	
275	30643	C	282	22	321	
276	30644	B	283	1	843	
277	30645	B	284	142	2796	
278	30646	B	285	458	7217	
279	30647	B	286	84	186	
280	30648	C	287	67	229	
281	30649	C	288	15	245	
282	30650	C	289	125	232	
283	30651	B	290	1	594	
284	30652	B	291	376	670	
285	30653	C	292	82	405	
286	30654	B	293	35	651	
287	30655	B	294	56	487	
288	30656	C	295	313	498	
289	30657	C	296	118	261	
290	30658	B	297	198	1868	
291	30659	B	298	1	1665	
292	30660	C	299	73	108	
293	30661	B	300	1	408	
294	30662	B	301	1	444	
295	30663	B	302	8	311	
296	30664	C	303	144	350	
297	30665	B	304	1	669	
298	30666	C	305	416	820	
299	30667	B	306	253	837	
300	30668	B	307	44	475	
301	30669	B	308	185	885	
302	30670	C	309	206	337	
303	30671	B	310	1	393	
304	30672	B	311	1	1259	
305	30673	B	312	24	434	
306	30674	B	313	44	2687	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop endon, /=possible nucleotide deletion, \=possible nucleotide insertion)
307	30675	B	314	1	154	
308	30676	B	315	288	770	
309	30677	B	316	85	683	
310	30678	B	317	1	873	
311	30679	B	318	1	1737	
312	30680	C	319	1	690	
313	30681	B	320	58	1487	
314	30682	B	321	1	816	
315	30683	B	322	25	772	
316	30684	B	323	42	271	
317	30685	C	324	16	159	
318	30686	C	325	74	280	
319	30687	C	326	221	545	
320	30688	B	327	192	364	
321	30689	C	328	390	638	
322	30690	B	329	151	4215	
323	30691	B	330	1	2076	
324	30692	B	331	1	465	
325	30693	B	332	40	1350	
326	30694	B	333	1	489	
327	30695	B	334	285	744	
328	30696	C	335	96	347	
329	30697	C	336	213	326	
330	30698	B	337	776	4384	
331	30699	B	338	201	317	
332	30700	B	339	1	2713	
333	30701	B	340	1	894	
334	30702	B	341	1	3842	
335	30703	C	342	745	1131	
336	30704	B	343	82	411	
337	30705	B	344	126	2123	
338	30706	B	345	57	1641	
339	30707	C	346	211	654	
340	30708	B	347	44	266	
341	30709	B	348	1	927	
342	30710	C	349	20	124	
343	30711	C	350	9	455	
344	30712	C	351	188	304	
345	30713	C	352	1	333	
346	30714	C	353	140	298	
347	30715	B	354	73	2171	
348	30716	B	355	1	1374	
349	30717	B	356	150	398	
350	30718	B	357	1	585	
351	30719	B	358	1	1716	
352	30720	B	359	81	1912	
353	30721	B	360	249	770	
354	30722	B	361	474	2875	
355	30723	C	362	1	483	
356	30724	C	363	1	251	
357	30725	C	364	28	407	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
358	30726	C	365	88	204	
359	30727	B	366	474	684	
360	30728	C	367	41	394	
361	30729	B	368	253	1044	
362	30730	B	369	468	1111	
363	30731	B	370	1	558	
364	30732	B	371	21	345	
365	30733	B	372	1	744	
366	30734	B	373	1	795	
367	30735	B	374	1	685	
368	30736	B	375	94	414	
369	30737	C	376	86	268	
370	30738	B	377	1	1003	
371	30739	B	378	41	1385	
372	30740	B	379	1	510	
373	30741	B	380	40	746	
374	30742	B	381	100	1991	
375	30743	B	382	1	267	
376	30744	C	383	168	278	
377	30745	C	384	173	208	
378	30746	B	385	141	4538	
379	30747	B	386	1	4086	
380	30748	C	387	398	474	
381	30749	B	388	1	762	
382	30750	B	389	1	1584	
383	30751	B	390	1	2703	
384	30752	B	391	1	489	
385	30753	B	392	527	780	
386	30754	B	393	1	4050	
387	30755	B	394	859	2958	
388	30756	B	395	639	2307	
389	30757	B	396	1	642	
390	30758	B	397	1	3639	
391	30759	B	398	219	540	
392	30760	B	399	1	3225	
393	30761	B	400	1	7552	
394	30762	C	401	626	1201	
395	30763	C	402	627	827	
396	30764	C	403	1	243	
397	30765	B	404	335	538	
398	30766	B	405	41	409	
399	30767	B	406	160	540	
400	30768	B	407	1	597	
401	30769	B	408	1	1605	
402	30770	B	409	1	351	
403	30771	B	410	65	601	
404	30772	B	411	1	870	
405	30773	B	412	91	2867	
406	30774	B	413	33	410	
407	30775	B	414	298	343	
408	30776	B	415	70	310	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
409	30777	B	416	64	1929	
410	30778	B	417	1	298	
411	30779	B	418	37	2612	
412	30780	B	419	1	510	
413	30781	B	420	44	1111	
414	30782	B	421	26	175	
415	30783	C	422	7	57	
416	30784	C	423	27	230	
417	30785	C	424	7	144	
418	30786	B	425	1	1746	
419	30787	C	426	318	486	
420	30788	B	427	896	1115	
421	30789	C	428	106	309	
422	30790	C	429	52	402	
423	30791	B	430	1	309	
424	30792	B	431	167	492	
425	30793	C	432	144	296	
426	30794	B	433	1	786	
427	30795	B	434	336	1303	
428	30796	B	435	333	419	
429	30797	B	436	1	489	
430	30798	C	437	1	199	
431	30799	C	438	110	239	
432	30800	C	439	175	303	
433	30801	C	440	35	181	
434	30802	B	441	1	1896	
435	30803	C	442	1	331	
436	30804	C	443	71	344	
437	30805	C	444	25	135	
438	30806	C	445	406	595	
439	30807	C	446	148	228	
440	30808	C	447	80	106	
441	30809	C	448	7	375	
442	30810	C	449	300	437	
443	30811	C	450	1	357	
444	30812	B	451	1	729	
445	30813	B	452	58	1287	
446	30814	C	453	1	410	
447	30815	C	454	1	411	
448	30816	C	455	1	420	
449	30817	B	456	1	555	
450	30818	B	457	376	1035	
451	30819	B	458	678	807	
452	30820	B	459	88	1485	
453	30821	B	460	300	2082	
454	30822	B	461	1	819	
455	30823	B	462	780	998	
456	30824	B	463	1	1871	
457	30825	B	464	1	1703	
458	30826	B	465	1	594	
459	30827	C	466	120	245	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
460	30828	C	467	1	387	
461	30829	B	468	1	1678	
462	30830	B	469	1	533	
463	30831	B	470	347	656	
464	30832	B	471	1	1098	
465	30833	B	472	224	1518	
466	30834	C	473	44	244	
467	30835	B	474	1	1251	
468	30836	B	475	1	428	
469	30837	B	476	1	495	
470	30838	C	477	233	373	
471	30839	B	478	8	950	
472	30840	C	479	1	813	
473	30841	B	480	1	1071	
474	30842	C	481	224	418	
475	30843	B	482	39	851	
476	30844	B	483	1	2006	
477	30845	B	484	1	561	
478	30846	B	485	167	227	
479	30847	B	486	1	777	
480	30848	B	487	1	645	
481	30849	B	488	1	1749	
482	30850	C	489	26	847	
483	30851	C	490	243	392	
484	30852	C	491	303	407	
485	30853	C	492	23	300	
486	30854	B	493	131	336	
487	30855	C	494	64	156	
488	30856	B	495	180	712	
489	30857	B	496	1	1104	
490	30858	B	497	24	917	
491	30859	B	498	65	228	
492	30860	B	499	1	2172	
493	30861	B	500	1	1338	
494	30862	B	501	1	795	
495	30863	C	502	181	410	
496	30864	B	503	69	1322	
497	30865	B	504	531	1315	
498	30866	C	505	24	320	
499	30867	B	506	1	791	
500	30868	B	507	1	3256	
501	30869	C	508	361	549	
502	30870	B	509	729	3252	
503	30871	B	510	424	1710	
504	30872	C	511	247	750	
505	30873	B	512	11	124	
506	30874	B	514	116	1079	
507	30875	B	515	1	766	
508	30876	B	516	185	796	
509	30877	B	517	1	456	
510	30878	B	518	99	435	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met. hod.	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
511	30879	B	519	1	834	
512	30880	B	520	54	246	
513	30881	B	521	1	372	
514	30882	C	522	78	305	
515	30883	C	523	329	484	
516	30884	B	524	1	459	
517	30885	B	525	630	889	
518	30886	B	526	95	343	
519	30887	B	527	353	610	
520	30888	B	528	113	529	
521	30889	B	529	362	1400	
522	30890	B	530	1	441	
523	30891	C	531	1	327	
524	30892	B	532	1	909	
525	30893	B	534	669	1268	
526	30894	B	535	293	826	
527	30895	C	536	12	155	
528	30896	C	537	1488	1706	
529	30897	C	538	26	211	
530	30898	C	539	30	185	
531	30899	B	540	1	789	
532	30900	B	541	63	358	
533	30901	B	542	1	900	
534	30902	B	543	1	728	
535	30903	B	544	112	220	
536	30904	B	545	49	386	
537	30905	B	546	1	585	
538	30906	B	547	328	531	
539	30907	B	548	10	987	
540	30908	B	549	49	248	
541	30909	B	550	131	368	
542	30910	B	551	80	1098	
543	30911	B	552	1	1364	
544	30912	B	553	1	1294	
545	30913	B	554	1	1995	
546	30914	B	555	1	279	
547	30915	B	556	175	715	
548	30916	B	557	1	636	
549	30917	B	558	1331	1600	
550	30918	B	559	32	406	
551	30919	B	560	38	206	
552	30920	B	561	1	1266	
553	30921	C	562	359	501	
554	30922	B	563	315	465	
555	30923	B	564	94	1683	
556	30924	B	565	1	1570	
557	30925	B	566	139	1734	
558	30926	B	567	1	810	
559	30927	B	568	658	1548	
560	30928	B	569	9	395	
561	30929	B	570	1	567	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met. find	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
562	30930	B	571	1	567	
563	30931	B	572	1	789	
564	30932	B	573	49	3187	
565	30933	B	574	1	1824	
566	30934	B	575	49	1413	
567	30935	B	576	1	1572	
568	30936	C	577	372	468	
569	30937	C	578	58	225	
570	30938	B	579	79	299	
571	30939	B	580	1	645	
572	30940	C	581	582	749	
573	30941	B	582	170	463	
574	30942	B	583	311	520	
575	30943	B	584	1	1074	
576	30944	B	585	39	140	
577	30945	B	586	60	1685	
578	30946	B	587	106	879	
579	30947	C	588	67	362	
580	30948	B	589	45	126	
581	30949	C	590	1	390	
582	30950	C	591	49	240	
583	30951	B	592	1	496	
584	30952	B	593	94	482	
585	30953	C	594	12	341	
586	30954	B	595	1	354	
587	30955	B	596	1	711	
588	30956	B	597	123	412	
589	30957	B	598	1	1107	
590	30958	B	599	1	800	
591	30959	C	600	82	408	
592	30960	B	601	1	3174	
593	30961	B	602	1	444	
594	30962	B	603	1	1671	
595	30963	B	604	1	603	
596	30964	B	605	339	443	
597	30965	C	606	237	380	
598	30966	B	607	1	771	
599	30967	B	608	1	1767	
600	30968	C	609	1	801	
601	30969	B	610	1	1062	
602	30970	B	611	450	3131	
603	30971	C	612	178	435	
604	30972	C	613	164	319	
605	30973	C	614	1	385	
606	30974	C	615	392	853	
607	30975	C	616	24	200	
608	30976	C	617	34	327	
609	30977	B	618	1	624	
610	30978	B	619	179	1222	
611	30979	B	620	1	916	
612	30980	B	621	151	339	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
613	30981	B	622	135	218	
614	30982	B	623	126	300	
615	30983	C	624	258	467	
616	30984	B	625	58	1038	
617	30985	B	626	246	4677	
618	30986	B	627	1	583	
619	30987	C	628	65	283	
620	30988	B	629	162	909	
621	30989	B	630	1	1062	
622	30990	B	631	1	909	
623	30991	C	632	160	297	
624	30992	B	633	352	1143	
625	30993	C	634	301	459	
626	30994	B	635	1	906	
627	30995	B	636	1	654	
628	30996	B	637	1	528	
629	30997	B	638	1	1102	
630	30998	C	639	81	299	
631	30999	B	640	1	345	
632	31000	B	641	39	360	
633	31001	B	642	22	293	
634	31002	C	643	1	504	
635	31003	B	644	107	3786	
636	31004	B	645	1	576	
637	31005	B	646	66	152	
638	31006	B	647	226	522	
639	31007	B	648	1	49	
640	31008	C	649	50	172	
641	31009	C	650	1	516	
642	31010	B	651	1	615	
643	31011	B	652	1	495	
644	31012	B	653	1	663	
645	31013	B	654	1	1812	
646	31014	B	655	1	1401	
647	31015	B	656	102	1151	
648	31016	B	657	1	385	
649	31017	B	658	232	987	
650	31018	B	659	1	1221	
651	31019	B	660	296	496	
652	31020	B	661	57	285	
653	31021	C	662	203	271	
654	31022	B	663	1	711	
655	31023	C	664	351	542	
656	31024	C	665	420	695	
657	31025	B	666	1	1860	
658	31026	B	667	71	2167	
659	31027	B	668	6	344	
660	31028	B	669	217	693	
661	31029	C	670	1	417	
662	31030	B	671	1	990	
663	31031	B	672	109	1169	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
664	31032	C	673	40	117	
665	31033	C	674	301	560	
666	31034	B	675	1	396	
667	31035	B	676	483	1033	
668	31036	B	677	673	3407	
669	31037	B	678	4	672	
670	31038	C	679	39	116	
671	31039	B	680	1	459	
672	31040	B	681	19	370	
673	31041	B	682	112	704	
674	31042	C	683	387	578	
675	31043	B	684	175	254	
676	31044	B	685	1	501	
677	31045	B	686	290	389	
678	31046	B	687	1	486	
679	31047	B	688	1	651	
680	31048	B	689	181	401	
681	31049	B	690	117	406	
682	31050	B	691	1	169	
683	31051	B	692	1	1539	
684	31052	B	693	1	475	
685	31053	B	694	1	1575	
686	31054	B	695	1	507	
687	31055	B	696	1	498	
688	31056	C	697	253	492	
689	31057	B	698	1	588	
690	31058	B	699	75	291	
691	31059	B	700	1	1355	
692	31060	B	701	112	259	
693	31061	C	702	492	833	
694	31062	B	703	297	483	
695	31063	B	704	45	471	
696	31064	C	705	175	318	
697	31065	B	706	1	1074	
698	31066	B	707	94	1180	
699	31067	B	708	1	3866	
700	31068	C	709	215	424	
701	31069	B	710	1	499	
702	31070	B	711	210	325	
703	31071	B	712	1	786	
704	31072	B	713	1	777	
705	31073	B	714	174	1804	
706	31074	B	715	17	368	
707	31075	B	716	769	1831	
708	31076	B	717	76	301	
709	31077	B	718	1	825	
710	31078	C	719	1	396	
711	31079	B	720	93	2449	
712	31080	B	721	408	687	
713	31081	B	722	97	662	
714	31082	B	723	169	610	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
715	31083	B	724	1	2511	
716	31084	C	725	104	410	
717	31085	C	726	75	527	
718	31086	C	727	7	263	
719	31087	B	728	40	1725	
720	31088	B	729	290	1671	
721	31089	B	730	46	465	
722	31090	C	731	378	644	
723	31091	B	732	48	2331	
724	31092	B	733	1	738	
725	31093	B	734	1	1051	
726	31094	B	735	1	840	
727	31095	C	736	291	551	
728	31096	B	737	1	1308	
729	31097	B	738	1	291	
730	31098	C	739	1	702	
731	31099	B	740	1	379	
732	31100	B	741	80	2747	
733	31101	B	742	1	1992	
734	31102	B	743	293	1296	
735	31103	C	744	769	1017	
736	31104	C	745	166	294	
737	31105	B	746	928	1483	
738	31106	B	747	247	375	
739	31107	C	748	47	582	
740	31108	B	749	47	388	
741	31109	B	750	53	458	
742	31110	C	751	32	277	
743	31111	B	752	1	1641	
744	31112	C	753	1	483	
745	31113	B	754	1	1518	
746	31114	B	755	1	321	
747	31115	C	756	604	779	
748	31116	B	757	695	967	
749	31117	B	758	1	768	
750	31118	B	759	101	531	
751	31119	B	760	1	1014	
752	31120	C	761	424	564	
753	31121	B	762	1	333	
754	31122	B	763	15	165	
755	31123	B	764	1	555	
756	31124	B	765	344	476	
757	31125	B	766	1	648	
758	31126	B	767	1	981	
759	31127	C	768	22	162	
760	31128	B	769	1	225	
761	31129	B	770	232	1671	
762	31130	B	771	166	504	
763	31131	B	772	473	1694	
764	31132	C	773	232	414	
765	31133	C	774	374	463	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
766	31134	B	775	1	1128	
767	31135	B	776	337	1284	
768	31136	C	777	25	282	
769	31137	C	778	4	63	
770	31138	C	779	496	1041	
771	31139	C	780	234	365	
772	31140	B	781	1	669	
773	31141	B	782	228	305	
774	31142	B	783	102	755	
775	31143	B	784	1	465	
776	31144	B	785	45	336	
777	31145	C	786	220	366	
778	31146	B	787	332	456	
779	31147	B	788	169	450	
780	31148	B	789	1	1173	
781	31149	B	790	36	355	
782	31150	C	791	354	482	
783	31151	C	792	328	708	
784	31152	B	793	1	829	
785	31153	B	794	14	182	
786	31154	B	795	307	1412	
787	31155	C	796	3	332	
788	31156	B	797	57	704	
789	31157	B	798	1	2406	
790	31158	C	799	1	759	
791	31159	B	800	1	351	
792	31160	B	801	142	272	
793	31161	B	802	34	2951	
794	31162	B	803	92	994	
795	31163	B	804	115	1746	
796	31164	C	805	292	408	
797	31165	B	806	1	880	
798	31166	C	807	156	329	
799	31167	C	808	119	328	
800	31168	C	809	1	492	
801	31169	B	810	1	516	
802	31170	B	811	1	624	
803	31171	B	812	24	1868	
804	31172	C	813	164	208	
805	31173	C	814	91	249	
806	31174	B	815	1	1059	
807	31175	C	816	80	106	
808	31176	C	817	283	408	
809	31177	C	818	1	357	
810	31178	C	819	1	909	
811	31179	B	820	26	71	
812	31180	B	821	1	714	
813	31181	B	822	1	678	
814	31182	B	823	1	675	
815	31183	B	824	24	1046	
816	31184	B	825	1	933	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
817	31185	B	826	1	363	
818	31186	B	827	112	1655	
819	31187	B	828	1	417	
820	31188	B	829	88	1485	
821	31189	C	830	1	411	
822	31190	B	831	114	277	
823	31191	C	832	671	1039	
824	31192	B	833	63	342	
825	31193	B	834	3530	4798	
826	31194	B	835	1	333	
827	31195	B	836	1	831	
828	31196	B	837	1	2514	
829	31197	B	838	98	250	
830	31198	B	839	1	5247	
831	31199	B	840	1	531	
832	31200	B	841	167	466	
833	31201	B	842	160	417	
834	31202	B	843	215	380	
835	31203	B	844	706	1262	
836	31204	B	845	41	368	
837	31205	C	846	252	578	
838	31206	C	847	18	380	
839	31207	C	848	14	349	
840	31208	B	849	1	1176	
841	31209	B	850	244	1174	
842	31210	C	851	27	146	
843	31211	B	852	217	1866	
844	31212	B	853	98	242	
845	31213	B	854	52	2112	
846	31214	B	855	98	242	
847	31215	C	856	237	518	
848	31216	C	857	1	528	
849	31217	C	858	213	365	
850	31218	B	859	86	478	
851	31219	B	860	1	903	
852	31220	B	861	191	539	
853	31221	C	862	283	480	
854	31222	B	863	248	738	
855	31223	B	864	7	1602	
856	31224	B	865	113	375	
857	31225	B	866	50	435	
858	31226	B	867	50	646	
859	31227	B	868	1	2292	
860	31228	B	869	1	2385	
861	31229	B	870	184	852	
862	31230	B	871	1	408	
863	31231	B	872	218	484	
864	31232	B	873	90	588	
865	31233	B	874	445	625	
866	31234	B	875	138	618	
867	31235	B	876	1	753	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
868	31236	B	877	1	489	
869	31237	B	878	113	366	
870	31238	C	879	271	489	
871	31239	B	880	918	3257	
872	31240	B	881	185	631	
873	31241	C	882	3	194	
874	31242	B	883	80	3219	
875	31243	B	884	213	1835	
876	31244	C	885	132	224	
877	31245	B	886	1	741	
878	31246	C	887	132	224	
879	31247	B	888	1	1281	
880	31248	B	889	125	1910	
881	31249	B	890	1	1449	
882	31250	B	891	284	696	
883	31251	B	892	139	390	
884	31252	B	893	1	1308	
885	31253	B	894	1	594	
886	31254	B	895	1	678	
887	31255	B	896	19	240	
888	31256	B	897	47	330	
889	31257	B	898	1	388	
890	31258	B	899	52	564	
891	31259	C	900	310	672	
892	31260	B	901	1	1338	
893	31261	C	902	77	214	
894	31262	C	903	213	467	
895	31263	C	904	202	426	
896	31264	B	905	68	567	
897	31265	C	906	32	205	
898	31266	C	907	513	701	
899	31267	B	908	1	1083	
900	31268	B	909	787	1633	
901	31269	C	910	40	288	
902	31270	B	911	178	330	
903	31271	B	912	129	520	
904	31272	B	913	2267	2626	
905	31273	C	914	34	87	
906	31274	B	915	23	610	
907	31275	B	916	1	1011	
908	31276	B	917	1	156	
909	31277	B	918	1	754	
910	31278	B	919	1	679	
911	31279	B	920	149	761	
912	31280	B	921	38	1175	
913	31281	C	922	542	724	
914	31282	B	923	31	283	
915	31283	B	924	21	341	
916	31284	B	925	199	361	
917	31285	B	926	293	427	
918	31286	B	927	56	145	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
919	31287	B	928	21	341	
920	31288	B	929	199	361	
921	31289	B	930	293	427	
922	31290	B	931	305	465	
923	31291	B	932	280	457	
924	31292	C	933	45	562	
925	31293	B	934	130	618	
926	31294	B	935	418	1620	
927	31295	B	936	115	252	
928	31296	B	937	1	573	
929	31297	B	938	1	2661	
930	31298	B	939	1	1345	
931	31299	C	940	747	1220	
932	31300	C	941	249	429	
933	31301	B	942	1	363	
934	31302	C	943	390	589	
935	31303	B	944	437	1553	
936	31304	B	945	1	1521	
937	31305	C	946	84	347	
938	31306	B	949	80	315	
939	31307	B	950	1	537	
940	31308	C	951	181	330	
941	31309	C	952	55	123	
942	31310	C	953	52	195	
943	31311	C	954	55	123	
944	31312	B	955	336	648	
945	31313	B	956	1	894	
946	31314	B	957	239	1008	
947	31315	B	958	126	308	
948	31316	B	959	1	747	
949	31317	B	960	101	351	
950	31318	B	961	179	1161	
951	31319	B	962	1	138	
952	31320	B	963	8	791	
953	31321	C	964	218	358	
954	31322	C	965	155	454	
955	31323	C	966	124	303	
956	31324	C	967	1	246	
957	31325	B	968	208	364	
958	31326	C	969	95	256	
959	31327	C	970	312	467	
960	31328	B	971	92	424	
961	31329	B	972	88	147	
962	31330	C	973	434	775	
963	31331	B	974	26	1781	
964	31332	C	975	363	692	
965	31333	B	976	201	563	
966	31334	B	977	348	687	
967	31335	C	978	529	660	
968	31336	C	979	418	738	
969	31337	C	980	25	177	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
970	31338	B	981	308	388	
971	31339	C	982	230	580	
972	31340	B	983	101	342	
973	31341	B	984	1	2341	
974	31342	C	985	1	642	
975	31343	B	986	1	1173	
976	31344	B	987	39	6743	
977	31345	B	988	1	516	
978	31346	B	989	1	756	
979	31347	B	990	1	912	
980	31348	B	991	310	441	
981	31349	C	992	58	300	
982	31350	B	993	80	1344	
983	31351	C	994	325	414	
984	31352	B	995	80	1582	
985	31353	C	996	143	499	
986	31354	B	997	173	375	
987	31355	C	998	126	268	
988	31356	B	999	1	762	
989	31357	B	1000	1	642	
990	31358	B	1001	1	1980	
991	31359	B	1002	67	456	
992	31360	B	1003	48	335	
993	31361	B	1004	1	1251	
994	31362	B	1005	1	642	
995	31363	B	1006	1	570	
996	31364	C	1007	1	687	
997	31365	B	1008	1	5450	
998	31366	B	1009	586	852	
999	31367	B	1010	299	530	
1000	31368	B	1011	1	1659	
1001	31369	B	1012	2	550	
1002	31370	C	1013	2	97	
1003	31371	B	1014	1114	1476	
1004	31372	B	1015	22	822	
1005	31373	C	1016	646	903	
1006	31374	C	1017	1	351	
1007	31375	B	1018	226	1284	
1008	31376	B	1019	138	997	
1009	31377	B	1020	341	527	
1010	31378	B	1021	157	1415	
1011	31379	B	1022	55	211	
1012	31380	B	1023	55	211	
1013	31381	C	1024	18	197	
1014	31382	B	1025	1	876	
1015	31383	B	1026	276	487	
1016	31384	B	1027	1	294	
1017	31385	B	1028	273	377	
1018	31386	B	1029	1	936	
1019	31387	B	1030	1	1158	
1020	31388	C	1031	104	283	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1021	31389	B	1032	1	720	
1022	31390	B	1033	1	219	
1023	31391	B	1034	1	170	
1024	31392	B	1035	300	831	
1025	31393	C	1036	1	456	
1026	31394	B	1037	1	1149	
1027	31395	B	1038	1	627	
1028	31396	B	1039	161	375	
1029	31397	B	1040	1	360	
1030	31398	B	1041	1	549	
1031	31399	B	1042	1	384	
1032	31400	B	1046	1	675	
1033	31401	C	1047	379	675	
1034	31402	B	1048	166	388	
1035	31403	B	1049	26	66	
1036	31404	B	1050	1	897	
1037	31405	B	1051	30	1359	
1038	31406	B	1052	1	990	
1039	31407	B	1053	52	1507	
1040	31408	C	1054	66	290	
1041	31409	B	1055	158	2072	
1042	31410	B	1056	1	654	
1043	31411	B	1057	51	1143	
1044	31412	C	1058	66	290	
1045	31413	B	1059	547	1510	
1046	31414	B	1060	1	1499	
1047	31415	B	1061	1	3347	
1048	31416	C	1062	116	235	
1049	31417	B	1063	1	1185	
1050	31418	C	1064	221	823	
1051	31419	B	1065	235	359	
1052	31420	C	1066	1	360	
1053	31421	B	1067	49	386	
1054	31422	C	1068	63	383	
1055	31423	B	1069	60	213	
1056	31424	B	1070	1	919	
1057	31425	B	1071	294	557	
1058	31426	B	1072	1	486	
1059	31427	B	1073	1	450	
1060	31428	C	1074	28	207	
1061	31429	B	1075	1	585	
1062	31430	B	1076	60	213	
1063	31431	B	1077	18	457	
1064	31432	B	1078	112	177	
1065	31433	C	1079	1	375	
1066	31434	B	1080	39	91	
1067	31435	B	1081	91	237	
1068	31436	B	1082	255	376	
1069	31437	B	1083	18	431	
1070	31438	B	1084	98	552	
1071	31439	B	1085	1679	1964	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
1072	31440	B	1086	132	1200	
1073	31441	B	1087	95	418	
1074	31442	B	1088	26	56	
1075	31443	B	1089	1	873	
1076	31444	C	1090	107	196	
1077	31445	B	1091	157	777	
1078	31446	B	1092	1	1273	
1079	31447	B	1093	1	202	
1080	31448	B	1094	1	382	
1081	31449	C	1095	189	449	
1082	31450	C	1096	325	429	
1083	31451	C	1097	3	80	
1084	31452	B	1098	50	691	
1085	31453	B	1099	1	474	
1086	31454	B	1100	3	335	
1087	31455	B	1101	137	617	
1088	31456	C	1102	69	134	
1089	31457	B	1103	369	886	
1090	31458	B	1104	1	1332	
1091	31459	B	1105	106	584	
1092	31460	C	1106	97	420	
1093	31461	C	1107	142	381	
1094	31462	B	1108	214	2544	
1095	31463	B	1109	238	1323	
1096	31464	B	1110	1	3000	
1097	31465	B	1111	203	313	
1098	31466	B	1112	288	375	
1099	31467	B	1113	1	480	
1100	31468	C	1114	286	351	
1101	31469	B	1115	59	376	
1102	31470	C	1116	287	504	
1103	31471	B	1117	878	2032	
1104	31472	B	1118	52	648	
1105	31473	B	1119	1	207	
1106	31474	C	1120	1	492	
1107	31475	B	1121	46	830	
1108	31476	B	1122	1	525	
1109	31477	B	1123	1	930	
1110	31478	C	1124	157	606	
1111	31479	C	1125	70	405	
1112	31480	C	1126	247	411	
1113	31481	C	1127	339	590	
1114	31482	B	1128	1	1881	
1115	31483	C	1129	258	452	
1116	31484	B	1130	241	733	
1117	31485	C	1131	294	530	
1118	31486	B	1132	1	439	
1119	31487	B	1133	16	612	
1120	31488	C	1134	234	377	
1121	31489	B	1135	134	763	
1122	31490	C	1136	1	228	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
1123	31491	B	1137	63	443	
1124	31492	C	1138	30	269	
1125	31493	B	1139	44	151	
1126	31494	B	1140	69	199	
1127	31495	B	1141	347	2830	
1128	31496	B	1142	1	576	
1129	31497	C	1143	49	129	
1130	31498	B	1144	1	1107	
1131	31499	B	1145	17	153	
1132	31500	B	1146	277	694	
1133	31501	B	1147	1	735	
1134	31502	B	1148	1	1110	
1135	31503	B	1149	55	552	
1136	31504	C	1150	463	591	
1137	31505	B	1151	136	266	
1138	31506	B	1152	1	795	
1139	31507	B	1153	128	880	
1140	31508	C	1154	178	366	
1141	31509	B	1155	1	654	
1142	31510	B	1156	1	3294	
1143	31511	B	1157	16	854	
1144	31512	B	1158	1093	1185	
1145	31513	B	1159	1	930	
1146	31514	B	1160	1	3969	
1147	31515	B	1161	1	4173	
1148	31516	B	1162	1	2187	
1149	31517	B	1163	47	993	
1150	31518	B	1164	1	1241	
1151	31519	B	1165	46	2170	
1152	31520	B	1166	1	1781	
1153	31521	B	1167	179	583	
1154	31522	C	1168	167	442	
1155	31523	B	1169	44	1848	
1156	31524	C	1170	1	417	
1157	31525	B	1171	1	198	
1158	31526	B	1172	231	452	
1159	31527	B	1173	219	326	
1160	31528	B	1174	212	302	
1161	31529	B	1175	748	1084	
1162	31530	B	1176	1	540	
1163	31531	C	1177	21	143	
1164	31532	B	1178	76	1300	
1165	31533	B	1179	1	1324	
1166	31534	B	1180	1	1065	
1167	31535	B	1181	1	1263	
1168	31536	B	1182	1	1809	
1169	31537	B	1183	10	406	
1170	31538	B	1184	65	287	
1171	31539	B	1185	25	337	
1172	31540	B	1186	59	698	
1173	31541	C	1187	329	527	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1174	31542	B	1188	1	1068	
1175	31543	B	1189	72	330	
1176	31544	B	1190	14	239	
1177	31545	B	1191	1	919	
1178	31546	B	1192	462	786	
1179	31547	B	1193	1	3468	
1180	31548	B	1194	16	457	
1181	31549	B	1195	1	697	
1182	31550	C	1196	1	145	
1183	31551	B	1197	91	450	
1184	31552	B	1198	1	1050	
1185	31553	B	1199	101	428	
1186	31554	B	1200	41	205	
1187	31555	B	1201	358	1082	
1188	31556	B	1202	1	183	
1189	31557	B	1203	1	1053	
1190	31558	B	1204	73	336	
1191	31559	B	1205	553	1587	
1192	31560	C	1206	118	366	
1193	31561	B	1207	1	423	
1194	31562	B	1208	120	338	
1195	31563	B	1209	1	1665	
1196	31564	B	1210	1	639	
1197	31565	B	1211	1	660	
1198	31566	B	1212	11	434	
1199	31567	B	1213	1	567	
1200	31568	B	1214	1	801	
1201	31569	C	1215	56	177	
1202	31570	B	1216	439	678	
1203	31571	B	1217	20	201	
1204	31572	B	1218	74	267	
1205	31573	B	1219	74	325	
1206	31574	B	1220	37	340	
1207	31575	B	1221	1	588	
1208	31576	B	1222	136	294	
1209	31577	B	1223	238	392	
1210	31578	B	1224	109	1394	
1211	31579	C	1225	300	653	
1212	31580	B	1226	32	3327	
1213	31581	B	1227	497	1306	
1214	31582	C	1228	1	333	
1215	31583	C	1229	1	249	
1216	31584	C	1230	1	249	
1217	31585	B	1231	147	297	
1218	31586	B	1232	1	714	
1219	31587	B	1233	1	1587	
1220	31588	C	1234	103	243	
1221	31589	C	1235	133	509	
1222	31590	B	1236	1	1594	
1223	31591	B	1237	1	628	
1224	31592	B	1238	1	948	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
1225	31593	B	1239	382	1020	
1226	31594	B	1240	163	5459	
1227	31595	B	1241	1	1386	
1228	31596	B	1242	44	344	
1229	31597	B	1243	6	398	
1230	31598	B	1244	77	468	
1231	31599	B	1245	520	2001	
1232	31600	B	1246	1	645	
1233	31601	B	1247	91	690	
1234	31602	B	1248	70	382	
1235	31603	B	1249	183	427	
1236	31604	B	1250	159	621	
1237	31605	B	1251	34	259	
1238	31606	B	1252	155	496	
1239	31607	B	1253	1	1416	
1240	31608	C	1254	18	355	
1241	31609	C	1255	665	826	
1242	31610	B	1256	1	559	
1243	31611	B	1257	343	1329	
1244	31612	B	1258	1	265	
1245	31613	B	1259	1	5081	
1246	31614	B	1260	373	1395	
1247	31615	B	1261	83	373	
1248	31616	B	1262	298	1252	
1249	31617	C	1263	142	327	
1250	31618	B	1264	1	237	
1251	31619	C	1265	1	330	
1252	31620	C	1266	20	358	
1253	31621	C	1267	347	493	
1254	31622	B	1268	220	1314	
1255	31623	B	1269	1	1244	
1256	31624	B	1270	35	368	
1257	31625	B	1271	145	444	
1258	31626	B	1272	1	657	
1259	31627	B	1273	84	273	
1260	31628	C	1274	47	148	
1261	31629	B	1275	1	528	
1262	31630	B	1276	34	1370	
1263	31631	C	1277	81	299	
1264	31632	C	1278	22	201	
1265	31633	B	1279	1	672	
1266	31634	B	1280	1	753	
1267	31635	C	1281	14	79	
1268	31636	C	1282	61	227	
1269	31637	B	1283	95	1124	
1270	31638	B	1284	1	891	
1271	31639	B	1285	1	1323	
1272	31640	B	1286	11	127	
1273	31641	B	1287	281	437	
1274	31642	C	1288	62	136	
1275	31643	B	1289	251	874	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
1276	31644	C	1290	16	231	
1277	31645	C	1291	299	412	
1278	31646	B	1292	310	968	
1279	31647	B	1293	237	1802	
1280	31648	B	1294	337	1143	
1281	31649	C	1295	75	176	
1282	31650	C	1296	193	414	
1283	31651	C	1297	98	679	
1284	31652	B	1298	186	260	
1285	31653	B	1299	1	732	
1286	31654	B	1300	123	268	
1287	31655	C	1301	1	420	
1288	31656	C	1302	86	223	
1289	31657	B	1303	1	594	
1290	31658	B	1304	1	4464	
1291	31659	C	1305	1	531	
1292	31660	B	1307	1	780	
1293	31661	C	1308	1	249	
1294	31662	B	1309	1	139	
1295	31663	B	1310	1	156	
1296	31664	B	1311	38	403	
1297	31665	B	1312	128	1089	
1298	31666	C	1313	262	429	
1299	31667	C	1314	209	592	
1300	31668	B	1315	1	684	
1301	31669	C	1316	1	339	
1302	31670	C	1317	71	310	
1303	31671	B	1318	1	476	
1304	31672	B	1319	133	198	
1305	31673	B	1320	1	227	
1306	31674	C	1321	612	977	
1307	31675	C	1322	65	523	
1308	31676	C	1323	35	121	
1309	31677	B	1324	8	430	
1310	31678	C	1325	1	438	
1311	31679	B	1326	1935	3296	
1312	31680	B	1332	254	462	
1313	31681	B	1333	1006	1540	
1314	31682	B	1335	127	1799	
1315	31683	B	1336	221	402	
1316	31684	C	1337	1	567	
1317	31685	C	1338	193	342	
1318	31686	B	1339	652	775	
1319	31687	B	1340	1	552	
1320	31688	B	1341	83	318	
1321	31689	B	1342	166	352	
1322	31690	C	1343	1	228	
1323	31691	B	1344	25	244	
1324	31692	C	1345	58	285	
1325	31693	B	1346	34	822	
1326	31694	B	1347	1	1563	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1327	31695	B	1348	229	1185	
1328	31696	B	1349	59	819	
1329	31697	B	1350	1	5955	
1330	31698	B	1351	1	654	
1331	31699	B	1352	1	1299	
1332	31700	B	1353	943	1872	
1333	31701	B	1354	1	942	
1334	31702	B	1355	444	560	
1335	31703	B	1356	1	1605	
1336	31704	B	1357	1	831	
1337	31705	C	1358	48	383	
1338	31706	C	1359	1	318	
1339	31707	B	1360	186	470	
1340	31708	C	1361	1	321	
1341	31709	B	1362	1	720	
1342	31710	B	1363	1	939	
1343	31711	B	1364	1	576	
1344	31712	B	1365	1	114	
1345	31713	B	1366	129	588	
1346	31714	B	1367	24	724	
1347	31715	B	1368	1	1840	
1348	31716	B	1369	14	350	
1349	31717	B	1370	1	3187	
1350	31718	C	1371	1	261	
1351	31719	B	1372	117	890	
1352	31720	B	1373	1	438	
1353	31721	B	1374	1	217	
1354	31722	B	1375	1	160	
1355	31723	C	1376	6	191	
1356	31724	B	1377	1	759	
1357	31725	B	1378	10	251	
1358	31726	B	1379	1	719	
1359	31727	C	1380	425	886	
1360	31728	C	1381	1	216	
1361	31729	C	1382	38	229	
1362	31730	B	1383	38	672	
1363	31731	B	1384	1	1845	
1364	31732	B	1385	1	2590	
1365	31733	B	1386	32	108	
1366	31734	C	1387	215	460	
1367	31735	B	1388	1	1008	
1368	31736	B	1389	1	368	
1369	31737	B	1390	44	2402	
1370	31738	B	1391	80	1617	
1371	31739	C	1392	199	531	
1372	31740	B	1393	1	465	
1373	31741	C	1394	415	612	
1374	31742	B	1395	16	147	
1375	31743	B	1396	1	1314	
1376	31744	B	1397	1	465	
1377	31745	B	1398	1	1569	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1378	31746	B	1399	1	490	
1379	31747	B	1400	405	573	
1380	31748	B	1401	1	2106	
1381	31749	B	1402	1	1593	
1382	31750	B	1403	1	666	
1383	31751	B	1404	1	652	
1384	31752	B	1405	352	1239	
1385	31753	B	1406	1	3184	
1386	31754	B	1407	467	1433	
1387	31755	B	1408	95	428	
1388	31756	C	1409	164	208	
1389	31757	C	1410	118	511	
1390	31758	C	1411	339	431	
1391	31759	B	1412	1	396	
1392	31760	B	1413	1	663	
1393	31761	B	1414	1	864	
1394	31762	C	1415	1	471	
1395	31763	B	1416	1	642	
1396	31764	B	1417	594	1764	
1397	31765	B	1418	1	771	
1398	31766	B	1419	1	5131	
1399	31767	B	1420	60	617	
1400	31768	B	1421	587	1202	
1401	31769	C	1422	336	638	
1402	31770	C	1423	30	200	
1403	31771	B	1424	1	1363	
1404	31772	B	1425	1	1113	
1405	31773	B	1426	1	1101	
1406	31774	B	1427	575	805	
1407	31775	C	1428	1	149	
1408	31776	C	1429	1	294	
1409	31777	C	1430	228	469	
1410	31778	B	1431	182	518	
1411	31779	B	1432	239	448	
1412	31780	B	1433	1	434	
1413	31781	C	1434	24	290	
1414	31782	C	1435	334	459	
1415	31783	B	1436	69	320	
1416	31784	B	1437	1	426	
1417	31785	B	1438	605	1423	
1418	31786	C	1439	9	113	
1419	31787	B	1440	1	58	
1420	31788	B	1441	1	210	
1421	31789	B	1442	1	2985	
1422	31790	C	1443	152	292	
1423	31791	B	1444	57	849	
1424	31792	C	1445	41	142	
1425	31793	C	1446	38	341	
1426	31794	C	1447	220	450	
1427	31795	C	1448	154	469	
1428	31796	B	1449	139	1023	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
1429	31797	B	1450	55	2370	
1430	31798	B	1451	1	1707	
1431	31799	B	1452	566	2356	
1432	31800	B	1453	72	255	
1433	31801	B	1454	51	182	
1434	31802	B	1455	466	600	
1435	31803	B	1456	481	1209	
1436	31804	B	1457	1	1638	
1437	31805	B	1458	8	874	
1438	31806	B	1459	1	552	
1439	31807	B	1460	1	2566	
1440	31808	B	1461	85	270	
1441	31809	B	1462	159	392	
1442	31810	B	1463	88	459	
1443	31811	B	1464	131	406	
1444	31812	B	1465	69	194	
1445	31813	B	1466	59	3134	
1446	31814	B	1467	1	3097	
1447	31815	B	1468	328	519	
1448	31816	C	1469	40	436	
1449	31817	B	1470	1	981	
1450	31818	B	1471	30	285	
1451	31819	B	1475	93	932	
1452	31820	B	1476	1	369	
1453	31821	C	1477	102	227	
1454	31822	B	1478	613	679	
1455	31823	B	1479	51	587	
1456	31824	C	1480	3	188	
1457	31825	B	1481	1	1434	
1458	31826	C	1482	27	173	
1459	31827	C	1483	294	503	
1460	31828	C	1484	506	718	
1461	31829	C	1485	97	504	
1462	31830	C	1486	27	185	
1463	31831	B	1487	50	3247	
1464	31832	B	1488	1	1032	
1465	31833	B	1489	8	95	
1466	31834	B	1490	17	303	
1467	31835	B	1491	34	81	
1468	31836	B	1492	1	1110	
1469	31837	B	1493	1	928	
1470	31838	C	1494	498	704	
1471	31839	B	1495	4	747	
1472	31840	B	1496	1	933	
1473	31841	B	1497	137	687	
1474	31842	B	1498	1524	1676	
1475	31843	B	1499	1	156	
1476	31844	B	1500	1	1126	
1477	31845	B	1501	122	765	
1478	31846	B	1503	95	304	
1479	31847	B	1504	1	156	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1480	31848	C	1505	12	173	
1481	31849	B	1506	10	252	
1482	31850	B	1507	25	301	
1483	31851	B	1508	34	267	
1484	31852	B	1509	10	366	
1485	31853	B	1510	536	2776	
1486	31854	B	1511	1	276	
1487	31855	B	1512	1	420	
1488	31856	B	1513	235	363	
1489	31857	B	1514	664	741	
1490	31858	C	1515	312	452	
1491	31859	B	1516	1	504	
1492	31860	B	1517	52	346	
1493	31861	B	1518	458	1283	
1494	31862	B	1519	324	473	
1495	31863	B	1520	137	286	
1496	31864	B	1521	1	2682	
1497	31865	B	1522	352	1132	
1498	31866	B	1523	245	397	
1499	31867	C	1524	371	661	
1500	31868	B	1525	69	325	
1501	31869	B	1526	38	997	
1502	31870	B	1527	1	1753	
1503	31871	B	1528	215	2588	
1504	31872	C	1529	38	124	
1505	31873	C	1530	33	317	
1506	31874	C	1531	224	379	
1507	31875	B	1532	1	480	
1508	31876	C	1533	145	256	
1509	31877	C	1534	64	198	
1510	31878	B	1535	1	394	
1511	31879	C	1536	1	696	
1512	31880	B	1537	67	246	
1513	31881	C	1538	95	253	
1514	31882	B	1539	145	476	
1515	31883	C	1540	1	361	
1516	31884	C	1541	1	276	
1517	31885	B	1542	1	658	
1518	31886	B	1543	1	623	
1519	31887	C	1544	187	465	
1520	31888	C	1545	1	207	
1521	31889	C	1546	24	512	
1522	31890	C	1547	20	121	
1523	31891	B	1548	1	785	
1524	31892	B	1549	1	498	
1525	31893	C	1550	17	118	
1526	31894	C	1551	1	291	
1527	31895	B	1552	1	504	
1528	31896	B	1553	62	413	
1529	31897	B	1554	1	282	
1530	31898	C	1555	236	408	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1531	31899	C	1556	220	398	
1532	31900	C	1557	1	732	
1533	31901	C	1558	1	372	
1534	31902	B	1559	1	1086	
1535	31903	C	1560	286	642	
1536	31904	B	1561	8	339	
1537	31905	B	1562	16	88	
1538	31906	C	1563	227	405	
1539	31907	B	1564	253	693	
1540	31908	C	1565	1	129	
1541	31909	B	1566	1	390	
1542	31910	B	1567	1	1377	
1543	31911	C	1568	16	264	
1544	31912	C	1569	51	269	
1545	31913	C	1570	39	266	
1546	31914	B	1571	200	260	
1547	31915	B	1572	220	372	
1548	31916	B	1573	1	377	
1549	31917	C	1574	280	441	
1550	31918	C	1575	50	131	
1551	31919	C	1576	47	265	
1552	31920	C	1577	10	291	
1553	31921	B	1578	1	522	
1554	31922	B	1579	756	1166	
1555	31923	B	1580	382	1228	
1556	31924	B	1581	63	229	
1557	31925	B	1582	1	452	
1558	31926	C	1583	299	556	
1559	31927	B	1584	1	870	
1560	31928	B	1585	1	708	
1561	31929	C	1586	1	420	
1562	31930	B	1587	1	1011	
1563	31931	C	1588	84	176	
1564	31932	C	1589	52	201	
1565	31933	C	1590	55	154	
1566	31934	C	1591	1	390	
1567	31935	C	1592	15	317	
1568	31936	B	1593	1	501	
1569	31937	B	1594	306	398	
1570	31938	B	1595	204	402	
1571	31939	C	1596	30	155	
1572	31940	B	1597	1	2274	
1573	31941	B	1598	1	486	
1574	31942	C	1599	148	504	
1575	31943	C	1600	82	282	
1576	31944	C	1601	82	282	
1577	31945	B	1602	66	395	
1578	31946	B	1603	114	237	
1579	31947	B	1604	1	1326	
1580	31948	B	1605	1	1900	
1581	31949	B	1606	1	1548	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1582	31950	B	1607	1	1440	
1583	31951	B	1608	1	1878	
1584	31952	C	1609	402	563	
1585	31953	B	1610	1	2964	
1586	31954	B	1611	1	1284	
1587	31955	C	1612	144	449	
1588	31956	B	1613	1	1050	
1589	31957	B	1614	1	561	
1590	31958	B	1615	127	330	
1591	31959	C	1616	202	443	
1592	31960	B	1617	1	924	
1593	31961	C	1618	60	419	
1594	31962	C	1619	285	602	
1595	31963	C	1620	1	93	
1596	31964	B	1621	1	480	
1597	31965	B	1622	96	416	
1598	31966	B	1623	78	1581	
1599	31967	B	1624	1	2259	
1600	31968	C	1625	180	371	
1601	31969	B	1626	1	852	
1602	31970	B	1627	1	204	
1603	31971	B	1628	37	2613	
1604	31972	B	1629	66	1505	
1605	31973	B	1630	1	1792	
1606	31974	B	1631	100	522	
1607	31975	B	1632	252	2347	
1608	31976	C	1633	294	450	
1609	31977	C	1634	118	372	
1610	31978	B	1635	1	799	
1611	31979	B	1636	1	2496	
1612	31980	B	1637	100	1188	
1613	31981	B	1638	35	1654	
1614	31982	B	1639	46	783	
1615	31983	B	1640	8	1428	
1616	31984	B	1641	1	2121	
1617	31985	B	1642	92	667	
1618	31986	B	1643	1	339	
1619	31987	C	1644	79	434	
1620	31988	C	1645	592	921	
1621	31989	C	1646	1	171	
1622	31990	C	1647	76	264	
1623	31991	B	1648	157	912	
1624	31992	B	1649	10	462	
1625	31993	C	1650	10	333	
1626	31994	C	1651	763	1001	
1627	31995	B	1652	202	701	
1628	31996	C	1653	215	572	
1629	31997	B	1654	261	399	
1630	31998	C	1655	623	749	
1631	31999	B	1656	198	1524	
1632	32000	B	1657	108	575	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
1633	32001	B	1658	40	2173	
1634	32002	B	1659	1	479	
1635	32003	B	1660	1	1542	
1636	32004	B	1661	1	849	
1637	32005	B	1662	1	684	
1638	32006	B	1663	1	318	
1639	32007	B	1664	1	406	
1640	32008	B	1665	1	393	
1641	32009	B	1666	1	210	
1642	32010	B	1667	1	450	
1643	32011	B	1668	1	471	
1644	32012	B	1669	1	471	
1645	32013	B	1670	282	580	
1646	32014	B	1671	1	789	
1647	32015	B	1672	1	324	
1648	32016	B	1673	1	465	
1649	32017	B	1674	1	948	
1650	32018	C	1675	24	401	
1651	32019	B	1676	46	401	
1652	32020	B	1677	251	1041	
1653	32021	C	1678	1	177	
1654	32022	B	1679	1	189	
1655	32023	B	1680	65	769	
1656	32024	C	1681	1	564	
1657	32025	B	1682	65	769	
1658	32026	B	1683	1	1743	
1659	32027	B	1684	1	615	
1660	32028	B	1685	1	323	
1661	32029	B	1686	1	618	
1662	32030	B	1687	1	579	
1663	32031	C	1688	142	216	
1664	32032	C	1689	145	432	
1665	32033	B	1690	1	729	
1666	32034	C	1691	1	192	
1667	32035	C	1692	1	474	
1668	32036	B	1693	326	1662	
1669	32037	B	1694	50	1462	
1670	32038	C	1695	1	432	
1671	32039	B	1696	173	375	
1672	32040	B	1697	1	1917	
1673	32041	B	1698	57	365	
1674	32042	B	1699	78	1250	
1675	32043	B	1700	8	2210	
1676	32044	B	1701	1	474	
1677	32045	B	1702	47	879	
1678	32046	B	1703	1	465	
1679	32047	B	1704	65	473	
1680	32048	B	1705	89	1908	
1681	32049	C	1706	1	612	
1682	32050	C	1707	80	226	
1683	32051	B	1708	992	2023	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
1684	32052	B	1709	1293	1497	
1685	32053	B	1710	29	1480	
1686	32054	C	1711	1664	2179	
1687	32055	B	1712	183	8544	
1688	32056	C	1713	60	472	
1689	32057	B	1714	202	735	
1690	32058	B	1715	532	661	
1691	32059	B	1716	1	453	
1692	32060	B	1717	24	320	
1693	32061	B	1718	59	583	
1694	32062	B	1719	1	369	
1695	32063	B	1720	51	204	
1696	32064	B	1721	318	849	
1697	32065	B	1722	1	597	
1698	32066	B	1723	1	325	
1699	32067	B	1724	1	675	
1700	32068	B	1725	1	631	
1701	32069	B	1726	1	1017	
1702	32070	B	1727	158	727	
1703	32071	B	1728	296	798	
1704	32072	B	1729	1	1128	
1705	32073	C	1730	237	356	
1706	32074	C	1731	393	519	
1707	32075	B	1732	1	6432	
1708	32076	B	1733	124	402	
1709	32077	B	1734	35	421	
1710	32078	C	1735	203	385	
1711	32079	B	1736	16	406	
1712	32080	B	1737	21	306	
1713	32081	B	1738	97	352	
1714	32082	B	1739	64	7164	
1715	32083	B	1740	553	1197	
1716	32084	B	1741	553	720	
1717	32085	B	1742	1	4029	
1718	32086	B	1743	63	422	
1719	32087	B	1744	342	451	
1720	32088	B	1745	1	1238	
1721	32089	B	1746	1	2393	
1722	32090	B	1747	1667	1833	
1723	32091	C	1748	33	287	
1724	32092	B	1749	1	469	
1725	32093	B	1750	75	166	
1726	32094	B	1751	120	756	
1727	32095	C	1752	1	1098	
1728	32096	B	1753	1	486	
1729	32097	C	1754	25	374	
1730	32098	C	1755	149	394	
1731	32099	B	1756	1	660	
1732	32100	B	1757	26	391	
1733	32101	B	1758	282	419	
1734	32102	B	1759	132	717	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1735	32103	B	1760	127	698	
1736	32104	B	1761	56	549	
1737	32105	B	1762	325	2681	
1738	32106	C	1763	465	893	
1739	32107	C	1764	123	764	
1740	32108	B	1765	206	402	
1741	32109	B	1766	393	900	
1742	32110	C	1767	1	360	
1743	32111	B	1768	285	482	
1744	32112	B	1769	1	405	
1745	32113	C	1770	304	399	
1746	32114	B	1771	1	273	
1747	32115	B	1772	67	1464	
1748	32116	B	1773	1	1122	
1749	32117	B	1774	1	1185	
1750	32118	B	1775	44	145	
1751	32119	B	1776	1	1050	
1752	32120	B	1777	250	762	
1753	32121	B	1778	1	390	
1754	32122	B	1779	172	867	
1755	32123	B	1780	327	637	
1756	32124	B	1781	1	1101	
1757	32125	C	1782	10	216	
1758	32126	B	1783	1	1449	
1759	32127	B	1784	1	402	
1760	32128	C	1785	134	418	
1761	32129	B	1786	1	417	
1762	32130	B	1787	1	384	
1763	32131	C	1788	1	738	
1764	32132	C	1789	68	280	
1765	32133	B	1790	101	327	
1766	32134	B	1791	1	1257	
1767	32135	C	1792	168	311	
1768	32136	B	1793	33	120	
1769	32137	C	1794	1	150	
1770	32138	C	1795	1	378	
1771	32139	C	1796	100	267	
1772	32140	C	1797	1	318	
1773	32141	C	1798	1	429	
1774	32142	C	1799	194	379	
1775	32143	B	1800	1	363	
1776	32144	B	1801	1	384	
1777	32145	B	1802	1	4462	
1778	32146	B	1803	235	425	
1779	32147	B	1804	8	1187	
1780	32148	B	1805	1	480	
1781	32149	B	1806	1	240	
1782	32150	B	1807	1	891	
1783	32151	C	1808	1	366	
1784	32152	B	1809	376	776	
1785	32153	B	1810	304	876	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
1786	32154	B	1811	1	939	
1787	32155	B	1812	4	744	
1788	32156	B	1813	1	717	
1789	32157	C	1814	67	366	
1790	32158	B	1815	185	847	
1791	32159	C	1816	1	315	
1792	32160	B	1817	87	297	
1793	32161	B	1818	1	1190	
1794	32162	B	1819	1	848	
1795	32163	B	1820	934	1158	
1796	32164	C	1821	1	477	
1797	32165	C	1822	6	125	
1798	32166	B	1823	335	536	
1799	32167	B	1824	157	324	
1800	32168	C	1825	176	361	
1801	32169	C	1826	1	120	
1802	32170	C	1827	25	360	
1803	32171	C	1828	246	377	
1804	32172	C	1829	4782	5015	
1805	32173	B	1830	1105	3034	
1806	32174	B	1831	818	874	
1807	32175	C	1832	1	444	
1808	32176	B	1833	589	734	
1809	32177	B	1834	1	264	
1810	32178	B	1835	46	112	
1811	32179	B	1836	1	360	
1812	32180	B	1837	589	734	
1813	32181	B	1838	1	675	
1814	32182	B	1839	1	1194	
1815	32183	B	1840	121	880	
1816	32184	B	1841	35	853	
1817	32185	B	1842	1	426	
1818	32186	C	1843	1	252	
1819	32187	B	1844	1	323	
1820	32188	B	1845	1	789	
1821	32189	C	1846	337	1521	
1822	32190	C	1847	1	345	
1823	32191	B	1848	331	3385	
1824	32192	B	1849	1	1584	
1825	32193	B	1850	1	957	
1826	32194	B	1851	226	1794	
1827	32195	B	1852	52	594	
1828	32196	C	1853	1	615	
1829	32197	B	1854	1	318	
1830	32198	B	1855	297	450	
1831	32199	C	1856	87	404	
1832	32200	C	1857	1	171	
1833	32201	C	1858	1	171	
1834	32202	B	1859	34	831	
1835	32203	B	1860	1	1375	
1836	32204	B	1861	1	546	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1837	32205	C	1862	36	182	
1838	32206	B	1863	392	1043	
1839	32207	B	1864	1	1283	
1840	32208	C	1865	283	591	
1841	32209	C	1866	97	108	
1842	32210	C	1867	25	250	
1843	32211	C	1868	142	448	
1844	32212	C	1869	1	576	
1845	32213	C	1870	1	396	
1846	32214	B	1871	1	885	
1847	32215	C	1872	321	848	
1848	32216	B	1873	82	871	
1849	32217	C	1874	1	723	
1850	32218	C	1875	1	426	
1851	32219	C	1876	624	803	
1852	32220	B	1877	1	588	
1853	32221	B	1878	39	58	
1854	32222	B	1879	1	1011	
1855	32223	B	1880	1	654	
1856	32224	C	1881	1	498	
1857	32225	C	1882	1	249	
1858	32226	C	1883	507	785	
1859	32227	C	1885	310	404	
1860	32228	B	1886	448	618	
1861	32229	B	1887	1	388	
1862	32230	B	1888	106	414	
1863	32231	B	1889	82	4206	
1864	32232	B	1890	1	240	
1865	32233	B	1891	1	324	
1866	32234	C	1892	243	447	
1867	32235	C	1893	139	228	
1868	32236	C	1894	61	300	
1869	32237	C	1895	271	429	
1870	32238	B	1896	545	1054	
1871	32239	B	1897	609	706	
1872	32240	B	1898	1	2521	
1873	32241	C	1899	152	517	
1874	32242	B	1900	217	313	
1875	32243	C	1901	86	193	
1876	32244	C	1902	29	271	
1877	32245	B	1903	1	522	
1878	32246	C	1904	37	225	
1879	32247	C	1905	84	308	
1880	32248	B	1906	36	1569	
1881	32249	B	1907	1	522	
1882	32250	C	1908	1	510	
1883	32251	B	1909	1	936	
1884	32252	C	1910	1	162	
1885	32253	C	1911	155	427	
1886	32254	B	1912	1	1282	
1887	32255	B	1913	165	270	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1888	32256	B	1914	513	9470	
1889	32257	B	1915	35	871	
1890	32258	B	1916	1	690	
1891	32259	C	1917	86	271	
1892	32260	B	1918	1	690	
1893	32261	C	1919	14	301	
1894	32262	B	1920	1	936	
1895	32263	B	1921	1	1901	
1896	32264	B	1922	36	238	
1897	32265	B	1923	1	738	
1898	32266	C	1924	5	364	
1899	32267	C	1925	43	494	
1900	32268	C	1926	96	263	
1901	32269	B	1927	1	207	
1902	32270	B	1928	1	290	
1903	32271	B	1929	52	482	
1904	32272	B	1930	271	408	
1905	32273	B	1931	114	309	
1906	32274	C	1932	218	398	
1907	32275	B	1933	1	1011	
1908	32276	B	1934	1	702	
1909	32277	B	1935	1	1305	
1910	32278	C	1936	141	374	
1911	32279	B	1937	1	834	
1912	32280	B	1938	47	363	
1913	32281	B	1939	73	558	
1914	32282	B	1940	373	864	
1915	32283	B	1941	96	377	
1916	32284	B	1942	55	2711	
1917	32285	B	1945	833	1352	
1918	32286	B	1946	1	1101	
1919	32287	B	1947	865	1070	
1920	32288	C	1948	1	285	
1921	32289	B	1949	1	642	
1922	32290	B	1950	124	813	
1923	32291	B	1951	1	654	
1924	32292	B	1952	180	303	
1925	32293	C	1953	15	170	
1926	32294	B	1954	245	646	
1927	32295	B	1955	100	824	
1928	32296	C	1956	52	348	
1929	32297	B	1957	1	678	
1930	32298	B	1958	1	954	
1931	32299	B	1959	1	675	
1932	32300	C	1960	52	348	
1933	32301	B	1961	71	251	
1934	32302	B	1962	427	747	
1935	32303	B	1963	1	453	
1936	32304	B	1964	1	375	
1937	32305	B	1965	117	1109	
1938	32306	C	1966	47	133	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
1939	32307	B	1967	79	1149	
1940	32308	B	1968	1	693	
1941	32309	B	1969	1	1179	
1942	32310	B	1970	1	639	
1943	32311	B	1971	502	1294	
1944	32312	C	1972	670	1185	
1945	32313	B	1973	1	1044	
1946	32314	B	1974	1	3645	
1947	32315	B	1975	1	2877	
1948	32316	B	1976	1	1579	
1949	32317	B	1977	1	750	
1950	32318	B	1978	1	438	
1951	32319	C	1979	122	307	
1952	32320	C	1980	71	271	
1953	32321	C	1981	151	363	
1954	32322	C	1982	122	307	
1955	32323	C	1983	55	282	
1956	32324	C	1984	89	385	
1957	32325	C	1985	48	275	
1958	32326	C	1986	246	557	
1959	32327	B	1987	394	2565	
1960	32328	B	1988	1	432	
1961	32329	B	1989	46	483	
1962	32330	B	1990	150	482	
1963	32331	B	1991	10	265	
1964	32332	C	1992	40	162	
1965	32333	B	1993	1	3639	
1966	32334	B	1994	83	179	
1967	32335	B	1995	39	1452	
1968	32336	B	1996	50	384	
1969	32337	B	1997	256	351	
1970	32338	B	1998	1	771	
1971	32339	B	1999	1	489	
1972	32340	B	2000	37	447	
1973	32341	B	2001	1	1272	
1974	32342	B	2002	1	2559	
1975	32343	C	2003	221	589	
1976	32344	C	2004	415	1033	
1977	32345	B	2007	318	694	
1978	32346	B	2008	31	819	
1979	32347	B	2009	1	276	
1980	32348	B	2010	1	369	
1981	32349	B	2011	85	628	
1982	32350	B	2012	19	178	
1983	32351	B	2013	217	393	
1984	32352	B	2014	1	779	
1985	32353	B	2015	107	650	
1986	32354	B	2016	313	527	
1987	32355	B	2017	32	258	
1988	32356	C	2018	51	345	
1989	32357	B	2019	1	393	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
1990	32358	B	2020	647	1362	
1991	32359	C	2021	16	378	
1992	32360	B	2022	32	349	
1993	32361	C	2023	256	425	
1994	32362	C	2024	134	382	
1995	32363	B	2025	138	171	
1996	32364	B	2026	1	1626	
1997	32365	B	2027	509	810	
1998	32366	C	2028	1	513	
1999	32367	C	2029	7	375	
2000	32368	C	2030	1	410	
2001	32369	B	2031	1	864	
2002	32370	B	2032	110	928	
2003	32371	B	2033	1	1026	
2004	32372	B	2034	1	1008	
2005	32373	B	2035	1	588	
2006	32374	B	2036	1	412	
2007	32375	B	2037	1	1851	
2008	32376	B	2038	309	663	
2009	32377	B	2039	1	525	
2010	32378	B	2040	1	2214	
2011	32379	B	2041	1	486	
2012	32380	B	2042	1	774	
2013	32381	B	2043	1	596	
2014	32382	B	2044	305	395	
2015	32383	C	2045	27	185	
2016	32384	B	2046	1	1071	
2017	32385	B	2047	1	1326	
2018	32386	B	2048	1	3761	
2019	32387	C	2049	55	189	
2020	32388	B	2050	1016	1683	
2021	32389	C	2051	942	1130	
2022	32390	B	2052	1	598	
2023	32391	B	2053	1	768	
2024	32392	B	2054	1	999	
2025	32393	C	2055	1	252	
2026	32394	B	2056	154	606	
2027	32395	B	2057	1	846	
2028	32396	C	2058	334	690	
2029	32397	B	2059	268	5712	
2030	32398	C	2060	117	662	
2031	32399	B	2061	1	3504	
2032	32400	B	2062	816	927	
2033	32401	B	2063	1	342	
2034	32402	B	2064	1	1443	
2035	32403	C	2065	53	102	
2036	32404	C	2066	271	528	
2037	32405	B	2067	1	843	
2038	32406	C	2068	187	408	
2039	32407	C	2069	174	320	
2040	32408	B	2070	31	534	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2041	32409	C	2071	183	329	
2042	32410	B	2072	3	389	
2043	32411	B	2073	78	974	
2044	32412	B	2074	467	692	
2045	32413	C	2075	605	965	
2046	32414	B	2076	1	555	
2047	32415	B	2077	1	390	
2048	32416	B	2078	1	2522	
2049	32417	B	2079	24	94	
2050	32418	B	2080	78	593	
2051	32419	B	2081	1	612	
2052	32420	B	2082	42	342	
2053	32421	B	2083	1	477	
2054	32422	B	2084	57	1640	
2055	32423	C	2085	110	307	
2056	32424	B	2086	1	591	
2057	32425	C	2087	14	355	
2058	32426	B	2088	47	998	
2059	32427	B	2089	1	498	
2060	32428	C	2090	357	560	
2061	32429	B	2091	1	522	
2062	32430	C	2092	231	659	
2063	32431	C	2093	36	167	
2064	32432	B	2094	394	2695	
2065	32433	B	2096	61	2215	
2066	32434	B	2097	204	572	
2067	32435	C	2098	476	652	
2068	32436	B	2099	1	190	
2069	32437	C	2100	1	259	
2070	32438	B	2101	1	2625	
2071	32439	B	2102	1403	2950	
2072	32440	B	2103	672	1955	
2073	32441	C	2104	1	351	
2074	32442	B	2105	1	567	
2075	32443	C	2106	176	304	
2076	32444	C	2107	27	308	
2077	32445	C	2108	68	307	
2078	32446	C	2109	322	567	
2079	32447	B	2110	1	1297	
2080	32448	B	2111	281	1488	
2081	32449	B	2112	12	2497	
2082	32450	C	2113	90	284	
2083	32451	B	2114	1	2466	
2084	32452	B	2115	1	603	
2085	32453	B	2116	1	954	
2086	32454	B	2117	205	441	
2087	32455	B	2118	68	2052	
2088	32456	B	2119	271	639	
2089	32457	B	2120	1	1356	
2090	32458	B	2121	247	1326	
2091	32459	B	2122	1	1041	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
2092	32460	B	2123	1	1695	
2093	32461	B	2124	1	1767	
2094	32462	B	2125	1	2286	
2095	32463	B	2126	1	1167	
2096	32464	B	2127	1	2343	
2097	32465	B	2128	1	1056	
2098	32466	B	2129	1	1379	
2099	32467	B	2130	1	1839	
2100	32468	B	2131	1	5460	
2101	32469	B	2132	133	549	
2102	32470	B	2133	1	534	
2103	32471	B	2134	1	537	
2104	32472	B	2135	1	49	
2105	32473	C	2136	1	432	
2106	32474	B	2137	1	615	
2107	32475	B	2138	146	556	
2108	32476	B	2139	133	1434	
2109	32477	B	2140	1	357	
2110	32478	C	2141	1	429	
2111	32479	B	2142	1	411	
2112	32480	B	2143	1	459	
2113	32481	C	2144	224	550	
2114	32482	B	2145	1	1035	
2115	32483	B	2146	1	342	
2116	32484	C	2147	1	321	
2117	32485	C	2148	1	317	
2118	32486	B	2149	1	495	
2119	32487	B	2150	146	556	
2120	32488	C	2151	1	390	
2121	32489	C	2152	461	643	
2122	32490	C	2153	198	416	
2123	32491	C	2154	258	500	
2124	32492	B	2155	291	1034	
2125	32493	B	2156	1	834	
2126	32494	B	2157	1	7852	
2127	32495	B	2158	1	1320	
2128	32496	B	2159	1631	1756	
2129	32497	B	2160	500	8643	
2130	32498	C	2161	193	475	
2131	32499	B	2162	1	795	
2132	32500	B	2163	1	663	
2133	32501	C	2164	1	303	
2134	32502	B	2165	266	385	
2135	32503	B	2166	1	704	
2136	32504	B	2167	1	720	
2137	32505	B	2168	364	507	
2138	32506	B	2169	44	197	
2139	32507	C	2170	72	224	
2140	32508	C	2171	228	393	
2141	32509	C	2172	241	396	
2142	32510	C	2173	415	552	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *≈Stop codon, /≈possible nucleotide deletion, ≈possible nucleotide insertion)
2143	32511	B	2174	64	268	
2144	32512	C	2175	1	462	
2145	32513	C	2176	1	357	
2146	32514	B	2177	1	3213	
2147	32515	B	2178	119	682	
2148	32516	B	2179	1	405	
2149	32517	B	2180	297	769	
2150	32518	B	2181	1	1314	
2151	32519	C	2182	156	287	
2152	32520	B	2183	1	756	
2153	32521	B	2184	1	645	
2154	32522	B	2185	1	948	
2155	32523	B	2186	1	660	
2156	32524	B	2187	186	518	
2157	32525	B	2188	1	3570	
2158	32526	B	2189	1	3354	
2159	32527	B	2190	1	2232	
2160	32528	B	2191	1	1356	
2161	32529	B	2192	1	1103	
2162	32530	B	2193	1	1902	
2163	32531	B	2194	1	2232	
2164	32532	B	2195	1	2991	
2165	32533	B	2196	1	2136	
2166	32534	B	2197	1	1524	
2167	32535	B	2198	1	2106	
2168	32536	B	2199	1	1224	
2169	32537	B	2200	1	1935	
2170	32538	B	2201	1	1428	
2171	32539	B	2202	1	858	
2172	32540	B	2203	1	2162	
2173	32541	B	2204	1	1374	
2174	32542	B	2205	205	3666	
2175	32543	B	2206	59	4311	
2176	32544	B	2207	1	1311	
2177	32545	B	2208	1	2742	
2178	32546	B	2209	1	1878	
2179	32547	B	2210	1	1074	
2180	32548	B	2211	1	2217	
2181	32549	B	2212	1	1945	
2182	32550	B	2213	1	1941	
2183	32551	B	2214	1	1737	
2184	32552	B	2215	1	1422	
2185	32553	B	2216	22	9087	
2186	32554	B	2217	1	4954	
2187	32555	B	2218	1	1812	
2188	32556	B	2219	1	939	
2189	32557	B	2220	1	2895	
2190	32558	B	2221	1	6223	
2191	32559	B	2222	109	4966	
2192	32560	B	2223	3807	9479	
2193	32561	B	2224	1	4903	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met lod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
2194	32562	B	2225	210	516	
2195	32563	C	2226	185	292	
2196	32564	B	2227	1	657	
2197	32565	B	2228	1	1011	
2198	32566	B	2229	1	1303	
2199	32567	C	2230	69	182	
2200	32568	B	2231	1	321	
2201	32569	B	2232	88	522	
2202	32570	B	2233	527	1207	
2203	32571	B	2234	118	375	
2204	32572	B	2235	8	148	
2205	32573	B	2236	609	1121	
2206	32574	B	2237	1	1500	
2207	32575	C	2238	121	330	
2208	32576	B	2239	1	591	
2209	32577	B	2240	125	471	
2210	32578	B	2241	64	909	
2211	32579	B	2242	13	579	
2212	32580	B	2243	249	531	
2213	32581	C	2244	107	928	
2214	32582	B	2245	213	322	
2215	32583	C	2246	373	441	
2216	32584	B	2247	54	2723	
2217	32585	B	2248	94	529	
2218	32586	B	2249	57	260	
2219	32587	B	2250	674	1972	
2220	32588	B	2251	1	1053	
2221	32589	C	2252	186	347	
2222	32590	B	2253	26	193	
2223	32591	B	2254	1	5442	
2224	32592	B	2255	428	3792	
2225	32593	B	2256	9	199	
2226	32594	B	2257	421	2932	
2227	32595	B	2258	305	547	
2228	32596	B	2259	1	891	
2229	32597	B	2260	1	641	
2230	32598	B	2261	108	542	
2231	32599	B	2262	105	440	
2232	32600	B	2263	553	729	
2233	32601	B	2264	1	645	
2234	32602	B	2265	291	452	
2235	32603	B	2266	143	348	
2236	32604	C	2267	310	426	
2237	32605	B	2268	1	1344	
2238	32606	B	2269	237	2834	
2239	32607	B	2270	1	2922	
2240	32608	B	2271	109	3499	
2241	32609	B	2272	1	1611	
2242	32610	B	2273	1	1575	
2243	32611	B	2274	1	1314	
2244	32612	B	2275	1	1209	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2245	32613	B	2276	1	2022	
2246	32614	B	2277	1	1938	
2247	32615	B	2279	1	1806	
2248	32616	B	2280	1	2361	
2249	32617	B	2281	1	2732	
2250	32618	B	2282	1	3703	
2251	32619	C	2283	1	507	
2252	32620	B	2284	118	316	
2253	32621	B	2285	1	272	
2254	32622	B	2286	37	388	
2255	32623	B	2287	1	660	
2256	32624	B	2288	431	633	
2257	32625	B	2289	1	1032	
2258	32626	B	2290	1	1227	
2259	32627	C	2291	27	296	
2260	32628	B	2292	58	370	
2261	32629	B	2293	1	1275	
2262	32630	B	2294	1	1299	
2263	32631	C	2295	227	613	
2264	32632	B	2296	1	297	
2265	32633	B	2297	126	206	
2266	32634	C	2298	1	387	
2267	32635	B	2299	19	279	
2268	32636	B	2300	1	612	
2269	32637	C	2301	81	191	
2270	32638	B	2302	120	308	
2271	32639	B	2303	1	2145	
2272	32640	C	2304	270	416	
2273	32641	B	2305	31	627	
2274	32642	B	2306	128	499	
2275	32643	B	2307	61	388	
2276	32644	B	2308	744	2094	
2277	32645	B	2309	241	669	
2278	32646	B	2310	1	285	
2279	32647	B	2311	137	307	
2280	32648	C	2312	168	362	
2281	32649	C	2313	8	394	
2282	32650	B	2314	1	489	
2283	32651	C	2315	1	204	
2284	32652	B	2316	1	2361	
2285	32653	B	2317	1	2265	
2286	32654	B	2318	1	2268	
2287	32655	B	2319	1	2337	
2288	32656	B	2320	1	2196	
2289	32657	B	2321	1	2298	
2290	32658	B	2322	1	2880	
2291	32659	B	2323	1	2562	
2292	32660	B	2324	1	2835	
2293	32661	B	2325	1	2172	
2294	32662	B	2326	675	2515	
2295	32663	B	2327	1	2709	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
2296	32664	B	2328	1	2478	
2297	32665	B	2329	1	2748	
2298	32666	B	2330	877	4763	
2299	32667	B	2331	1	2590	
2300	32668	B	2332	1	597	
2301	32669	C	2333	279	412	
2302	32670	C	2334	507	878	
2303	32671	C	2335	1	147	
2304	32672	B	2336	52	573	
2305	32673	C	2337	211	446	
2306	32674	B	2338	1	1669	
2307	32675	B	2339	69	418	
2308	32676	B	2340	1	2778	
2309	32677	B	2341	1	1896	
2310	32678	B	2342	1	1836	
2311	32679	B	2343	1	2463	
2312	32680	B	2344	287	1785	
2313	32681	B	2345	1	2860	
2314	32682	B	2346	1	1281	
2315	32683	B	2347	1	1176	
2316	32684	B	2348	1	1431	
2317	32685	B	2349	1	2361	
2318	32686	B	2350	592	1815	
2319	32687	B	2351	1	2764	
2320	32688	C	2352	309	581	
2321	32689	B	2353	99	5619	
2322	32690	B	2354	133	3213	
2323	32691	B	2355	1	3193	
2324	32692	B	2356	1	3291	
2325	32693	B	2357	1	4019	
2326	32694	B	2358	167	4093	
2327	32695	B	2359	1	3534	
2328	32696	B	2360	1	3405	
2329	32697	B	2361	1	3555	
2330	32698	B	2362	1	3786	
2331	32699	B	2363	1	3414	
2332	32700	B	2364	1	5130	
2333	32701	B	2365	1	8244	
2334	32702	B	2366	1	7995	
2335	32703	B	2367	1	1980	
2336	32704	B	2368	1	4269	
2337	32705	B	2369	1	169	
2338	32706	B	2370	1	573	
2339	32707	B	2371	388	1101	
2340	32708	C	2372	1	354	
2341	32709	B	2373	134	1057	
2342	32710	B	2374	91	1464	
2343	32711	B	2375	117	767	
2344	32712	B	2376	1	486	
2345	32713	C	2377	1	726	
2346	32714	C	2378	31	447	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2347	32715	B	2379	1	402	
2348	32716	B	2380	22	427	
2349	32717	B	2381	351	560	
2350	32718	B	2382	1	1122	
2351	32719	B	2383	1	1035	
2352	32720	B	2384	1	309	
2353	32721	B	2385	80	673	
2354	32722	B	2386	160	659	
2355	32723	B	2387	1	858	
2356	32724	C	2388	228	365	
2357	32725	B	2389	1	531	
2358	32726	B	2390	218	670	
2359	32727	C	2391	182	484	
2360	32728	C	2392	1	738	
2361	32729	C	2393	27	316	
2362	32730	B	2394	291	498	
2363	32731	C	2395	230	409	
2364	32732	B	2396	228	1361	
2365	32733	C	2397	210	548	
2366	32734	B	2398	309	1202	
2367	32735	C	2399	100	406	
2368	32736	B	2400	440	2579	
2369	32737	C	2401	102	359	
2370	32738	B	2402	1	414	
2371	32739	B	2403	717	976	
2372	32740	B	2404	1	777	
2373	32741	B	2405	1	208	
2374	32742	B	2406	1	570	
2375	32743	B	2407	187	525	
2376	32744	B	2408	20	499	
2377	32745	B	2409	1	210	
2378	32746	B	2410	41	166	
2379	32747	B	2411	29	348	
2380	32748	B	2412	1	564	
2381	32749	C	2413	250	366	
2382	32750	B	2414	164	430	
2383	32751	C	2415	141	340	
2384	32752	B	2416	304	422	
2385	32753	B	2417	1	2031	
2386	32754	B	2418	1	1527	
2387	32755	B	2419	1	2892	
2388	32756	B	2420	218	4186	
2389	32757	B	2421	203	655	
2390	32758	C	2422	1	346	
2391	32759	B	2423	299	433	
2392	32760	B	2424	172	525	
2393	32761	B	2425	1	3270	
2394	32762	B	2426	202	481	
2395	32763	B	2427	148	3473	
2396	32764	C	2428	182	460	
2397	32765	B	2429	116	2953	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2398	32766	B	2430	153	332	
2399	32767	B	2431	267	2752	
2400	32768	B	2432	1	848	
2401	32769	C	2433	54	350	
2402	32770	B	2434	160	531	
2403	32771	B	2435	159	184	
2404	32772	B	2436	44	293	
2405	32773	C	2437	129	438	
2406	32774	C	2438	255	469	
2407	32775	B	2439	292	456	
2408	32776	B	2440	86	225	
2409	32777	B	2441	1	603	
2410	32778	B	2442	305	402	
2411	32779	C	2443	117	332	
2412	32780	B	2444	1	642	
2413	32781	B	2445	50	238	
2414	32782	B	2446	350	1331	
2415	32783	B	2447	1	867	
2416	32784	B	2448	1	498	
2417	32785	B	2449	40	849	
2418	32786	B	2450	187	404	
2419	32787	B	2451	1	921	
2420	32788	B	2452	439	517	
2421	32789	C	2453	143	682	
2422	32790	B	2454	87	401	
2423	32791	B	2455	44	277	
2424	32792	B	2456	1	639	
2425	32793	B	2457	1	816	
2426	32794	B	2458	100	454	
2427	32795	C	2459	717	923	
2428	32796	C	2460	1	412	
2429	32797	C	2461	80	394	
2430	32798	B	2462	278	323	
2431	32799	C	2463	9	239	
2432	32800	B	2464	1	537	
2433	32801	B	2465	1	798	
2434	32802	B	2466	1	861	
2435	32803	B	2467	611	979	
2436	32804	B	2468	56	166	
2437	32805	C	2469	40	495	
2438	32806	B	2470	1	216	
2439	32807	B	2471	273	385	
2440	32808	B	2472	77	489	
2441	32809	C	2473	480	791	
2442	32810	B	2474	110	1318	
2443	32811	B	2475	114	563	
2444	32812	B	2476	813	3193	
2445	32813	C	2477	198	650	
2446	32814	B	2478	1	234	
2447	32815	B	2479	7	174	
2448	32816	B	2480	1	1035	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2449	32817	B	2481	1	564	
2450	32818	B	2482	16	894	
2451	32819	B	2483	1	207	
2452	32820	B	2484	1	2742	
2453	32821	B	2485	1	1071	
2454	32822	B	2486	58	1228	
2455	32823	C	2487	51	179	
2456	32824	B	2488	1	1119	
2457	32825	C	2489	147	398	
2458	32826	C	2490	1	504	
2459	32827	C	2491	4	240	
2460	32828	B	2492	190	388	
2461	32829	B	2493	1	594	
2462	32830	C	2494	299	477	
2463	32831	B	2495	1	2328	
2464	32832	C	2496	1	924	
2465	32833	B	2497	1	2703	
2466	32834	B	2498	504	1392	
2467	32835	C	2499	649	1239	
2468	32836	B	2500	46	842	
2469	32837	B	2501	251	555	
2470	32838	B	2502	258	326	
2471	32839	B	2503	49	386	
2472	32840	C	2504	63	383	
2473	32841	B	2505	150	585	
2474	32842	B	2506	65	678	
2475	32843	C	2507	477	634	
2476	32844	B	2508	80	337	
2477	32845	B	2509	1	1233	
2478	32846	B	2510	1	2526	
2479	32847	B	2511	192	2617	
2480	32848	B	2512	1	921	
2481	32849	B	2513	1	1650	
2482	32850	B	2514	79	1587	
2483	32851	B	2515	1	657	
2484	32852	B	2516	1	1260	
2485	32853	B	2517	1	762	
2486	32854	C	2518	1	729	
2487	32855	B	2519	1	1299	
2488	32856	B	2520	1	882	
2489	32857	C	2521	1	369	
2490	32858	B	2522	52	573	
2491	32859	B	2523	1	570	
2492	32860	B	2524	1	2376	
2493	32861	B	2525	1	786	
2494	32862	B	2526	1	760	
2495	32863	B	2527	73	714	
2496	32864	B	2528	1	2976	
2497	32865	B	2529	1	1021	
2498	32866	B	2530	1	1386	
2499	32867	B	2531	352	1239	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
2500	32868	B	2532	1	1740	
2501	32869	B	2533	1	915	
2502	32870	B	2534	392	1393	
2503	32871	B	2535	1	4868	
2504	32872	B	2536	1	2667	
2505	32873	B	2537	1	825	
2506	32874	B	2538	1	735	
2507	32875	B	2539	88	469	
2508	32876	C	2540	1	390	
2509	32877	C	2541	113	328	
2510	32878	B	2542	475	848	
2511	32879	B	2543	472	1482	
2512	32880	C	2544	42	593	
2513	32881	B	2545	470	998	
2514	32882	B	2546	83	339	
2515	32883	B	2547	1	501	
2516	32884	B	2548	1198	1432	
2517	32885	B	2549	1	486	
2518	32886	B	2550	454	1626	
2519	32887	C	2551	227	388	
2520	32888	B	2552	25	687	
2521	32889	B	2553	569	753	
2522	32890	C	2554	147	384	
2523	32891	B	2555	210	419	
2524	32892	B	2556	1	1185	
2525	32893	C	2557	93	257	
2526	32894	C	2558	41	375	
2527	32895	C	2559	155	579	
2528	32896	B	2560	1	375	
2529	32897	C	2561	37	351	
2530	32898	C	2562	39	518	
2531	32899	B	2563	310	493	
2532	32900	C	2564	83	373	
2533	32901	B	2565	120	843	
2534	32902	C	2566	327	468	
2535	32903	B	2567	1	732	
2536	32904	C	2568	243	434	
2537	32905	C	2569	117	347	
2538	32906	C	2570	1	363	
2539	32907	C	2571	1	219	
2540	32908	B	2572	82	390	
2541	32909	B	2573	1152	1737	
2542	32910	C	2574	294	524	
2543	32911	B	2575	1	345	
2544	32912	B	2576	106	1073	
2545	32913	B	2577	1	313	
2546	32914	C	2578	1	594	
2547	32915	C	2579	16	102	
2548	32916	C	2580	1	441	
2549	32917	B	2581	1	462	
2550	32918	B	2582	113	1257	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2551	32919	B	2583	1	402	
2552	32920	B	2584	489	570	
2553	32921	B	2585	218	356	
2554	32922	C	2586	225	345	
2555	32923	C	2587	472	621	
2556	32924	B	2588	1	984	
2557	32925	B	2589	1	1119	
2558	32926	B	2590	1	771	
2559	32927	B	2591	97	681	
2560	32928	B	2592	112	202	
2561	32929	C	2593	1	381	
2562	32930	C	2594	115	321	
2563	32931	C	2595	3	200	
2564	32932	B	2596	212	303	
2565	32933	C	2597	236	396	
2566	32934	B	2598	119	625	
2567	32935	C	2599	68	334	
2568	32936	C	2600	85	351	
2569	32937	B	2601	1	723	
2570	32938	C	2602	235	463	
2571	32939	B	2603	1	498	
2572	32940	C	2604	179	346	
2573	32941	B	2605	21	486	
2574	32942	B	2606	20	600	
2575	32943	B	2607	172	294	
2576	32944	B	2608	130	1200	
2577	32945	B	2609	61	243	
2578	32946	B	2610	1	753	
2579	32947	B	2611	1	2274	
2580	32948	B	2612	1	1848	
2581	32949	B	2613	1	1263	
2582	32950	B	2614	412	654	
2583	32951	C	2615	176	658	
2584	32952	B	2616	310	628	
2585	32953	B	2617	1	579	
2586	32954	C	2618	145	309	
2587	32955	B	2619	298	353	
2588	32956	B	2620	163	594	
2589	32957	B	2621	1	468	
2590	32958	B	2622	1	552	
2591	32959	B	2623	1	876	
2592	32960	B	2624	140	1333	
2593	32961	C	2625	1	222	
2594	32962	B	2626	1	645	
2595	32963	C	2627	49	339	
2596	32964	B	2628	1	1944	
2597	32965	C	2629	79	189	
2598	32966	C	2630	513	767	
2599	32967	B	2631	114	230	
2600	32968	B	2632	24	629	
2601	32969	B	2633	98	230	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
2602	32970	B	2634	99	462	
2603	32971	B	2635	127	1498	
2604	32972	B	2636	22	105	
2605	32973	B	2637	1	1173	
2606	32974	B	2638	403	660	
2607	32975	B	2639	58	507	
2608	32976	C	2640	103	480	
2609	32977	B	2641	1	657	
2610	32978	B	2642	1	508	
2611	32979	B	2643	1	999	
2612	32980	C	2644	1	756	
2613	32981	C	2645	1	675	
2614	32982	B	2646	1	810	
2615	32983	B	2647	1	334	
2616	32984	B	2648	1	781	
2617	32985	B	2649	76	211	
2618	32986	B	2650	1	687	
2619	32987	B	2651	1	753	
2620	32988	B	2652	37	1038	
2621	32989	B	2653	1	456	
2622	32990	B	2654	1	168	
2623	32991	B	2655	1	786	
2624	32992	C	2656	571	1278	
2625	32993	C	2657	96	548	
2626	32994	C	2658	391	504	
2627	32995	B	2659	1	183	
2628	32996	C	2660	1	381	
2629	32997	B	2661	1	642	
2630	32998	B	2662	1	1164	
2631	32999	B	2663	1	471	
2632	33000	B	2664	1	972	
2633	33001	C	2665	75	182	
2634	33002	C	2666	125	226	
2635	33003	B	2667	1	462	
2636	33004	B	2668	1	422	
2637	33005	B	2669	81	616	
2638	33006	B	2670	197	713	
2639	33007	B	2671	1	882	
2640	33008	B	2672	1	507	
2641	33009	C	2673	176	274	
2642	33010	B	2674	250	446	
2643	33011	B	2675	19	118	
2644	33012	B	2676	21	120	
2645	33013	B	2677	373	389	
2646	33014	B	2678	1	1452	
2647	33015	B	2679	70	148	
2648	33016	C	2680	7	96	
2649	33017	C	2681	360	550	
2650	33018	B	2682	55	1618	
2651	33019	B	2683	1	309	
2652	33020	B	2684	100	528	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
2653	33021	B	2685	1	1191	
2654	33022	B	2686	52	834	
2655	33023	B	2687	1	933	
2656	33024	C	2688	80	322	
2657	33025	B	2689	127	415	
2658	33026	B	2690	74	190	
2659	33027	B	2691	150	380	
2660	33028	B	2692	1	1098	
2661	33029	C	2693	185	502	
2662	33030	B	2694	1	180	
2663	33031	C	2695	257	498	
2664	33032	B	2696	88	409	
2665	33033	C	2697	720	902	
2666	33034	C	2698	201	437	
2667	33035	C	2699	16	189	
2668	33036	B	2701	1	2286	
2669	33037	B	2702	1	1026	
2670	33038	B	2703	777	1035	
2671	33039	B	2704	1	1200	
2672	33040	B	2705	332	462	
2673	33041	B	2706	351	480	
2674	33042	B	2707	10	327	
2675	33043	B	2708	108	1325	
2676	33044	B	2709	36	189	
2677	33045	B	2710	54	3192	
2678	33046	B	2711	1	3423	
2679	33047	C	2712	5	280	
2680	33048	C	2713	1	88	
2681	33049	C	2714	1	153	
2682	33050	B	2715	70	231	
2683	33051	B	2716	11	427	
2684	33052	B	2717	74	943	
2685	33053	C	2718	109	315	
2686	33054	B	2719	1	335	
2687	33055	B	2720	108	506	
2688	33056	C	2721	1	486	
2689	33057	C	2722	87	441	
2690	33058	C	2723	85	276	
2691	33059	C	2724	86	280	
2692	33060	C	2725	108	254	
2693	33061	B	2726	1	930	
2694	33062	B	2727	23	847	
2695	33063	B	2728	19	182	
2696	33064	C	2729	190	300	
2697	33065	B	2730	67	650	
2698	33066	B	2731	1	1149	
2699	33067	B	2732	1	263	
2700	33068	B	2733	73	676	
2701	33069	B	2734	1	414	
2702	33070	B	2735	4	256	
2703	33071	B	2736	29	493	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2704	33072	B	2737	1	1323	
2705	33073	B	2738	1	4209	
2706	33074	B	2739	538	728	
2707	33075	B	2740	344	1447	
2708	33076	C	2741	223	477	
2709	33077	B	2742	1	1091	
2710	33078	B	2743	1	2865	
2711	33079	B	2744	1	1203	
2712	33080	C	2745	120	401	
2713	33081	B	2746	1	688	
2714	33082	B	2747	1	549	
2715	33083	B	2748	196	1647	
2716	33084	B	2749	1	378	
2717	33085	C	2750	2	166	
2718	33086	B	2751	1	807	
2719	33087	C	2752	343	532	
2720	33088	B	2753	1	885	
2721	33089	C	2754	32	247	
2722	33090	B	2755	1	1152	
2723	33091	B	2756	1	885	
2724	33092	B	2757	87	359	
2725	33093	B	2758	71	418	
2726	33094	B	2759	117	1983	
2727	33095	B	2760	176	1045	
2728	33096	B	2761	25	187	
2729	33097	B	2762	1	315	
2730	33098	B	2763	1	351	
2731	33099	B	2764	1	396	
2732	33100	B	2765	12	350	
2733	33101	B	2766	1	411	
2734	33102	B	2767	1	1020	
2735	33103	B	2768	72	359	
2736	33104	B	2769	1	526	
2737	33105	B	2770	1	1233	
2738	33106	B	2771	1	1563	
2739	33107	B	2772	1	246	
2740	33108	B	2773	1	747	
2741	33109	B	2774	1	861	
2742	33110	C	2775	1	1278	
2743	33111	B	2776	1	630	
2744	33112	C	2777	22	147	
2745	33113	B	2778	242	744	
2746	33114	B	2779	54	178	
2747	33115	B	2780	1	2277	
2748	33116	B	2781	1	204	
2749	33117	B	2782	1	447	
2750	33118	B	2783	1	819	
2751	33119	B	2784	1	720	
2752	33120	B	2785	1	444	
2753	33121	B	2786	1	519	
2754	33122	B	2787	1	864	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
2755	33123	B	2788	1	654	
2756	33124	B	2789	1	772	
2757	33125	B	2790	1	930	
2758	33126	B	2791	1	3594	
2759	33127	B	2792	1	654	
2760	33128	B	2793	1	444	
2761	33129	B	2794	403	1560	
2762	33130	B	2795	1412	1495	
2763	33131	B	2796	536	2770	
2764	33132	B	2797	417	1025	
2765	33133	B	2798	108	326	
2766	33134	B	2799	1	694	
2767	33135	B	2800	380	541	
2768	33136	B	2801	1	916	
2769	33137	B	2802	509	1643	
2770	33138	C	2803	40	180	
2771	33139	B	2804	1	345	
2772	33140	C	2805	170	361	
2773	33141	C	2806	1	312	
2774	33142	C	2807	307	450	
2775	33143	B	2808	1	993	
2776	33144	B	2809	1	321	
2777	33145	B	2810	1	321	
2778	33146	C	2811	604	779	
2779	33147	B	2812	52	646	
2780	33148	C	2813	7	177	
2781	33149	C	2814	118	294	
2782	33150	B	2815	337	1512	
2783	33151	B	2816	32	335	
2784	33152	B	2817	1	1026	
2785	33153	C	2818	1	1044	
2786	33154	B	2819	1	1575	
2787	33155	B	2820	1	1356	
2788	33156	B	2821	1	3726	
2789	33157	B	2822	158	627	
2790	33158	B	2823	814	3116	
2791	33159	B	2824	1	2667	
2792	33160	B	2825	1	2778	
2793	33161	B	2826	96	662	
2794	33162	C	2827	163	245	
2795	33163	B	2828	1	381	
2796	33164	B	2829	47	378	
2797	33165	B	2830	1	614	
2798	33166	B	2831	277	528	
2799	33167	B	2832	1	1059	
2800	33168	C	2833	354	491	
2801	33169	C	2834	161	466	
2802	33170	B	2835	78	2700	
2803	33171	C	2836	37	111	
2804	33172	B	2837	1	1929	
2805	33173	B	2838	36	612	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2806	33174	B	2839	189	498	
2807	33175	C	2840	302	430	
2808	33176	C	2841	58	219	
2809	33177	C	2842	56	275	
2810	33178	C	2843	21	293	
2811	33179	C	2844	337	543	
2812	33180	B	2845	1	507	
2813	33181	C	2846	232	489	
2814	33182	C	2847	314	476	
2815	33183	C	2848	572	937	
2816	33184	C	2849	259	528	
2817	33185	B	2850	1	597	
2818	33186	B	2851	1	564	
2819	33187	B	2852	368	732	
2820	33188	C	2853	58	375	
2821	33189	B	2854	608	1222	
2822	33190	C	2855	41	358	
2823	33191	C	2856	73	177	
2824	33192	B	2857	1	582	
2825	33193	C	2858	1	543	
2826	33194	B	2859	1	1538	
2827	33195	B	2860	40	704	
2828	33196	C	2861	303	407	
2829	33197	B	2862	131	336	
2830	33198	C	2863	64	156	
2831	33199	B	2864	180	712	
2832	33200	B	2865	1	1104	
2833	33201	B	2866	65	228	
2834	33202	B	2867	1	2172	
2835	33203	B	2868	1	1338	
2836	33204	C	2869	181	410	
2837	33205	B	2870	1	1137	
2838	33206	B	2871	69	1322	
2839	33207	C	2872	24	266	
2840	33208	B	2873	1033	1089	
2841	33209	B	2874	367	463	
2842	33210	B	2875	1	3256	
2843	33211	C	2876	278	466	
2844	33212	B	2877	323	4268	
2845	33213	B	2878	424	1711	
2846	33214	B	2879	567	643	
2847	33215	B	2880	1	258	
2848	33216	B	2881	1	806	
2849	33217	B	2882	56	984	
2850	33218	B	2883	1	807	
2851	33219	B	2884	1	396	
2852	33220	C	2885	107	411	
2853	33221	B	2886	1	678	
2854	33222	B	2887	1	246	
2855	33223	C	2888	41	316	
2856	33224	B	2889	1	300	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2857	33225	C	2890	1	273	
2858	33226	B	2891	78	169	
2859	33227	B	2892	1	882	
2860	33228	C	2893	1	246	
2861	33229	B	2894	1	639	
2862	33230	B	2895	1	411	
2863	33231	C	2896	427	522	
2864	33232	B	2897	158	826	
2865	33233	B	2898	275	310	
2866	33234	B	2899	429	933	
2867	33235	B	2900	1	560	
2868	33236	B	2901	1	798	
2869	33237	B	2902	45	384	
2870	33238	B	2903	845	983	
2871	33239	C	2904	171	422	
2872	33240	C	2905	139	360	
2873	33241	C	2906	188	436	
2874	33242	C	2907	76	303	
2875	33243	C	2908	362	574	
2876	33244	C	2909	42	347	
2877	33245	B	2910	1	766	
2878	33246	B	2911	170	1381	
2879	33247	B	2912	274	543	
2880	33248	B	2913	768	2001	
2881	33249	B	2914	140	279	
2882	33250	B	2915	1	2858	
2883	33251	B	2916	1	321	
2884	33252	B	2917	1	552	
2885	33253	B	2918	1	603	
2886	33254	C	2919	122	406	
2887	33255	B	2920	508	679	
2888	33256	B	2921	1	942	
2889	33257	B	2922	1	753	
2890	33258	B	2923	136	326	
2891	33259	B	2924	445	625	
2892	33260	B	2925	1	639	
2893	33261	B	2926	1	1850	
2894	33262	B	2927	76	1341	
2895	33263	C	2928	184	495	
2896	33264	B	2929	1	226	
2897	33265	B	2930	1	972	
2898	33266	B	2931	57	1493	
2899	33267	C	2932	207	404	
2900	33268	B	2933	664	1647	
2901	33269	B	2934	1	1305	
2902	33270	B	2935	1	639	
2903	33271	B	2936	59	1108	
2904	33272	B	2937	276	1311	
2905	33273	B	2938	1	708	
2906	33274	B	2939	123	309	
2907	33275	B	2940	1	957	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
2908	33276	C	2941	199	357	
2909	33277	B	2942	319	355	
2910	33278	B	2943	574	1044	
2911	33279	B	2944	1	426	
2912	33280	C	2945	1	381	
2913	33281	C	2946	145	301	
2914	33282	B	2947	1	1644	
2915	33283	B	2948	1	906	
2916	33284	B	2949	249	317	
2917	33285	B	2950	388	655	
2918	33286	C	2951	228	379	
2919	33287	C	2952	200	343	
2920	33288	B	2953	1	600	
2921	33289	B	2954	123	719	
2922	33290	B	2955	1	879	
2923	33291	B	2956	88	445	
2924	33292	B	2957	518	1508	
2925	33293	C	2958	1	414	
2926	33294	C	2959	202	408	
2927	33295	B	2960	1	351	
2928	33296	B	2961	1	378	
2929	33297	C	2962	84	194	
2930	33298	B	2963	1	306	
2931	33299	B	2964	238	354	
2932	33300	C	2965	326	331	
2933	33301	B	2966	1	1005	
2934	33302	C	2967	31	408	
2935	33303	B	2968	48	335	
2936	33304	B	2969	1	241	
2937	33305	B	2970	1	768	
2938	33306	B	2971	93	728	
2939	33307	B	2972	25	88	
2940	33308	B	2973	1	414	
2941	33309	B	2974	1	555	
2942	33310	B	2976	83	3457	
2943	33311	B	2977	59	1280	
2944	33312	B	2978	1	414	
2945	33313	B	2979	1	354	
2946	33314	B	2980	1	477	
2947	33315	B	2981	1	357	
2948	33316	B	2982	182	394	
2949	33317	B	2983	148	1104	
2950	33318	B	2984	494	641	
2951	33319	C	2985	44	310	
2952	33320	C	2986	303	395	
2953	33321	C	2987	229	407	
2954	33322	B	2988	195	707	
2955	33323	B	2989	713	1063	
2956	33324	B	2990	67	746	
2957	33325	B	2991	468	1010	
2958	33326	C	2992	1	258	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2959	33327	B	2993	1	282	
2960	33328	B	2994	139	767	
2961	33329	B	2995	1	133	
2962	33330	B	2996	136	291	
2963	33331	B	2997	172	634	
2964	33332	B	2998	1	435	
2965	33333	B	2999	503	1294	
2966	33334	B	3000	1	495	
2967	33335	B	3001	1	1416	
2968	33336	B	3002	1	321	
2969	33337	B	3003	1	378	
2970	33338	B	3004	1	337	
2971	33339	C	3005	1	474	
2972	33340	B	3006	1	633	
2973	33341	C	3007	142	423	
2974	33342	C	3008	226	360	
2975	33343	C	3009	45	281	
2976	33344	B	3010	1	369	
2977	33345	C	3011	2082	2558	
2978	33346	C	3012	99	356	
2979	33347	C	3013	312	467	
2980	33348	B	3014	89	463	
2981	33349	C	3015	16	357	
2982	33350	B	3016	239	541	
2983	33351	C	3017	176	345	
2984	33352	B	3018	1	2238	
2985	33353	C	3019	40	309	
2986	33354	B	3020	80	835	
2987	33355	B	3021	1	741	
2988	33356	B	3022	1	1005	
2989	33357	B	3023	185	3661	
2990	33358	B	3024	1	1539	
2991	33359	B	3025	1	1197	
2992	33360	C	3026	258	584	
2993	33361	B	3027	103	905	
2994	33362	B	3028	1	159	
2995	33363	B	3029	72	642	
2996	33364	C	3030	195	424	
2997	33365	C	3031	350	454	
2998	33366	B	3032	1	1494	
2999	33367	C	3033	1	336	
3000	33368	C	3034	169	423	
3001	33369	C	3035	131	307	
3002	33370	C	3036	80	423	
3003	33371	B	3037	1	663	
3004	33372	C	3039	619	1068	
3005	33373	B	3040	1	441	
3006	33374	B	3041	1	453	
3007	33375	C	3042	174	431	
3008	33376	B	3043	236	1145	
3009	33377	C	3044	99	215	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
3010	33378	B	3045	1	675	
3011	33379	B	3046	1	479	
3012	33380	C	3047	18	272	
3013	33381	C	3048	800	1097	
3014	33382	C	3049	1	231	
3015	33383	C	3050	1	777	
3016	33384	B	3051	194	328	
3017	33385	B	3052	1	633	
3018	33386	C	3053	431	838	
3019	33387	B	3054	1	450	
3020	33388	B	3055	684	1367	
3021	33389	B	3056	112	423	
3022	33390	B	3057	28	420	
3023	33391	B	3058	28	280	
3024	33392	B	3059	1	1335	
3025	33393	B	3060	516	1396	
3026	33394	B	3061	1	1563	
3027	33395	B	3062	1	903	
3028	33396	B	3063	191	628	
3029	33397	B	3064	1	534	
3030	33398	B	3065	1	1134	
3031	33399	B	3066	1	1248	
3032	33400	B	3067	1	1479	
3033	33401	B	3068	1	1635	
3034	33402	B	3069	46	447	
3035	33403	C	3070	1	624	
3036	33404	C	3071	25	330	
3037	33405	C	3072	132	253	
3038	33406	B	3073	4	1011	
3039	33407	B	3074	392	814	
3040	33408	C	3075	414	557	
3041	33409	C	3076	74	328	
3042	33410	C	3077	1	678	
3043	33411	B	3078	1	5130	
3044	33412	B	3079	1	985	
3045	33413	B	3080	1	1671	
3046	33414	B	3081	146	556	
3047	33415	B	3082	1	732	
3048	33416	B	3083	136	753	
3049	33417	B	3084	1	1500	
3050	33418	B	3085	300	2678	
3051	33419	B	3086	1	1221	
3052	33420	B	3087	58	1287	
3053	33421	B	3088	1	933	
3054	33422	B	3089	1	1317	
3055	33423	B	3090	1	771	
3056	33424	B	3091	1	2241	
3057	33425	B	3092	1	642	
3058	33426	B	3093	1	2664	
3059	33427	C	3094	1	513	
3060	33428	C	3095	52	174	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3061	33429	C	3096	44	428	
3062	33430	C	3097	300	437	
3063	33431	C	3098	1	576	
3064	33432	B	3099	1	864	
3065	33433	C	3100	1	801	
3066	33434	C	3101	298	480	
3067	33435	B	3102	503	720	
3068	33436	C	3103	1	756	
3069	33437	B	3104	1	355	
3070	33438	C	3105	1	1143	
3071	33439	B	3106	1	2256	
3072	33440	C	3107	537	966	
3073	33441	B	3108	1	2009	
3074	33442	B	3109	1	3021	
3075	33443	B	3110	1	1085	
3076	33444	B	3111	180	2069	
3077	33445	B	3112	1	375	
3078	33446	B	3113	31	127	
3079	33447	B	3114	47	452	
3080	33448	C	3115	149	440	
3081	33449	B	3116	119	538	
3082	33450	B	3117	1	900	
3083	33451	C	3118	1	270	
3084	33452	B	3119	1	344	
3085	33453	C	3120	72	245	
3086	33454	B	3121	1	822	
3087	33455	C	3122	69	242	
3088	33456	B	3123	2129	2289	
3089	33457	C	3124	1	255	
3090	33458	B	3125	2129	2289	
3091	33459	B	3126	1	306	
3092	33460	C	3127	1	255	
3093	33461	B	3128	82	1254	
3094	33462	B	3129	1	468	
3095	33463	C	3130	2	250	
3096	33464	C	3131	166	357	
3097	33465	B	3132	423	3286	
3098	33466	B	3133	63	436	
3099	33467	B	3134	1	4578	
3100	33468	B	3135	1	4322	
3101	33469	B	3136	46	325	
3102	33470	B	3137	58	289	
3103	33471	B	3138	1	1695	
3104	33472	B	3139	89	1195	
3105	33473	C	3140	317	541	
3106	33474	B	3141	314	992	
3107	33475	C	3142	95	222	
3108	33476	C	3143	26	172	
3109	33477	C	3144	40	255	
3110	33478	C	3145	277	508	
3111	33479	B	3146	12	1358	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3112	33480	B	3147	602	780	
3113	33481	C	3148	1	306	
3114	33482	C	3149	1	771	
3115	33483	B	3150	149	360	
3116	33484	B	3151	1	567	
3117	33485	B	3152	1	345	
3118	33486	B	3153	1	1233	
3119	33487	B	3154	144	773	
3120	33488	C	3155	1	417	
3121	33489	B	3156	85	525	
3122	33490	C	3157	251	679	
3123	33491	B	3158	1	1185	
3124	33492	C	3159	541	729	
3125	33493	B	3160	211	382	
3126	33494	C	3161	200	409	
3127	33495	C	3162	85	423	
3128	33496	C	3163	243	455	
3129	33497	B	3164	152	437	
3130	33498	B	3165	1	816	
3131	33499	B	3166	79	294	
3132	33500	C	3167	6	353	
3133	33501	C	3168	82	405	
3134	33502	B	3169	3	191	
3135	33503	C	3170	204	413	
3136	33504	B	3171	75	1449	
3137	33505	B	3172	1	738	
3138	33506	B	3173	1	324	
3139	33507	C	3174	299	1009	
3140	33508	B	3175	1	447	
3141	33509	C	3176	1	570	
3142	33510	B	3177	1	703	
3143	33511	B	3178	142	744	
3144	33512	B	3179	1	237	
3145	33513	C	3180	63	254	
3146	33514	B	3181	185	330	
3147	33515	B	3184	214	1333	
3148	33516	B	3185	61	423	
3149	33517	B	3186	19	2467	
3150	33518	B	3187	4	1085	
3151	33519	B	3188	157	341	
3152	33520	B	3189	222	656	
3153	33521	B	3190	249	999	
3154	33522	B	3191	416	2447-	
3155	33523	B	3192	187	1855	
3156	33524	C	3193	38	166	
3157	33525	B	3194	1	1449	
3158	33526	B	3195	286	663	
3159	33527	B	3196	255	556	
3160	33528	B	3197	85	591	
3161	33529	B	3198	32	404	
3162	33530	B	3199	185	253	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3163	33531	B	3200	202	2862	
3164	33532	B	3201	448	833	
3165	33533	B	3202	1	1275	
3166	33534	B	3203	1	591	
3167	33535	C	3204	1	291	
3168	33536	B	3205	1	744	
3169	33537	B	3206	338	523	
3170	33538	B	3207	1	435	
3171	33539	B	3208	1	477	
3172	33540	B	3209	1	2943	
3173	33541	B	3210	1	1719	
3174	33542	C	3211	113	280	
3175	33543	B	3212	1	1092	
3176	33544	B	3213	1	1470	
3177	33545	B	3214	1	426	
3178	33546	B	3215	1	747	
3179	33547	B	3216	321	2234	
3180	33548	B	3217	1	3057	
3181	33549	B	3218	1	537	
3182	33550	B	3219	1	2496	
3183	33551	B	3220	94	273	
3184	33552	B	3221	302	1432	
3185	33553	B	3222	35	1657	
3186	33554	B	3223	2	901	
3187	33555	B	3224	82	1479	
3188	33556	B	3225	224	411	
3189	33557	B	3226	328	429	
3190	33558	B	3227	27	1098	
3191	33559	B	3228	508	1765	
3192	33560	C	3229	1	321	
3193	33561	B	3230	251	415	
3194	33562	B	3231	695	1011	
3195	33563	B	3232	1	416	
3196	33564	B	3233	45	1340	
3197	33565	B	3234	65	2087	
3198	33566	B	3235	1	1149	
3199	33567	C	3236	1	108	
3200	33568	B	3237	1	384	
3201	33569	B	3238	80	383	
3202	33570	B	3239	200	409	
3203	33571	B	3240	14	419	
3204	33572	B	3241	1	888	
3205	33573	C	3242	165	435	
3206	33574	B	3243	452	593	
3207	33575	B	3244	1472	4415	
3208	33576	B	3245	103	207	
3209	33577	B	3246	242	292	
3210	33578	B	3247	1	306	
3211	33579	B	3248	1	684	
3212	33580	B	3249	1	838	
3213	33581	B	3250	215	2593	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
3214	33582	C	3251	80	376	
3215	33583	B	3252	1	639	
3216	33584	C	3253	52	288	
3217	33585	B	3254	1	1197	
3218	33586	B	3255	39	2809	
3219	33587	B	3256	1	609	
3220	33588	C	3257	269	418	
3221	33589	B	3258	1	561	
3222	33590	B	3259	347	922	
3223	33591	B	3260	52	339	
3224	33592	B	3261	235	434	
3225	33593	B	3262	74	2676	
3226	33594	B	3263	90	675	
3227	33595	B	3264	1	1440	
3228	33596	B	3265	288	752	
3229	33597	B	3266	1	804	
3230	33598	C	3267	109	451	
3231	33599	B	3268	1	1122	
3232	33600	B	3269	1	768	
3233	33601	B	3270	380	2743	
3234	33602	B	3271	1	1296	
3235	33603	B	3272	322	591	
3236	33604	B	3273	174	464	
3237	33605	B	3274	1	384	
3238	33606	C	3275	320	385	
3239	33607	B	3276	53	485	
3240	33608	C	3277	175	205	
3241	33609	B	3278	216	316	
3242	33610	B	3279	1	921	
3243	33611	B	3280	22	453	
3244	33612	B	3281	168	817	
3245	33613	B	3282	1	477	
3246	33614	B	3283	190	1062	
3247	33615	B	3284	116	787	
3248	33616	B	3285	130	697	
3249	33617	B	3286	1	901	
3250	33618	B	3287	1	342	
3251	33619	B	3288	1	677	
3252	33620	B	3289	1	624	
3253	33621	B	3290	1	756	
3254	33622	B	3291	1	624	
3255	33623	B	3292	130	429	
3256	33624	B	3293	95	516	
3257	33625	B	3294	120	524	
3258	33626	B	3295	51	425	
3259	33627	B	3296	647	1015	
3260	33628	C	3297	518	841	
3261	33629	C	3298	67	294	
3262	33630	B	3299	1	1212	
3263	33631	C	3300	187	453	
3264	33632	B	3301	188	492	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,400,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3265	33633	B	3302	123	647	
3266	33634	C	3303	1	219	
3267	33635	B	3304	1	690	
3268	33636	B	3305	1	930	
3269	33637	B	3306	552	722	
3270	33638	B	3307	84	304	
3271	33639	B	3308	328	1104	
3272	33640	C	3309	300	593	
3273	33641	C	3310	1	87	
3274	33642	B	3311	1	819	
3275	33643	C	3312	122	334	
3276	33644	B	3313	1	318	
3277	33645	B	3314	764	977	
3278	33646	C	3315	379	471	
3279	33647	B	3316	1	1194	
3280	33648	B	3317	1	1800	
3281	33649	C	3318	273	506	
3282	33650	B	3319	1	1689	
3283	33651	C	3320	48	212	
3284	33652	C	3321	1	507	
3285	33653	C	3322	117	251	
3286	33654	B	3323	89	845	
3287	33655	C	3324	1	651	
3288	33656	C	3325	48	212	
3289	33657	C	3326	1	864	
3290	33658	B	3327	223	839	
3291	33659	C	3328	1	189	
3292	33660	B	3329	36	144	
3293	33661	B	3330	56	389	
3294	33662	B	3331	1	597	
3295	33663	B	3332	1	606	
3296	33664	C	3333	1	426	
3297	33665	B	3334	1	696	
3298	33666	B	3335	1	417	
3299	33667	C	3336	1	594	
3300	33668	B	3337	1	228	
3301	33669	C	3338	1	879	
3302	33670	B	3339	1	405	
3303	33671	C	3340	33	152	
3304	33672	B	3341	224	429	
3305	33673	B	3342	578	4588	
3306	33674	B	3343	1	288	
3307	33675	B	3344	77	1479	
3308	33676	B	3345	132	875	
3309	33677	C	3346	120	395	
3310	33678	B	3347	1	729	
3311	33679	C	3348	8	133	
3312	33680	C	3349	171	359	
3313	33681	B	3350	1	1098	
3314	33682	B	3351	1	1547	
3315	33683	B	3352	1	933	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
3316	33684	B	3353	1	1989	
3317	33685	B	3354	1	595	
3318	33686	C	3355	62	559	
3319	33687	B	3356	1	153	
3320	33688	B	3357	1	768	
3321	33689	B	3358	1	969	
3322	33690	B	3359	217	358	
3323	33691	C	3360	449	961	
3324	33692	B	3361	1	1799	
3325	33693	B	3362	80	1327	
3326	33694	B	3363	111	258	
3327	33695	B	3364	112	429	
3328	33696	B	3365	147	390	
3329	33697	B	3366	1	585	
3330	33698	B	3367	1	2290	
3331	33699	B	3368	19	4071	
3332	33700	C	3369	1	183	
3333	33701	C	3370	1	183	
3334	33702	C	3371	44	283	
3335	33703	B	3372	1	954	
3336	33704	B	3373	1	384	
3337	33705	B	3374	709	773	
3338	33706	B	3375	1	3294	
3339	33707	B	3376	83	1229	
3340	33708	B	3377	1	1512	
3341	33709	C	3378	30	200	
3342	33710	A	3379	3	322	
3343	33711	A	3380	530	1489	YAGNESHPPSLPRYLRRSRHCG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPVSVP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMPFA/SPGQVPAQQD LSQEDSSDSPAEQVLPPSSGSH NTLYLGCKRFSFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRDGPCSTGRQSAKTPPPPS HPHTGHSLWSEEK*KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP APFSRMGPQHLPVVVLPTGA FAVVLPCLFLVSSSAWHFKVKH PSIPLLRGEK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
3344	33712	A	3381	296	1255	YAGNESHPPSLPRYLRRSRHCG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPVSVSP YLVLSQCQEQPHHCCPPSTPRPS WSPLPGMPSA/SSPGQVPAQGD LSQEDSSDSPAEQVLPPSSGSH NTLYLRCKRFSAFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRDGPCSTGRQSASKTPPPPS HPHTGHSLWSEEK*KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP APFSRMGPQLPVPVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK
3345	33713	A	3382	81	702	RAAFSPAPVSSLPAPVSSPPAS TSCPPAPVSSI PAHASSPPASTSS PPAPLSSAPHTSSLPAPVSSPP ASTSSPLVAGSGGSTTRSLPPGL GALLTHSVAPYPGGQPPAAAD DP*TMAPAGWGSNPRGCSCSP VAAGAGPFPASF*GPLR*AGSQ TFQILQVEVFLVVRHFSPTP/PS VMLYPPPPSTPTLRAPRPPIPPS P
3346	33714	A	3383	3	231	PMILLEVSVADRDV*TFWQAPI GESQQGALGFWSKALQSSADN NS/PFQITMQPELPIMNWVLSVP SSHKMGHAQQH
3347	33715	A	3384	3	355	KIPGTSTSVKFLGVQ*CGTCQDI PSKVKDKLLHLAPTIKKEAQR LVGLFGFWSQHPIHLGELLRIY RVTRKAASFEGWPEHEKALQQ VQAALQAALPLGPYDPADQPL CNLNCLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
3348	33716	A	3385	2	1076	LCQRLLAEPNEKPGSLGNVM AVARIEIGICEY YHEKTT EKALD SHGVL AGSTIKGVRSFQRNLEL KL PATERATANAIFII.TVLDQA YENFAPQILPSTGSPTSQETAQF KANQNKPLVRGKGPHEAIRYI SAAHREWKPAILTSAIRSFCSCT WLVTFSKNFPKLVTQHGSGTIAG NGQSSDETQVQGAAWKSDSRG TKRQIPTWILAEGNNAGAQLDI PGPTIPAPNCSLKVPSQSWSTTPS MPSSLGKAYWLLACYWALVET E/RLAMGHQVTMMKPEL PVMN WVLSDPSSHKVGGAAQQHSINK WKWYIRNRARAGPEGTTLP KALTWLKKYSNVLMLEVTG LTMFPDILKQLE
3349	33717	A	3386	1	1416	MAQYPILDFKVGQLLGNAL GKGNDQTFRGLDGTGSELTLP GDPKHCDPPVKCAIDLANA FFSIPVHIKAHQKQAFGWQQQ QYTFVTVLHQGCMNSLALCHNL QRELDCLTLPEDITLDHYIDDIM LIGSSEKEVANTLDLLFPWYR EPLRLANYSPPERQLLACYWAL VETECLMMGHQVTMRPEL PIM NWWLADPSRHKVGNAQQHWK CAVHT/IHKWKWYIRDWAQAG LEGTS*LYWPRASRYQQGHQD LFILRSDLPSQVFIRDKLMERRN RRTGRTEKARIWEVTDRTVRT WIGEAVAAAAADGVTFSPVPT PHTFRHSYAMHMLYAGIPLKV LQSLMGHKSSISTEVYTKVFAL DVAARHRVQFAMPESDAVAM
3350	33718	B	3387	50	693	
3351	33719	A	3388	153	578	ARIQ/GSRNQGVVEVAPLTVT PSDPLANVLLPVPATLPSAGLEI LVPEEGRLP PGDTTMMPLNWN LRLPHGHFGLLLPLNQAKKG VAVLGGVIALDCQDEISLLLYK GDLTVMVEDKEEQNHILHGS RQREPSKTGSPL
3352	33720	A	3389	3	402	GRHVGDI EAEDGGGVGRGPH GGVYGLQQSHPGGDPVWED GHPGLPGAQQRGQ* RQACAH HKSPSGAG*G*LPGP/AQS/AGN PDPKSPGPAPCLVGSSRNETPG AMGAPSRNGSPPTAGLVGVDG TGSPSEAV
3353	33721	A	3390	141	320	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
3354	33722	A	3391	1	464	HLKGLGNDTPRVCSCLIG*T*LC DCH*LQAEASPTSVREPRTSV NKD/SPKSLLYSCSYFDEPVE LRSSSFSSWDDSSDSYETHLL HLKLV*PNLAVFNCRPTARRKP DYEPVENTDEAQKTFCKTAHN LWSLTFPPCL*YETRARLER
3355	33723	A	3392	3	1189	
3356	33724	A	3393	1	867	PGRPT/LSEWIQNTLGVNVEHK TTSKASLNPRDTPPSVVNEDFL HDLKETNISYSQEAADDRVFAH GHCLHEIFLLTEGMFERIPDIVL WPTCHDDVVKIVNLACKYNLC IIPIGGGTSVSYGLMCPAETR IISLDSQMNRLWVDENNLTA HV*AGITGKELERQLKESGYCT GHEPRFPWSSSTVGGWVSTRA SGMKKNYGNIEDLEIVHFSN DLSCIELDRLEIVLPSSGIPLLD GYSTEIHMPVHLETSITMCIVTP IHSSMKLETLRMSMSINCRKDK
3357	33725	A	3394	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLSHFQWGTLDTCVV MRDPNTKRSRGFGVITYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYQKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGGGSGGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGSSSSSYGSGRRF
3358	33726	A	3395	2	441	DGMEKVDTAMNARPHKVDGR FVEPKTAVSREDSQRPGAHLTV IKM/FKE/DTEEHKLRDYIEQYQ/ GGNFGSACAGGGRSGGGR*GG SGNGYNRFNDGSNFGGGGSY NDFGNYNDRSSNFGPIKGGNFG GRSSGPYGGGGQYFAKPNQ
3359	33727	A	3396	3	404	

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3360	33728	A	3397	2	762	MNARPHKVDGRVVEPKRAVSR EDSQRPGAHLTVKKIFVGGIKE DTEHHLRDIFYEQYQKIEVIEI MTDRGSGRKRGFVFVTFDDP\ DSVDKIVIQKYHTVNGHNCEV RKALSKQEEMASASSISQGRGRS GSGNFGGGRGGGFGGNDNFG RGGNFGSGGGGGSRGGGGYG GSGDGYNGFGNDGSGNFGGGGS YNDFGNYNNQSSNFGPMKGGN FGGRSSGFPYGGGGQYFAKPR\ NQGGYGGSSSSSYGSGRRF
3361	33729	A	3398	1	3737	
3362	33730	A	3399	5	633	DLREWSWARRTAWEPGRKRV RGK*AFKEIQCP*QKQK/MSGL LLLKVYAKEMTWLPLSAIQAP GKVEPTKFPFNKLMFSWWYIE TTTASAKVIGYKPSVLNCATLR VQIMSHYHSYRHLASLLVEGSA TLPGHSHILGPLIRHPDKVSAGK PRVLGLQLLKEDCSSQPAAKPQ GPHRLCSSLILHRARARLGEQ RETKVPFSGKGTTH
3363	33731	A	3400	2	816	QVPTMVDWAGWSPGLWTTCS GTGGGGAEQGWANWSLVLP VLAGTSLETFSPLS*GLTFSSLLL MQISAASLNFSSENGIFSTTLP GCKFSKFLCSASLLKWNAFSST QVTS*MLCCSEISSTRYPKSSL* SSKFHKSLEQGQNAASLFAKT* QESPLLQLPTSSSSPSETTSAWIS LSISLSVFLSKLFDKSLLESSKLS TFSSVLLSPPNCSNLCLLPSEFV ACTFLGTFRLRSTSLHWYQFTVL VCFHPADKDLKSEKKRCKEK
3364	33732	A	3401	1	485	LFAVYLDHDPHLKLLSLYGTSL HTDVSHLCETLKHTTCKIEELM LGTCDISDEGCEDIASVLACNS KLIHLSLVENPEKDKRM/CCCA LETLMMLMYCLICVSCEDISHV LFCSKSLSLDLGNSFLEDNEV\ HLLCEALKH*DACKTWRSLNF DWVGYLGC
3365	33733	C	3402	952	1164	

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3366	33734	A	3403	3	163	IAVSKQDPITSLQEKEPWNMK ICEMVDESPAMCSSFTRDLWPE QDIKDSFQQVILRRHGKCEHEN LQLRKGASVDEYKVHKEGYN ELNQCLTTTQSKIFPCDKYVVKV FHKFLNANRHKTRHTGKKPFK CKKCGKSFCLMLHLSQHKRIHI RENSYQCEECGKAFKWFSTLTR HKRIHTGEKPFKCEECGKAFKQ SSLTTHKIIHTGEKPYRCEECG KAFNRSSLTTHKIIHTGEKPYK CEECGKAFNQSSLTSTHKFIHA GEKPYKCECDKAFNRFSYLT HKIIHAGEKPYNCEECGKGFN WSSTLTTHKRIHTGEKPYKCEV CGKAFNESSLTTHKMIHTGEK PYKCEECGKAFNRSPQLTAHKII HTGEKPYKCEECGKAFSQSSIL TTHKRIHTGEKPYKCEECGKAF NRSSLTTHKIIHTGEKSYKCEE CGKAFNQSSLTTHKRIHTRQK PYNCEECNTFNQSSNL/N*/HK IIHTGEKLYKQCECGKASKQSF TLTKH*ILFNK
3367	33735	A	3404	3	345	
3368	33736	B	3405	282	694	
3369	33737	A	3406	586	1403	VSETALADGRWFRKQCQSHLC LASTTGKC*TSLTQSGRDYTEN GESAQEGETGLPERRLAHCT*L AEVHRRQPD*TOENRP/SKMG MTSS/AAKDHLDNKCRQDSIP GSSRGPSPLTMGAQDTLPVAAA FTETVNAYFGADPSNTPSVLV EQLLSKRNSNPIMDHGGHKVPC SLPPLTTHPNRRQRELKMYGSH KAVAQPSPLQDRLLQCAVPTP VTGWTNSRAALGDFSTWGSLL LRTSTPKKAAARARMPCCPGA YNTSYPLAPYFWR
3370	33738	A	3407	1	421	FRHSMNGCEKDSSTDSANEKP ALIPREKKISILEEPSKALRGVT GPNIKSVKDLQRTVS.LTRYR VMIKEEVDSSVKIKAAFAELH TCHIDKEVSLMAEMDKVKEEA MEILTARQKAEALKRLTDLA SQMAEMQL
3371	33739	A	3408	1	403	MEILTARQKAEELKRLTDLAS QMAEMQLAELRAEK*/WFSN ELGNSDLCYSYCYLAQKLS QCYLGGTAHSAPGIAKRRKTSQ L*PLP

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3372	33740	A	3409	1	756	
3373	33741	A	3410	2	1849	QRRRRNTPGWSGFQGLTRAPALFPRLLFQSSSETRLLSGTLLWIPRAYSTRSKMAELNTHVNVKEKIYAVRSVVPNKSNNIEIVLVLQQFDFNVDKAVQAFVDGSAIQVLKEWNMTGKKKNNKRKRKSKQHQGNKDAKDKVERPEAGPLQPQQPQIQNGPMNGCEKDSSTDSANEKPAIIPREKKISILEFPSKALRGVTEGNRLQQLSLDGNPKPIHGTTERS DGLQWSAEQPCNPSKPKAKTSPVKSNTPAAHLEIKPDELAKKRGPNIEKSVKDLQRCTVSLTRYRVMIKEEVDSVVKKIKAAFAELHNCIIDKEVSLMAEMDKVKEEAMEILARQKKAEELKRLTNLASQMAEMQLAELRAEIKHFVSEKRYDEELGKVAARFSCDIEQLKKAQIMLCGEITHPKNNYSSRTPLQAPCWPLLNAAHANLWGKQSNFSRKSSTTHNKPS EGKAATPKMVSSLPSTADPSLRAMPANKQNGSSNQRRRFNPQYHNNRLNGPAKSQSGNEAEPLGKGNRHEHRRQPHNGFRPKNKGGAKNQEAASLGKMTPEAPAHSEKPRRRQHAADTSEARPFRRGSGRVSQCNLCPTRIEVSTDAAVLSVPVTLVA
3374	33742	A	3411	1	489	MAEVQVPVLHGRGHLLGRLLAAIVAKQVMLGWKVVVVRCEGINISGNFYRNKLNCSFRTPSIFRWTVRGMLPHKTKRGQAVLDHLQVFDGISPLYDK/K/KRMVVPAAALKVVRLLKPTRKFAYLGRLAHEVGWKYQAVTATLEKKRKEKA*IH YRKKKQLMRLRKQA
3375	33743	A	3412	2	260	
3376	33744	A	3413	1	612	AEVQVLVLDGRGHFLCRLADI VAKQVLLGRKVVVVRCEGINISGNFYRNKLLKYLALRKRMTNPSRGPAYHFRAPSRIFWRTVRGMLPHKTKRGQAALDRLKVFDGIPPPYDKKKRMVVPAAALKVVR LKPTRKFAYLGRLAHEVGWKYQAVTATLEKKRKEKA*IH YRKKKQLMRLRKQAELNVEKKIDK YTEVLKTHGLLV

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3377	33745	A	3414	734	1488	MTKDPWLKQSGSSDTPAASP GHFRAVPRAARGTVVHHRH/ LCLSSWPSS/RVPPGCASYTPA STAAGALPYQAQRQGVLRRY TTYLRV*HFLPRGLPEGFQGRP RVPPPPPCPMAAEPGLGHAKL LDLREIVSFLYFYFFFFLRRSLT LSPGWRDLGSLQPLPHGFKAI/ /SCFSLLSGWDYRHTATHAQLI FVFLVEMGF/TPMFARMASIS*P CDPPDSASQDAGITGVSHQVW RERLFLDEGGGGCP
3378	33746	A	3415	48	966	WSQVVTVTVVTVTSGSNHGN HTQASHEGYRHPMRAQVSH/G ECR/PSHEGHRHPMRTQASHEG HRRPMRTQASHEGHRHPMRTQ ASHEGHRHPMRTGTGP*EHRH PMRAQASH/GEHRR/HH/GEHSC PMRAQASHEGTGP*EHRC/HH ENTGVP*GHRCPMRMQASHAG HRHPMRVQASHEGHRCPMRTQ VSHEGHRRPMRVQASHEGNTGV P*GAQASHEGTGP*EHSHPMR AQASHENTDVP*GVQASHEGY RRPMRTQASHEGHRCPMRAQT SHENTGVP*AAQYRP*EAGAPQ GGQGWQETGADRST
3379	33747	A	3416	8	432	NSKLPPVVTSSQMRFMY/DPQT DQHMKNFPEQLPLDEFLOKTD KDPANYILHAVLVHSGDNHGG HYVVYLNPKGDGKWKCFDDDD VVSRICTKEEAIEHNYGGHDD LSVRHCTNAYMLVYIRESKLS VLQAVTDHDIPOQL
3380	33748	A	3417	38	2865	SFRWDSKKHTGYVGLKNQGAT CYMNSLLQTLFFTNQLRKKLL MGALPWEGALAPVW*ALDTP SLPCSTCLTARTCTSL/QQCHA DQCRWQTRWQGSRRW*WQOE EIGQEREVEGYAKRVLLGPPY SISDCTHMESSLPPCSS*DPGSF QFHIEERADEKSEGRGPSCST QPPPW*SLGEGLGECR*ESSSY CSLAGLSLIIP*ETRGERLQEA SQGPESPFGEV*HPALVSLDLA E*QGAEKHGCTETH

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3381	33749	A	3418	2	3515	YVRVSLPPPPPAACRPGA AVAD DAREEEEEAAPPPPPPPRLAA ARPPGSQRP PPAAGEAQAAAD MNHQQQQQQKAGEQQLSEPE DMEMEAGD TDDPRITQNPVIN GNVALSDGHNTAEEDMEDDTS WRSEATFQFTVERFSRLSES VLS PPCFVRNLPWKIMVMPRFYPDR PHQKSVGFFLQCNAESDSTSWS CHAQAVLKIIINYRDEKSF SRRJ SHLFFHKENDWGF SNFMAWSE VTDPEKGFIDDDKV
3382	33750	B	3419	36	335	
3383	33751	A	3420	2	1602	CR LKTTAFSSPSRHITACLPRF WQICSLPKHLIPEAPPV GMS*R RRKPVWVKSMMLG*RIP*GKR DPPTTAKCRTCSPQEETGPAGT QGQAARQLERRKLP PYVQT/PP RPDQLKGVCSLQTD AISLAPTA ERHSRLPPPSRQQPTSAGTEA GACPNTRRPSGLQLPAAVQTPS GQTPSVPKGLEPTSLPVGSG/PI SASHSQ/PVSKINKK**VCESPY METFP*DAKRTRHKRADTARR GEPLRPRTSVPRRTVPAPSEKLR GSRRGEP TPAAPRRDPRRAGSL THAGPPGG*RHR*PGWPRGTA/ AKTPVAAEALIAAALPLAHRI PLGAPPQLPAAPAP/RLALALRG ASAA/RPRVAPSAASPQRCLL R\ GPPSPQSPAPGPVAPSAQGRG AVPGGVLAVL LPGA PRLSGKRP AAPRGGDTPAQGQVPLAARAP REGPHG GREPVIEELERRGAEL RSGKGGTRSEGVRGGRARGIV YGGAHGPEVGKDKMPLKPRNL SAPVAIGGLLHGAGIRFLNLAL HSPAVDFGQIT
3384	33752	A	3421	3	498	IIDPTQYRPMVPNKVSSPC*WLP TITQVHPDNEAEPIS/PARSCAP ICGV P/AYGSPLSQSSVS*TRQ*F PSCSQSL**GSPITLVNPKTAYT* NSGSRGG/VSFDEDT SQHCYPG TG*GQQLQ*SRNHAGPPGG*M T*VTGVAERDK/PPKTPVGRRG THSQPPRRSP
3385	33753	A	3422	1	270	

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3386	33754	A	3423	1	1899	MGFCHIGQAGLKLTSKDLPAS AFQSAGIAGFWLLDGISGPILGQ REACCPAGNSNKLKQENSAL AEQLQVVLIDKAGMQCDLFEI KKKLELTELTLQQLSSWCEAPD ANQQLQOQPTDERAQLAHLGQ VMEWLKYLQMEREQYAEYLH GESAMWWORMREMSEQIGHLI VPGICEMGGAQPEVVMGLGFV EVHITLREERVHSMRSRVQLETI LAELRNQVAEPLPPEPPAGPSE VEQKLQAEAEHLWKELENLAG QLQAQVEENEGLSHLNQEQEG LLRLLEQEELKLEQEERLLEQE ERLLEQEERLLELQESLLEQKR KAASFLS*TPTPGAPSRALRGK YVTSYQSQRSV/REDVDRENEY ISRLAQDKEEMKVKLLELVLQL VGDCNKWHGRFLAAANQPAD EPAPWDPAPEIGAANKQGGFLF PGCCI.VTPGGFHGDCRGA YGA QSSPDSQQAQNPDLAVAGKAA FWFEKHEQESLTLKSWGRRK SGSGQAAQLREGSRCAAARRH LARALPAARMPPKRVISTEGAA KEEPKRTSASLSAKPPAKVEAQ PKKAAAKDKSSDKKTQTKGKR GAKGKQAEVANQETKEDLPAE NELSSLSFYARSLILAFIHLRM
3387	33755	A	3424	198	364	FLII*YEGINCSRIVNLTRTAWCF FSG*IFRQKKCKQKKGGEQREN RPEVANPRN
3388	33756	A	3425	3	238	GVCPPRGSRSCDFKADSLYSFP CPSRCGS*ESSTQTCSGFWTGCT ALHRWRGMPERCPPESRDS*TR FPQSSLPGHKT
3389	33757	A	3426	3	681	HIRGPRYSGHHSAGFCPPYSDMN LKKEATLHDLRLREQTQANLES DSSHSKSKSLCSLNFNGKHEKV NSQPRLVQQAQCLKIKGKEDID LDNLFREYSVEQAQQVLHQS SMSTVSAHPFRDPLPLGREQHCK LLPGVADIRASQVARWTVDEV AEFVQSLGCEEHAKCFKKEQI DGKAFLLLTQTDIVKVMKIKLG PALKIYNILMFRHSQELPEEDI ASGQEVRG

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3390	33758	A	3427	30	981	TQDPWPSLPVLWSRASSDPAAG HRAEHI*TYWPWKLEGTNDIWL VLYMPLVQPDNFIKKHSHLPTY CLFKEDVKFPFRCTRLTYCWLN YTEEITYLHTKKVSVGQSAVRE EFAAACTWSIRIGEKLAILLSLY LCRQQALLNMMSVPIHESGV AQRSPVMDKLAQYSVEQAQQV LHQSVMSTVSAHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLIQTQTPHIDESIS KGESPALVVTELRMCMTATEP LVPTKNPYQERGHIGDSFLHYT DQEPQPWDQSSVHPPTAPIYSV SSGFRVTRGSDI
3391	33759	A	3428	1	864	MVSALPEVGRAQILRLIAYIRSP APPVVGVERAARRPAQAFGLV ALPSTDATVFANQPLARACIGA ARHREPDAPGQSAWVGEECLK DALRSPETPKLGSLSPQCQDTRP GRASNDFSLEMGYSLSAARLK IHGQVFQCCGPGPLRLTLHWTQ S*TYLNILALET*GAQNQP*EW QAVD*GAPGLFSHTLGVFPR/RL PQHPKQIICFQNYEYSVEQAQQ VLHQSVMSTVSAHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSAPRGPELSAGANS SRGA
3392	33760	A	3429	201	336	QQTTPGKAVHAPFIADQSLT*EL VSVFPQFQLFPYRR*DSHSGKS
3393	33761	A	3430	600	768	TDTSYHSGS*PARNG*MHSFI RCLLLK*GIEPCALNGDSVLKS RTDVTFTPNITTKVKSVEMHN EALSRLPGDNGVGFKNVSKMF VMATLLFSDCIHNTFDQMWR KEHNARWLSQSSGDKVMKEN DELSDSVSLQKQTLKSPKI ALGESLISCRERAIEIIVDKQTQ ALIMGVADLQGRVNAQLHQVS TVKVRDWKRMGPYNLECGTV GRTLKLWTLSSL
3394	33762	A	3431	1655	1841	EHQAEAEAGDGGPRSLPMKPG SPLMPDKAQRKQVRSRHGRGG RGGG*AGPGIPGKPGSPVSP
3395	33763	A	3432	1	1773	

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3396	33764	A	3433	648	1884	LDPEVAWAKWOHSTVKGPOK QFAFSWQQQYFTFTGLPQGYIN SLSLCYNLIPRDPD/RL/SLQNI TLVHYIDIMLIGSSEQLAYTL DLLVRRLLCAKGWEINL.TEIQEA STSVKFLRVQWCGACQDIPSK MKDKLLHLFPPTTKKASLFGF RRQCIPHLECGPEQEKA.LQQAQ AAVQAAVPLERYDPADPMVL/ V/ELTWLWPLLSAQFASSGDQH *ALHMAPFLGVVSQLPGGKLIL DIFHHGKGRVLFSL*TLTPDM GLPILHIMLLPRLPSVNSQNALS TVMPGFTGPGIKGWKWHHS PLVIH*QNFCLFP*HYVLLA*R S*FQRKEPCHQET*Q*FH*TGS* GCQLDTLGSCYF*VNKLRLRELQ CWLG*LTQTIKMKSVYYSITEN CWMKRSPVKRRKILEEEA
3397	33765	A	3434	1	2223	
3398	33766	A	3435	1	1078	MNKEMSGQTFVGKQNSVRMP KIIISGLGVQKPNRQWRLVQDLR IINEAVVPLVQAVRNPYTLLSQI PEETGWFTVLDLKDALFCIAVH PDSQFLAFEDPLNPTSQTLWT VLPGGFRDSPHLFGQALAQDLS QFSYDLTLVLRVVDLLLAAPS ETLCHQATQVLLNFLTACGYK VSKLKAQICSQVVKYI.GLKL GTRALSEERIQPILAYPHKTRK QLRGLLGHGFCQIWIPRYSEIA RPLHTLIKKTQKANTHLVRWTP EAEAAFQVLKKALTOAPVLSLP TGQDPSLYVTEKTGIALGVLTQ HYGEERNS*LPTEYLSNIRKPLG DYYWLYRNLRWQSYTARVIR KERKKG
3399	33767	A	3436	1	1677	

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3400	33768	A	3437	1	2052	MVLVVVAVVVVVLVVAIVVV VVVVVAAVVVGAVVVVVVV MVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLLKKHSGVKNKIPRNPTYEG CEGPFQGELOTTAQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAWEF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLD LVLRYMDLLATHSETLCHQ ATQALLNFLATCGYKVSQPKA QLCSQQVKYGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAF GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPAEVAF QALKKALTHAPVLSLPVGGNFS LYVTEKVTGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIENRQADIEARR AARODPPLEMLTEGPLAFELA MATARAELSIAIHHCLPPPQ TRCWLPRLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEQGPPVTQTHILRSHL

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3401	33769	A	3438	294	2340	EKCRHNCSSRVWQSLVVSQSVW ATEGQYGRTKNARPPQVKIDS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPI GVQKPNGQWKLVDLRINEAI VPLYPAPNPYTLQSIPPEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVRLYRDDLLAAHLETLCH QATQKKTGIALGVLTVQVGTSTF QPVAHLSKEIDVVAKGWPHCL WVVAAVLVSEAVKIIQGRE LTVWTSHTDVSGLTAKGDLWL SDNLLNQALLFKRPVRLHTC ATLNPATFLPNNKEKIEHNHQQ VIVQTYTIQGDLEVPITDPL NLYTNGSSFVEKGLRKAGIHPS RQWTPLPWPKAGPEMLSKRQVL ESGILKAFLVPYLLVAVLGSIDF NGKPPVAVFSLSQAHRFCLCAT WLLGYGEVWIHSHTAIKTYQ RRRSQDGRIGTAPVYSSQRERR RRRVISAFPSEGIPTDLQLRVLS VRRKTNKQKGHPHQPCTSPS SRPKVDKTTKMGKKQNRKTGN SKTQASAPPPKERSSSPATEQSW MENDFDELREEGFRSSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSAMED
3402	33770	A	3439	2	350	YKVKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIPR*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
3403	33771	A	3440	1	897	
3404	33772	A	3441	1	429	

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3405	33773	A	3442	3	957	NKIPRNPTYEGCEGPFQGELQT TAQQNKGGHKQTEDHSMMLMD RKNQYCENGHTAAQAVPNPYTL LSQIPEDA EWFTVLDPKHAFVC IPVHPDSQFLFAFEDPSNPMSQL IWTVLPQGFNRSPHLFGQALAQ DLSQFSYLDLTVLRYMDDL ATHSETLCHQATQALLNFLATC GYKVS KPAQLCSQQVKYLG KLSKGRTRLSEERIQPLGYPHP KTLKQLTAF LGITGFCQIWIPRY SKIARPLNTRIKETQKANTHLV RWTPEAEVAFQALKKALTHAP VLSLPVGQNFSLYVTEKVTGIAL GVL TQELVLSWQN
3406	33774	A	3443	146	1303	EKCRHNCSRVWQSLVSQSVW ATEGQYGRTKNARPVQVKIDS ASFPYQRRYPLRLEAQGLQKI VKDLKAQGLVKPFNSPCNTPI GVQKPNQWKLVDLRIINEAI VPLYPAVPNPYTL SQIPEAE WFTVLDLKD AFFCIPVHRESQF LFAFEDPSNPSTQLTWTVLPQ FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLAAHLETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTS HDVSGTLTAKGDLWL SDNLLNQALLFKRPVLR LHTC ATLN PATFLPNKKEIEHNHQ VIVQTYTIQGD LLEVPLTDPDL NLVTNGSSFVEKGLRKA

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3407	33775	A	3444	1	1647	MNKEDYNDDDDNGDIKYLDPDI KTGYNKTVQIPITSENSIVGLSN TEADEMDRLKCRDDALKEVN TLKRRTKGGKHLTLKVTVTLSE TNLHKNYLWECILMGQLGCYE ILRKPSPALGLTPEHKGNGVGH GEKTGAG/PATSRPPDSFPN**G PPFNPNGTKGDRQRGKQQTKE CQYSPIMPPTSSGRRRIWSSQIR HVPFSLSDLIDLAVPNPYTLSSQ IPEEAWEFTVLDLKDVFPCIPVH PDSQFLFAFEDPLNPMSQLTCT VLPQGFSDSPHLFGQALAQDLS QLSYLDLTLVQYVDDLLAAC SETLCHQATQALLNFLATCGYK VSKEKAQLCSQQVKYLGKLS KGTALSEECIQPILAYPHLKT KQLREFLGITGFCRIW/NFQALL LERPVLQLCTCATLNPTFLPD NEVEEYNCQIISQTYATRDL EVPLTDPDLNLYTDGSSFVEKG PQKAGERRAVLASQTSLTPLGR NGRSIPATLALESKELVKSVR LLDMDCAIFFLVGTSIVDPYLYK YEPTTKNHLIMVQGEKNCITGR
3408	33776	A	3445	1	2217	
3409	33777	A	3446	1	749	MNQSDQEMTGAFVHMKSYYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEAWEFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDLTLV RYMDLLAAYSETLCHQATE ALLNFLATCGYKVSFKPAQLCS QQVKYLGKLSKGTDLTTLFL VNEEKIE/P*LSNCSKLCRSRG TSRGSGLG

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3410	33778	A	3447	1	1374	MPLLQMIATPLQQSLISTEDEM DELTEVGFERWVITNITEPSPA LGFTPEHKGNGVHAGKGPLESS SPDPFLCGQEKQKAGLLHRQ YPLRLEAKQGLKIVKDLKAQ GLVTPCSPCNTPTLAVQKPNG QWRLVQDLRIINEAVVPLYPAV PNPYILLSQIPEAEWFTVLDLK DAFFCIPVHPDSQFLFAFEDPSN PMSQLTWTVLPGGFRDLSHLFG QALAQDLSQFSYLDLVLQYM DDLLLVTHSETLCHQATQVLLN FLATCGYKVKSLKAQCSQQVK YLGKLSKGTALSEERIQPILA YHPKTRKQLRGLLGITGFCQI WIPRYSEIARPLHTLIKKTKKAN THLVVRWTPAEAAAFQVLKKAL TQAPVLSLPTGQDFSLYVTEKT GIALGVLTQHYGEERNS*LPTE YLSNIRKPLGDYYWLYRNLKR WQSYTARVIRKERKKGK
3411	33779	B	3448	1	2862	
3412	33780	B	3449	94	1248	
3413	33781	A	3450	1	3805	MQWEEAEKDPSGSCVFQRPPV ALVFLHSHKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGT QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGLTSTRTNPLKKEKSPEDL KQIKIDLKGFSDN
3414	33782	A	3451	1	444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFAFV*YVNE RNARAAVGGDIDSSSFDLDHDF QRDYYDRMYSYPAHVPPPIAR AVVPSKCQHVSNGNRRGKSGFN SKRGQRGSSKSGKLKGDDLQAI KKELTQIKQVDSLLENL
3415	33783	A	3452	3	93	
3416	33784	A	3453	117	316	SSATFSAL*ETLPSNTMASSSFD LDYDFQDYYDRMYSYPARVP PPPIARA VVPSKRQRVSGNTS

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3417	33785	A	3454	102	1059	ETLPSNTMASNVTNKTDPRSM NSRVFIGNLNTLVVKKSDVEAI FSKYGKIVGCSVHKGFVQY AYERNARA AAVAGEDGRMIAG QVLDINLAAEPKVNRGKAGV KRSAAEMYGSVTEHPSPLLS SSFDLDYDFORDY YDRMYSY PARVPPPPPIA/RAVVP SKRQRV SGNTSRRGKSGFN SKGQRGSS KSGK/LKGDDLQA/KELTPD KTKKWDSLA/ENLEK/KEQSK QAVEMKNDKSEEEQSSSSR/VK KDETNVKMESEGGADDS/EE GDLLG*MNDNE/DRGDDQLE/LI KDDEKEAEEGEDDRDSANGGG
3418	33786	A	3455	299	509	
3419	33787	B	3456	16	101	
3420	33788	A	3457	1209	1828	GNCDSPARPARPPHRGQCPRPS PPPRGRPRALGPTRASAAAP DLPPPAAPHAPAALVPHTAAP KA/RNALPGSPGALTEGAVLLP NAGARPRRPSSEKPGAPSWP RIPGFRGTAPPATPVLAAGGL APPSGLAGQQVALPSQVPADT QSGVKSGSQRGRN*QSAGSA GGGARTQVPGPLRMWKRAVW PGDWAPHANI
3421	33789	A	3458	387	772	PHRKQAEPPRHHRLGRRVRH HARHGRGSRPDAAEAAGCG DPRAFQQLERRLRHPPLRWQGL LRRQRLREEPRRSL/QTS*S*C SPVTRPSSGCSPRSWMETRRG APAPPAPSRNKPTTWPH
3422	33790	A	3459	362	608	FFFFLNRVLLCHPG/WS*SGNH QWQSWLNS*PQTPLGK*SSFLC FRKWWDYKHEPLYPAKPHFEF LFGSSLQVREFFGKIKV
3423	33791	B	3460	1	612	

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3424	33792	A	3461	1277	2152	SRAAPTCFSWLPCCGASTCPWL MWAMSGRMVAPLQRVLRAP GLEGLTGGRQHPGTPPSVLHFS LTMNSMFGI.QDFNVTPLAAQA TLPPGSPGRPTLPVSTAAAPNSLQ MFTGGHGA*FPRWQPPSPGVS /SHGAPPGVPHYCRQGRSPGKR/ QRKWLESEVQAQGP*EPDPTQL QTSTRACG*GPPSQADPDPPD TRPRTPDLDPNCMLRTPKPGR RQSRPHGPRTPPTQTDPPVPVQ PAPEVKPQRP/WAARAPSDTA AS*GGLTCNSRPIREGQMGSPP AGSLLLGAL
3425	33793	A	3462	1	2064	MDGQCSHYCVKTDLRVHSPFT TGAVHADQSCCKTTSARWEDT CDLTGSKKTLVISNIVIRTSDD KLENEWETQSQNRNRVKPTAA DPCRNE/NEHSS*EKHPEVLQES ANDRLRDNERVSQRQSQPTTVS QRQSQPTTESEPTTES/RQRQSQ RQRQSQPMTESETMTLQKMT ESANDRVSRQSQSQQRQSQQR QSQRQSQSQSQ*QSQSQRQSQS QRQSQQRQSQSQSQQRQSQS QRQSQSQSQSQ*QSQSQ*QSQPTT ESEPTEVSQRQNRQRQSQP/ DDRIRDNRVSQRQNRQRQSQ QIQ*QSQRRQSQSQSQPTTES EPTTESANDRVSRQSQSQSQRS QIQRQSQSQ*QSQPTTESANDR VSQRQSQSQGQSQSQSQSQ/D DRVSQRQIQSQHQEDRPPKYQN KNVQVHA/DDKPRSDPQRRRNL TPPVKTAERRPHQEHVVKGEK ATSPSRHSTSTAPTRPPSAETAH VNMCGGDMAHINQGHVEAP QGSHEKHVGAARDQYERRDA QSEKQQVQTTGLRVHVSRRPP HDGSLTSTGLRVHVSRRPPHDG SLTSTGLRVHVSRRPPHNGTVT STGLRVHVSRRPPHDGSLTSTG LRVHVPRRPPHDGSLTSTGLRV HVPRRPPTTALSHPLDVSICTL NAYPEMLTGERSTFPCVNVKN EKAVESKKDTPFKCESKESWI
3426	33794	A	3463	1	424	

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3427	33795	A	3464	1	492	MDESSFRGSIQTQSGSAKTAGLT GFCKLCKTSSWHTGAAQIL.EGG MEKANSPQYADPQTHLSWHTL PPGSQATSANESNVNFLSLPDT NSPEIRPDHSPVPDRSVSPLEHI PRTFPKPGTG/PPHINTVTNP GAPR*E*PS*SGFNPGCFQLVRP SRISGTPV
3428	33796	A	3465	107	543	KREGWKEESDFWDGSHLPPLN SRCSTRKGRKTGRCGAATAAA SSPREGRPPPSWAGHPCLGSC QWLRSCR/RGLAMAPGALPAL GEEEGPGASGLSAL/RASERGL GQGLGPAALHS*ASFTPWAPVR PEPPRRAPPPAPWRPVPL
3429	33797	A	3466	27	1021	STQTWPVSEETGSPQQRNRC*SS HQPD TASWVLQREYSHRKGT PRGMQGTLPCLPSLSGCRSPSCP AAARPPRPRAVRFPFPATAAAS SPREGRRPPPSW/RRPPLPRGLP VASELPEGLAMAPGVLPALFGS TLPL*AVT/PH*ECL/PASLLKPA RP*THREK*TPDVQP*EL*HSP *RSAASLQEGPOLHS*SQ*DQEP TNSGHTYTLGTGR*FYTVQCFL WLG*TYRSSHRPGFACRCLEPG SAAPCPHCLSAPEGTL*AAAC LGKVPGRSAPRSDQWSPGGRA PRGVPPPLSRGHCKALASCAP SADA REPPH RALLGSPKVHTP
3430	33798	A	3467	807	1428	GSDRLQPQPLLFGRDVLVLLPS GPAIPASGLASVFGAAGRAHG SGGSA*TWGRGTRRRERPLGG AGASEPGSVGPRGA/GWVSGP VRAPPRAAPGTLAPSSGRCRAP PPRRAQACVALTCGPGGRCPL PMDR PALAMP/SHL/HPRPGQV APRWSPCSRREEKGRHERVDI GHSHLVFALTFLP*FGGGGKT EAAQNSWRIPPAG

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3431	33799	A	3468	68	1153	LLKMFRAKAACTLSMAWVLP LSLIVLVILSPGSFILQITFTLLEP VLRPPSSAEKPLEPGSSSPSSG RARGAIRPALPAAPKPLASPEA GMAVPGWGRRISPSRREEAGA VACLSTVFSGKWICQAP/SA WGCCC*D*GKLVHRST*RCAR* KYPGLKPDQEGYCPGAPVEV HPRCRDFPS/VLRRNLGFSALAQ SEYLW*DHS/CLVVG/PVLC* TLFASFIRLYPEELLA/HKVTQ CPSLVSPCNWLSAGGGRKFEP LRRPSSAERPLAPYSPSSPGAGR APQPWPALPAAPKPLASPEAG MAGPGGRRRTTSLPKRRGCGCS RPASSCFSSLSGWAARVERRQM ASIPALFFPSPL
3432	33800	A	3469	1	248	FRPAPISSAPRGPTPEVLRPPSS AEKPLEPGSSSPSSGRGAM ASPPSSSEATGKPRGRDGS G/VGGRPSRKEEAGAVAGGK RTARGLRGRGPAATGQEGDR HPYRWRQRSGILHEF*AASGF PPPNHGRHTVQAEPPWPAL PAAPKPLASPEAGMAGPGGRR TTSLPKRRGCGSCCGEAHSPT TARTGEDAPRGREETGTQTGG DRRGAA/RGSP/RSPWA/CIRAPL PSLGVA PG/VPSGRLAHGDILISP CTLPHELSELSPGH*TQANFL*DP GRRRTVLWKVFQGRSRK*EG RGPGRGHNYDGSVTPGNFIA*S PS/PLPLPPSFTWLPKTRIPES GVTKCSGLTGRVW/RPGSWG LHPGSAFP*LRRPSSAEKPLEPG PSSSPSSGRGAMASPPSSSEA TGKPRGRDGSPRMGEDVPPE
3433	33801	C	3470	365	589	
3434	33802	A	3471	1	465	MVTTCYCKKAKPIPRRCSAKE WSCQLPCGQKLLCGQHKCENP CHAGSCQCPRVSRQKCVCGK KVAERSCASPLWHCDQIKE/CR SQSCS*RRKTKTTG/LEAFENR LKGRKKNRKRDEVAVELSLW QKHKYYLISVCGVVVVFAWY ITHDYN

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3435	33803	A	3472	1	444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFVAVVNE RNARAAVGGMYSSSFOLDHDF QRDYYDRMYSYPAHVPPPIAR AVVPSKQCHVSGNRRGKSGFN SKRGQRGSSKSGKLGDDDLQAI KKELTQIKQKVDLSLENL
3436	33804	C	3473	190	265	
3437	33805	A	3474	144	316	
3438	33806	A	3475	3	342	
3439	33807	B	3476	180	1370	
3440	33808	A	3477	102	1054	ETLPSNTMASNVTNKTDPRSM NSRVFIGNLNTLVVKKSDVEAI FSKYGKIVGCSVHKGFVAVVNE VNERNARGIYVAGEDGRMIAIG QIVLDINPGLQSPKVNRRGKARC ETDLQAEYGLLF*PWTYDFQ RDYYDRMYSYPARVPPPIA/R AVVPSKRQVSGNTRRGKSGFN NSKSGQRGSSKSGKLGDDDLQAI AIKKELTQIKQKVDLSLENLEK IEKEQSKQAVEMKK**SQKEEQ SSQLR*KKDET*C*RLEVLKGG AD/DSA*GRGDL/DDDDN*RS GGIDQLE/LIKIDDEKEAEE/GED DRGQRPMMGGDDSLST
3441	33809	C	3478	216	350	
3442	33810	A	3479	1	3048	MGLMVLNVENCSSFGWIGRAP PRNTTVDLNSGNDVPPNMTSW ASFHNGVAAGLKIAPASQIDSA WIVYNKPKHAELANEYAGFLV ALGLNGYLTKLATFNHIDYLT GHMTSISGLLLGVSAAKLGT DMSITRLLSIRIPALLPPTSTELD VPHNVQVAAVVGGLVYQGT AHRHTAEGPVGLR*DGLLFLKC NTALTGSHTP*AAGLALGMVC LGEQGPCCGVWEELGERETFK DLIFNRKAPEGSNAT
3443	33811	A	3480	173	422	AAAERGAEASGGAPPGILEDA GRERRSGGGR*AGPVGDSKD GVGAV*PPQPHSHRDHHQ*PGP LGGPGCSG*PHILREGLET
3444	33812	C	3481	241	426	

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3445	33813	A	3482	3	826	RGEEAVSGKAGPDSRAVLRG QGQVWGAAERGAEEASGGG TQEGGREGVFDSD*GTCSLGFPS* PGEQLMGLVYTLGG*PHSHRD HHQ*PGPLGG/HGCSG*PHLRW VPSALGGRGVGADQLVRVAQ GSPETPCSLSGESWPA/GLPGPT PPGWQ**PGP*RAPGLQKAPKG PSYQQGPAPPSHRQSTAQRGV PRTKRCPSLGGDLSSLAVP VAQAPRCAYRMLPLLFLGRL TPVPSPLSSDKVIYNLHLQFIVF TSIKFSATPFKKKKK
3446	33814	A	3483	135	396	LCWLQIHRQGRKPCSPSLKG* *ATCMPPRRRKGGFLSSVMDII THSPGNEKIKMPPPTMSKQPGV LQDQCREKLSHCLVCSLSG
3447	33815	A	3484	256	1860	RAPETPRKILGEAGGCRGDGR PAFQPVNRNRPFLSKLLGQCGR STLCRLCFRSLNHLFWLFPGGP WRGPGGHSTEDGSLQGKAGQD FSC*NLEISFFP*PSPTCSPTLHC GQKPRAGQGHLSVPGAPCW AEVPALLPRRVGDIPGPDILPPS TRV*RCPLDRNSPILL*VHFLKD RATTONTARPPMGWRPLQQR QISPAVGGKLCSLPVM*ASPH SASVVGTEPA*IGGWGW/P*GF QLIG/LPHVRGTQPLLESRVPS VRGTQPLPGLPESRVPSVRRT QPGLLESRVPSVRGTQPLPGL PESRVPSVRRTQPLPDARVPY VRGTQPLPGLPESRVVPYVRRT QPGLPDARVPYVRGTQPLPGF RPSRVPRSFCEGDAAGPPRRPRS YVRGTQPLPAFPSPAFLVRVP SLRGTQPLPGLPESRVPSVRRT QPGLPDARVPYVRGTQPLPGL PESRVPSVRGTQPLPDARVPY VRGTQPLPGLPESRVVPYVRGT QSSLPGLP/GVPRSFREGDVAGP
3448	33816	B	3485	111	258	
3449	33817	A	3486	1	4455	

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3450	33818	A	3487	1	2302	MTECLDRFIDSIAAVPRSTKSTV QKCLPCLSDGEDKIPDLIAITWT PRQGELLEKNVISEGTLLPTPC LDTSTKETADKSTSGKTIHQSIK TVLKDLSGSIDDLPFGTEATLSS AVSASGSTSSQGDQSNPAQSPF SPHASPHLSSIPGGPSPSPVGS GSNQSRSGMSPASIPGQDPGYG NS/DKSMGHEYSQR/SFLEDRFP IAVWWPRPLRLKNCLSVLSYSS PSEVTPHPKSESSGTS/SAQDL QGCSQDVGGQPASSSGGSTREQS TSSFIRIVAASSPSSCWKLQVLL SG/AGGDYSPVLLIGGYSRVCLP Q*SDASAAATREP/GQNPVPIPP* ASHQCHRKEGPPCRQQAGASQ MLSRD*AKQLKPSSSHTLKHK TT/GTRKSLLFGIKKAYNFTNKY YSELMTQTRFQSTPSIPSPLPLD DAGLERSQGNVSASSFMVLGN RERGEDTTGAGFGRSRNKEEVP CTIYVGAESP/EMC*WMDHT*R KEGKGGLVGVPCV/SREHLEEW QYQLQR*ISLKTQV*RRKSEV LLGRS/SNTAQACSCWQLTCFM AGTQRNPQMAQYGPQQTGPSM SPHPSPGGQMHAIGSSFQQSNSS GTYPQMSQYGPQDGGGDVSD VVMAIDDDGSHLLGSAVPGA VLVTFNLLLIIVVTLQMTPEQFR EYITGDPLESTCRHASLALAVV LHQETAMTMITDSLAVVPHSG

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3451	33819	A	3488	2	1427	EEPSRREPR/PPGHAPGAVAGG AGPMARAGARLLGGRRPPGL RL/CARASARVAAG/CGRRRRA REPPRRRVPRRPARQPRRGATA AAATTT*WASGTRPSTAAPPT ASAAAR/RLPLLPRRAAPRPE PLFQLRHAGLGPDRPAARPRPR HRSAPGPRPRAQPYGLRRCVRR RSAAGDGG/EPGLAFDEVGDRG PPLTAVPAGADRASEAAGPPG ATASHPGPTER*QGRSEPGHR TEPRLTPRSRQEAPOQRAPGVG RPGAPARPAAGRRDPLSSPEL GCSARRHSSLPCRRGRPAAGL/R QRFPALEPSRQPPARAPR/HPR TCLRRWTPAPGPRRSTRPLPRR APMPGPPVAPRGP/PLLSHPTA RAF/HGTPATRARGAPVQCED A*DLQPAAPRPLRQGRPVVP KDQ*QDRGHRVKRGRGA/RRG MGWGPVCPSEPQATGRGAPAV RPALLSASTAVVWSLQAAGSS CK
3452	33820	A	3489	1	262	
3453	33821	A	3490	411	1919	RSYGVRRWRHAPGRRSSPRIG KVKSASRAWRLRCCGCRPPSR TGMRWQMRWPMVTLARQPFW RRSVSWRGAWGSRKSWRRS RATRSCSMATATASCRLSRID DISNYEVNLEPGHDDITSCQG RGRSLPQRAPIGLCCSLGGGAV LADTPLFLPRPKRDGPGSRF QKRQQQSALRVMQRNCAAY LKLRLHWQWRLFTKVKPLQ VTRQDEVLQARAQELQKVQEL QQQSAREVGEQGRVAQLEEE RARLAELQRAEAELECAEAEETR GRLAARKQELELVVSELEARV GEEECSSRMQTEKKRLQQHIQ ELEAHLAEEGARQKLQLEKV TTEAKMKFEEDLLLEDQNS KLARLGA*QGLGKWWGALV G**MVNFTPWGLPHCGSQERK LLEDRLAEFSSQAEEFEKVKS LNKLRKYEATIDMEDRLRK EEKGRQELEKLRRLDGESSEL QEQMVEQQQRAEELRAQLGRK EELQALARRRQFQ

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3454	33822	A	3491	3	266	KMRRLIKSKKDIINRERQKSLSL TPTRSDSGEGFLQLPHQDSQDS TSVGTNS*EDGQTQHPRPI*DA QSSVCCAGSQHGM*ANHSEQ
3455	33823	B	3492	1	241	-
3456	33824	A	3493	1	1486	SRLHLKCNKPRRS GTTNAKR V GPDCHPMGREGAR*HHALRGR RGEAGTRGGRQRRREQDWREA GPGPRAEVGRTAASARRARG S APGPRGPSRGRSRWNIGQPRR NRGRGAERPRMQRSRPENGAR GTGAGLRGFQRRRHPGFPSRV* GSKDIPAAARRRVETCPGPEPRQ PQLPPRPWKGGGDARGDPKFP QAPNAVPGFCVIPAGGVLGAPT AAGLRPTGDVALRRPAGSVEPS GS/AGSQSQCLLCGPVPYRQQT STGP*PGGWGSPSDVPCSALIS GTGC/PKAQHVSGSLSQRSLSL VDFGRPAS/RGSLFPWPLGTGG KS/PAAPSPQTLWQSS/P/GFLYF PGE/RKGKG*SGPGAGCEP/PIA VGCQEQRGAEGNLPPKPADPC AGTKQPRARQGVQQGTSQ*PST VVMTSGRGAHSRGGPVRRGAH SREVPAAVHGGD/GLLVEGHTA GRVQQPSTGG*PLVEGPPAGEG PFAEGHTAGRSSQLSTVLTTFP
3457	33825	A	3494	3	393	
3458	33826	A	3495	145	1089	VYRTEFLQDRNYFFLSLVVSAP RTVPGTWTCLLSE*RNE*ILGCD SLFPKAGQAP*VAHITLGFQSSE YSKWKFNTNSPTFLELLEFP SLQ VSAGFLLSLLPILKPRFYSSSSQ DHTPTAIHLTVAVLMYHTRGL QPARATLMSTHSSHPGLPA AVSQAQACAGFRLPEDPSHPRV LIGPGTGIPPLSFVWQRLHDSQ QKGVAGGFPVQGGRMTPVFE CRSPNEDHIYQEEMLEMARKG VLPVAVPTAYSCLPKPKVCVQ DILQQLASEVLRVLHKEPGHL YVCRAVCMADVAHT/L/KQL VAA*NLNL
3459	33827	A	3496	292	478	

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3460	33828	A	3497	87	992	TACGFIACIG*QRLEYCV*DHK GKQQEVLSKHLQAMMDISHIR RNVSCSGRNKASSKAYGTGGS QGRACDLGHNF/TPSSWERHC TLTSQGVDDFLNAKATFKIFDF SDAFVL SKVGFSGILIKDENKE ELSDKDIYMEAGIFVSANRGP VDYCGNRGLSIQGHGGWTLRP SILVSPGVEVRGNEDSVDTAAC IPAAPAPAPTLAERCTGTAWVT ASEGASYRPWLLHSHVKPVSPH STSLETWEPPYIFQKMYENAWC PDRRLPKKQSLMGNLYLGS AE GKYGVGAPTLETTIMQTPDS
3461	33829	A	3498	1	382	TADCAKPVPLAVVSLDSRYGQ WESRSSIHARH*LNSSSSSSSS SSPPAVYPRFIEFIHFDIQSTGQK SHRVNTRRGPIRDALF*LN SLIP LVRTSSKSAARRRP/GEAPRGTA VPGADPAGGTRPR
3462	33830	A	3499	229	367	
3463	33831	A	3500	233	525	WYFPAGRAGPADPGPGLAGT PDAGAGGLPTYSTPLRVSSPVP RLESSTG/SSFPADSAPVPLA VVSLDST/RRDSGNSRSFHSWG VIN*MTRHLVH
3464	33832	A	3501	386	729	TGRGCCLPCTWRIRAQTCLT*T QCC/SCPTTYPGGGERRERERK RRGEKEKQKVLKRYKEAMSNK VCKYFDEGCGSCPFGENCFYKH VYPDGRREKQQRQKVGTSRY WAQRSNHF
3465	33833	A	3502	63	559	HSSTCECT*DSRCGCKWRSKQ FESKIKSCPECRITSNFVIPSEY WVEEKEEKQLILKYKEAMSN KACRYFDEGRGSCPFGGNCFY KHAYPDGRREEPQKQKVGITSS RYRAQRNNHFWELIEERENS N PFDNDEE/ALSPFELGEMLLM LLAAGGDDELTD
3466	33834	A	3503	374	656	RRVGCRCFHPSQTCTCT*RP PW NVHH*PATCHLAYNRHWS PRA/HWHIATAIQLSAHV/ACHY QQLHHYQHSHHHHHHYRHHH HHHHHHYCHHH

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3467	33835	A	3504	1	1337	MQLQILITFLDLHHNTNICNELE SSNVDDPCDIWEKVHISLIFTAK GSKIPKSSDFQADRELNMFDIIS QYDGCPSIGLTSAGSTHRA PWTQTYPQGPTHLSGSPGCILA SITGRVTKMPESSSPA WELPRF TEFLSLIKDEWTCIFLQLCCPTM LLSGFPPIRIEPWSPSLDQNLPIP LEAAIATHSRIHHCLVFTASLP GPLTAGNQMAADRLVATVSN RHFIHNLTHVNASGLKCRYSNT WKAAKAIQRRPTCQKRKIK/PD QEOPVQPV* AEGVRFWREDH*P /SHIRSRHSRMTSVSRQSTW/W LPSVTWT/CPTTEALEYGSAC LGCPISGVSKGNKTRSGAAGFH /SPAFKSAICJWRFKQQHANRP YVCWGMHRSPYSLLPRSSSS HPQIHGNLSDDLQVQRGECFI CRPCFHLRLRSVPDITDTCQPQR
3468	33836	B	3505	1	1158	
3469	33837	A	3506	35	369	
3470	33838	A	3507	345	564	PCASRTVPSSWPVP*PQPTSARR SPRCLPMVQ*AAASHDSQLCS CRFCVVVTPCAPQGGCTCTRQV CARVTHG
3471	33839	A	3508	437	946	SFSSKIVQRMSSSCTENMHMSP SAPSSPQRPGALSLS/RPSGVGG LLKDPAPC/SR/RLPGILSLSPQN PRAASPDSPAGFWDVSLCTCRL LRVACLCAVRSPRRLCTRSC GRGSSMVR*GGGLPIFSSSFAT SLQLSSETVARVTPADECPAES LPSHGPVSCQGIT
3472	33840	A	3509	1259	1497	KSNMSLLMVFISSGITV/TMCSS WGHLQCRQIFLSLEGLMKTSRS GPWAVL/RGWFSHT*ALDEDA ALGHPWASTRKQAPS

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3473	33841	A	3510	268	1278	SPSGPSSSHQPPALKGQVLQCL LSP*ISLRNLHLWDVYLVEGE QVLMPMACTAFKV*WSKSTCA QWHWAFLLCLFFLLFLLDSKK DNRPPVLRAGAQCMTAHVEV LPD\PSVFLSAKPRQGSAAARAV LASRGRKALCSG\IHVPTPSGLG CGGPLVP**FQTELLSSCPF*MC PGQPSCAIPDTLEN\AVQ\EEAG PVKAMREKGEHIGIPAAQPASS\ SPGSLVPTCGTVSPSQGTIRRP GA WPRQPRLTPLL\SAAPPWMR HLH/RSLWVGTSIQEDQLATCW QANHTVEGA\IGFHCTKPCQGR GFAGPQGLGSATSTWNVLSLQ ASRSIWDTAH
3474	33842	A	3511	1	1557	MSRISDDCSELCPLKA\KIKERR KEKKQEKWETYRE/REKRQRG QRRNRNGERKKRKN\TKKR*NAG REGEKKRQKGKTEERKRRGGR RRRETKEEGGS*RNKKQA*SEE KKGRTGKNRKERRKEEGREKE RK\REKDRRGGRK\NKTRERD WGGEQKQTEREEEWARKRWK VPGGWEREAPHRELEKNEQLD KHSSSR\AKLYDAGQLD\CSNLI QSCDPEC\PMQATSLTRYPTTTQ IFLRGAQGWVCVELFRSYGVE D\TSA WERDMRNF\GCMTREKQ GKPGQLLAHRLCAH\QKMSLL CADNSQKGCLSPANAA\PCYGV QVAILTSA\PTCPYHLEPLCRSFS LSDQQA\ISDPRTA\VR\IARSGAS SNPRLCVTLTFPRVLQPPFPPPPQ RWGEATKGGRLPAK\GSPARTA AGRCGRSAGMPPDARA\IFTSA ALPKSRLVPSN\IAFKGKRKDL TKAAAPNLLALRYPRPSA\PVGG SHA\PSPGQQLQPEEEGN\EEEE EEEGDRAPVFTTGRKDRDSLAE
3475	33843	A	3512	1	525	
3476	33844	A	3513	69	707	LRQ\NQHEVLKDP\RTHTHGGQM GTSSPEQRSTASGAPGW\RA\TSS CVLLASPHHVHHAHGSQEAAS TPPVW\TQREYHGWPPIYFES SHLHK/RLLPNPAREEL*RRQQA PWKRHCWRDVTTP\ESTKNLVE SSMVNGGLTSQTKENG\LS\TSQQ VPAQRKLLRAP\TLAELDSS EPRTAVHSSCTA\HRCSAWCLA VSAVCPSPCQSQRGLALS

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3477	33845	A	3514	81	446	TQGGRIKRHLGTSASPTGIMKY PPYCTPCFQSQALHPVPGGLSG KEAESQ*LSPHHPSSQAPGEDPT P/SQP/RLPKHSTLPALGFATCG RISPSKPALPPRGTAAPPHPHY CCYYFPNRSHE
3478	33846	B	3515	58	1034	
3479	33847	C	3516	1	1470	
3480	33848	A	3517	1	606	MAGEDETPVPLPCGTRPI/DA AAHMAPVPSHLRKHQRVEVHG FCQVQPSYCGPEDRGLADRGST DEHNPGAAQPRAAALHAHPGG VSQLPAPAH*AGQPPTEPQLP VSPA*SNPQVSAPLSKQLPSP GS*DPAPVGLAE*K*TNCPRD YTAAVAVLGSAPAAPAQLHPA CTLRAPSLRALQEAGAPQPPMG GSGQR
3481	33849	C	3518	76	1275	
3482	33850	A	3519	1	508	MTRQLSNCWVAEECCDPLRHV TQQVLQEAPIVSQAVGGSRTN LATTPGSHRSTYCLSGAVSSRN LIEPAGEEAGATRAAREEPPGR LRAPSGGVPSRPLCCRPVAG CGSGLKMDDEGGGEGGAVY CNLELKASGVILAVAAEKPSG QAVLTNTEHSEPSHLKGSSEK SYLHATPKEDIASFIPLNVYKQ QGPP*APSYSTL/PPPPSPSSSI LRPLQPATGGRQQRGLGTP PEGARRRPGGSARARVAPASS P/DGLDEVPRRDSSGETVSRMT AARGCGQVGPAGASYSL
3483	33851	A	3520	451	487	SPLEKSWPGTSHTWFP*SRP*NP GRPLPDPLPADP/LRGVPPNPQR KGMSESSRALITPFHPPLTPAPL *NRPFLWSLF
3484	33852	A	3521	1	758	TPRAPLCRGAASAARSICKWAP WPSRPRRHP*SCEAREGSAA QIPPASKLKHGGSPPA/PRRG HPRLLPAPP/VVPLPATAPAAVP SAPGKPFPTPPGLPKADPG/PIG GPLSAFSGSPFPVH/EPTVLGSP QSTRNLPRPPAA*PPVAWARDA PGSSPAAAAAKQTFASQTQTP KIT*EPRSPTGPAPALAKLFLTP GTCAPGQPSRKILPSRPVAPM GTIENIGYITKAFDWNVLFSDTT KGYRVDCMVQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met box	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
3485	33853	A	3522	3	801	TLLMSHQKLLPLPQIKTPRSFHH SRHLHHQHRHHQKQHKKHH HHFYHHH*NHHHHHHHCHTSP PHHHHRHHYYHHHHHHHPQH HQHHNNHHYHHYHHHHQH QRHHHPCTVCPQEE*/HNEHR KRPHRCWKVQDPR/NLGYLYIP TTSELRLALSKHLPFL*NVVS IYYRQSPDLCPHLNLNPHQYHH RYHHQYHHHRRHKHYPHHH HHLHHHHHHHHQNHHHHQE TPLHRTLGLPQGPRRRSSAAQP PPPPPPPLLSRRH
3486	33854	A	3523	3	229	WDPPPEFGRPRRESSGFPASI LLVTEPGARSPRPAAS/HPPS PLHRTLGLPPRHPDGAAPRSS PPPPPPSP
3487	33855	A	3524	1	1257	MKAIEKMFETNENKDTTYQN LWDTFKAVCRGKCIALNAHKK KQERSKIDTLTSQKLEEEQEQ TPSKASRRQEITKIRAEKSWFF EKINKIDKLLARLIKKKREKNQ DAIKNDKGDITSDPTEIQTIRE YYKHLKYANKLENLEEMVEFLD TYTLPRLSQEEVESLNRPIGTGEI EAIHNSLPTKKSPGPDGFTAKFY QMLEVLAIRIQEKE/VKGIQL GKEEVQLSLFADDMIVYLENPII SAQNLLKLISNFSKVSQYKINV QKSAFLYTNNKQTESQIISLP FTIASKRIKYLRIQLTRDVKDLS KENYKPLLNEVKEDTKKWKNI PCSWVGRINIEKMAILPKVIYRF NAIPIELPMTFFTELEKTTLKFI WNQQRARIAKSILSKQKNKAGGI TLPDFKLYYKATVTKIA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3488	33856	A	3525	2	2133	WRRYQANGK*KNKQKKAQV VILVSDKTDKPTKIKRDKEGH YIMVKGSIQEEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLNIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRK YKRTIITDCLSD HSAIKLELRKLTQNSSTTWK LNNLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCCKA VCREKFIALNAHKRQERSKID TLTSQLE/LEKQEQTHSKASRR KSRNG*IPGHIHPKTKPGRI* VPE*TNRRV*N*GNN*LTNQK KFRTRRIHSQILPEHSAGSSGQG NQAGERNKGYISIRKRGQIVPV CR*HDCIFRKP HHLSPKSP*AVK QLQQSRLIQNRKAKITSSPIHQ* QTNREPNIH*TFIHNCFKENKIP RNPTYKGCEGPIQGEQTATAQQ NKRGHKQMEEHSMLMDRKNQ YHENGHSAQGNL*IQCHPHQAT NDFLHRIGKNYFKVHMEPKKSP HCQVNPKPKEQSWRHAT* LQ TILQGYSNQNSMVLVPKQTYRP MEKNRGLRNNTTLRPSSL*QT *QKQEMGKGFPI**MVLGKLAS HM*KAETGSLPYTLYKN*FKM D*RLKC*T*NHKNLRRKPRQYH SGHRHEQGLYV*NTKSNNGKS QN*QMGSN*TKELLHSKRNYH
3489	33857	A	3526	1	1896	
3490	33858	B	3527	1	1296	
3491	33859	A	3528	1	1095	
3492	33860	B	3529	1	1413	
3493	33861	A	3530	1	1539	
3494	33862	A	3531	1	1167	
3495	33863	A	3532	1	1575	
3496	33864	B	3533	1	1653	
3497	33865	B	3534	1	1932	
3498	33866	B	3535	1	2451	

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3499	33867	A	3536	1	2502	MTELTGIQQPQIVLFEHKGHKL VQGSSSDAGKVNRIYQHYEAS DKFNYTTGLAWKTAPEQTGKT VRKQIKLNVKKMESRSKMQE HSSPPMEQSWRENDFDELREE AFRRSNYSELQEEIQTGGQEVK NFEKTLDEYITRITNTEKCLKEL MELKAKARELREECRLRSRCD QLEERVSVMEDEMNMKREG KFREKRIKRNEQSLQEKWDYV KTPNLRLIGVPESDGENGTKLE NTLQDIHQENLPNLVRQANIQI EIQRTPQRYSSRAIPRHIVRFT KVEMKEKMLRAAREKEIQTTR EYYKHLIYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPTGS EIVAHINSLPTKKSP/GPVGFTAE FCQRK/EGILSISFCEASILIPKL GRDITTKENFRPISLMTIDTKIF NKILANQIQHKKLIHHDQVG FIPGMQGWFNICKSINVIQHINR TKDKNHMIISIDA EKAFDKIQQL FMLKTLNLKLGIDGTYFKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLGAIR QEKEIKGVQLGKEEVKLSLFAD DMIVYLENHIVSAQNLLKLISNF SKVSGYKINQKSLAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLEIK EDTNKWKNIPCSWVGRINIVK MAILSKVIYRFNAIPNLPITVFT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
3500	33868	A	3537	1	2197	MNNAKENFLGRFDGRIGTAP VYSPQHQRRRRVISALPTEPPL VIPRQTGFQVLDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGRNQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRLVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDLME KTMAREL RDSCTFSRQFDQVE ERVSVIDQMNMEREKREKRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLFADNM TVYLENPI ISAQNLKLI SNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL SFTIASKRIKYLGIQLKRDVKEL FKNYKPLLKEIKEDTNKWKNP CSWVGRTNIVKMAILPKIIRFN AIPKPPMTFTTELEKTTLKFI QKRAHIAKTILSKKNKAGGIML PDFKLYYKATVTKTAWYWYQ NRDIDQWYRAEASEIMPHIYNY LIFDKPEKNQWGDLSFNKW CWENCLAICGKLKLDPLTPYT KINSRWIKDLNVRPKAIKILEEN LGNTIQDTGMGKDFMSKTPKA MATKAKIDKWDLIKLSFCTA KETITRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NSINKRAKDMNRHFSKEDIYAA KRHMKKCSSLAIREMQIKTTM RYHLTPPEVEVVLLET/LNH/RSW
3501	33869	A	3538	3	242	NLEEMDKYLDITYTLPRLNQEEF ESLNRPIGTSEIEAIINSLPTKKSS GPDGFTAKFYQSIVLEVLARA RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIISAQNLKLLSN FSKVSQYKINVQKSQAVLYTN NKQTESQIMSEPSFTIASKRIKY LGIQRTRDVKDLFKENYKPLL KIKEDTNKWKNTPCSWIGRINI MKMAIVPKVIYRFNAIPKLP TFTTELEKTTLKFIWNQKRARIA KSILSQKN

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3502	33870	A	3539	281	3228	KPRLNYMKNAEASRADAINW KKGYYLVMDKMNEMKREGKF REKRIKRNKQSLQEIWVYVKRP NLRLISVPESDRENGTKLENTL QDIHQENFPNLARQANIQIEIQ RTPQRYSSRRATPRHIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHYRANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEEY QRYKEELVPFLKLFQSIKEGI LPNSFYEASII
3503	33871	B	3540	295	2804	
3504	33872	A	3541	83	480	
3505	33873	A	3542	159	729	PTIVGVVIFKSVCISSPWSHLKP TFHATSWLADGDTDGCVLVFA SSCSSYQ*HPCSSVPEPRYGRRI GSEFSAGSIVRFECPNGYLLQGS TALHCQSVPNALAQWNDTIPSC VAPELREECRSLSRCDQLEEM VSVMEDENMEMKREGKFEK RIKRNEQSLQEIWDYVKRLNLR LIVVPERDRDNGTK
3506	33874	A	3543	1	1116	MMARGAGVLIRKIYPLNYKHS AVEQVSRAYSFYQRPVVPPEPR YGRRIQSEFSAGSIVRFECPNGY LLQGSTALHCQSVPNALAQWN DTIPSCVPCSGNFTQRRGTILS PGYEPYGNLNCIWKIIVTEGS GIQIQVISFATEQNWDSLEIHDG GDVTAPRLGSGSLTPH/WKLS RCMAC/DPSERGLSCTWALV/I/H KMEPEQPVCQKQHPEDSQGR/K GPGPGPNHLLPGF*VSDGRG RSRSELTAGSFQWQHSRPNV *LIHQPSAQVPQRLFKWRLLCP QFP/GDFVKYQCHPGYTLVGTD ILTCKLSSQLQFEGSLPTCEATP SSQCWVSPHRPEARLPAHGPA PKRHVCQKASLLICGKEGMQL
3507	33875	A	3544	373	1051	RHLLGAQCLSRAPWCWNNQAS FPFPRCPRAKGQGTARASFSWL GCRIQHEGPIRVQGRRRPHRRE PAWAHLHPPMPCRQPNLR/PG SLRVWPC*KSLC*PSPRPARTHP PGQRCHPYRVSPSPSPSPRPPS*F SRTFPQPPGPRTLTSGPRTQETL SPENVPGPGAP/PAPRHRSSGPK ADVALRMRGLSRAPPSAARKE RGSPESEPLNLSGSGCKHF TTVRA

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3508	33876	A	3545	1	411	RGREARNAAAVGAAQACT*FH RTQGPSRLGGVRGQLALPLRA GLGDCIFPV*AKSEFS/HSP/LHAP ASLCWGP/PPHPVL/WATHRRQ DCGTLILQGSPAVSN*DSAPPAL ACRLSCGGGGERTAPPSCRGE KTPWEVPG
3509	33877	A	3546	107	550	TFQMNSLTECCPSLRGWGAPOS LPMALQTPGSAHLRCQGLLSV ETEVLWCHPTVIQSAVALKLH* AISPCF*LPPNYPLSGSSL/PTPH ACLSLPLNQCASPL*QPPPCPRE VAPLSLEIPESFVYIGLTHITGC LCISL.VLPLSP
3510	33878	A	3547	54	825	VGGCLAGQDDPDGVFQTSRLK GVNRAQQQRQLLPGPTPSKA KDSHP*EGG*GASPNAALLSGA GELPRACQCRLSRHLALPTCAA RVC*NPVKPRKRSEPRSGWAS QLPGGDSRLPLRPGTSQGVFSP HRLG/EGGKLVGLVLSLQKQR GFPGE/WGAAVLSVPRGPRTGW GE/DLPRALPDQSDGSGMRKRS AAEAETGPGARSAAGRSDSDS GGRPDSCQTVPAAR/SPPCLRRQ KLPRERLRPRANP*GPRPLGR
3511	33879	A	3548	1	1335	
3512	33880	A	3549	1	903	MPAGYHVLSDVVSSETPGCPA EFLNIRIPGDPVFDPPDQRGDVP EPPRRVPPPAARRPIPSTTQGLR SVGARCGTGKQLHLQPQCEIH WVKPAGLLSLVGTWRTFMSSS ELVNIPIGTRYLAQAVTLTVKV CSFTAESAETSPGGGTNSRR AALRAVTLTAKVCSFTPEPARP RTHQKEETPNTSEHQEQTPDT SAFKNCNTHGEGQLHLSPGR PPTPPGRPNWNRNPGLKSWNT YPGKVRNFWLFSKKEIEDIRN TTLRDVLVAVINIDPSALQPNVF VWHKGGFLP/CPQFFP

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3513	33881	A	3550	1	797	ATRFGGNLVLVLGFGEMTTVP LHAAIREVDIKGVFRYCNNTVT LTAKVYSFTPEARETTNPPGGT NNCRNAGLRAVTLTAKVRSFT AEPARPRTHQKEETPNTSEHQ EQTPDTPPLGTVTLNARVRSFIV EVNSQNPLLMWAAPDPAPGQN GPRGLYAFGAERGNREPFLQAL GLVLVRLHNLWGQRLARQDPA DWEDEELFQQPQRQVVIATYQI TSPHTCTYSRTRCFVPKEDIKEQ SLTSHHYLSCSHCFGHEQSDIIP
3514	33882	A	3551	23	3990	HGHFWLGHGPLWLSAPSWTLI LFNTTGSRRGIVWGTRCPRKRA KSSTSPVQSLRLRTPFRGRCDL MGGTTTSWSTDG/CSKGYHYLS DLVSVETPGCPAEFLNIRIPPGD PMFDPDQRGDVVLFPQRSRW PETGRSPSNRPDPANQVTGWLD GSAIYGSSHSWSDALRSFSGGQ LASGPDPAFPRDSQNPLLTGPG GCTQRGNREPFLQALGLLWFR YHNLWAQRLARHPDWEDEE LFQHARKRVIATYQV
3515	33883	A	3552	2	663	VLLDERSAALDGAKRDGTLAL AAGALCREARAQVFFLKGGY EAFSASCPELCSKQINVSANCP NHFEHGYQYKSLCGMTTHKA DISSWFNEAIDFIDSIGNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRIISP SFMGQLQLLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNPV SIPDHSTNSALSYLQSLITTSHC
3516	33884	A	3553	3	669	GYEAFSASCPELCSKQSTPMGL SLPLSTSPVPSAESGSCSSTPL YDQVSRCPCHREEVRTGKGME E* CQGGI*KVTCIIYNGGDTGI* FIPQLSGLTEPSLQL*ALRK*TC WSCP GKWA*FPIYLSSNRTEFT RYLKLTFPAESFCGYGHW PWL *ASLMNVGYFWISG/GPVEILPF LYLGSAYHASKDMLDALGIT ALINVSANCPNHFEHGYQYKS

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3517	33885	A	3554	3	1377	WAVCATRVGGAVGGTAKKPR SPEPRVTLSSQSKSGFWGAER PGGLAFPRKAPPCWPREQTKS TAGPITLGAIRPAMVMEVGTL DAGGLRALLGERAAQCILLDC RSFFAFNAGHIAGSVNVRFTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAGVLD GAKRDGTLALAAAGRA/LCREA RAAQALLPSKGGYEA/FSASCP EL/CSKK/STPMGLS/LSLSTSV P/DSAESG/CASSCSTP/LYD/QGG PVEILPFLYLGSAYHA/SRKDML /DA/LGITALDPNVLSQIVPNHFE G/HF/QYKSIPVE/DNPKADISSW /FNEAIDFIDSIKNAGRRVFVHC QAGISRSAT/ICLAYLMRTNRVK LDEA/FEFVK/QRRS/LSLPNFSF HGASLLQFESQ/VL/APHC/SGR GWGAPANAGLDRGTSTTTVFN FPVSI/VHSTNSALSYLQSPITTS
3518	33886	A	3555	450	719	
3519	33887	A	3556	63	332	
3520	33888	A	3557	573	1309	WCKGEGEATEKGPRAEQAQSP LSEEAGAGRCPCGPYRDAQPLL GSGHTLKRAIQDICYGPGHYQA RAAREVHPPGRKIGKQSLRRPC KLETDHLSRSLRELD/SW*FGR KCAGAGLTERTQGRLLRRKRTL SSEALPQVLELSAEASKRGS GKPRKFGKKNPBGHGAQPQVVF QSRQCLQRILGEHPRTRPCLRN DNPAGASSAPAQATFISPSDFSS SSQARSALSLSFREGLVMTHG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3521	33889	A	3558	1	1797	KDSAGPGPPVALLPGAA/CLSP APGCRRAAPRWSSGPRTAAG* RRMWACASASLA*SPCRPPRSRW WRDAGSGWTPHCPASAAWGA EQEPVRSWGPASQSHCPGGLR APPPGSRVRCSTQ*DCSSVRPAW SRS*GAC*QV*PRCPCRTPATG WAPPPQGRCGPTTAPGSTGPAG RASLCCPRRAHLPG*WPQKLIC AHPGAKSLGLACQPHRGVKGTP IEG/PACGT*GGRGSGGCPGRPH TRRRC*PPAPCGRRSAGSAHPA RPWPHPGGGQQRDPGPAYRGG QGGRSASPGRRLPASRAGRS RAARGTGRPEPRSPQRRGTGTV QPACRPWPPHRAAAGPPRRGS GAPAPLGRTRSFGTAGKAHPW PRRRPGHW*SAAAPATGVPA CRAGSWVSAAPAEGRPARAR RHIPGRCEASGPRGRSAAHGH GARAGSPQGPAPCHLPGIPAR QPLGLPRRTRCFGGIAQGRGAA RHCLLSRPSAKAKRNSSYREPG MGGWRSPPALGEYGGKGSQAG SARLSGAASQGRRAHRLRGKA PAWNPAPPPSPPPALGLPLRTQ REATRKPRREEARRPRPLRP GGANGSPGPRAARA
3522	33890	A	3559	1443	1871	PFVYTSSLGRPPSIS*QPFVSGSG CSCP*RSRPSGAWRA/RSASSPA PPP/KAP/SPRPGPRATAGASRRT AGPALCGRPR*GSRGRHLFSRP GGTRRRRRAAR/SAGLPAPGGS EPPKSGSGFPSSPYASSGLIPGN RSPAAAGEL
3523	33891	A	3560	62	864	ALAESRGDLEAGPSSNTWEFW ELAGFSVLFLGNRRRAALGLCEL PSLRAGVEFTAVQRLWSSAGA TWWSKLAVPLAGSAGRENPGS LLDGLLFTLENNLSRGQGAPST PPAARRAAR*DGGQSASS/PAL ESPPERHRRLLALVSEQKPQEPAL RSSRRSCGTRLPRLVFCSKVCR RAEPGGSVTRREGGAEREAEER KRGR*GEARR/RQGGRKSTRRK KQAIKGRRESQKRRGGRQGRG RAASPPL*EPRARQPRGSAAPSL LRGLSGCL

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3524	33892	A	3561	3	2701	TGLWCRCPRASRRSVGRRP GTGPGGRILRPGGWGCF ¹ AGPRGT EDADQRAARGPVGAGTQQHG RAVPRIG ² QNEPDETL ³ LP/GGPS PRGGELRGRSGARGLP*SLTGP APGPQRGG ⁴ G*SPSPGRASSKAG PWKRPGASRASLQRASSM/PAS QVDWGG/PGGSPRCNRCRERKP GTGPGWPPRLRSPGNLRPGVGG LGLALPARTAAAPRRERWRS PGAPCLGAQ*PSL
3525	33893	A	3562	2	905	HEGFFFFILGCPFPNFI ¹ PNLVSV RKLGVKPAWGAA/RPRLPLAP MPSREGAARSREMRRPRGIRRS PKEGLFHP ² EGSQGKSQNGADPQ RM*REP ³ SSKSSEPLRLLGVH QTA*RWETGETGPAIGGPAELD AVHVGL*CNRGFPSSKQRRRR ARVWPGPKRPPARAARMARL ASDQRDFSVSRKAGDGRFPVIG IRSGGGAATGSSSRLSVSSAVL RKPGR ⁴ TTGAVPAGGSARKGPSL APMLGPGSVRSASSPSGHNPG AGS*ERAGLGERPRQKPLAVPA AAIDFPQSPASRSNI
3526	33894	B	3563	149	283	
3527	33895	A	3564	269	452	AGILFLSSSQ*SNARRPTHGALL GDWGPCRSPSPYANRSPSSSLA RQCRTGRGSTRDLRVRT

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3528	33896	A	3565	1	1877	MDPOLERQMETTQNLVDSYAA IVNKTVDLWVGVTPTKIMHV MINNRHAPPHGSRGLLWHWGC RWPCWPGGDAGQPYGTSILIEK KREKNQIDTIKNDKGDITTNPT IQTIREYYKILYANKVENLKE IDKFLDTYTLRLNQEEVESLN RSITGSKIEAIVNSLPTKKSPGPE QFTVEFYQRYKEELVFLFLKLF QSIEKEGILPKSFYKASIIIPKPG RDTTKKENFRPISLMNIDAKILN KILANQIQQHIKKLIHHDVGF PGMQGWFNTRKSINVIQHRNR TKDKNHMIISIDAFAFDKIQQP FMLKTLHKLIGDGYLKIIIRAIY DKPTANIMLNEQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLA RQEKIKIGSLQRVLSFLTTRG LRRSLQPSIFSIILVRAMFLLS GLVAVTLGSPSAGNQSTVLSSW SLVAQQEKA VPTLPLQ SARPPH GSAVQA AVWPDTLYQSCPLA ENQTHFWMTGKCVLCWLCSL WSSGEGKGQAISRVLFGGVKRP YPFQGTFLFESPNWLAGSCPVK PALATRGQG*SSAYSTEPVIVQ RNAT*LKGKARVQLGAKKESG
3529	33897	A	3566	770	949	IRYVLCGGALRIMELLTKQG*SS AYSTEPVIVPRNAT*LKGKARV QLGAKKMMSQSVTPD
3530	33898	B	3567	507	1436	
3531	33899	A	3568	43	421	TSAHPGGEAVPS/LTTSTTWSRS SSLVTFTLMPRGCSGPPVTSP LCRMPRTTTMPASPVGSSIGQT STTLPCPQRQT*PSACTGSG*A SAVRCAPKSSSPATSSSMTTTT PGRATTTTTQTRC
3532	33900	A	3569	210	610	TRKSRRNG*IPRIHHSPTKPKGR S*ISE*ANNRTEIVAINSLPTKK SPGPDGFTAIFYQSTRRS*TTT MPASPVGSSIGQSTTLPLSLAPR QT*PSACTGSGNHKSLTVKSFS QGCAGLPASLTGPLWVRC

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3333	33901	A	3570	1	718	MENAGEREDPTVGNCEVRLA GPVLRITQDELSWEDEANPTSY PKGADSYCHSDCQTIMDFSNFN AFSTPNTFALMNTYSCQHPNS KQFQLPTFFVKMGEAVSVFFIGL PHATPIVEHQNDLIAGSVRMQN QPKGSTLQCILMPQRPQGQTL DMDYYSFCFSDEKNLGTCKLS SFPWSHSKEVKATFKGRYPGSH ALNRHTTLPGTAWILLGGELA FLTVDGSPALALPSRPADGMRG RNKARVLSLNLASWG*QAQ SSELRTSSPGKRMKQTQLLIQK EQILIVTRIARP*WIFPTSMHFLP QTHLLS*THTA/VPOHPNSKQFQ LPTFFVKMGEAVSVFFIGLPHAT PIVEHQNDLIAGSVRMQNQPKG STLQCILMPQRPQGQTL DMDYYSFCFSDEKNLGTCKLS SFPWSHSKEVKATFKGRYPGSIQPLT ATPHYALALPGFSF*VGNLHSSQ* RMEALWPCPPAQLMG
3334	33902	A	3571	719	1643	IQKRACSVSARRGLRTGRCGT AGTTTMAPSPVGGSSIGQSTTLP SCPQRQT*PSACTGSG*ASAVR CAPKSSSSPATSSMTTITTPGRA TTTTTQTRCASTPPSPSTPGAAT AAGGPLVQGHGRHRVRVQSES HEGHPHGMRPQPHCSTSTSGM SAGPRVPGQV*ASSRMLTHTNG LRPGPGFKLPISHGVLDLQNGT GMPGGA*VCCSTVRGPATGPAQ TGQRREPRPTRCPWSSVPLRR GKKDLARRQVESKPVWPGPWE GTPWSLLLGCNLPALSLCCIGTS ADRSFRKFYFQTRIPLLLTDVL
3335	33903	A	3572	1	933	MPEPPP*PWAPARPKPPRRAPP PAPRRPVPSSTQQLRSAGT/PAR DWQAAPPAALSSPEPHFNLIAS VQTVMCPVGAPAGMQGSG*PK PSGRLVLWTPG**KGSIWGTA ASMTRRRWTRMSRTAMSPGPQ RVPSAPKPSSAPCA*MEGKRSL LPA/VTPGCKKRYKVTWVAVG GPDPTREASLCQPSLLGTDQDL QSSPFHWHLRIRQKMYRTPRP HAEQGMGEGSHCLMSEHHFEK TQRQFSPDYYPNPSSQLNVNGI KYHAKNGHRTQIRVRKPFKCR CGKSYKTAQGLRHHTINFHPV SAEIRKMQQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
3336	33904	A	3573	2	316	CLSLPTPPWTPVVRPEPPRRAPPP ALRRPVPSTTQGLKSAGARRGT GRQ/PPPAAPDCVAQSSVHLA ARATK*PSAHSVSSSPMGVLF LHGLDFPRMTRSQLR
3337	33905	A	3574	3	1078	SLPPPPWAPVRPQPPL*VPPAP RCVPVSTTQGLRSAGA/PARDW QAAPPAQVFTLLKNIKMLPCL EKPFGFSLVIMREFNNHMQ VELKMPVPSDLPKGTGKTLILP ECIQAPCMKSNNAPSSSSAPSP WML*A*A*AWLCRYCRASCGLSSI PTASPVTMACC*RYMRWGILPI SEPPQTFSPAGANQRGPLAAT LSGPGGEGQSAVARLTGEKKN HPGAQYANRLSPRVGRFINAAG TTGFPTGKRAGHKKEPIQSFIT RAARRSR*PSKASELGRKQRRP V/PVR*LLRSAQEISAVGKTPG FCQGGNTGYQSQR/RRK*PANR PVKRLP*GGI*SLPGSKTYAVSV RCPDQKI
3338	33906	A	3575	2	969	VSTWETPQYRRPPSPS*RGSRQ PCSFSSPRDTPGENHWLSLPQR D*AGPPVRRALGAS*PHATRRP NRGGAS*PDLPNHTRPFRPFPS KNPCFRFPEPLRAPTLVPGCKP HSPAASGRVPPTHPGRGLGKSE G/SKEKPMRRTAAPTPIRFPKIT GT/PSTQTAADHALLGMRDQSL SGQSPGPKSPDADDQLQNRDH TETEQRISGRSSALA PESLQQ GCAGIHFGRGFCKAPPLVCERL RGW/PRGKRKGVCESAAQASP MSAAPCSTVSPINHPRAEECG RTARDWQAAPLAALVRDPLDE ASWAPESGGDVENLYV
3339	33907	C	3576	1	444	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method in US 09/540,217	SEQ ID NO: 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
3540	33908	A	3577	227	2141	FCPVATSA SVTPVQTRCATRPT TAPSA D C V S P R A A G G L P S G H C F R S E P * G K N W A P C P Q P A L T P S S / P S Q T S D S E E H P S S E N I P P G Y E V V S L L E A L N G L T P S P A V P P L H V L / E R W P P L R N A P F I W Q * W P P A P R Q D D L A S * P P V * / P A A V R D S N S K R V S P N P L P K T L P C C M K R K M S I P A A S / T E T Q L S Q R P S V Q H L G E E C G V T P E S E N L T L S S S G A I D Q S S C T G T P L S S T I P P Q K A L P A A A W P S L S C P W H P P R S A L T P S P P C L A P T S P L A L K R R E R L S L P P S L P A G P P Q K K / R E G L P A E S P D S N F A G L P A G E Q D A E A A L S S H Y Q P I S H A S K G D C K S G M E Q Q G V C E R E W G P A T V Q S D T P A A A V G L A A P G R Q A V E G L S V C S L R P P C S S R C D G S G S G Q P T T V I N I S L R R P T S P R T R E D S E K P G Q Y P K G H T E A R Q M P G Q K D K V A K R S R K V A * E E K E N G K G I R R Q * K Q A A P R Q L G Q A G L T H S L K A R V / R G G T G G / A A G V L G / G A W A W R A P H Q W / P G L I A L P A R G N E G L S T R A S G C G G C T G S P S S A P P A L R S I S R R A L A A F P R G R A R D L Q P A M P E P T P S V G S C A A P A S P M S A A P C S T A / L Q S H R P P K G * G V R A H G A G L A G S S T C S P S A G S T G * S * L G S * V W W G R G E P L C P A Q G L
3541	33909	A	3578	26	1141	V L Q L L R W R V W S L F F L M F R C V R S F F L L T Q K P S W L H P V D P A P G L Q V E L P A S P A P C A R T P Q P L G G R W D W A P W S R G R R S S G R L G L H R N L R R P G A Q A W R A A G P G P C P A G R Q L R P G E K S S A A P V G W H C W G T E Y T F P S S R W P G C * A P H C P L A G P A G / S P S A G P A K P T P T W N S S W P A S A A R S P G S Y S / P P L P P Y / P L Q A E G A G S G L G Q P R K G L L H L * D V P A E P V L A G P L A S G S I P L A A P P A G R G L L A P G P C P G L D L R L L * Q L P P P S V F P T T P K T E L V L G T P G H G Q P H R G G H E S S D S A G G / A P T P R A L R S G W D P S P P S S V C A T P T S S G L S S T P Q L P L H Q R T S S S T A S W S P G W G M G S C * V I V T S G A A T V G C * R L P S I S T S * S P I
3542	33910	B	3579	1	1234	
3543	33911	A	3580	443	865	

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3544	33912	A	3581	2	1524	CLSLSPRP RPHPWAPVQPEPPR RAPPPARCPVPST/TPGAEEGR RTARDWQAAPPAAPKEETPNA SEYQKEQTPDTPPLRTVTLTVT VHGFILEVSETKNPPIPD TGLQV VPKPLPRHTRGRVASSIHHRF PVSPSARAG/APPGHTPCQGTW QIQSSPAQGGGAPNPLY SAGSA LVSSLVLVLFVDFVRSPEHS VIARPSPARPGTWELGRRRTRP SQDPPRPGSGGPWPGRGRGPW RSKTDAAAPGKA VARSAPGASC ELARRGASPGREGLAVGRAAG RGVASG/APSPAEGPQAALGAP PGTHRSSPSAQVPSSGARTESP W*P*LLASAGRPRPQPGYHAQE WRKRPRRPVTRRRFPPTKAPAR SAGSFETSTFSAHDPGSRGHPW GPKPLPAGGDRTPPGAQGRGS A\SKAPARIHEPALRGHSGSRGG TPGIGSSALLCAKNCAPGDPGT AGVGR*SGTQLPPRAPLEPLSAP RRVRPVGSGRRREK VPRPGRP
3545	33913	A	3582	1	3339	MSVRKDV EKLPSDIVCGNVQ CYSCMETNLTVSQVKHEVTV GPREGATKPNRMKGEGRS LLGEGDFFKDESVMSQSSKD GEKRRGKAQRW WPMQIGICR QLGVAKSMEGYQSRDQGR GVSDKW PQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPK VNDIITDISSSGSGA GKFQVSKSDISEVLLQMDAG HSSKDDPNEYGGWKSPRPRC
3546	33914	B	3583	1	503	
3547	33915	A	3584	1	787	MIKVVSYQGC RDGLTYGWSCS VETVRWLPEVHAADTSLKISA CLSSFSYKAPSVVAQAAPPSS PHKTSSLCTTSA PLSRPSMRTTS APP*VSSAARPSI*NISS/PESSAA TI*N*NMSSSPGLQLHDTQTRTS APPRVLNSA/T/SQITTSAPPRAR TPVPPGSPAPRPSQKNSHGTGSFV VFSSTT*DISGSTGSHGPPAQR LS*T*KAAPAPPGGSITTPDLN SGSTTS/SSRSSAPRPSLNNPFS* NSAVKKSAAEVNE

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3548	33916	A	3585	746	2018	THPOERGTWGNRQLFAVLPLFF YTSLETMSMGCAVAVAGQYQ KCPFFITPSANFPWQKQEGMSG NPPRVRRHISLSRSLTLAVPMT IRRSWEGAPFVGAQDGCRLPL GRRALLHLGLAPLL/GPPPPPV SPPWPPCKATWVSAGGRCLY/G CPSAPAPR\APPEFPAPPGFAPP AASSPSTRCSRGT*SCGPGRPGP LGPASAWGQRGLAVPEPLQA VLGALGLLRPLGERR/PAQAGT FSPTAPGRGAPGASA*GGRISG HSSGDIPRRGPSRGHPPLLAQGS DAIRSTLIH/ERLSTRTRPSFKIKT PSPHQRPQQPHASWTPSSGTL KPSTPCSSSSCAPRSGDGGG/EG HAGLPSQPAAGSQPAAPCQRPE AWAGGRGNRPGKPGAPQGPCF SLPRPQRSR*LPPPARQKPPFFTL LSLFSF
3549	33917	A	3586	1	1911	TIYAVNLFPIPLQGDLPFTMTVT MHWGEGNGQIFRGLLDTSSEL MLIPGDPKCHCGPPVKVGAYES QVINGVLAQVQLTVVPEGPQT HPVVISPVLECIIGDILGSWQNP HVGSLTGKVRATMVEKAKWK PLEQPLPRKIVSQQYRIRGEIA EISAKIKDLKYAGVVIPTTSPFK SPIWPVQKTDGSTKIPGTSTSVK FLGVQ*CGTCQDIPSKVKDKLL HLAPPTIKKEAQLVGLFGFWS QHHPHGLLELRPIYRVTRKAASF EWGPEHEKALQVQAAALQAAL PLGPYDPA/DQATVQLKLPVIN WVLSDPSSHKVVMHKLREEV GQMTMVFTPATLSSLPQHMM VSWGVSVDQLEEEKTRAWLT DRSARYAGTTRKWWTP/HQSLS PATPVI/SQWA/HGHGGRGGGY AWAQHGLALINADLATASAE CPICQQRRPKMSTRYGTPGKV LQKAVCDLNQHPHYGTLS/PIAR IHRSRNQGEVEVAALTITPSDP LAKFLLPVPTTLRSTGLEVLVPE GGKLPFGDTTITPLNRKSLPPG HFGPLPLSQQAKKGVPYPPKKK SLYQKHALSYMSLFTAVPFTIA KTWNQPRFPMYVNIENMWYI YTMEHYTAIKMSEIESFAAIWM QLEAI
3550	33918	C	3587	44	310	

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3551	33919	C	3588	20	328	
3552	33920	C	3589	288	542	
3553	33921	A	3590	332	528	
3554	33922	A	3591	3	1717	NVCQSHRIPEHCYDSLNVCS* GIPEYSCCDLNICPSHWTPHCY EGLNDPCSSNIPEHCWGLNDC SSRSIPQHCWGLHVCPLHRIPE HCSWVLSVSPSQRILEHCENL NVCL*HRIPEHSRCCLNVCPSHR IPEHCCL/ESELSLTQDSRTLRL L*GSECLSET*NSIILPPLFECLSH T*YSKTLHLGSECLSLT*DSRTS LLWSECSSYD/VENTTA/EGLSI CPSHRVPEHCYEGLNDCPSRRIP EHYRWGKNVFLSQRIPEHCYE GLHVFRSRGIPHSRCCRLNVCP HRIPEYYYECLNICPSKRIPCYC CLVPSVYSSHRIPEHCY*VLNV PSQRIPEHSCGGLNFCPSHWIPE HRYEGLNVCLSHRIPEHCYEG YDCPSHRIPEHSCGGLKVCPSHS IQEYCCWVLSVCPSHRIPEHCY HCLNVCPSHRIPEH*EDSRTL LSECPQRISEHCYEGLVFP SHRIPEHCYEGLNDSPTHRIPEHCY EFLNDCHSHRIAEHCFSGNLN LSHRIELHFRWGLHVCPSHGILE HCCWDLVSVSHSH/SNSRSL*RV
3555	33923	A	3592	3	191	
3556	33924	B	3593	58	477	
3557	33925	A	3594	19	367	AIQSWCHHVLQAQPHVELLP RFIEELGSLVGH*PRHRLPPAH SHVLHHCQLQLGHTLRPRHCIL QEHACG/RVRCLLQROAGSPGG WCKRECLFLQE/VKPSVRICTVE MCTISIS
3558	33926	A	3595	55	555	NHFVAEASCPPCPRFLDAKK LVRSPSGLRMVPEHAFGSPFG LEEPQWVPDKECRRCMQCDAK FDFLTRKHHCRRCGKCFCDRCC SQKVPLRRMCFVGPRAAVRGS APWVFPQGGGVFTD\NSSKCS* AEPSSS/QFGNSEKPEMT/VSS FQ*PEILVSGWRQPL

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3559	33927	A	3596	182	696	PVFWIRNL*SMASRGLRRD*EH LKEAILAHL/KAKRGGEAAEE ESEASRGWLVRFKGRRLRNIE VQGETASAAAGEAAAGHPGDLA KITGAGGYYTQQIFSVDETTLH WKKMPCRTFTATEEKISAYFKA SKDGLNLLGVNAPGTYVLR NISVFLSEEMSSDKRLTEMGY
3560	33928	A	3597	74	2521	RERWAAGPVTCTQVTTWPGAAT TRVTWPMTRPATPCAVHGCSC PRSHWSQKCGQPAKRAV/SPHP PSTCGSSA/APGPTPKQEAPSA WPLSGFPN*EPGPGQPGD/VVE KATERMAAMKTEAGVPLVEV QDPVEVPSGR/PAGTCPAQPH RTPACTADP/PALDPTTTTHPA PAPCPAIAASWPAVWLPQPG Q*PRCPRLIATCEGQTPAGEEPQ AAATAGEGR/VKASVSPAPRGT PCCGIRWVARPAFSGHRSSPCP GSQGCWA/PSSGVPEASEPRPGE QEPIFRKREFNKEIKSL/PEPAGV PRPAWLLSAP*APSHAELPG*PP PLPCPAKRGQPGCG*APWRPLP RRPSSV/PPPAWSP/QLPPLGS EPAKPTNGG/PALCFPPPHSLQP QDASEKTQG/PEEAPPPCLVPR WPPDSNSR*HPRRSPMSPAPHS TPGRRHLTQIPNYKTHLFP*APA RGPSGRACTSPCPRQGLWWR WPAARATSGALSHLHFPPTPA LPATFSLSSLQLPLHLPCHVQR APAAAAAGSRRRRCPPSRSPA CLTSPTAFMRSSPTS*PSRQPPW SSASTSSKRTSVSSWASSPSPSP TCSGTFPWA*RR*KAPASTCPR RPTGAACCVNWRSPKGPGRPP GSAPPTAAQRHPLCSRNQPPTL PRTRPQSPAAPSTPTCQAPAGSSA LWSPSSTCLPAPAVVPVPPSPR
3561	33929	B	3598	1	588	

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3562	33930	A	3599	357	1011	FLPLGELYAEGSRMIWSDGFW AGHLHSCSHPRSSSFSPCTCTYPL PPPPWVVERQGTGSGVP*PGKR TSSPFRVSPGSNTRECTPS/GLLD CIPSCISLSEKPNQDSSSESA*KIP ASSLVTSGLGFCKNPQWSNTSC TSLSCDA/CPPWND/CCQMPVPC SWTFQPEP*AK*TSVPYKLP WYSVSQSGKDSPPAPPGPGR AQPASRAAAPAVGP/SDRAA DPLSPLQAPIWAPRHQHGSRP/ VR*GLRWLHGALRVVVILEGG RAQ*PPWNDFVRCQCHALGLSS LQNHPEPKLLFLINYPVCGILCP NAGKTARAPPLRARVGPAPLPA ALLLLLLWDR
3563	33931	A	3600	63	660	KPQVNKSASCAQLAGPVSQRG KDSPPAPPGPGR/CPACQPRC CCSSCCGTADRAAAPLSPLQAPI WAPATSMDDARRVPVRVFALTE ART*GRAPWAFPGDVNPSLAPI P*TCSTELIPVVSFSPSTSGN SPTACLDGSQLASPSGSRGTGA TGGAAHSPARAPA/PPQPLGSR WDQGLRWLHGALRVVVILEGG RAQ
3564	33932	A	3601	202	515	FCKHEAAVSSGKAVGTRSQCR HSGPLRVAMKFPARSTRGATN KKAESRQPSSENSVTDNSDSED ESGMNFLEKRALNIKQNKAML AKLMSELESFPGSFRGR*PRGCS AAPRSKRSGHPPPAWT/CSPR AAERS/PE*RRT*RNDSM*S*FP ARSTRGATNKKAESRQPSNSV TDSNSDSEDESGMNFLEKRALN IKQNKAMLAKLMSELESFPGSF RGRHP
3565	33933	C	3602	40	186	
3566	33934	A	3603	1	3189	

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3567	33935	A	3604	1	1821	MLKNFKKGFGNDYGVMTTPG KLRTLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAA VLVAKGQIVKEGSRSTHRGKSTPE VLFDPSTDDPLQEMAKVIPVVP SPYQGERLPTEFTSVLVPPQDK HIPRPPRVDRKGGEASGETPPL AARLRPKTGIMPLREQRYTGI DEDGHMAERRVFCQPFPSAD LLNWNKNTPSCTEKPQALIDLL QTHQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGEHAP ADYQNPQEQYEGKEESPAQFYER LCEAYHMYTPFPDPSPENQRM NMAVLSQSAEDIRKQLQKQAG FAGMNTSQLLEIANQVFNVRD AVSHTGAHVSVTGPVAPLSK KTIDHIGAMGVSAAQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAQWEDPESGVTTQYTWTV LPQGFKNSTPFGALARDLQK FPTRDLGCVLQYVDDLLGH P TAVGCAKRTDALLRHLEDCGY KVSCKKVAQICQQQVRYLGFTI RRGVRLGSEKQVICNLPEPKT
3568	33936	A	3605	1269	2463	GVQEESSDLPTAVDSSRPDIRD QAWASVHWELVYVHGSSFIN* GERGAGY/AVITWT/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHARQG PAVPPGIAQYGAAPFEDLQVDF TEMPKCGDIRKIVTGDVNTPAI LGVVSSSPSHIGNNITEDPELQ PILAGLSLSMYLVTVLRNLLIL AVSSDPHLHTPMCFFLSNLCWA DIGFTLATVPKMIVDMQSHTRV ISYEGCLTRISFLVLFACIEDML LTVMAYDCFVAICRPLHYPPVIV NPHLCVFFLLVYFFLSLLDSQL HSWIVLQFTHKNVEISNFVCDP SQLLKLACSDSVINSIFMYFHST MFGFLPISGILLSYYKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
3569	33937	B	3606	1	1830	
3570	33938	B	3607	1	459	
3571	33939	B	3608	30	440	
3572	33940	A	3609	1	279	
3573	33941	A	3610	2	500	

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3574	33942	A	3611	370	464	GHACGAERDHLQPHSPAHL LLL SV*AVW*PRYTVKMATAC HQW
3575	33943	B	3612	1	780	
3576	33944	B	3613	1	610	
3577	33945	A	3614	1	1896	
3578	33946	A	3615	2	1418	
3579	33947	A	3616	314	720	GVQEESDLPTAVDSSRPDIRD QAWASVHWELVYVHGSSFINT* GERGAGY/AVITW/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHHARQG PAVPPGIQAYGAAPFEDLQVDF TEMPKCG
3580	33948	A	3617	1	1029	
3581	33949	A	3618	1199	1758	KTLSFLSDQPLRARSCLPFSGKI RS/RALAKTVRQRCVSCRQHHA RQGPVPPGIQAYGAAAFEDLQ VDFTEMPECGGNKYLPLVLRGT YSGWVETYPTRAERKAREVTRV LLRDLIPRLELPRIGSDNGPAF VADLLQKTATVLGITRKLHAAS RPQSSGKGIONNRTGGVYTPCD IESHVILFRSGY
3582	33950	C	3619	499	831	
3583	33951	A	3620	410	1144	LSIQYLTRP/PLLGFPFAEDSW FTCLDLKDAFFPIRLAPERQKLF AFQWEDPESGWPPCWRALAAAT ALLVQEANKLTGQKLNIAKSR AVVTLMNTKGHHWLTNATLT DYQTLLENPRITIEVCNTLHPA TLLPVSKSPVKPGCEVLDSDS SRPDLWDQPWASVDWELYL DSS/FLQPPRRGGGYA/VGDTSE LPPCWVCQIPALTQRLEKQHLP PSGHQGLKHLIWDLLLLTKKR TFSSMI
3584	33952	A	3621	1244	2690	
3585	33953	B	3622	1	1114	
3586	33954	B	3623	1	1863	

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3587	33955	A	3624	3	2056	REALQGIQVRLKHLRTFGIIVPC QSPCNTLLLPFPKPRTKDYSQV QDLRLHLHQATLTFHPTVPNPPT LLGLLPAKDSGFTCLDPKDAFF PIRLAPERQKLFAFQWEDPESG VTQYTWGTGLPQGFKNSPTIFG EAWARDLQKFPSRDLCVLLQ *VDDLLGHPTAVGCAKGTDA LHRHLEDGCGCKVSKKKAQICR QQALAAATLRVQEANKLTLEQ NLNIKASRAVVTLMNTKGHHW LTNARLTQYQTLWCENPRITIE VCNSLHPATLLPVSESPVEPRC VEVLDITDSSRPDLRGQPWASV DWELYVDGSSFFNPQGERGAG CAVITLDTVVEARSLSQATSAQ KAELIAFIRALELSEGRKGLSPG RGKDK*WRKDGFGYRMGEYC ATAARSCSCGTCARNHPSTSGV TGKVVRPVFLHLAFVSAFAKTV RQRCVTCRQHDARQGPVLPGL GAYGAAPFEGQVDFTEMPKC GGNKYVLVLVCTYSGWVEAYP TLTEKAREVTRVLLRDLIPFRFP PLRIGSDKGPAFLAALLQKTAK MGTRSDTQLAHIGTVLRDIHVS VCSDGPNLRTGLNVILGGVEW QSTPGNLVRRQGETGLHLHIYH WWQAVAIFFPVYLGSSLHMKVG GRSFEQEEDTEHIPVSYDREGQ ECDTELKGQEGDELEAGSVVP
3588	33956	A	3625	491	964	RIQLCCRTRGTAQKKRMKVS SRCTPAPATRGTAQWQPQAQ APGVRAATEAPRL*AHDEVSQA PAPPSTRHSPRR*PVAGKEHLE AAVDKERHEVAQAVVTHVLEG QLEDVAPAHAAQ/GSPPWAGK RLRTNPAPRPCHPIQTLSSRLGP QNHTLLH
3589	33957	A	3626	131	351	NVGLKGTAGER/GSGSPPS*PPA GRNSGPAGRRPPAARAPPGSA AR*PAPPGP RP RPAGRAAAAA GPAGGGA
3590	33958	A	3627	3	428	GEWEAPPLLRHTRPGPA/PAPPA PSGASCAPCGQTCRPRPLRQA PPSPITTGARIWLGQPRPRSSS ATPPKELP*GPTEPHTGELWVA SGSCPSGTKLPEEGSGSNITYFSA VSAGDTQSNIIWNGPPANSNRP AAEGPDC

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3591	33959	A	3628	2	425	YLASAAIFRNMSSVCLVCFFF TSQICLQTDNAPYTVLSINENLS VLGSMFNFRLRSFLRSTKASAK PFIVTLRLSSFFSVSSSLASSAM HSCSSSNSSFFNSSRTTSKSSST SSSFTPS/SESF/SS*VSSSRFHST PW
3592	33960	A	3629	81	594	LPAGFGPCGAWNQNRQKRFPQ SPGAESAA*SGGGQQRGRAG AGGHGACASLGSE/PQGREPAL GAGGETALPSGSGSRPQR PRDSGPEALPSAAFWRKR*AS ASAPALTPVPDSVRGAQPQGGG GAEPGKAVMRGASRPALSQ LSGREIGPCPQGRVVPSTGATC
3593	33961	A	3630	317	778	PMVWSCASAAARLPEPENGALL RTSSPRCSP/CPASAA*LTRLPPT/P /PGDPSAAPSQRPAAGLAGAG GAERSGA VEVGPREPGRDGAG S*S*W/AGPPGRLEAGSA/GVLR SPVAGWRPGTCAGRP/GKAGDL GPSAPPQAPHPPPPSWPLSPLA SPPTK
3594	33962	B	3631	1	1068	
3595	33963	A	3632	1	730	LALTARSSHQRATVPKASVVA AASPTKFRHSGAALQWRNLGP VRAQGRRLSTAAPAAPSRLFP PPFRGGGRGGVWSGRGRRGA EPGRSHGAGGPGDDGRCGWGE GAGTSTPARPSRGPGRPEIWTR GGGSAKSQG/PAGAPGCAGPR GASSFRGRQAPAVLGP/SSA VCPLPRRTWNLRAPGGAPSYA QVAAAHQAPPGRPPWSPRGAR GSGRSRTFAPSTPAVVAGAASA VAPPRLRPSPPAPAPAAAATA AERRGREAPRGCGSGRAEPP PLGPDGTQVSPQRSSRVTEFC GGSGGHYARFWHSSPLRVGAS RSQS
3596	33964	A	3633	70	792	HGLVLDVVRGLPSHAAPYWAPY PAATAAAARTAPLPPRSAIV*/S GPQPDFQELRKTWPSQC/GMAR REPLLPITAIPRVVETTP*GFA KQEPSVAGLRCRGSEAPA*LLH GVHRNVSETPGPEMGRPG*GN HRQRPQKQRGIPSSGLPGRCSG SRGPHSSPGQKPHGSTLSGRRG ADPRPRRRVYLSTPLCEKPKPH HDTILKRKPGMGDGNNPCWVN AGLYGQATRFAPLPLCPRRRHG

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3597	33965	A	3634	2	339	WPCGWTGRGGCRQ RGRERRL GSGVRFQDVFSFRGRGRGRARA SWKPPHQGPGEPSGTRNRP*\n GGGAPAGIRGPELGTGNMCKL LLSLPIVYHLAGEKGQVAKIVRI PSADV
3598	33966	A	3635	31	438	MVTDVVTGGELGQRHVPPGE SSGLFCGQCGERETRDPSYRG/ WSRRFRFRALKNGAHWSPLRA VFGDLGADNPKAVPRLRRDTQ QGMYYDAVLH/VGNFSNYKARF SMPGDNEGLWYSWDLGPAHIIS FSTEVHFFLH
3599	33967	A	3636	1	422	LRRTDQQGMYYDAVLHVGDFA YNLDQDNARVGDPRFMRLEPV AASLPYMTCPGNHEERYNFSN YKARFSMPGDNEGLWYSWDM GPAHIISFSTEVYFFLHYGRHLV QRQFRWLES DLQ/QSQ*EPGSP AVDHHYGAPAHVLTk
3600	33968	A	3640	1	319	FRREPPRGA AAAAALPRNRNEN KRSKNRPCCGPRGSARMKELE *PRPLQVLCLLPEMCSPLADS YSPVSVRPISAPVRFRLHRCPPPP FAEFACRLLQHRSRVPL
3601	33969	C	3641	214	363	
3602	33970	A	3642	1	3390	
3603	33971	A	3643	396	766	ERGLGRSEIPRKEVEHFMLQGS AVAGP*LLPLVGPAGECFHGW LEPLLARIAEDKTVVVSPDIVTI DLNTEFAKPVQGRVHRSRGNF DWSLTFGWETLPPHEKQRRKD ETYPKQPVGVIGD
3604	33972	A	3644	105	786	VGPEHCAGAARWVTSPPRS WP DAGQSVN*PDLP*REKHPEG/G* KLQGGQAKTAGNAVVKPLS K/PQGSSALSGGHWDRLPAPDP GKMPNCDRAPPKIASRVSPQAC FPRPSPVPSPAGPLRASTPADQA RRPARAARPPDALS KRGPGRIS AKLHSGGGGGGCREKAQEFP EGRTARSLTPPLPLAPRPGPAGR RLPPAHTTTPPGRTGCPSPAGR DTSQLPYFLK
3605	33973	A	3645	313	546	RNKVGSRGRAKQLKFSQGSTR VHRSESEEEEEKEDEEEEEEE EEEEYEKEEEEEEEEEERDLEF SKGPFLSS*SSQKG/GTRVHRSE SREEEEEKEDEEEEEEEEEYE KEEEEEEEEEERDLEFSKGP

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3606	33974	A	3646	3	1332	PLGPRRQQSECGAPTLTWPPGS NGLPGQQGASPLSASPGAGAGS GRGPAAAGSGASCTPSRGPAS WSRSAAQVPRSSRWAGSASS* NAGSP/TPPTSQPPRA/PALCAA AGTLAPVEKGVVEVPAGRGLSG APS**GKCLPEAPSGGSAPLS* GGTESGAGAPEPRKATGRPGPR VPGGAGAA/RGLPAPTSAGCAAP FPPRCPGCLCVLRARFAGAAHP CPGPGWPG/PGGAHQTLRAAL REPSPLASPLVSGRPGPRLVFNR VNG/AAGPLHVILRGDPGDLH SGPRGECPLCVRLAAGATAA\ DGGPAGEGRPVYTMERTAN PRLQNFVPH*PR/PSGGRKQFLA RITSFPGSGWEGGAATRPTCRQ EKGMAALPTHCAWLGAHT*K CQHLDFCTFFPGPGCGDGRCH VQGPNSDLSAHPACGQATSP WG/WQGGAPG
3607	33975	A	3647	102	788	GHCGGGTQCSWPAPWCQNLLP PSASPTLSTQRQLWHIAPGAH RNPV*QVPSLDS*ARAQLSVPA QGSLLPLC/ASLTASPWCSGSSLA VLLFGK*PFCVNL*F*RASLMKS SSRARVLPRLRPVRWPAVGIRG WQGMERGQGAWPWLCGAVCS RA*SVHMTTLPSGPAALCGIQR LQSSSTQRRPESLHPLQLGWEEA QAGEGLPHPAVVHLPASPRLQL SQLHQSRRLPPG
3608	33976	A	3648	114	1309	TNCSCLDRPLDSSHVPWVEEA QSAHNKEIVPQKGPWSSKHN QARGPPRSESNNTKAVNCAGRS TKTQTPRGTSQT/TEGNT*VIHTR HTKMSTTNTNTSSLDAPTTQ MRSTRERGTS/PAPPSSALKNTY TLPLPTS/NDTTIYQLTVVPGP GPRTGELPRCHARTVTRVSGEE ALPPPPRSPENSNTHLRTPSQTR TPTRARPPL/PETSPQPPWDPDR VGFFLRSPVWAPSSQQYPWW SPSLSTNMTPPESS/SLLPTLAY YTSLSHHGQRMPA/PADHA*A QSTPSAHRHRPQYVQWTTDPPS THGTFEESGR/YPQHTVAVK KKTGTGTPARDSHSFPTPTTRM VKSLKTTGTSTDLSSRSILKS PTSSIFTSLTIFSWRDPDSMDLC V

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3609	33977	A	3649	3	1777	NVAGNPARSMAETQSRAGTAG PGPRTKQTPGTWGSQGAGAPA HPPCYIQESRSGFSAPGRARNA\ PGAANPLCMAPGGAEGSGVIQ REVEGRPRSHSAPMLSLWSERP PSCVCLGPDGAADFPRRGRGPR PPLQDSPASPSAPRCSPARCSRL PL*PRPRDKDAPGTGGRPG/PPG TLPDSRLECSASRPGEGCETL VQFPDRRGPGCGPLQGPRGRNP ARQPRLTRAAPGPTAPAAALVS SGGAAVPPRRTR*PLLAGAVEV ASPRGVSQSLVPEHPGPFKELR NIVLSNSPEASYAPAN*RPPPA EIRRREWQELRGGVLGGGLVFS FPHSCVSGTGAWGLPTWRGV GSGIQGFFSVPR/SGRETSRGG TATAPWSSTPDCPSHWREPSAG SLRRG*GRRDAAPGAR*SRAPP TRPGRSAPGIGAGEAGVEGEL LGPGRQVVTG/PGRPTAPGIYRP GGRRKASAGSRCATGGSRSSC PRRGRSPGWRWTRWGV/GR RGTLPAPGPGCPYRRRPGGA PRGAGGRPSTGCGSRSQWLA GQLLPRPSMLGALPGLAPLQPP PAPPVPPPPPPPPMPLSAAALSS
3610	33978	A	3650	3	922	NVAGNPARSMAETQSRAGTAG PGPRTKQTPGTWGSQGAGAPA HPPCYIQESRSGFSAPG/PRETHS GAANPLCMAPGGAEGSGVIQ E/GKAGPDPTARLCSAFGPSGR PAC/RLGPDGAADFPRRGRGPR PPLQDSPASPSAPRCSPARCSRL PL*PRPRDKDAPGTGGRPGRLG HSLTRAWSAQHPGP/AGEGCE LVQFPDRRGPGCGPLQGPRGRN PARPQRLTRAAPAPDSAGSSG/ APPEGCCAPAKDEMTPAGRSC GGCLAETRICPVARP*APLEKSF PNVVPNGKKKAQPTLSPSNMT
3611	33979	A	3651	1	542	LPGAGHRRVLDAGGPRGAGLQ PQLPARQVGAVAEHLVSGPPG AGLA/GSGSGASGVGLGAAGW GSGPRGVRAEGEGAYSGPGQV FPVQGNVGNADAGTTGVGVPA GWWPPLPTRLQTLVSAWPLCP *AAASARSPPSGLSGE*TLFYTF SFLPPVVIAASPPAGLASEARPC FPRFHSYP

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3612	33980	A	3652	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFPVQNCLS LARSDSREQGLVLMESRNRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSFQSFISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSST GLSPSGNMEKNKVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
3613	33981	A	3653	1	847	MENKKVASPGWTCWECDRLF MQRDVYISHMRNEHGKQMKK HPCRQCDKSFSLSHSLCWHNRI KHKGIRQGPDSRRTFTKRLMLE KHVQLMHGKIDPDLE/TDRCH P*GGNRNKRQPRSPVPSRSWK NQFWSSGLPKEQSLNH*KS*KS MFLRFTSALVRGFTTENLLQFH EHIPQHKSDGSSYQCRECGLCY TSHVSLYMHFLFVHKLKEPQTV FKQNGAGEDNQENKPSHEDD SPDGTVSDRKCKVCAKTFETEA ASNTHMRIHGMAFIKSKRMSSA EK

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3614	33982	A	3654	854	3009	VNSHSQLQRE*NT*ESNLQGM *RTSSRRITTNHCSMK*KRIQTN GRTFHAHG*/RVNIVKMAILPK KIQSDLTSHSISLEEMKKHNQG KEAAQRVLSQIDVAQKKLQDV SMKFRL.FQKPANFEQRL.QESK MILDEVKMHLPALETKSVEQE VVQSQLNHCVNLYKSLSEVKS EVEMVIKTGRQIVQKKQTENPK ELDERVTALKLHYNELGAKVT ERKQQLKCLKLSRKMRKEMN VLTEWLAATDMELTKRSAVEG MPSNLDSEVAWGKATQKEIEK QKVHLKSITEVGEALKTVLGKK ETLVEDKLSLLNSNWIAVTSRA EEWLNLLLEYQKHMETFDQNV DHITKWIQADITLDESEKKKP QKQEDVLKRLKAELNDIRPKV DSTRDQAANLMANRGDHCRR LVEPQISELNHRFAAISHRIKTG KKPSWRRGVSNLGEMLVEVYL KALMSDELKRGINQDEFSPITY YFPITVFGSEGDLLLGKIRWIGQ AYCLMIGQDVFMDFRLRVASAC FLTKMKTVLVVFDQNEQNEG TVKELLQRGDNLQQRITDERKR EEIKIKQLLQTKHNALDKLRS QRRKKALEISHQWYQYKRQAD DLLKCLDDIEKKLASLPEPRDE RKIKEIDRELQKKKEELNAVRR QAEGLSEDGAAMAVEPTQIQLS KRWREIESKFAQFRRLNFAQIV
3615	33983	A	3655	44	953	GVHNGVEELILVRRMQKSPGP GEMESGSLEKEPLGTGTGPVPS E/EYIGIGLSQSISTKHPETSPKDS RIRENDVTADGRTTEDHITADP GTTEDSVTADPGTTEDNVTVD GTTGEGSVTADPATTKDYVSADP GTTKDSVTADPGTTENFVTADP GTTKDSITADPRTTENFVTADP GTTKHSITVDPGTTEDSVTADP GTTKHSITADPGTTEDSVTADP GTTDEETTKHGDTHLL*TTSVT AVKPTRLTPMGILISLAATT TVVLVFGLVGFIKCFPLPLNPS TRVIYHPHVMYDSTP
3616	33984	A	3656	200	542	CSPPSTRPGPGP/SGTAWPGPRG TKRSSPSSSSSPSTTTSSSSS SSSSSSSAPPRGFSSTRPSPLRR LLPPSSSPSSSSSPSTTTSSS SSSSSASAGGRRAGTRG

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3617	33985	A	3657	132	853	EIDKKHRLFLVSLNSPSK*GEG DTPSRPHRARTGASVVPSPKFPPT SLGRSALSRRHPHQTTNPTRLPLR KAGAAAFNAPRACPLGTAWPG PRGTRKSSPSSSSSPSTTSTTTS SSSSSSSSSSAPPGRFSSSTRPSP LRRLLPSSSSSSSPRSSSTGDEA AAAAPVA/SRGAGPGA/AAAAA AAAASSSPG/SGAGAGPGTGGG SPGRAASLAGAGAPAGCSAA PPRRLPLRLRLARRRAC
3618	33986	A	3658	222	373	
3619	33987	A	3659	3	513	IPAALSCCPEWQALV*QILQDS SCCQSPRVPGHSCGKGTTLCVF SREWSLVSGSRC\SDGETSCTGR CCNAFLCYDLRFSLFCTLDVR RGVA/GQGGRLGLDLGLSAVCI HQV\WMGSRGC*QLLAPGRVS RPRGRERGTHWSCWCRSPWM GSGWEAHSGAACLSGVFVP
3620	33988	A	3660	3	463	
3621	33989	A	3661	263	1020	SGLREPKQLQMLEL*RKMSQLS LEG**SSHNM/V*RL*KKCSQDYS YRDYILSWYGNLSRDEGRTPS ALGR\FWEIARQLHDLRLSHVDV VRSLQGCCEDLYSLISVT*KLP MPDMKNSQDLLCCT/PCLRNDS DEVRFLLQTCRVLVFCLLPSKD VQSLSLRIMLAELTTKVLKPVV ELLSNPDYINQMLLAQLAYREQ MNEHHKRAYTYGPSYEDFIKLI NSNSDVEFLKQLRSVEGTVEKS GRRCVLVVFNN
3622	33990	A	3662	1	4314	
3623	33991	A	3663	2	492	ISAGVTGTSGLSAEATGIPGLSA GVTGKTGLSAGVTETIGLSAGL SARVTESTGLSAGVTGTIE*SAV VTETTRLSSGVTGTIGPSAETG ATGLSAEVTGTTGSLAEVTGTT GLSAGVTGTIGSSAAGLSS/A* IPSAFSGLVFILSCSTKFKAKE WLFFV

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3624	33992	A	3664	1	959	AGLSLMGSI*ACHTGLESSLVPV WLSAPSFPPHPVTSSPPISFHLG/ KLSLSH/CT*LGTVGALLPASSA THVHQAWPQWPATLMSHWNC YPREGEEIGVLTSHPTPIYIPV LTSTA/HSAAPSHFGSQAPIRL PPPPGAPISLSPLPQNLCCKGYE RDPLFSRPPPLRAVRSKKQKLGW RLAGPLSKSPDGINLPFLTSPLG CLDLSLPPGPGPTVLFVSLSLWH STKLCCQHQSLLTGLGGQPGQQG SSSPSAVFRGSRDVSQVIAQRQT SQEKELESGL/CVLTSGAPSPSSP HPPYRGTSLLFLYL CILEKKGKM VNKRDLCC
3625	33993	A	3665	2	2180	CPQSLIAVEQRKPPPTGSGVLLQ PRAAQGTPLPTATPHGTSGDAQ KHLQLQIW*NTWP*KKPGSPPT/ VRRQTQDQTTAQHPEGAKVQ GHIDQFPGGSVHFGCRPAPSPPR RQG/PLAWHGAGADGFPH/GSP FPSSLTRRCTATPSVLKTSPIRK PLLHSCPSN*MYP*PTRPPSPPTS PTQLSLRT/ANVATCPPLWPLPL RRHLQWVPPNWEFGAASGSS REHGGI/PAMPQPQCSAPSY/PPT EACLQADGDQALSKHSADTN ASVRPKPRGSWCPPVTDEDAES DRGSGQQSQRTPAEVLGKPKQ VLERFLLPTQTKQEGSHDEETR HVHNCREGSTEKQGRHPLPARP SPASSKRLL/TPGSPPAAKRLL RQGLLRPAATPCSASGGYLGTR QALGAGALGGCEPTPATGEES RPCHLR*PLSPDSSSLCPLGFA K/PHQARNAGLLGASTGMKAT KWAGACRQRTAKTEAWASSW QRVSDTKP/GSTRQKNKDSGSH PQYQAFDLRLTITAGFSAEAS ELEGSCAAATQISSLQVACHGT SRPHNHVVDDIMNSTAGPPSGV CGELENVMSGKPTQLVSEMLQ VR/PSPSGASFQQLRMT*VSVN WTPPRPCI*NRPAAPAEETSPAPR TA/STPNASPPQGSARGFVEKW NGSHAARHPRYKPGTQ*PSGA ASTG/SPGTPPSPALPFCRASSLV
3626	33994	A	3666	3	426	
3627	33995	A	3667	3	266	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
3628	33996	A	3668	2	1256	CHCGPP/VKVEAYGSQVLKGVLAQVQLTVGPVGPRTHPVVFVPECHIGDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPRKIVNQKYHIPEGIVEISATIKDLKDAGVVIPTTSPFNSPIWPVQKTDGSRWMTVGYCKLNQVVTPIAAAVPDVVSLLEQINTPPGTWYAAIDLANDFFPIPVHKAHQKQFAFRWQGRQYTFTVLPQGRWEINMTKIQQPSTSVKFLGVQWCGACQDIPSKVKDKLLHLVPPTTKK/EAQCLSGFRREHPIHLPYIRVSRKAAANFEWSPEQEKAQVQVAAVQAAWPLGPYDPADPMVLEVSVADRDADWSCWQASI/GHKVGHAQQHSIIKWKWYIRDWARADPEGTTKGQGRWWQLAERQDSRDREAIGERQETA VGKTARDGEAVCD
3629	33997	A	3669	349	718	AGPEGTTTAECP/I/CQQQRPILSLRYGTISWG/DQSATWWQVDYIRTLWSKWSASAKTTIHGLTKCLIHHDIPHSIASD*GTCFMAKEVWQWYCFSHSQDSRVQESRGGIGSCTTHHPCSFNP
3630	33998	A	3670	667	960	
3631	33999	A	3671	1	1371	
3632	34000	A	3672	1	942	MVGKAKWKPLELPLPRKIVNQKQHHIPEGIAEIAATIKDLKDAGVVIPTTSPFNSPIWPVQKTDGSRWMTVDYCKLNQVVTPIAAAVPDVVSFLEEINTSLGTWYAAIDLANAFFSIPVHKVHKPFASFQQG/QQYTFTVLPQDYINSLAL*HNLWRDLDFYFLLQDITLVHYIDIMLIGSNDHKVGGAAQQHSIIKWKLYIHDQAQTGPEGTTTSVIQQAWEHQSGPSRDGGYAWAQQHGLPLTKADLATTAECPVCQQQRPTLSPRYGTIPSLPLTKALTLQLKKCSSGPMLEFTGLAMPFIILKQLD

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3633	34001	A	3673	1	1270	MGDPSRRRTCRAMQAKYPLVF KCGGVCWGS LDP RCRVASQV WPIPKRLSRGWPFHNAVGRQV SDWKSQDFADFGTTHQTGFS PAGANQRGPLAATLSGPGGEG QSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAACTTGFP TGK RAVSATQLMILCLLPGVYLCNGK RKL SAIQGLLDNGSEL SLPENP KRHCGLPVKV GAYGGQKTDRS WRKTVDYCKLNQV VAPIVAAV PDV/VVSLLEQINTSPGTWYAAI DLTNAFFSIPVHKAHQKQFAFS WQQQYTTFTVL PQGRWEINMT KIQGPSTSVKFLGVQWCGACQ DIPSKVKDKLLHLVPPTTKKEA QHLTGLFGFRKRYIPYLGVLCC PIYQVTRKAASFQWRPEQEKAL QQVQAAMQAALPLGPYDPAGP MVLEIAVADTEAVWGH
3634	34002	A	3674	1	1978	LTIIYAVNLSLILPQGDLPWPFTRV TVH*GKGNDQTFQELLD TGSEL TLIPGYPKRHCCPPVKVRVYGG QVINGVLAQV*LTVGVPVGPRT PVVISVPPECINLSSWQNP HIGF LTGRARAIMVGKAKWKPLELT LPRKIVNKKQYHILGGTVEISAT IKDLKDT EAVTPTTSPFNSPIWP VQKTDGSRWMTVDYCKLNQV VTPIAAVDPDVVSLLEQINTSPG TWFEWSPKIKALQQVQA AVQA ALPFGPYDPADPMVLEVSAD RDAIWSLWNAAI GESSRRRLGF WSKALLSSADNYS PFERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSGAQ RSIIKLKWIHDWVRAGPEGTS KLHEEVAQMPMVSTPATLP SLS QPALMASGGVPYYQLTEEEKT RAWFTDGSARYAGTTQK WTA AALQPFSTRPLKDSCEGKSPHH PVIAQWAHEQSGHGGRDGGYL WAQQHGFPLTKADLAMATAE CPICQQQRPTLSPRYGTIPQGDQ PATWWQVDYMGPLPSWK GQR FVLTGIDTYCGYGSAYSARNAS AKTTIHGLTECLFHCLGIPHSIA SDRGTHFMDKEAPSA SVLG LA LALLAPQLADSLLED PVIVKGT DEAEYFQSVREEDPSGVKRRK MLKSGKNY

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3635	34003	A	3675	1	746	MGKIVQPEKAVSAKAGVCLKG CDCSEYKVQCEWQDTSPLYG IVLSFGEEPVTLRWDLHAWSY ALSKVISTICRRGKFSEFKAHTA PVRSVDFSADGGFLATASEDKS IKVWSMYRQRFLYSLYRHTHW VRCA/KFSPDGR LIVSCSEDKTI KIWDTTNKQCVNNFSDSVGF NFVDL*PPSGTMP*PSAGSDQT VKVWDVRVNLPTALPRMVY YGAKCHLWGCWSFTENSELSF QLFCTSIPIWF
3636	34004	A	3676	5	812	AAGSAGLPATPQPRARRVGR RLGPGARGAGGAGGAAGCRAL RATARAAGSQPGPHSPGRTARS ARK*RLRRPESNKVRVCGPHSP APRTPPSPGIQHAGKPRARRPL PPPGAGVGLGIVPGLGLGRAGA DVAGRVGPGAGVPGCCREGAR RPGSGRRAPVLSPLC/PGLQTA RAAAGPAPGA/GWP*VRRLEPA EALPSGMFMMRKSCSVALTSSL SSSSSSSSSSSSSSPSTRPDVS PRVTAATGDMYRGSFSLGTLKA LRTWPR
3637	34005	B	3677	1	1071	
3638	34006	A	3678	1	169	
3639	34007	A	3679	2	189	
3640	34008	A	3680	3	352	SKHNLKLTATSQPHRPMQLKP ACVPPVLSPPHMGWGRSDTSEGP AH*PPAAWRVCVVLGL*ASPP AKLQAQHQAGSTRPVDRQAPS VLTAPPLVWPPFQGICSKWGA QHIGKRQGH
3641	34009	A	3681	8585	9026	ERYKFFSAASPNILILLTFKIVV RPLITKENLYLEILIRHLLCSVL TLVCVFCCPVFIGSCSSKRLTTA WTHSTGLCAAMSSRPGGGGG KGGPAPWAGKAGSGG*GEGR GKERVCGVQAPSVPTGVGMGG QRRAGVGGPRAAP
3642	34010	A	3682	2	484	
3643	34011	A	3683	1499	1793	IHSIESSPIPHWIGGLRLMLCIVT RLNFEICLVKHFQCKVVEHT QQYEWHRVLHLKK*QALNLK KNLQT/GDKL*VSSLVHGETN SCRKALAL
3644	34012	C	3684	1	1044	

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3645	34013	A	3685	8504	8970	ERYKFFSAASPNILITFFKIVV RPLITKENLYLEILIRHSLCSSLV TLVCVFCCPVFIGSCSSKRLTTA WTHSTGLCAAMSSPRPGGGGG KGGPAPWAGKRAGSGG*GEGR GKERVCGVQAPSVPTGVGMGG QRRAGGGEKGALARRLGGG
3646	34014	B	3686	I	2178	
3647	34015	A	3687	I	2424	MLTVIHSEMQAAKVSDDGNEELI GKWNLLGIERPWGPRRDWSGL HGPGPPTPTARPRPLRDSSQNT WRLQKPRLKGGPGAQNARM NEAWQPLPRFQRIYEKTWVPW QKHADGAEPSQRTSTRAVPRGS MELEPPHRAPRVRRVPQFSRF QNGRSTSIHHPVPGKAAGTQLK PVRADLVAALYKATGAELPKA LGAHPLHQCLDVTDELLEKIA SRSQNIIEINISDCRSMSDNGVC VLAFCPCGLLRYTAYRCKQLS DTSIIAVASHCPLLQKVHVGNQ DKLTDEGLKQDNQPCIEGNFE SRMHAQGRITLVQERPKKTVNF TVCLLPVQAGSKGQGRVYNG KVLSTANLRRISVDGKSEKSV KDAEKAFDKIQPFMLKILNEL GIDGMYLKIVRAIYDKPIANIIL NEQKLPWVVDGTGRGAGGS VTGEARAMQGPQWKGRLRH GGLQVPFALQGGG*GPARN*A QQLLAQRKYL*IQLTRDVKDL FKEN*KPLLKEIKENTKKWKN PCLWI*RIINIVKIAL/PKVIYRFS AITIKLPLTFTTKLEKKTTLNFI WNQKRACIAKTLGKKKNKDDG IMLPDFKQYYKPTVTKRAWY YQNRIDQWNRTEITSEITPHIY NHLIFDKPDKSKQWGDSSLN KWCWENWPAIYRKLRLDPFLT PYTKINSRWIKDLNVRCTTVKI

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3648	34016	A	3688	453	1508	KAPQAPNINSYCLQVEECCQKG ISVDLSTGMTSTGVVP/HYNEQ VAGEKEEETNSVATLSYSSVDE TQVRSLYVSCSSGKFSSVHSR ESQHSRSQRVTVLQTNPNPVFE SPNLAAVEICRDASRETYLVPSS CKSICKNYNDLQIAGGQVMAIN SVTTDFPSESSFYGPLLKSSEIP LPMEDSISTQPSDFPQKPIQRYS SYWRITSIKEKSSLQMNPISNA VLNEYLEQKVVELYKQYIMDT VFHDSSPTQILASELIMTSVDQI SLQVSREKNLETSKARDIVFSRL LQLMSTEITEISTPSLHISQYSNV NP*RGCFHYCLAFT*T*NTLSI YSENVQEGLVKGN
3649	34017	C	3689	57	230	
3650	34018	A	3690	2	123	WWKV*KKYSGFKVFL*HQH** PRRPLQSLFS*MPWKRIAK
3651	34019	A	3691	94	360	LMSLLTSPHQPPPPASAPSA VPNGQSPKQKQEPKLSHRFNEF MTSKPKIHCFRSLKRGVSSAPE SCLSGVLWLHVWFCITNFVCE
3652	34020	A	3692	1	2037	
3653	34021	A	3693	2	1079	NLSKKYQPKKNSKEEEEKYTS CKAFISNLNEMNDYAGQHEVIS ENMASQIIVDLARYVQELKQER KSENDHRVSGASRRAPLPGPFR RLRPFTPDVGGEEAANQAE/Q *VPSLKWNSKGKTNGTRNGTK CGKEHSPTLHQSRQGTVIQSAN RPSVA*SYRAPLHPSPH*KLAP* VPAFSSSRVFPMLSSFSL/YISTD DQEGLYSLYFHKCLGKELPSDK FTFSLDDSQLVIEAYKSGFEPPG DIEFEDYTQPMKRTVSDNSLSN SRGEGKPDCLKFGGKSKGKLWP FIKKNSPKQKQEPKLSHRFNEF MTSKPKIHCFRSLKRGVSSAPE NEKQDDTMASSTFSLSLDYEM PVIEKAE
3654	34022	A	3694	1	215	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVLSRHQAP/C*PPA FAHAAVAASHKVFSNIVRERV KTQEAERA
3655	34023	A	3695	1	208	MAQDYGAMGDLVLLGLGLGLA ALAVIVLAVLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT

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3656	34024	A	3696	1	164	MRYRYPVPRMAEVRT/SDETKC W*ECGATGTGFIHCWLNIQQHT LSRLFTCLCSC
3657	34025	A	3697	146	659	LAGPRCTTSLTPSEGG/LPPDLSL GYTVHPPDSQGHGTGPLAREGT GSHRFGVE/VRQRRWERGEAPL LQLSPAPGRPPRRPHPCRPQHLP SAAISEAATARGPRNRSQAAAA AADPDNLRVARG/PRSTRSSAV DAGPPPSASPGFP*SSSQQRPS EKTGSEVYSAYIPANC
3658	34026	A	3698	32	376	
3659	34027	A	3699	1	2148	MALSPWTPGLGAGEKLVQAAA VSTGPSLELCTLPSTLGSSVAVE ALEQLFVVECVRDARRNLFEI NTIKMRITRTENEIELKKKITD LTKYNEALGEKQELARKHAR FVLSLNTQTMKKATTYYINET YTKINLKREDIALQKKCIQEAEE LMEKERAELYLRKQELTAQINE FENTREVKRMETYQKK/QRIG*I TN*NVKNKRNSYFSAAVLSDH NLEIARLHESIRYWEQEVSELK KDLAILEAKLCFFTDNKEKLLD ISNDEKNEFLNKIKQLVETLHA ARMEYKDLREKMKTLARQYKI VLSEEEKAFLOKQKIHDENQKQ LTFISQKEYFLSQKRVDIKNME EGLITLQELQQVILSFMSSVYSK PNLSHSGRLTCCSFPLYLQMMT PFPCVITQWMACLRKKHARW TAKIKAEIQATEKIQNAEVRRI ELLNETSFQQEISGFVAQIEKL TTTELKEEEKAFVNKEKMLMKE LSKYEEIFVKETQINKEKEEELV EYLPQLQVAEQEYKEKRRKLE ELSNITTEIHWGLFEQEDVKQEL QQLRDQESKKNDHFETLKNL ENGFIYINDQADLLLLENKKLK EYILYLKNNIEKYREGQEALMH TSSDLSQLIAQEGLLQVEEQGI QWWIRQSPKASQVGKPTVQPS VCGQRKSPCQTGTGVNPRVQK LKNLESNVRGQEAASSTGERGIL

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3660	34028	A	3700	1	2658	MQAPYRCQRTGWLQQRKKA GLWGLESSWSLGLGQAAQQ ELTSAPGQFRLPPPPQAPERPTA GGSASLGPLP/PGKLSEVPEPS RPRGRPRPPSTWAPPGGP/GASA LPVVP/HRGARTRGASTRGAS/ EAGPHLPVPVTSNAPGHAGGW/ GAPSHQNHASPTGRGPQPAGE LRQA/GEQFPNSWGRRGSCRTC SVVLGHTEPRPEPAHVLVR/GN PGSPVGAAWGNEA/GHPRAPG AQRGG*RSPLGRE
3661	34029	A	3701	31	556	
3662	34030	A	3702	3	1394	RKKELQHKIDEMEEKEQELQA KIEALQADNDFTNERLTALQEN QTRAKESDFSDTLSPSKEKSSD DTTDAQMDEQDLNEPLAKVSL LKDDLQGAQSEIEAKQEIQHLR KELIEAQELARTSKQKCFELQA LLEERKAYRNQVEESTKQIQV LQA/QWQRFHIDTENLREQKD/ NEIASARDELHSARDEMVLVH QAAAKVASERDTDIASLQEEELK KVRaelERWRKAASEYEKEVT SLQNSFQLRCQCEDQQREEAS RLQGELEKLRKEWNALETECH SLKRENVLLSSELQRQEKELHN SQKQSLLELTSILQMSRKELE NQVGSLEQHLRDSADLKTLLS KAENQAKDVQKEYEKTQTVLS ELKLFEMTEQEKQSITDELKQ CKNNLKLREKGNPSILQPVP ARIHRPIPGFPMVIRSIVERKK PWPWMPMLAALVQVTAIVLY VPLGARASP

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3663	34031	A	3703	1	1133	LEEKEQELQAKIEALQADNDF NERLTALQEHLLSKSGDCTFI HQFIECQKKLIVEGHLTKAVEE TKLSKENQTRAKESDFSIDAVSP GKD*GSDDSDAQMDHDLNE PLVKVSLKALLEDYRGGYRN QVEESTKHQVLQAQLHRLHID TENLREEKDSEITSTRDELNAR DEILALHQAAKVASERDTDIA SLQEELKKVRAELERWRKAAS EYEKEITSLQNSFQLRCQQCED QQRREATRLLQGDHTDEAADLP LSRHSVSDPGVSCTQEEIQEAR GLTLLCFSKIKCSQKQSLTSD LSILQMSRKELENQVGSLSKEQH LRDSADLKTLLSKAENQAKDV QKEVKRKDIMSPIMVGLKAKS
3664	34032	A	3704	1	540	
3665	34033	A	3705	1	280	
3666	34034	A	3706	2	416	
3667	34035	A	3707	309	908	LPSRGAGLGTCTRPCLSLPLLP WAPVLPPEPPRRVPPAPRRPVG STTQGLRSASTRR/VDWQAAPP AALVWDPLGEASWAP/GVWCA AIDLANAFSIPVHKACQKQFA FSGQQQYFTFTVIPQRYISFPAL CHNLI/RRDIDCFSLLVVHFAWK EKWSDVRLGTDSWAAASGLA GWSGTWKKHDWKTSPVIEHQ KFCFLFP
3668	34036	A	3708	1	2973	
3669	34037	B	3709	1	1053	
3670	34038	A	3710	1	1178	
3671	34039	A	3711	3	247	DCLRVLWCPPV*F/QRSPSLQQP L/RPGFEPLVGRHLMRPARSWR PQPSSASAGLPSSPFRDGCCHRFR ASWALGGRAAEGEVAI

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3672	34040	A	3712	137	2176	LKNPPQTHPRRGHLLLSIVWGH ILRACGAWQEAQKPAKWPQIP EEKEEGQAPRACTLPGCWRL RRGQEEKEENWVPPACTLSGC WRLEAVRQQQREGDGFGAAS CSDLAFRCASSQNPRSLPVA PERRRRQPSRAPLQWALKEPGS ERSPLLSCEALQPPFLGLGS GAFCLTRGEKGSPPQDPFCLHS PWMLEAGGSDAATARGDFGA ASYDLAFRCASSQSPKSPPEPVA SISERRRRQPSRGFQILRSSGAFL LDREHVCLASSASTTGLGSPRP SWSHQVASNKGLKPLRGCSW DGERGTTLEDTRVLLSNPLLR KGGKRVSTSRMLQCSVVEKY CPWFLDQGTMNIEIWEKVARA LKKAYRDGAEDIPINIWSVWAL VHPTLEPFHTDHDEEESEEGE YNEVTKEVTEQFCLPAKAAKE GGNPSLTSPQQLTTETEAEIQLI EKQVHKAQINRIDPEKTLDLLIF PTQHSPTGGVVQEQLVWELF LPHSNSWTLTPYLDQIATLIGN GRTQIVKLHGYPGKIIVPLTK AQIQQAQFINTLNWQTHLADF GVLHNFHFKTKLQFLKLTNWI LPRITKFKPIECSENVFTGRSSN GKASYSRSKNKVFQTSYTSQA KAELVAVIEVLTAPEMPVNVIS DSAYMAHSTQLE/TAQL*FHTD
3673	34041	C	3713	1	784	
3674	34042	A	3714	87	447	AVQRRSGVGPACLSGCSANPGP PPGTPSGAGAAPGGGRWARAK SGPESPPGT/GPPQPA*APQ/AA PKTRAGVSFLSPPLASSPGHANF GPDSDLGDGVMRQA*RSNKQ DPA/GTPGTWVR

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3675	34043	A	3715	3	1435	RGPSGPRTVSPSPAGASSVGGPP VQAWPCSLCVGSLPRGSIGGP PKGLQLWGPRASWFLGDYACP LLASAPVLAACKTLCQTPAVPA SLAG*RPLVAVKTHVAAQPFLRI KHLAAVLADKSAPGLRPVCGT A/GFAGYLCLPHSL.PSPDG/EPV DVSTLDSAEYCQLGLGGICRGP GR*EGGHGY/RGSEKPHSTYPSS PSLSG/EPENRG/DPGVAAQEP*P PPREQAGPSPFVILEAAPFSAG ACFPGEAPGGSSPPNGSAVGL WRGRCPPGPRSL*RIAAAWEPEK RCLDSWK/RRDGAARGVGT ATFSPPFASRLVLPGEASLGTGP VVFLLRAGEPSASGFGPAWRE STAGASGGGCCGHGPGSLRA AGLPSGAGSW/RGDCCHLGMG EDPLG/PW*SSGTPASARGSQEV PAT*GRAGGRAARHPQGARLPS GPPG/EPGSPGFWRKESQSTLT FLGAQSSSPLADLGLSGLASAG
3676	34044	A	3716	1	756	MNDAGNHSHQTNTRTGNQTP HALIHKRLJNENTWTQEGEHH TLEPFGGTTDRIVSPSHTRSPDM AIA NFQSSGCSVVPDTIPRPQYQ CRSRHSVLLTSNLTVPMSQCVK PPYMLLVGNIKIWMNNQTVRCI NCHVYTCTSHFDSRKSVMVLV AREGIWLVTLRPWESSLSIRLI NEVLQRIKRSKRFVFTLIAVIM GLITVTALATTAGMALHQSVC TAHFANDWQANSNQMWNSQQ GIDQ*EHMDTGRGTSHTGAFW WNNRQNSFFPYQSQRHNSQF PKFWVFCCPRYPHPSPVQCRSR HSVLLTSNLTVPMSQCVKPPY MLLVGNIKIWMNNQTVRCINC HVYTCTSHFDSRKSVMVLAR EGIWLVTLRPWESSLSIRLINE VLQRIKRSKRFVFTLIAVIMGL ITVTALATTAGMALHQSVCQA HFANDWQANSNQMWNSQQGI DQILAAI
3677	34045	A	3717	3	131	

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3678	34046	A	3718	2	424	CGRKSRGTALPTGSSPOS GPAA PGHSAASALHPTP/SPPPHPL/PP AATGDIDGNRYPATPMTKYPS ASARRPVHRPTCSGGGSHTNHA ESLPPLTPLEEADTHPPGGSQ*T RPPHCIRTGSCLP PPRAPYTRR ERRRHPP
3679	34047	A	3719	1	418	
3680	34048	B	3720	361	1371	
3681	34049	A	3721	1	469	PGTCRGSTGQP*EACWRSP*SV RNTRCPVREEPASPGWSSCLTS PSARGVWVACS*RLPSSSCPGST AGSSSGTLCREAAPCHR*AACS DGKPPGMPRSTRRLGPSGARSG SARRCPCGDGPESLRGHAPARA ATQAPDPSTQSSASSATPRAPPL L
3682	34050	A	3722	117	871	GPQSSAGNAGPQRRRTTLGVPR TWHPGPAA*AGNSCHISFYSSR FQPF LGVTS VLRGSSVSVSGIPD HLGQPRSSQEPSRPENAAAQM* TGCPGYAGCTVA*MKGRAELQ GLRTIAAQPGQWLTLLPRCPST RRLGPSGARSGSARRCPCGDGP ESLRGHAPARAATQAPDPSTQS SASSATPRAPPLGLCGGGC*G DRRSQQGTE*A/VA VP GMLGGP SPFSQPEHPSAFAQPSCLPLGL DFKLLIPSQ
3683	34051	A	3723	110	1017	EAANEPKHLHLRHAAGLGQHR QAPRPQGRPFARPHIQGDQTD RLHHLQGGGRHGARGHLHQA GAGQSAPAPKGAHVQGPCGCH ESTGPVEH*SHGERPKHRCRP AL*EHGHENPHK*SSPHDQR*Q TADPEGDN*SQCCPTAN*IPLRK LWLRG*DLGRSHGQ*PHQG W/HLDAQLLTPASSSTLCPTPLQ QPLHLQLRHAALAQHRQSPAA RTPLARPHQGQDQDRLHHLR GGGRHGARGHLHQA GAGESAP APKGAHVQLVSKQLGGVAAEA HVDSSGLWVSPGRHN*YKKS SRL

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3684	34052	A	3724	3	1092	LVEPGRLLLEAQGFDPKNNK*RRR GRVCGRGGEAPAPGQGGQPD *NKGKEEV*NSSE/EESSEVSLP KTSREQEIPSLACEFKGDHLKV VTDSQLQDDASGQNESEMFV PLTSLTISNEESLTCNTEPPKEG GEARPCVGDASATPKVHPGDN VGTKVETPKNFTVEENMSVQ GGLESAPQSNFSYTQAMENI QVRETQNSKEDKQGLVCSSEVP QNVGLQSSCPAKHGFQTPRVK KLYPQLPAEIAEAGEAPALVAVKP LLRSERLYPELPSQLELVPFTKE QLKILEPGSWLENVESYLEEFD SMAHQDRHEFYELLNYSRCR KQLLLAEAEELLTSLDQNAKS RLWQFKEEQMSVQVF
3685	34053	A	3725	182	771	QTALSCARHGRSAAFVWRPNR APVWRSGFRGVAAGSALVHST ALPSRRQPPERRSEHDCLRCRA LCGTKPQGLSY/TGP/WGLGV PEAAAAALDLGVH*PLFHLPLD SESRKPGRGLAAPPMPARWGL SCLEQVGHTRKEGGGQGCRRPW PPCWSPPVSGTRGGPITTLRRGS AALHVRASYCLMENPEPPSIV
3686	34054	C	3726	769	981	
3687	34055	C	3727	70	197	
3688	34056	A	3728	1	158	LGSVSSFASCTLGAPGYSTAP VAL*SVGPWGRIVKVPGHGGS WEMHFIISM
3689	34057	A	3729	229	496	VTGLQNLVLSIVTESGKTHLLSF SSHGLEEIIISQLPGCSGTLTVRP QGPT/GSQGNRGCDRVAQGSQ GAGGERGDRSQAPVPAARDS
3690	34058	A	3730	167	769	FLTRETGDPTRSSSHGKHPVA VF**PTRPP*TIWEITHGCGRR AGRCPTGPDGPGSGRGGPRCW PSGHAAATGGLGPSCGRGLGAN RGEAGPAGFTVCSPLSGWRTPY THHFPASRMSWHLDYASPTY RSQGNRGGERVAQGSQGAGGE RGAGSQVPPVAPARNKDPKR QKPRPPLLSSPTARLIGLFPRAD SCRSC
3691	34059	A	3731	234	543	ALDQVASLPIMVPASKQNTATS CCRLGYNSFDLGPAAATIFFSP AMVISQLPGCPGLTMRPQGPT /GSQNSGCERVAQGSQAGD ESDGSQVPPVAPARD

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3692	34060	A	3732	1	3695	MGKRSFERVLVDKCDSGRSL RKQHENECAFIQILDTQSLMIPG QRGSFRLADSQHTDRVLCTLM AEKWDRKALSYTRNSFRAQIRL RKTRFQGGKCMICKKSRVLPY QAAYVSQHGSAQPPSHLPVSG SLSSSTGDDEEEIEIVHMGNAIM SFYSALIDLLGRCAPEMHLIQTG KGEAIRIRSILRSLVPTEDLVGII SIPLKPLSLNKDGSVSEPDMAA NFCPDHKA PMVLFLDRVYGK DQTFLHLLLEVGF
3693	34061	A	3733	1	2523	MKQFLLYLDESNAIGKKFIIQDI DDTHVFVIAELVNVLQERCHTR LGYTEFLVAVRVTFGLCVEAV TLHLKYQILIRGLLEMMMSFSDA DILKQLPVTVPGLFPASLSPSSL LGNPPSWLRHNSKVS AVSS PSATKTLSTGIGKLDPGHKEMA EESLLKNKMQA PPLSRCPESQ KCQHQLRLHHWKPSVRHQVKR RSPAVLRSAMPADCPAVLEAT TATHPEKGTALSKHLPSSDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKEQGKGLDKKKKK GKLPKNYDPKLTDPERWLP QECSEFYQGRKKGKKKQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIPRH QRPAGAPATKKKQKQKKKKG GKGFVPLREITVVKVDTLVVFQ ILEERLSVFHIIQYDTSYPFSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQQPFMLKTLNKFVVDGTY LKIIIRAIYDKPTANIILNGQKLE AFPLKTGTROGCPLSPLLFNTV LEVLRARIRQEKEIKGIQLGKEE VKLSLFAAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTESSQIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL

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3694	34062	A	3734	1	6208	MILDQAFKYITELKRQNDLELL NGGNNEQAEIEIKLRKQLEEQ KENGRIYELLKANDICLYDDPTI HWKGNLKNKSVSVIPSDQVQ KKIIVYSNGNQPGGNSQGTAVQ GITFNVSHNLQKQTANVVPVQ RTCNLVTPVVISGVYPSENKPW HQTTVPALATNPVPLCLPAAI SAQSILELPTSESESNV LGATSG SLIAV SIESEPHQHSLHTCLND QNSSENKNGQENPKVLKKMTP CVTINIPHSSSATA
3695	34063	A	3735	164	415	EYWGWLRRNINILTGNCRLG/ WPSLLPQAEESLSPQTKVERLK AAWIEEGILPLLGMRLFLAR KVHQSLQAQCPQLHQGPPT
3696	34064	A	3736	1	886	MLDLPWFNVVEEGIQLREIGML EWLSHRFPTRLREDPEDIPFTN TLPNKFVRGVPASLKSSFIGLLC MPDLTKTVGSRWMTVDYHKL NQVTPIAAAVPDVVSLLLEQIN TSPGTWYAAIDLANAIFSI PVHK VKDKLLHLAPPTTKKEAQCLV GLFGFWRQHFLHLGVSLWVIY RVTLKAASFEGWSEGEKALQQ AGQAAVQAALPLGP/HKDPAD PMVLEVS VADRDAVWSLWQA PIGESQQRPLGFWSKALPSYAD NYSFPERQFLAYY WALVETERL TMG/HQVTT*PELRIM
3697	34065	A	3737	1	1815	
3698	34066	A	3738	1	988	MPAEFFQRCSVIMVQLPWKEA HVERPHGERDYTPDLQPDWWE KFPGLRRALRPVVKTLVQLEY RQAEKCEKRDWPSLPDYIFLLC WMLPALEYRTPSSSVLELRLAL RAPQPADSLWDLVIVPITSLKS WQTPRGEVEGVTHEEICASLKS LAVALLSMSDLTVGTPTVTPQT LNTMGHIGSRGGRGQVAALNR QRQVPELIIGIDILSSWQNP HIGS LNGRGYNSLALCHNLIRRDLD RFLLPQDITLVHYIDHIMRLDSV KDKWLHLAPPTTKKEAQCLVG L/FGFWRQHSHLETAL/ RPVTG LWVKLNI*LWAIKSPCNLCLS
3699	34067	A	3739	26	318	RTAWMQYSPHLSAYGRVPTVT SSH*LLPLRSHPRDSRPAPCP/RA GPARNRQSSA/SRNRSRPRRNPE ASRGRPPGRGVASPA SPPTPRE TRTAATRRP

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3700	34068	A	3740	425	588	IWSVPFAPWRRRGHAGSRCSRR SRSR/TPRRNELSTAALGAARG HARIWREAGNWP
3701	34069	B	3741	465	1623	
3702	34070	A	3742	667	960	
3703	34071	A	3743	1	2021	MTVLTTQTSSQHSTGCHAKPAIT TPWLLAVFFQGGVGLQSVGGK ASQADIIILGLSPVSAIFQLYDVS FPPGKQGRPGLGSAGRIEVAR CGMLWKQRGYLISSSQPIKNGQ QVSDLFEAIPEPKSLAIHKISGYS TLETPESKHNHFTNTLAAIDL NAFFSIAVHKVHKQKQFAFIWQ GQQYTFTVLAQQGYINS/PPALC HNLTQRDLDCFWLLQDNTLVH YIDDIMLIRSSEEAANTLDLLV RHFCATGWEINPTKTQGPSTSV KFLGFQWCGACQDIPSKVKDK LLHLAPLASKKETQRLVGLFEF WRQHSPLRMLLQLIYQVTRK AARFEWACTDGLMRSPYDQLT KEEKTRARFTDGTQCEGTTQK WIAAALQPLSRCTCLKDSVHOR VSSAEEDFNNQVDRMSRSVDII HPLSPATPVITQWVHEQSGHGG RDRGHAWAQQHGLPLTKADL AMFTAECPIFQQQRPTSPQYG TIPQGDQPATWWQVDYIGPLPS WKRQRFVITGIDTYSRYRFAYP SFNASAKSTHIGLMECLIHSHGI PHSIAFNQGTTHFMAKEVWQWS HAYGIHWSYHVPYPEAAGLIE LWNGFLKSQLQYQLSDNTLQY WGKVLQKVVYALNQCSIYGT SPIARIHGSRNQGVVEVALLT VTPNDPL/GKY*LPVPVTLHSDR

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3704	34072	A	3744	3	1197	TLGPGTGPRAGTGSSSPSSPG TGSVPGAGPGANSVVHPGADS GVRAGAALAPGLC*VKLLGQM SPPGGALGPHNARQSAVAGGF GRARRPGRHE*LQGTWWSGPG QPLGAALQTATGPVVMNQFLR *TWHHEGHSRAPCPRFWGWF* TYSGEKPLPAAVQPSSSVF*SL QQRCPFFLGVPQCACSSACPLL F*GL*W*PGVHEDQ*ASPAGSA LTWP*LHHDPPSSGA*SDATG PGGPGSALAGFQQQLGSGGQVL QQGQLGSQTCRGGSPRRRHC* ASSWG*G*AGRLLPWA**PPAR SAGSPHRLRGLS*ARPCGCAPR CRAAGGAGP*SSAPRTGDGDV GQLGERE*EAHPARVGGQWGW GSRCPQGQGVAFSGSESYMOW SSRNRFRNT
3705	34073	A	3745	1	98	
3706	34074	C	3746	439	1053	
3707	34075	A	3747	48	751	EGDLVFPLGRGMLRLVFSKMF KLLKRTMDYSGSPSVSGHIPL PQACGPPQLVCSRRVRGQRPRP HSVPGSRAAPGLSGDTGRFLSG FGKFCFGSRKGALLTKGFSVSS GWPAAKFPPAQRVQTIVRSR/P RRPGKRVL*GEK/GEWAASLPT PLPLAGPSLPSVPGVPVPAQTV RAVSPVTPQGPSSPPFLREHSTQ PRPGCREIYQHPRMGGTGRMRTP WPWRLSARPAAAAA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
3708	34076	A	3748	1279	2791	QAAGGAAGAERDEGAGVAGA HGSRSTARRGGRGAGPRPPPP PRSLGTGSAGRGAAEGTGRAR RPAGAAAGRALRAGRAGRLGA CGGVAAVGARGRLRAAAAGAR RRGAPATGAPPP/PSAAA SPTA P PGPRHPGRVSGAAARAPPGTAP RIGERRPGGGAPATEPPDSRTPA AARASSA/PGAVSGPAAAPGPP GRRENAEGR*PQDAG*RGLWE GALPVPGSSPQTSSSTGRTSGG SRAPSHMVPGTGSPPGRGGEA GAR*AAAPAGVKPSSLWKK*L ALFRPCFQEP TPG/SVGC RGPL E CFTHSSPVG/VNGHRHCDNCCR/ PLKPPSPKAAWAVPRAAVPEA HA*K*RAEDQRLRLVLPNVTL SNPPTRGFR*LGTGVPGFQDPC VDS/GL*VEEGLCEASRGNGE RNKGTWGIPPQPLRPSSRWLQ E*PTPLPGSP*DATSPAGGGRH RSRLPKPALVGNAGTSSLPAPE PCFPHLYFTTFLLS.DSSLKFRD LAGILIPE
3709	34077	B	3749	71	285	
3710	34078	A	3750	417	1208	GPQRVPTLWVEDAEARSQRDG VGGRAEAPGARIPRDLGAAGG LRGHPRLVRGHCRRLRCSMA RTLVLRLVTPVPGGAPLALRQPP VPGGSRQEWPAFSRVGTGLPLT PTAGPSRARGARRPCPPALPGH CLLDRTYTGQLTLGAETLLAVV NSAAMNVGVQVVDVELHRHS LGEDCIYPQSSESDISDAPPSLPL TIPAPVKASSPIKQSHPEVPDTS VEKGS/PGSCPFL*GPLSHLGS SPGFLWWRPGLLSSVALVASC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
3711	34079	A	3751	10	932	LQLCSMWLLRSWVQAEQAVSI SDSPFSLHQCWAVLHKAWCVF LQLPGGFTFTLNLPLSDNLGKR VDSAPSWGPLGSFRGVHMP VGAAWEGKGNLLRPSGKLG SGSRPTPIGQQQLPEVPRAKGP GPAAVICQ/HMPAPSTGGKRG FSGRYLSASLELGGLPMAPTGP SALSAPPSVSRGAR*STREKPGV YASAT*AAEIREGQALGG/PRPS RNG/SGGPLGPDFGPNPKLRRS KAGCPWWHLSSVDAGE*LWK QHSTAVFSMPGTQPPWRGLITM PISPRGTPTAHPGPRSPGLAYS LTA
3712	34080	A	3752	3	650	GTVLDDPHLTGYCWHPPCPNNS VCNGLSPLVREEAESSEAPVQ SPQRSWTPSAKSPPLPASPPCSQ LKAGGDOEGLQRGALPVGMD RGGPGCGGHCQCSRPRILSPV VPVPQVCPSEAPGPPRQVPHTP RPQEPSRTRGRLEA/SAPSWQ*P APPAAGSLPAWP/PG/RPAPTGS AR*AGLEASETT*WSTNGPTTVH P*TL*AGSLGAPQTSAAASEHSP CPNLLPL*KPWCATNLSRI
3713	34081	B	3753	1	1812	
3714	34082	A	3754	1	209	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVVLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT
3715	34083	A	3755	2	462	PPLPGCLGDTGAPWPGPGCTGP PPRTRSPRLPG*APASRLQNP PRGRWPWAGHSRCH*SQPWL GPTGS*HLPDASGFCGALTGS CLPLSGGAGGWQSPAPDVGS KWNTPRRSAGAPPPGGRLLPGP ACRAPPRLDPLS*AGRVGRPG
3716	34084	A	3756	129	616	NRIFLNCNMVHKCKCTPMVV AGASLVETGQDESIDK*LNIGP GPVATPSRLPPQRTWN/VGPH MP*RRPQSLPQPSQAPPGLS* GSEGETQPKP/P/GLPLGPPR QPGRCGFAVD/PPRCGVSPGPG VPGPAGPAAGAAPG*PKLRQRP GPSIGDCGDAP
3717	34085	A	3757	59	292	YCNVSFGPILSARKPASPRSS*T SATWLQNHPLMYLTPGTGLW RFLTTRENVYPGPVP*WNRITC GVANWPYWPVS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3718	34086	A	3758	177	448	GTGGWVAMLQQYFA/TAWIPH NDGTNNFYTANLANGIAAIGY KSQPALWVTGGLLVHHITFIVRGI VYPLTKSQYVISM\AKMLVL*P GA EGL
3719	34087	A	3759	1097	1206	
3720	34088	A	3760	2	505	QGSRAKLSLPLGISCTRSTAGP SRFARCSLGGCSHPSRHSPLHPP PPPVQFRAGPRGRQGSRSRGSPS \GAFAPAGPGGAAAAAVGDDQQ QQEQHGAHEGEENNEGNSVPC G/PGKTGGSSVSPGLPEPWPPAP LWTQPSWSAPCH/P*KPPIPPTR QVLGRGTGCELLPAP
3721	34089	A	3761	181	581	ADELNVPLT*APAIPLSKEMKL HVPTKPARKRLKWLHSQQPTC PSTGEPVSNCG\PPPVQPPTTQQ YQGLDAGATTRVPRSLRSEGS QTQKSPSCGSHSQDNSSG/SQSS PVTPQHLLSPRAQAAPSPDRA PV

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3722	34090	A	3762	18	2104	RWQGDKRDSA*RGNLRRARKPS KRGK/DR*RRVSPTRSGKRRGA EENRQEKKKGREKERREKRS ERQDRRRRRKEQRKEEQRRRA RTNERKPRQTQANGATSS*KAS AQQAGMWGGSP*TDAIARRG GAPCSSRRCLNQGTIATPSGR\
						RRHGDAG*PGLASEHDASGHG CLRTGAG*PSDSTESVCCRPLA MHVPTHESHGVPVTRLVSHTFH CGSKLPAVGRPVACRPTYSPSL CHNPQPAQALLAHSSALQCAPL SWDPQRCAPSPRPHRRGPPSP HPHRRAPSPPHRRRA/HTTART DPTTSAPPP/RQTQRRATREPAT KHTRNAHPRRSACNRGTHTHP RRRRTTERTTHHARPRNRGQAT PNTRQPTAGRHEETDGTATRRR QHGTTRGEGG/RRRGRAAKTR QRERQEPHDNTRTRRRPKRR DRTGAPAGTRNRRTSGHKRQRP GTRASTGTAPASQQQQTPTVLS RCISRFGVFYGPDPFSGGINSFCS LPLMSDSTLSTYGGQRRG/RSR ARKTQDTGVLSPLRRRRSCPPA HGRFPGLFLSTHRQVGPAALRP PELSCE*LPQDGDFCVWLPRLR SRLRGTRV VAPASSP/CGDWQV TAVAP*PQTQSPSLSQSRDVEK RHRGQHPSVGSV*LMKAA*RG PSGAKRPKTA PRPQCARVLPK RSGPTSPGRGSCGQSRTRGF*D
3723	34091	A	3763	1	446	MWESLELPRDLLNGFDQADN DMDNEIQAEVVS DGEELVGN WSKGKQLKSENLQLDDATEK KNLFSEEKFLAEETYLSNEEP NINSQDNGKNVSKACQRTLEQ AFPS/SGS/GGLGGKNGFVG*AQ SPSAV/CSLGTWYP/CPSCCSHG
3724	34092	A	3764	186	529	GTCWKLEQSTLPLHWAGLAC PLAPGTC/TSGLL/TAPQR*MQL CGSPGWHWKRSVV VAPGRQLP GSGECMFQLPLPCRQPSLCAIPP ILQANLPLNGRQNCQAQISCKE DQSFH
3725	34093	B	3765	73	1374	
3726	34094	C	3766	1	873	

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3727	34095	A	3767	603	1208	FTTCSKHQTRPGHREQQHPAE KSVSGIFCYAEEMESSQLPDGGS GQPPRGG/ALGPPYEPLSNRIPD APG/EAGPASTPGH*SLDQGI *PGLAPRGHRLWKSPEPTAPSP APRGVSGGLPGSRSAQVSGDP SPHHL*QPAAAGRKDSSSF*AT WRPP/GPPGPAAAAGRKDSSSF* /GHMASPRPPGAAAAGRKDSSS FMVLP
3728	34096	A	3768	872	1015	VIRSRMLIPKTMGKVSFGHVRG LHSRPSQHRPRLGGKNGFTAA PAMAEAGN/GALAVASEGASP KPWQLPCGVPS/IRRCMETPG* PGRSLLQEQVPHGEP/ARAAQ KGNVGLPPTVPTGVPPSGAV RRRPPSSRPQNGRSTDSLHHP GKATS/SSMPAPESSEYEGGTL QSHRGRAAQDHGNPLASAA*P GDLVKLQLLTPQSDNSCTHIGD NGTYRSQKAAFAEKLNMGLK TFFITGVNHKWLPLSLTWLPA NSWESLLSFPPSPQQNLNDKPG RRSNITHSSKEDKKTESLELPR DLLNGFDQNADNDMDNEIQAE VVSDDGDEELFGNWSKGDSCYV LAKRLVAFCPFRDLWDFGLER DDLGLYLVVEISKQCIQEVTRV LLKAFSFIREDTHKSENLQPDN AIENKIAFSKKFKPVAEICISN KEPNVNPQDNGESVSRACQRSS QQALPAQAQRPRRKWFHSCS
3729	34097	A	3769	234	636	GPVSGHHRVNCPLPLRR*R AKGHLCRLLCPAGEATGARWR HSPQPLALLQRAPEPAHHHPAA PPGRLLHAGLRCSVPVPAEEGR GPRPQQRARTASLQLLRRR/SLL QQPPD*VRDKMAEPQRRSRQP AHL
3730	34098	A	3770	1597	1878	DTPRFHSRSGITLQEQYASSRN *RTSSAVPVF*RMSSVRGMEVPC SNER**TQSISGDQVRPAEEGPGP RPQQRARTASLQLPRRRYFLQP QPPD
3731	34099	A	3771	97	471	GVEELRNVNFFPHFKYSMDT YVFKDSSQKDLLNFTGLPVM YQA*ICHWSSSSSPQVSRGTS HVFIS/TSDEARQVLLAYIAKVT LKVFQIQIRAGQIMRIKQSIKL LWLEVENSVLPAH
3732	34100	B	3772	1	1449	

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3733	34101	A	3773	1	927	MQRWFNICKSISVIHHINRVKT YMIISIDAEKAFDKIQHLFMIKT LSKIGIQGTYLHVIVYDKPTA NIILNGKKVEAFPLRTGTROGY PLSQLFFNIALEVLARAIQ/EEI KGIQISKEKVKLSLFGADMIFYL ENPKDSSKKLLELIKELSKVSRY KINVHKPVALLYTNSDLVENQI KNSTPFTVAAKIKYLEIYLINY MKDLYKENYKTLKKIIDNTN KWKHILCLWIGRINLV/KMTILQ KAINKLNTIPIKILP*FTELEKPI LKCIQNEKRAHIAKARL/SQKN KSGGIRLPDFKLYYKP
3734	34102	A	3774	1	639	MGRNQSKKAENSKNQNAFSP KENDSSTAREQNWMEFMDL TELDFFRSVITNFSKLKEHVLTH HKAENLEKRLDKWLTRINSV EKTLYLMEKTTLFMVDNG/C R*LENSHDL*AYFLHLLGNTGL *CCVRGQIGDGKEKREQDRSRS MG/EILRAQLEPFAFHQRSVQC GDIRDLMWGYFLLNLMKKLTF Q*FP*QDT*QLKELKKIAT
3735	34103	A	3775	3	1079	APGPRGAGAQKACGASAGGDP ECAAY*GGAQCECGPTVGPGE VPRAV*VWVHGGPWAGGYPV Q*CDAGGREGSFAGAAAAPGG AAGEPAGPCPGAAAAEPAGAG AQQPPAGREVCAAGDSGPGAAP EAGGAGGGGAGGTAVPGGDPR AAAGPASGPQGPGTAAAAAGG RARGTAGAAPRPQGQHAGTGA GPPGAAGPARAAAGPAGQRGG TGGGPAGRA*TPDARWASAAG PGGGA AEASERARQGS DAAGR VVSGAG*AAG*TRGATGPAGA AGAGAGTAGDAEPAAARVQPA AGPERLPADHAV* AIDTAAKCP GRGEPAAG*SSGPEPGEQGAP GAQPGESGPPAPRTAGVPGPA
3736	34104	B	3776	45	149	

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3737	34105	A	3777	3	442	EGKDERND\GKDEGKDEKKNE RNDGKDERNDEGKDEGKDERK DERNDEGKDEGNDEGKDD*KD EGKDEGKDEGKDDGKDERKDE GKDEGKDERKDEGKDEGNDEG KDERKDERKDEGKDEGKDEGK DERKDEGKDEGKDEGKD\EGK DEGKDEGKDEGKDERKDEGKD EGKDEGKDEGKDEGKDEGKDE RKDEGKDEGKDEGKDEGKDER KDEGKDEGNDEGKDERKDERK DEGKDEGKDEGKDERKDEGKD EGKDEGKDAGKG
3738	34106	A	3778	459	660	VRGHEWAQKKYHKFSLWSD ST*N*QPSPHASGCHWLEPPA FCHASPAASGIFAAAAADRPLLP SV
3739	34107	A	3779	2	440	RPLSLINIHANFLSKILANSIKQC LNRIIHHHDGVRIFEM*E*FNHR SINVTTYINRMKNKNMIIIDAEK AFDNIQHPFIILIKLGIEGT*LN TIKALLMAAAACLNSCKDKAR SSRGMAEGCRLSASSELWAP MSMGGGLR
3740	34108	A	3780	1	1145	RHPGWPTPAACPTTLRLWKAP VWTPGP/QKMEKEPAARGTPTG GKERLKAGASGFAGGMGPRSV PARKKAQTAPPLQPP/RAAPGPE RGAALGRPVAQQVPGARLAGG AAGLGFAVPRVLPFPFPCALSG DRSARERPPGALLRPLPC*GPPT VPVVGKNDQLKERADSGDPDV AADA VPGEAALQARVP/GALGP AKLSPEGAIVAPA*VRGPGRLH QPGLRPGPRQRSDPRFPGSREPA /GERGRGARRGHRGRPGGPCD PRRPGTQGEASERGEAAEGEAA EGGET*ER/GRGRKRRGHGPPG SPGKPYPSAGSHAKGATGRGH GTPGTSPGRSRPGCPRGVPTRS SGLGVARSSAQARGTEPAPRR SPGAPSGRPATLAK
3741	34109	A	3781	218	376	TRNKILYRQANAERFCHHQACP KG/RS*RKH*TWGTTGTSHCK NMPNCKDHQG
3742	34110	A	3782	2	187	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL*RILFLLHL* SLVWLDMDKWCWVENSFL

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3743	34111	A	3783	1	220	IALMVSTIWHVFAVAGTGCFPP CLVLPAGALVRQA**W*QNLSAF ACL*RILFLLHL*SLVWLDMMKF WVENSFL
3744	34112	A	3784	713	997	KFFSLRMLNIGPHSL/CLQSFC QRSASVSLMGFPLWEPDLSLW LPLTFFPSFQLW*I*QLGFL*LLF LRSIFVAFSVPEFECWPALLD WGSSPG
3745	34113	B	3785	1	1698	
3746	34114	A	3786	948	1121	
3747	34115	A	3787	1211	2437	LTKRWPGTNTSPESG*SRRAAC AGL/LIPFTSRSSPTWTRPLLS/ ACASSHDPGHNSP*VLVPPDG GTQGFVLHQADDLHRFLIKILI DIVRQRRENGVKILLGNRVMY HEHSPQVRGGQLEQLPLITVH GGGLQLLHHVLSHGSAVQNW GWTLPFIHAKLLMNLH
3748	34116	A	3788	1	1908	
3749	34117	A	3789	1	1788	MTGVSRSGLPISMAENRRPLP VSAGSKVPVILQSPQLQINTTH YFLKSLLTPTSSFAHVISSAEDL VQRRNVIGDVYSQGPASPFEIN NGLGSPKYTAWRKQEMGPW QWLWQQDFHLFLGAPLQRYAE PLPVGTISPGWGS CVVDSSES LPNDKHLRAAKEVPLQLQWQR SFQLPLGASPORNTIRLLTGMS WVWLNHHPGTLLGEKLGSGWS KGRITTAGAIAERLLVSSSEIPG NPEQLPRNAELPLTEVFRCG*IFI QGPCLVKS WGPAAAEPLQE P*RRGCWFLRA/AIPGNPEQLP RNAELPLTEVFRCGQCSYAAGT PQKAPCPVRSSRARDPCRKPSD CLLGTDEQKDSNLCRLKCPCL TALKRAVFLPARSWRSENGQT ASSSGSLSPQPKWEAPPSSRGL TPHTAGSLRSQCDQREEWVSA MEDEMNMKREGKFREKRIKR KEQTLQEIWYVYKRNLCIGV PESDGENGTKLNTLQDIIQENF PNLARQANIQIEIQTPTQRYSS RRATPRHIIIRFTKVEMKEKML RAAREKGWVTHKGKHRLTAD LSAETLQARREWGSIIFILKEK NFQPRISYPAKLSFISEGEIKYFT DKQMLRDFATTRPALKELLKE ALNMERNKRYQLQKHAKM
3750	34118	B	3790	116	885	

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3751	34119	A	3791	593	883	
3752	34120	A	3792	47	716	EAPACL*KALSPLAPTTISSVDC GFRASGTITLLPRTGAAHGAAG *DRGGGAGVLTMTASRACGAG P*SS*RYLRQ*TPNSLEGPTGRS LRSRASPGF/TLRDPVTQPSSPV AAVS/ALGVEPGLAPAL*SQRV* ALPR*TRRKSATAPTATKPN GHNTTKKARPGQGPTEIPALG SPREVDPEVAHPGAFLSQPERR RCVLGSSFPFGYQQRVDPPLPV
3753	34121	A	3793	2	829	GTRAGWRRRRSGRDGPVTPQ PPGAARDGAG*TGSPPRCAGP A/TAAPSGHPPPGDFIALGSKG QANESKASTLLTPAPSGLPSE KRDAALSSASALTGLTKRPI LSSTPPLSALGRLAEAAVAEKR AISPISKEPSVVPVIEVLTPTLLDEI EAA'SWRATMTGSRACGAGP*S S*RSPAPSLTAPST*ASCTWPRS SPTSSPLRASRLC/ASCGGTPP STSRPRGTAWCLCWPTTSSWPP TRRTGTGPRLSRCTSRTPWGS GSGWTALT
3754	34122	A	3794	114	254	
3755	34123	B	3795	1	2052	
3756	34124	A	3796	860	1090	
3757	34125	A	3797	2252	2557	LNPLSMGRRWPGEETVTDPGW KRLCHPLHWVAETVPVQAVGA PWSLQMGGWNWGGRCPOHLA PSKGVM*RLPGQGFRTPSWKE VPEVWGMFRRPACGPRLS
3758	34126	A	3798	444	854	VSHLEAQK*PSWTC*HQQCWA LPMFPHHSEADGLIE*WNLK SQLQCPGGNIL*G*GKVLQES VYAQNRHLIYGTVPISRTHRPL CSQSTQDSCLLVANPSQICLVH PPF*VQHSGLL*ISWDWTGEVG PFL
3759	34127	A	3799	1169	1881	LEHPATVIFCFSWETFDQGF SLPKVSGTCLISLLHAFPVVT SAPCPQEFPHSPHLCFHVPHHS EADGLIE*WNLKLSQLQCPG GNIL*G*GKVLQESVYAQNRHL IYGTVPISRTHIGHQVTHGQPV KTT/LL*SPMSGWGIALVLPPL DLLLSG*SLTLPLAFLLRTHPL TTVQRRAELPFTSWICFLSLFER GKGPGQPLVTWTECQALTLPS PGSHTQGTWRJPH
3760	34128	B	3800	65	1324	

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3761	34129	C	3801	1	1263	
3762	34130	A	3802	1	2845	MAPRSLRMEDIAESLAVVSSEY VGAGVNWMLPPSSKSTCKILT PHVMVLGEQGLAPPTVFLKALP IPLYHTVPPGGLQPRAPLVTGSL DGGNVFPILSPVLQPEGPGPTQ VGKPAAPTLTVNIVGTLPLVLS GLGPTLGSPGKVRNAGKYLC HCGRDCLKPSVLEKHRSHTGE RPFPCATCGIAFKTQSNLYKHR RTQTHLNNRSLSESEGAGGGGL LEEGDKAGEPPRPEGRGESRCQ GMHEGASERPLSP
3763	34131	A	3803	1	279	
3764	34132	A	3804	2	517	KGLAFEVSLADLQNDVAFRK FKLITEDVQGKNCLTNFYGMG LTCDKICSMVEKWSMTAEHV DVKTDDGYFFHLFCVGFKKH NNQILKTSYAQQQS/RQIQKK MMEIMT*EVQTNDLKEVNVKL IPDNIGKDTEK/CPIYPLHDVFI RKVKMLENPGER/MELRGGGS
3765	34133	A	3805	18	602	PAPWRLACNRLTKGGKKGAK KKG\VNPFSSKEWY\DVKAPA MFNIRNIGKTLVTRTQGTIAS DGLKGRVFEVSLADLQNDVAF FRK\FKLITEDVQGKNCLTNFH GMDLTR\DKMCSMVKK\WQTM IEAHVDVKTDDGYLLRFLCVG FTKRRNNQIRKTSYAQQQ\VR QIRKKMMEIMTREV\QTNDLK EVNVKL
3766	34134	A	3806	525	1173	GEPHSQATSGHFASSAGDTQAN RVWSGPPANTNRPAEGHDC* KEN*ETERTSTPKPHLYVTIJD QRKGISD*RSNE*NEARREV*R KKS KKK*TKPPRNMGCEKTK STSDWCT*K*RGWNQVGKHS SGYYPGERPQPRKAGQHSNSG NTENATKILLKNTNSKTHNCQI HQS*NEGKNVKGSRERSGY QREAHQTNR*SLGRNSTSQKRV

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3767	34135	A	3807	111	1329	RNRRRERHKERE GGGTGGTDW *RRGNRRKRTQGRDERRGR DDQNHHTNTTRRETTKTRTT NRTQQKREQKRNETS KRNETH RATEQNRRERTGTRSGRS AKRQ RTEPERERAARRARAKRTASAA RDRGLSSTFQLPTRSGNSVHTS KKPLSRKYE QDPWADS/GSEGV WKPVPRRLEAKVMRESQSSR SCCNSRTSARLI RTMR*ATLSS NKWSFCMPAGRCLTVTSPCCTP CALVTRKMLVTLGL*SRSELT T*GTFVRGKQKISVFSAAWGPG HQAQCSEQPSRGFRHRAQPM *EPCCSRHRPATPLHPRPSRPK SPPTPPPTRQANNNKGHNITHT KPRAPPEPQTTHQHEHTPQPPDS HAQDNNNNKNTPPQPPTKNAER PPRPTAHPPPAHKPLL
3768	34136	A	3808	2	517	
3769	34137	B	3809	1	1008	
3770	34138	A	3810	139	1407	WRGGLDSALRAAVTLQGCAGC DRPGSA*SNNYSI* R*RW*SN YSEK**GNEGNAVILLFHSNGT ASKWTVNRSADISKSLQASW GTEHTWPEGEYS'AGPSQHSSP AVSDSLPSNSLKKSSAELKKILA NGQMNEQDIRYRDTLGHGNGG TVYKAYHVP SGKILAVKVILLD ITLELQKQIMSELELYKCDSSYI IGFYGAFFVENRISICTEFMDGG SLDVYRKMPHEVLGRIAVAVV KGLTYLWSLKILHRDVKPSNM LVNTRGQVKLCDFGVSTQLVN SIAKTYVGTNAYMAPERISGEQ YGIHSDVWSLGISFMELALGRF PYPQIQKNQGSMLPLQLLCIV DEDSVPLVGEFSEPFVHFITQC MRKQPKERPAPEELMGHPFIVQ FNDGNAAVVMWVCRALEER
3771	34139	B	3811	1	1134	
3772	34140	A	3812	374	931	WRGGLDSALRAAVTLQGCAGC DRPGSA*SNNYSI* R*RW*SN YSEK**GNEGNAVILLFHSNGT ASKWTVNRSADISKSLQASW GTEHTWPEGEYS'AGPSQHSSP AVSDSLPSNSLKKSSAELKKILA NGQMNEQDIRYRDTLGHGNGG TVYKAYLCPEWENIICKGHTR YYTGTSEANYV
3773	34141	A	3813	3	444	

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3774	34142	A	3814	75	807	GIAGFVNIHLDSLFLTGVPGVK AERFE*RTAKHCAISLVGEPI MYPEINRFLKLLHQCKISSFLVT NAQFPAEIRNLEPVTQLVYVRVD ASTKDSLKKIDRPLFKDFWQRF LDSVKALAVKYLQRIGSRTPM DTKIYSYCPAVHPAEPIDMKS WPSLFEVPTSLEYCPFYLLQVES ADAEGTQKYRRLTAYYIPVYTE PPLITKEPCLWKQAEFGDLGK HVWLVEQFSSTRVQEHGVGW
3775	34143	A	3815	35	2088	KVMNKRSTQNGTRYMTPPPR SSHTKQHL\PTPPRSSHTKQH PLHDPITTKLTHRT/CTRYTTPSP RSSDTEQHPL\PA\PPSRSSDTEQ HPL\PA\PPSRSSDTEQHPLHDP TTKLTYRTAPATRPHHHEAHTQ NSTRYTTPSRSSDTEQHPLHGP ITTKLTHRTAPATRPHHHEAHT QNSTRYTAPPPRSSDTEQHPLH GPTTTKL RHTTAPATRPHHHEA HTQNSTRYTAPSRSSDTEQHP LHGPTTKLTHRTAPAT/PAPSP RSSHTEQHPL\PA\PPSRSSDTEQ HPLHGPTTKLTHRTAPATRPH HHEAHTQNSTRYTAPPPRSSDT EQHPL\PA\PPPPRSSHTEQHPL\PA PSPPRSSHTEQHPL\PA\PPSRSSHT EQHPLHGPTTKL/STQNSTRYT APSPRSSDTEQHPL\PTPSPPRSSH TEQHPL\PTPSPPRSSHTEQHPLH GPITMKLTHRTAPATRPHHHEA HTQNSTRYTAPSRSSHTEQHP L\PA\PPSPRSSHTEQHPL\PA\PPSR SHTEQHPLHGPTTKLTHRTAP AP/PTPSPPRSSDTEQHPLHGPTT KL RHTTAPATRPHHHEVQEQ KPIK*PPRSPETTRAQPREPAV TLLPSGALGQACPCDATABPHG TTLWPAVPPRWQQLTRELLH PVPRACP*QGQGPFTAGPGRG SHPYDPTGASPKGQSSIL
3776	34144	A	3816	83	184	RLTL\PDRLGSPPDTH*AQHITRA VLPQGFDTDSH

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3777	34145	A	3817	1	811	MAEEDSGNLQPEGEAGTSS HGGAGERVKGVQLQTFKQPD TKQTRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIHHPFKGVR PRRDACLGPSPLAASPAFLGKG QHALKRLKPIITRLLQHGLLKPI NSPYNSPILPVLKPKDKPYKLVQ DLCLINHIVLLPIHPMVPNPYTL LSSIPASTTHYSVLDLKHAFFTIP LHPSSQPLFAFTWTDPDTHQAQ QIT*AVQPQSFTDSPHYLNQAQI SSSSVTYLGIIHENTRALPADH
3778	34146	A	3818	2	324	HFEARRQAGPPKPSPPFR*LP TAGT/RGGGGEKAAGGFRWGR FAG/MGQGPDPGAHGNPASP SLDFWPGPICASQGVTDQSPSTF QGPLGEA*KPTAGAKPGAGAG
3779	34147	B	3819	206	1391	
3780	34148	A	3820	229	792	LGSSAGNSAPDPWRPTSSGVFS FHNTSHSHWILRLRTQERFSEV CVQGTWPTPLWALPPP*FPFPS PAPAAFASCQSLPPHSPQSPRPG AGIS/RPRSQEAPDSSQ/PAPTRP SVSPMANQSGGDDRQPPPPQD TPPRPNAASQSAGHNYASLPAP RGRVGVGIGFGSPACAGGGIW HFHTLSFFAF

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3781	34149	A	3821	3	1676	KDNERRLNTCRSTRSHKRAHTR RSIRAHRGSAAPPAQAQPGW RWASSCPVRQSAAGRGGRSGA ASGR*APRWGCP*CGSRPGKC SPSPAPLASTFPRPGTEPPCRL*R GTCLGSACSGGSGRG*RR*GTG TQRRCPGPSARPRTRRRQISCQG KFS*CPASSTNVCSPTGRGL*K PVPWAPGGRRRRPS*GRSSGDL SSGTWWP*S**ELGIPEYSHST/Q G/LVGVAAMPHRRRAVTGNVHIA GQARKKDS/GRSPAWL*SPL FCAPGGRGASHLLSFP*ESPAP *TARP/PLPARKLTPVVLLRDG LGRGGLGRR*PCSAEKS/GRGRS GWRRARRPSEAGTRGNRTSSS WRAPWRPGLGTGEPGPAPPGF APSSSPRRTPISPLSPASGSGSG LGRRQRAADRARTKPGGD*VG SWAGRRPPGGAEGP*GQRRPRP YAVLLSGWPGGEGGSLQPS VQLLVQGGPVGLTG*VSPRLLT REALKQNGATEAGEHWPSC PSH*/PGAGEHPGAADTLQVAS PA*GHGTAGRQGRAPAAHAPH RGQRAHSTRQ
3782	34150	C	3822	78	371	
3783	34151	C	3823	349	591	
3784	34152	A	3824	822	2114	AGRSVRIQAMTCLHPAHLGYP GSFQAPESSCPGQ*GRMHSQPT P/AGRDMQDEPSFNNIGVAG PGAMSR*YTCPGCKNSNQRTTEP KKMR*TF*SLSSFPWGSQSPH VPSFLWVPPSQLPNT*KLRAGL GTSGLAPGGTQKLRFMASLW QSKKRLCPRWGPSPVGVSV*G VEGVAE*ROGLGTAGSGHQPE RTGHRWPAAASG*SLACSAPSR KGSCFSRPSLRSTETSLPAPGSL SAVGH*GVESA WPAAGRAGNH FGPEVADNLNEMKPPEPVKVP GLGRRQRAADRARTKPGGD*V GSWAGRRPPGGAEGP*GQ/GGP GLTLSTFFQGGQSGEGGGS/PAA ECISGGDSVALQGSCHVHSEQ GCLAELEDPG*EPGVAVPVGW SQERNVAGTGGVSAHGDACR PAPPGHW*PTGRGDEIVEAKTK

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3785	34153	A	3825	3	452	PRHSPGCRCPVAEGQSSGRALP PRLLILAVLLLLLLCGVT/CWLCP VLLPPEAGTGPAATSTAAALR CGSHPYGQ*QPCTQ/P/GPPTAP CSTHWACGCPAFGSWNWTPW/ PPPAYSLYTPPEPTSYDEAVKM AKPREEGPALSQKPSLLGAS
3786	34154	A	3826	16	118	
3787	34155	A	3827	292	1047	SWQELSRQAQPNVQGRDGP RGLSYHYAAEVNELLVEGQHR LEGDKHFTGHSG*QGARGVKA AGRDP*PRGLVKA VGRGAMES RSSSPKGRGNRMPSGYCTEL*A AGNQSGFVEAGLAFTPAISTPT GGPLGTHRSQCCVQGHCP*G* LPRRRAAVLVADYAGPVPASG GSRTG/AQPAVTP/QAEAGPPA G*APLATGCSSGPRAGTGPRGR SCRPRSPAPAAAAGAAGAAG AAAAAAVGRSAAPGP
3788	34156	A	3828	2	462	GPVSI GEPEIGPPGPVSI GEPE*G PPGPVSI GEPEEGPPGPVGI GEPE EGPPGPVSI GEPE*EGP/ GPVSI TE PE*GPPGPVSI GEPEEGPPGPVGI GEPEEGPPGPVGI GEPEEGPPGP VSI GEPEEGPTGPVSI TEPEEGPP GPVGNEMSSR
3789	34157	A	3829	3	374	YRALVFSSSTQ*VSKNFLYSGSS SMLPVLASFLLSFLAIFWNGA NSATAGYSRPQVGEELEVVV CWQRAQLLLQLLGEARRQAA DDHLRGARGRSHRGGAWTRSS KGTA YRAGRPGRPRTK
3790	34158	A	3830	66	619	VRSLFSEMN VVEFQNGFWNMF PVKRPKISCSGRVCSIPEDSQKE AEKKRCQDWKHRR*SRI*EVFR NLARVVEEKTSANPETLLGEME AKTRELIARRTTPLL EYIKNRKL EKQRIREEKREERRRRELEKKR LREEEKRRISVEDRWLYTIRINR RKSQRKK*GLRSHSGS DKEHRD VERSQEQ
3791	34159	A	3831	253	482	QVSTCYHSQKEKKRISSTSKSL NKEKRRNEQ/KDQ*ALLSSPPSP PAESQGW HWSLPPISRF LKTS YILDL DIKK
3792	34160	A	3832	156	443	
3793	34161	B	3833	426	513	
3794	34162	B	3834	47	1311	

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3795	34163	A	3835	1503	1652	NCGNNG*LTNQKSRSRWIHS QILPDVQGGAGTIPSETIPINRKR GNPP
3796	34164	A	3836	1	1986	
3797	34165	A	3837	1	1116	
3798	34166	A	3838	1	546	ERSSSPAAEQSWMENDFDELRE EGFRRSNFSELKEEVRTGKEV KNLEKRLDKWLTRITNTQKSLK DLMELKTTARELHDECTSLTNQ FDQLEERLISNFSK VSGYKIN/G KNHKHSYTPITDKQRAKS*VNS HSQLLQRE/YKYLGIQ/AYNGCE GPLQGLQTTAQGNKRIQTNG RTFHAHG
3799	34167	A	3839	1	987	
3800	34168	B	3840	1	1593	
3801	34169	C	3841	1	1479	
3802	34170	A	3842	129	368	
3803	34171	B	3843	1	1884	
3804	34172	B	3844	1	471	
3805	34173	B	3845	1	675	
3806	34174	A	3846	1	410	
3807	34175	A	3847	250	880	GEVTKPQFAQFFHGSASLTIRP GKMESQKVISCLQACKEGLDIN SLES LGQGK YHFNPSQSILVME GDDIGNINRALQKVFIYINSRQFP TAGVRRLLKVSSKVQCFGEDVCI SIPEVDAVYVMVLQAIEPRIITLRG TDHFWRPAAQFESARGVTLFPD IKIVSTFAKTEAPGA*KPQVQN SEFSL*AFENPVSCQISNSGHVP NQFRV
3808	34176	A	3848	890	4889	
3809	34177	A	3849	1	799	MYAQPPNCKREKASGDVSLYW WKLAKGCLQMEVSEGAPNSAS TPTGNTVSQLNRPLP/QPPYPR RFSWVCSSLQA*VAESATKTS AFRAPNSFCRLQPRPCCRASPAS PATSCTCPGLSALWARPAPASH WARPHRPPPCPTSPRP/PRGRDA PER*AHGPPVPDAR*GALAPQA TGGGQPPGAQPHHARAGPGQP RTPLQ*GLCARPGEPQLRVTPH GPQAGG/HTQRLPPMGKPGVSG GVCPHSDFPQPMPTVEMTGPRS GVQRPT*DTGWLPDAESLV SFEFSSPT*VL*QQWK*RSQVQR PT
3810	34178	A	3850	212	361	

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3811	34179	A	3851	3	909	GGRQRGKDTGHMAKQEQERE VGGATHL*TTFRFSCSK\SALIP VIPITKSTGSRFRNSVEGLNQEIE IIIKETGEKEEQILIPQDIPDGHRA PPPLVQRSSSTRSIDTQTTPGGAD RGSNNSSRSQSVSPTSF.LTISNE GSEEPSCSADDLLVDPRDKENG NNSPLPKYATSPKPNNSYMFKR EPPEGCERVKVFEECSPKQLHEI PAFYCPDKNKVNFIPKSGSAFC LVSILKPLLPTPDLTLKKGSGHSL TVTGTMTTLLQPIAVASLSTN TSKTESLEEQVQSCHQLLYSHH QNQLRKIKD
3812	34180	A	3852	189	454	LWKRFNSWTSLRHPYQPYQAE QIAPQTCGSQSDGGLPSSSGPAP LHHAGLGYGTGSPGARRRVE GQDP*VLEQAAGPTPPRYLVLP
3813	34181	A	3853	17	561	IPGSWRQKMPVPPAA\PAHAQG RPGALQSPGSSTPAQPGSRWEV GGPAAPWGSRLHP*QPYQAEQI APQTCGLQSDGGLPSSSGPAPL HHGGLGYGTGGSPPGA/LEEGGR PRSLGPGAGSRAHAAEVSPFSG PPSRGLTGSGFCACSEERAGFP ELMVIKNTVTPTREATLILTKA PAILP
3814	34182	A	3854	1	540	FFQPIFWGKDPQSGTPPPHP/RPG PAPSGPEPSISMVTRRWLRAPN CSDRRGEGPRTEADRHGSCCRF RSRAGTAVHSCRRRHPRAAGLP SSLCAEAGPRET**LEGGCREG AEPRP*RPGSGAHAHTDPERAH RSGARTQ/HPERAHRSGARTQIR SAHTDPERAHRSGARHRSGAR RTLPL

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3815	34183	A	3855	1326	2409	GRPPGVPPATAPRAAPGADGDE AGTPAPGDHPEPVCRIPG*WG T*GWGASQHWGGH/PALALAG RRP*SRGLAGASGRSSEEPGVAT QRLWESMERSDEENLKEECST ESTQQEVLALEEERAQVLGHVE QLKVRVKELEQQ/LQESAREAE MERALLQGEREAERALLQKEQ KAVDQLQEKLVLETGIQKER DKDLQRCCGMMGDRAKASP SWTSTVILKFPLIKNCLNPKDIS LMAKELWSLRTMDALNRNQIG PGCQTQTMVQKGPLDIETGK GLKVQTDKPHLVSLGSGRLSTA ITLLPLEEDCLPSLVDDLVPRLG LKISLETRRRGQLMLCTPKFEN QWPTTDKMPETSTGSH
3816	34184	A	3856	240	639	DHGRSQ*EPNRPWMPDPDHGA ERTLGPDRDRQRAE/MQTDKPH LVSLGSGRLSTAITLLPLEEGRT VIGSAARDISLQGPGLAPEHCYI ENLRGTLLTYPCGNACTIDGLP VRQPTRLTQGLSMSLPSLIQET
3817	34185	A	3857	1	1758	MALLPTVLCLWAQAVGVQR HNHIFWNEKEHGHGKSGSCHN GASCSAEDGACHCTPGWTGLF CTQRKPHLLASQPLRIPCCGLL ATVGIVQTSREGGMQAAPGLV VPDSCPTRTEELCRGSSRPDWIQ GIDKPKVLQGCPAAFGKDCGR VCQCQNGASCDHISGKCTCRTG FTGQHCEQRCAPGTFGYGCQQ LCECMNNSTCDHVTGTCYCSP GFKGIRCDQGIMLLFLIV/CAA GPICLASAAAEREGPRPGSPCLL HTCHE/R*PAPITPSQDLTDHYL RFSMPIMVLT/CLQGAFFGSPGR VPG*TWAPLCGMNVNRPQT/HE LGCDSDHWGPHCSNRCQCQNG ALCNPTGACVCAAGFRGWRC EELCAPGTHGKGCQLPCQCRH GASCDPRAGECLCAPGYTGYY CHPVTGACTCQPGWSGHHNE SCPVGYYGDCQLPCTCQNGA DCHSITGGCTCAPGMGEVCA VSCAAGTYGPNCCSICSNNGG TCSPIDGSCCTCKEGNVPSLSPS LTYEHIPQVVLPAGESQDGTFG LNCSEHDCSHADGCDPVTGH CCCLAGWTDIQEGFLEKEGPKR
3818	34186	A	3858	2	2414	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
3819	34187	A	3859	1	852	DEEEVVAREEEEEEEEEEMVPE ESMASAGPEDFEQDGEEAALA RGAPAVDSLGMEEVDIETEPV AHEKRPSMLDEPLPVGVVEPA DSREPPEEPLSQEGAMLLSPEP PAKGLAHPNGSQKVIFRVPLRV IHGPKAVELQVFPGLHKQPTNQ PK/TEPCDPHSWFKSCYHLLFIP VGISRPP/HNPITATIFASTASV LW/PVLDTCMSSNSGYFKA VLE SYSSKVLVSTQYGNPRATGSAG LRGRPGSPVSGSGSRGPAWP*PQ AAPRCPPSSGRPGTSSQSPS
3820	34188	A	3860	3	1997	AQGSVVPGLFWAFLQLEVNCL LESPIQKGFFHRLERISVVEPQE RKRLSFRKSEI*P*K*SLVKKL*E RLKTRKQMQLANRLRRYGSV VES*FPNLKVSSTVSTPTTYIP MTHKAIFSSYFLWDGRSAFLT YKMMSSHPQEEEEEEEEEGGE GEERKRRKKEERKRRKRRR RMK*RRRRTRKRRKRRKMK*R RRRRRRNRMRKKEGKNMKK KM/REEIKRQNALYEIEMRKKL EKKREEMHESRRFLAPLFSSP TANCSTSLVPRLRLASLPAALPS NRVVRVTPPAGVRGAWRHS FSRSRSDTSSSEMLVRFGRRC GRAKESTGRDWNLSKSSEEDR KMWESLELPRDLLNAFDQNAD SDMDNKMQAEMVSDGDEELS GNWSKGDSYVLAKRLASFYL CPRDLWNFEKDDLGYLAEIISK QQSIQEAQRSSKKWFYGP GPG SLCCVQPIDLVPCVPAAPAMAE RGQCRAHAVASEGGSPKPWL PHGVEPVGAQKSRIEVEWPPPR FOKMYGNAWMSRQKFAAEAG PHGEPLLGQCRRELWGRSSHVE SLMGHYLVLLSIGAMGKIVQR PRCFFDIAINNQPGEKGTGKSTQ KPLHYKSCFLHRVVKDFMVQG GDFSEGNRGGESIYGGFFEGP AMGPNATNNFTKLAG

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3821	34189	A	3861	86	1120	LVLKSGKEHLLGIKEHEEEEEER RKKYE*KDAEEIKRQNALYEIE MRIKLEKKREEMHESRRRLFLEH MQDKHIIKAVEQQQRQRKKM KR*ENSSKQKKRLIQMGKEKEA ETHRLMEKRRERIHNFSELK EKLDNEDMIIARDIAEAEAEWE KREREKDEKNQAEKKTIAEYRA IVMKNKEEEERQRKIEAKEQLL AVMKADQIFWEHEKEKKCKA DKEHQEVQDAHIQQMAKNKFN AKQAKQAEALDYCRLEALVAE KEKEFQDYAREVIELESETPNK YIYPLVKAVQEGPGGGRGPVVF DRGGLRPSYQANDVTGVQLPF YNSQGPKNYFQKSKRRLGFTW
3822	34190	A	3862	591	2805	WVHPAGS*GEKPT*ISAPPWP EAPTELWLTTPPEAVQEAAR VGQEVPAAP/RGPLPSSATGAK SLGQGSPTPSTRMSLSQSCAGP QHP*TLRRGPLWGTSRWKMVL T*ASRTSSTPGLT/QGPRVTVLL GKAGMGKTTLAHRLCQKWAE GHLNCFQALFLFEFRQLNLITRF LTPSELLFDLYLSPESDHDVTFQ YLEKNADQVLLIFDGLDEALQP MGPDGPGPVLTLFSLCNGTLL PGCRVMATSRPGKLPACLPAEA AMVHMLGFDGPRVEEYVNHFF SAQPSREGALVELQTNGLRLSL CAVPALCQVACLCLHLLLPDH APGQSVALLPNM/YSALEYADG ARPPQPPWALAHLY/LYWTWGR WP*GAWRQGRSSMQKILLHP* *LLGLTAC*LPSASAQALGTS/ ETGYAFTHLSLQEFALALHLMA SPKVNKDTLTQYVTLHSRWVQ RTKARLGLSDHLPFTLAGLASC TCRPFLSHLAQGNEDCVGAKQ AAVVQVLKKLATRKLTGPKVV ELCHCVDETQEPELASLTAQSL PYQLPFHNFPLTCTDLATLTNLL EHREAPIHLDFDGCPLPHCEPA LVGCGQIENLFSKSRKCGDAFA EALSRLPTMGRQLMGLAGS KITARGISHLVKALPLCPQLKEV SFRDNQLSDQVVLNIVEVLPFL PRLRLEQGRSGAPGVGDSTPD
3823	34191	A	3863	1	2784	

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3824	34192	A	3864	727	1715	YLSKGLKEVREGSLQIPGEIIPG RKKLQMQLSEKTL*SQHHY*K GFLQRQIHQKMAHLEVRQNRK DCMFLQIMPAATS*/TEIQATIR DYKHLNANELENEPEEMDKFL DTYTLQRLNQEEVESLNRPIGT SEVEAIINSLPTKKSPPDGLTA EFYQRYKEEL/PKPCRDTTKKVE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQ WFNICKSINVQIHNRTKDKNH VIFSIDA EKAFDKIQPFMLKTL NKL/GIKYPGIQLTRDVKDLFKE NYKPLLSKIKEDTKKWKTLCS WVGRINIVKMAILPKAPLPLPP
3825	34193	B	3865	1	1908	
3826	34194	B	3866	609	1658	
3827	34195	B	3867	61	234	
3828	34196	A	3868	1	978	LFTDDLCPVEATSGQAMVQS RGATTHGGGRGGSCKLLGDRG QGSTSQVGRWGSSCHPPTGG/P ARSPCWPTARKPLRGVLQGASL GSTASMLGAASGTTPPPSWLV SVSPRAPCWGVPGAGEQGGP ETQPPGAREYPQAGREGRPQI LRFKSSSSQCLVEFCSLASSCF ALEAMKTRRSPSS/SGSSGSDG/ SQRTTRSGPAQRPRVSGSSEQ\A DGMRGSSSGMGRRVPKREP RTEAASSSTA*RQPPPPPSPLPH ARRHFRFRPCCGPARDAAPSRA QTEAPPPLRTQSALS WP LCSRT DGKLSRGQSRDGRAPTGV L

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3829	34197	A	3869	1	1919	TPVSDDEEGSLHHTTWRNLRIG VRIACPAGENAQSSESPVRACQ PGTKTQYGLNQAWSPGVRRDL IQGSAERPARYPAPGEMGVGAF IPLGHDKRRAASQHLHVSREG PEALGSRGSA LRKQVPAWLPHS LRTCVPDRNPQAPCARTGLMV ETPHHEQWVRGEHYRYKFSRP GGRHAAEGKWWVRKRIGAYFP PLSLEELRPYFRDPHTLMGQR VTERELDGEPRGPVTVEGRSAT TSGYPTKVTKIGGPLDPAGGLE GPLHGALGSDPLEVSDCPGPHL SRKVWENGSGFASDQQHTR/YT TDGSSWPTVAEKKAPSSKQYH SSMET*R*TGHSNHPRNRPCTG QVPPNENNRNRPHTARYLPT /ENNPRNHSTHATRYLLTTTTE IIPHAARYRPTRTTRYLPTRTTR YLPTKMTREIVPHAATYLPMT TREIIPHTATY/ASNENNQYLP RTTSQVPSNEDNPGCLPTRTTR HLPTRTTRYLPTRMTQEI VPHV AWYLP TKALRPFN GKRTAFSA NAAKRSEAPTLR*ALRT*CPVN PPDTEGTGPAMPSLECEQGNP QRRWAGRRRSSGAQDAGQGTR FTPSLWRAWGW SRLRP LPSAP GCWLTRKCRTEPPVVPQALMM AAVTDMQTLIH
3830	34198	A	3870	295	457	
3831	34199	A	3871	296	1057	GNEVKMPARETTPHVP TGAQ PSEAGEKGHHPPDRRMVDPLTL ALCTWKSCRHSPDCKAAGRE AVPCKVTGAERPRPRAPTSAP SGKLEGLSLWCTQSCSMLHR AGVISVFFTMEDVAPTRGLLH* RAAIGHSPTISVTKTSNNCRWC RVGGCAN*LRGALEAGG/WLQ NQKGRDAFNKRLRGMDKPG AGGTCGSGRRNRPLDRS/VPE VKGGTGTG*KTGSGGLKRYV GDGTTASFESLRVLKWPPL

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3832	34200	A	3872	3	913	GGADSGERLGPALGLGAGSG GGRGRYGPSRSRPSGRAADPGG VRPFVPAPRGARARRGRVVP AF*RPAGAA*AAQHVVVSEP AAAARGGGPGGQGSRAWRG VRLPGGAGGLAGPPGRVPVL GPPGSGPAAQRPPGRGQAGQ EPPPA GD AAAA/ PSSGSASCR/G PGAA/GPRALCPGPAPPARRGPR AGLGRPAADRGAPAAAAPVRAE PHGLGGAAGARPPHRLRGAG H/SGALVLLTLWTGGGDGD RASPGSPGLAT/GAGLVGNKA APS*RAARAPGGLGCRWARFSL TSQCPCPQL
3833	34201	A	3873	2	484	TPWRRKSTE*PTLGVRPPVPRN AMPHHCSFFTGRTPVSMATPG YNEGWDKFRMKCHLCVNYIE MQTDPANCDYVIVSGAQRKEE RWDMDADNEQVLTTHEKKQK LETDA MFRLEHGEADRSTLKK ALAHTDHIQEAQSAWKDDFAL NSMLRRRRFRVPSKP
3834	34202	A	3874	3	531	GRKRSKRMEKGERGEPYSLSLR NHQGSWEPEHMS*KPEGGVLA FKGDDGFSVWESNAIATYVSNE ELWGSAPAAAAQAVQWVNFA DDSQYQGVPTLGMHHDQQA TQDAGEEV/QPQFQAVLG/EMK LCENMAHFDAKIFAESQPKKDT PRKEKGSREEKQKQPAERKEEK KVATPAP

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3835	34203	A	3875	2	1326	TMAAGTLYTYPENWRAFKALI AAQYSGAQVRVLSAPPHFHFG QTNRTPEFLRKFPAGKVPAFEG DDGFCVFESNAIAYYSNEELR GSTPEAAAQVVQWVSFADSDI VPPASTWVFPITLGHMHINKQA TENAKEEVRRILGLDAYLKTR TFLVGERVTLADITVCTLLWL YKQVLEPSFRQAFPNITRWFL TCINQPQFRAWLGEVKLCEKM AQFDACKFAETQPKKGTPRKE KGSREEKQKQAEKKEEKIAA APAPEEEMDECEQALAAEPKA KDPFAHLPKSTFVLDEFKRRKYS NEDTSLVALPYFWEHFDKDG WSLWYSEYRFPPEELTQPFMSC NLITGMLQRLDKLRKNAFASVI LFGTNNSSSISGVVFRGQELA FPLSPDWQVDYESYTWKLDLP GREETQTLVREYFSWEGAFQH VGKAFNHGKIFK
3836	34204	C	3876	58	222	
3837	34205	A	3877	6	153	
3838	34206	A	3878	2	889	CPPWELILDQFRKSLGISPANTG PLCPAPPSCMYPPSPQMPAKAP/ PDHPPEGRPGTTPPEFPRVTCVT E/PVGKGLSRDSQ*ETRGLQE* SLAAPKSAPCFTHSAICPGAPSM SRHPERSVFLLFQAPVQEPAPAG PP*WVLRPEPDFGTGVFPEPSW* KAADFEPLGLCPGRSLSAQCPS WWPPTSSDPG*ALLKSGTGTPT VAPRQPAAPARFORPPQPRGL ASTCPAGPQKQKSDPPGRSAGS EGSVSGKSLKPCLSPLIPPPQS STQKKASVAKFVEFSPYTKQKS QLSVP
3839	34207	A	3879	1	391	MAKAVEKPESTLEATKSKESV MSRVEWIGTAHMMWVDETDG NASKTQQTLEPAELATKYANFS EGACKPGYASALMTAIFPRFC KPIRLSP*PRHLAHWCKKWAPK ILGSSAPVALQGAAPVAALMG WR
3840	34208	A	3880	1	346	
3841	34209	A	3881	249	474	VYLLIVLAVLYTNNRQTESQIM SELPTFIASKRIKYLGIQLTRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
3842	34210	A	3882	25	302	
3843	34211	A	3883	1	2235	

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3844	34212	A	3884	1	2724	MGGMVESRRHNWSGLDKQSDI QNLNEERILALQLCGWIKKGT VDVGPFLNSLVQEGEWERAAA VALFNLDIRRAIQILNEGASSEK GDLNLSNVVAMALSGYTDEKNS LWREMCSTLRLQLNNPYLCVM FAFLTSETGSYDGVLYENKVAV RDRVAFACKFLSDTLNRYIEK LTNEMKEAGNLEGILLTGLTKD GVDLMESYVDRTGDVQTASYC MLQGSPLDVLKDERVQYWIEN YRNLLDAWRFWHKRAEFDIHR SKLDPSSKPLAQVVFVSCNFCGK SISYSCSAVPHQGRGFSQYGV GSPTKSKVTSKPGCRKPLRCA LCLINMGTPVSSCPDRSTRQKV NKDIQELNSALHQADLIDIRTL HPKSTAYTFFSAPHHTFSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRIKTFTPNRSTTWKLN NVLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDTFKAVF RGKFIALNAHEKIQTIREYHK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIITGSEIAI LNSLPTKKSPGPDGFTAELYQR YKEELVPFLKLFQSEIEGILP NSFYEASILIPKTGRDITTKEN FRPISLMNIDAKILNKILANQIQ QHKKLIHHDQVGFIPMQGW NIRKKSINVIQHINRTKDKNHMII SIDAEKAFDKIQPFMLKTLNK
3845	34213	B	3885	1	1971	
3846	34214	A	3886	1	1146	METRPSRGPLTPHTARCQSETK LPEEGSGSNICCSAIFAILQPLV IPRQTGSGVDLQQTPTDLELRD LTVRRKTNKWKGIASSTKRTS TPKRHLSWFFEKINKIDRPLAKL IKKKREKNQIDITKNDKGDITTN PTEIOTTIREYYKHLANKLEN LEEMDKFLDTYTLRLNQEEVE SLNIPITVSEIEAIKSLPTKKSPG PDGFTAIFYQASILNGQKLEE FPLKTGTROGCPLSPLLFNTVLE LLTRTIRQEKETKGI/QLGKEEV KLSLFADDIMIVYLENPISALN LLKLSNFSKISGYKINVOQSHA FLETNNRQTESQIVSELPFTITTK RIKYLGIQLTRDLKDLFKENYK PLLNEIKEDTNKWKNLCS

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3847	34215	A	3887	66	1392	QVLLSFGTPLVLTTKREKNQID AIKNDKGDITDPTIEIQTISIEYY KHL YANKLENLEEMDKLLSDTY TLPRLNQEGVESLNRPTGSEIE AIINSLRPISLMNIHAKILNKILG N*IQQHKKLHHDDQVGFIPGMQ GWFNIRKSNVIEHINRTKDKN HMIILDAEKAFAFDKIQQPFMLKT LNKLGDIGTYLKIIRAIYGKPTV NIILNRQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAKAIRQEKEI KGIQLGKEEVKLSLFADDIMIVY LENPIISAQNLKLTGNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPTTIASKRIKYLGIQLTRD VKDLVKENYKPLLKEIKEDTNK WKNIPCSWVGRINILKMAILPK VIYRFNAIPKLPMTTFTELEKTT LKFIWNQKRACIAKSILSQKNK AGGITLPDFK
3848	34216	B	3888	1	2868	
3849	34217	A	3889	1	1218	
3850	34218	A	3890	1	1893	MKEIETQKTLOKINESRSWFFE KINKVDRPLARLIKKKREKNQI DAIKNDKRDVSTDPAVIQTITIRE YYKHL YANKLENLEEMDKFLD TYTLPRLNKEEVESLNRPTGSE IEAIIINSLPIKKSPPGPDGFTADFY QRYKQELVPFLKLFQSIEKEGI LPGSVYEASIIIPKPGRDTTKK ENFRPISLTNIDAKILNKILANRI QQHIKKLIPHDQVGFIPRMQS/W LEVLAIRQEKEIKG/IQLGKE EVKLSLFADDIMIIYLENPIISAQ NLLKLISNFSKVSGYKINVQKS QAFLYINNROKESQIMSELPTTI ASKRIKYLGIQLTRHVKEHFKE NYKPLVNNKIKEDTNKWKNNMPC SWVGRINIVKMTILPKIERIGKT KGTETQRGKSCKPTHPVSVISL AESIARDFCLQLNRARSCDQSS YNEVLEADNRAFSLCKGMPPFD RLSPISQTPGPSWYQSSPYQPMF LAAPIDIGSRPASMDPIHSRTWH YVTVVILARSRKHQELILSESKQ FEEAPPELRSRAPGGFSKPAAG QIKVGLRENLTASMQISPADAN LILQDSFLAIFLQALIVTIYKEN EKEEGQERREALRSTGKNNV WKNTDIDRPESISDSSESAGCDY

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3851	34219	A	3891	2	1562	WGEIRAEKLIKPKTGAPFLQRI AAPRQQRNKTGQRMSLTS*QK *ASEGR**QT/LSKLKEHVLTHC KEVKNLEKRALAKLIKKKREK NQIDAIAKNDKRDITTDPTIEIQT REYKHLHYANKLETLEEMDKF LDYTLRLNQEEVESLNRPTIG SEIEIINSLPTKKSPGPDGFTAE FYQRYKEEL/PDKQLQQSLRIQ NQCAKITSIPHIQ*QTNREPHE *TPIPNYYKENEIPRNPYKGC GPLQGLQTTAQR/KRGHKQM EEHSMMLMDRKKQYCENGHTA QGSTDGFEVQRLRLWQEDDVA EEVSGFEEFNLSVAQDPFWE SRQVKTFNCVDYIAGAKAIA GITQVCTGNGQFAEINQRLKL KKSWSLYRRFPQWQEECGPSW NPSWTHPSVASSRKDAAAQRE AQEGDLQGQEGAEASHAGGPA ADHYSGTAAHAGRGALDRGVC VRGHAPPITELSRPAGCGPHR QGEAAREGDANKNGFHIQRC SCCLSCKQEHVPLVFLGLD
3852	34220	A	3892	2428	6109	YPESTMNSNKFTRKSSNNPIKK CQASQLKALPTQSCSPSSNSY ETFLVSPLHPFQFYISFPHYTEM VPPLTPEDYNSRDFGDDTETN HIIKFKHRSLEQVQNAASRRSQ DGRIGTAPVYSSQRRRRRRVIS AFPSSEERSSSPAMEQSWMENDF EELREEGFRSSNSYSELREDIQT GKEVENFEQNLIEECITRINTTEK CLKELMELKTKARELREECRSL RSRCDQLEERISVMEDEMNM KREGKFREKR
3853	34221	C	3893	13	391	
3854	34222	A	3894	117	704	WLSAWPRACPCDRCVRFPHTSP CLPCGPEAEPGPGPALREL VQP LPGQLQPPFGMPLPLVPAGSFLI CTVWERPRPGLAVGSPPCFPSL H/PTVPVGCPPSPCLRPFA*PT THLHIWPSLLFGPLPALPPPLAA SASAGLRKPWLDGLHPSVEPSG LGAAPSAPPACAWTRPPHLHP SSFSSCVQISSLFLCF

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3855	34223	A	3895	1	1185	SAASSVLVYHNEPQVHGAHQK IHPIHPSLHYCLAHIIISQDLHTS MNALGLFGVG*EQGLQEKS SSTHHEPGHGGQDAAGARDGA RGRGGS/IGSAAGERGGRTVPH WA/GQPAEAGGAG*PRGPQLRR SPPP/RLPPRAGSSANTRNSVLL* FF*AVCLWADHYPL*TLISSS*M AGRWRSVPGIPTSPK/PPPPPP PPPPPPPPPGSFLSEP/VSTA* NSTCPRRCRSASGGPIWCPCRP /PAPPPAPPPPLEATEESLEEG IGGRASRSANMFAPAPAGSSW HRARWG*PAWKAGAAAGTRGA KCGQFVPSASSAP*LAGGWPGA GGQRGARRAQKAWCCRPGTSL /APGPELFPESALVQAGSAPPP PPPPPPPLCLLLRAESEGA VLM
3856	34224	A	3896	192	477	
3857	34225	A	3897	2	1782	RAAARKEHQGSAT/RAERA/PR TPKAS/GRGSPVPTSGTVTART GTAPRGLSAEDGRRRGRPIGIP FTDHSSDILSGLNEQRTQGLLC DVVILVEGREFP/THRSVLAACS QYFKKLFTSGAVVDQQNVEI DFVSAEALTALMDFAYTATLT VSTANVGDILSAARLLEIPAVSH VCADLLDRQILAADAGADAGQ LDLVDQIDQRNLLRAKEYLEF/ YYQSNPMNSLPAAAAAASF PWSAFGASDDDDATKEAVAA A/VAAVAAGDCNGLDFYGGP PAE/RPPTGDG/DEGDSNPGLWP ERDEDAPTGGLFPPPVAPPAAT QNGHYGRGEEEEASLSEAAP EPGDSPGFLSGAAEGEDGDPD VDGLAASTLLQ/MDVIGGPGG GRGGGQRRGVAGRRQGRHGL LPEVLQRRPRRRRLPGLVAEGG EEDPSQGLPEVPHLREGHPGRR QAAATHPHPHGREALRVQHLQ GPLHQDTSTSTLQKPGSPRPL*V TAGR*AGQAEGAHAEAHGRE VPVPAVRRRLCPQLRPEEPHAR AHGPAPLPVRQLQDLRLPLRPP AQTPQERRLQRRPLAPAVPASP CVLWAGGCPDPQFW
3858	34226	C	3898	162	356	

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3859	34227	A	3899	3	2289	GELHGVAEQAEGDPREGSPGP AEQASGTELEVPGPWPLHPP EAPVCQHYHRPMVQKGN*GSV WGRGESLVQG/AHGQTSQSV QMTGGGAWTGGTSQRSVQMT GGGGTPRGSRSSSPRTTTPGTA EDTEGEPAGAGEQAAGRPRP LHGHPGAGQEAAGVRELPPA EPAHLHPQALLIQHPISHAR SQHPRRPCCLPGGLRAGGTAE GLPCAFCSDRDERAEGREDDLE GGGEAASGGRQAQAPGQGGH LGPPLTPAAPLPWWLEGHIRE ATGRPRGG*GRPPGRGPTGRRK ASRAQDISSGQNLPRGHPA*VA SPRHEPPAHLQPAARDHCRGA\ PGSQACPADRGANGTPPPLPA RSSPSP*GMSVASPWTASCGPP GPPP*PUGPEALPEGGPALPPKP PPVPAPSEPPQQPPGCCSPQRP PAPGPEGQSRRLGGAHRTAG AAQCPCGGHAGSPGGGTAPAP GPAAGAG*QGGRQCQAKGPAH TRGDAALPTSLRL*GP*E*GD QGSSGVAAGLSGGRHTQAPAGP RAQRTEAAATQDCALDKPLDL SEWGRARGQDTPKPAQGHGSL SPAAAHATASPEPTTQSGPLTRSP QALSNGTGTRVPEQEEASTPM PPDL DGH*GPARKLC*QSPSTN WMRQTQAA\SGPELPGGGIPT STTGEPECICTQEHGQGPGRK
3860	34228	A	3900	3	3169	ASQLVLTLAYQANCVSVS YTD LLGKPGGSYFTFLYVLNIRSR LKKDYDDFRKQPDHDTFNREL WTTDEGEGLGKDSKGEISKS IDSTEPLDILEKDHFDSDMKLS EIDFPMARSKLLKKELPSKDL KTLKTLKRQSKQTDYVDDST KELSPRKKAKLSTNETTVENLE SDVQIDCFSESKHTEPSFPESFA SLDSVPVSTLQKGTKPIQALLA KNIGNKVTLTNQLPPSTGRNAL AVEKPVLSPEAS

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3861	34229	A	3901	33	1227	HHLRGTGQRAGQQQLPPGMKMG GRAGPPGPWCEHTT/PPSRGRPT SSGGPTLAPALAEISPRPQTSP SISSLPMITSLPGGTGPLCLRLPLS WEKPGSATGKVRGSQQEVDVG PSPGHTAPSKSIHQGGPVGSPSA RQGCGPASSALQRRREPGGGPR GHPAGPHGGCVLPWP/GCPCGN TMQRL*GFHTRAMNTQSGAGP RTAPSPRAQGAQGRPSKSCSGA SQGPCPAV/GPH*APGEDRVVRHP LASISGTTTRAHGRPSQQREPRN KSTRADSRSPRTVPPHGGPGPSL PRGR\PAQPGPGV*RNGISVGAG RFPFPTAPCGQARPGAG\NRG AGSGA\PEL*GGLGRDPGSSGCE VPGGRAGG/PPRT*HFLARPAPP SPPQGLPRPPKVGLQA*ASAPS
3862	34230	A	3902	124	1183	DNRAVFSPTGRKDRGGGGPAG TLARV*SAPGAFGV*STRTHVA GVQMPPVPGTCDVCTRPCSPVS RPPRASTAVAAAAS/SGPRQPR HPRHTSPMPPPAALRPPAGPRG LAPGG/HTAPPATAAPVELQHP LLRLQTGPPLGPPTGPA*EPRAH PCIRGLLPAGSGPPPRRQGHPEP PRLHTAACSPQPQRALESSCPP RAFPGTAHHWLLGTGDWLL*P AAQAALASQEWALPGICLNSL SEPTGRVILASQLAPCIRLGCRK RSLAKAPKLISGGAGAHTPTPE PTCFVSVLGTSPPAAGGPRGQ ESVVSVPVTMG/VPAAWAIPLSG CRGEASLDHPAGQLPARGQSR RH

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3863	34231	A	3903	174	1599	VLHAVGNQVQGCPGEVHVCG WRPGCVRLQLHVVGRADGPE CDLCAVWPGGGDV*PAVPGAV PHVTQCEPQGHYPYEGTGAGA YCAALCGPPGARGHCGQEARQ PQVRTCQGGERRRDCQDLL*E AGGQEAQGAERFSAQ*ASRGTP RAAATHPPRTASPGEGQH*VP AHVGGARPGAWQRHPGLHQY HRPQHLEPPAQDEPHQDP*HL PGQRPAPAVEAEPGQQAPS/KP CPPPEPSAQDGVPAENGLPQG DP/GAIAAPRAQAPDSPCGRCTSP GQQ*YWLGPAGPQRGSSPEWD RP*ATQDGRPRPRTTAAACDP G*PREPRGGAPQWAGWGRRR **RLRNPQ*PGQPSGSSGRPG PRRPSVASSVSE/RVLRGERALS PSPEAPLRASGQRANPTTAA ECPPYNPRDLCWTPGWLPMGP ESGKRRCVEEDAGPALHRQ GGTDGET**TGRGNNRPGPYGR
3864	34232	A	3904	331	1120	HKDRFWQLQNDSCFLHSPGER QWLGGPRSDTFGPQVLFGHVGI CSQRA/HPAGPGHRLPEGR*PP HRSQRHPPRSRKPYLA*PPDMC VATDRRTQTTPRDFPPLGR*KPH GTLRSAACPAGRVSPSPRGL PAPPPKSHLC/PGVRGR*QLLP PHPGSPKGERGWTASPGAARG GPGPAPAPRPARASWSQPSVTFF LPLAGLA/GHPGSRTEPAWKAG GAAARPGPELPRDLLQAGSTDT ASGEQLAAGPWTGKEISGRARP RL
3865	34233	A	3905	2	415	YTILTEK*KLSKLS*WVHQDQ LQKREELSMELNK*DQDSEAY PQRTVTGEETWLYQYDPPPLPR SLPPPQTHTAPVGA*S/DWGG*E LPPGLNGDKLAHHSPTPFLSFG LLFVDWL*SQLLSLFLFTQGV/ RIFI

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3866	34234	A	3906	1	4527	MGFCCRRCRPRLLKGRPCIQHA GPVAAFVATPYSLYVCEPGQ NVTLTCLRLGPDVKGDVTFY KTWYRSSRGVEQTCSERRPIRN LTFQDLHLHHGGHQAANTSHD LAQRHGLSESADHHGNFSITMR NLTLDDSLGYCCLVVEIRHHHS EHRVHGAMELQVQTGKDAPSN CVVYPSSSQDSESNHGNFNRIH VSNGLLMRGPRLDRERNSSHV LIVEAYNHDLGPMRSSVRMRK LRQSTALAQHWGTGALDR
3867	34235	A	3907	1	2180	MALTFPCRKFWEYGRQRPEVR YSVPASHQLKATDADEGEFGR VWYRILHGNHGNFNRIHVSNG LLMRGPRLDRERNSSHVLIVE AYNHDLGPMRSSVRMRKLRS TALADSTGQAQHWTESRSGSPG SPVAPTCSART*QTSASVHLCL SGKSHHAWPP*TPFKLYYVHIE YSAHHKENLVIVYVEDIND EAPVFTQQQYSRLGLRETAGIG TSVIVVQATDRDSGDGGLVNY RILSGAEGKFEIDESTGLIITVNY LDYETKTSYMMNVSATDQAPP FNQGFCSVYITLLNELDEAVQF SNASYEAAILENLALGTEIVRV QAYSIDNLNQITYRFDAYTSTQ AKALFKIDAITRILGTQMDTKM NKTLSPQRVLRLLEVEMELIQD ANQSATRRCAENYNRGVVEPL RAQQSYLAGEAGRLHGRGGFP VECEREELQQTCEPGEVMPDR GSDMEGVITVQGLVDREKGF YTLTVVADDGGPKVDSTVVS TRVYITVLDENDNSPRDFDTS AVSIPEDCPVGQRVATVKAWD PDAGSNGQVVFSLASGNIAGAF EIVTTNDSIGEVFVARPLDREEL DHYILQVVASDRGTTPRKKDHI LQVTILDINDNPPVIESPFGYNY SVNENVGGGTAVVQVRATDRD IGINSVLSYYITEGNKDMTFRM DRISGEIATRPAPDRERQSFYH

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3868	34236	A	3908	603	1395	RGRPRGSPFIPTAPREKKR*EE VGGHKREQTG*GGGERKKPPN PQHEPKERGWCSRVPPEEPQ/RK RRSARARPKKL*REKRRRGRPK RCLW*TRRHPSHHPRTIIQC*F* WRK/REEGKERKKEQPAHAGQ KRRKAARHRRRRRRRERTDEK NRTWTRRRREKAGQDEKREGE HGQKRSQQGRESRRDGRARTR KERRQKRENDNRARRRQQAER EKTYSVKRRQTTTQAAEEVRA RENEAREPQQRQHSRRRKEKE EMRAPRSKQ
3869	34237	A	3909	1	548	
3870	34238	A	3910	1	1803	
3871	34239	A	3911	1	279	
3872	34240	A	3912	1	506	MCYSRQSNLGTGEGKIKGSEV IDECPRSSRYQDLQELQNKTKL TVLEGDILDESCLKACQDMSV IIHTTSIIDIGVTHRESIMNINVK RTQLLLEACVQATVPVFIYTSTP EVAGPNSYKEIINSHHEEPLN TWCSPP/PYKKA/LARSGI*ATL QLGGSQEECT
3873	34241	A	3913	3	621	AGQQTVEIDLRRRIQLPDLENQ RNFNELSRIVLEVRERVRQEQQ EGGHEAGEGRGRQGPRESQSP AQPRAEAPSKGPDGTPGEDGGE PGDAVAAAEQPAQCGGQPFV LPVGVSSRNEDYPRTCRMWNS TFQTYKKEVCLPRHSMHPGPW AICCECQTRFGGRLPVSVEAA LPYWVPLSLRPKQHPWCWMA AGTAGGSVMMS
3874	34242	A	3914	1	430	RHRIQLPDLENQRNFNELSRIVL EVRERVRQEQQEGGHEAGEGR GRQGPRESQSPAQPRAEAPSK GPDGTPGEDGGEQPNVAAAAE QPAQCQGGQPFVLPVGVSSRNE DYPRTCRMW*GCGGYWGLKV GQHGLQRGQPHT
3875	34243	A	3915	2	1175	
3876	34244	A	3916	1	256	HLRIHTQESSYVDCDEGKALTS KRNLIHQHRIHTGEKPYCESKY IG*PFGLLPQLGHLHEHVSGEKP VLIDICRFLPEFFTPFW

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3877	34245	A	3917	1	1396	MRPOLAGRDHHRGAATLLER PGRLVTHFRQRRGAVRYGGGK STTQHLSSQRRLSGPNDHTKGLV WLLLEHILQRLVSFVKLQATRTF TRTYITYAWFLPWGFSGLVCGT PVDTCWALKHQRIHTGEKPFEC SFCGKAFNGNSLIHQRIHTGE RPYQCEECGRAFNANLIRHQ RIHSGDRPPYCTECGNSFTSSSE FVIHQRIHTGEKPYECNECGKA FVGNSPLL RHQKIHTEKPYEC NECGKSGFRTSHLSQHQRHTG EKPYSCKVCGQAFNFHTKLTR HQRIHSEKPF* ¹ /CVD CGKA FS AQEQLKRHLRHTQESSYVCDE CGKALTSKRNLHQHQRIHTGE KPYEC SKYEKAFGTSSQLGHLE HVYSGEKPVL DICRFGLEPFFTP FYWKEEKCCGRKMRNEVVHK VSFFLVVPALSSLLKKKWKML KKEKAQDPTVEYGNLEDDNSQQ
3878	34246	A	3918	1	547	MDSQRPRERQREERQSERQR HTQRMHREAETEDERD WKGH DTKTRRQRQRKRAEEGQCREH DRERRRD RTGERREKQKSTQ QSRKPSEEPHREKTQIKRERGPE QGELERGQCTERNRKA/GTPEC *TDPHIWTPHPARSAPAHPPDH TAAKYRPPYRSHHSIGITHQHPR AASTLKLWPKP
3879	34247	A	3919	1	399	
3880	34248	A	3920	3	872	KSKLKSEQDGISKTHKLLRRTC SSTVKTTDDVCVTKSHRTFGRLS SSDPRAEQAMTAIKSHKLLNRP CPAAVKSEECLETLKSHRLTRS WSGDP RCEHNTNLKPHKLLSRS YSSNLRMEELYGLKNHKLSSKS YSSAPKSSKT*/VFSKEP**RRRG RKALSLPQGLFGYP**HHLHPSSS QLAPNGAKCIPVRDRGFLVQTI EFAEQRIPVLNEYCEVCDEPHV FQNGPMLRRGRDVCWEAKKY ANSVVRKKFCRLSIARRSRYRA DMDLLRMSNFILTHYKQKQLNL
3881	34249	A	3921	3	218	CCRSHQGAGEGGHLSVQLLWQ YRWMCWCSWGPV/FQFHTDLEL VAWRCVGLDPGCGQLDIGMQT LIGDHICVF
3882	34250	A	3922	1	1055	

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3883	34251	A	3923	3	962	RSMRQKVNKDIQDLISALPQAD LIDYRTLHPKSTEYTFFSAPHR TYFKIDHIVGSKALLSKCKRTEI TTNCLSDHSAIKLELRKIKLTQN RTTTWKLNNLLNDYWVHNE MKAIEIKMLFETNENK/DETYQN LWDTFKA/PSILNGQKLEAFPL KTGTREGYLLPLLFNIVLEVL AMAIRQEKE/IKGFQLGKEEVK LSLFADDMIVYLEDP/ISAANLL RLISNFSKVSQYKINVQKSQTF YTNNRQTESQIMSELPFTIATKR IKYLGIGLTRDVKDLLKENYKP LFNEIKEDTNKWNIPCSWIGRI KIVKMAILPK
3884	34252	A	3924	1	1452	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDYRTLH PKSKEYTFFSALHHTYSKIDRT VGSKALLSKCKRTEITNSLSDH RAIKLELRKIKLTQNRSTTWKL NNLLNDYWVHNEMKAIEIKM FFETNENKDTTYQNLWDTFKA VCRGKFIALNAHNRKQERSKID TLTSQLKELEKQEQTSKASRR QEITKIRAELEMEIETQKTLQKSN ESRSWFFERJNKIDRPLARLIKK KREKNQIDVIKNDKGDITDPT EIQTITIREYYKHLNANKLENLE EMDKFLDITYTLPRLNQEEVESL NRPTGSEIVAIHNSLPTKKSPGP DGFTVEFY/QEGN*AGEGNKGY SIRKRRSQIVPVWR*HDCISRP HRLRPKSP*AGKQLQQLRIQN QCTKITSIFIHQ*QANRKSNEH* TPIHNCFKENKIPRNPYPKGCCEG PLQGLQTTAQ*NRGYKQME EHSMLMGRKNQYRENGHTAQ

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3885	34253	A	3925	1	1251	MKAEINMFFETNENKYTVYQN LWDTFKAVCRGKFIALNAHKR KQERSAMNTLTSQLKELEKQE KTNSKANRRKQETTKIRAEKKEI ETQKTIHQKINESRSLFFKTNKI DRPLARLVKKKREKNQIDAIAIN DTGDIITDPTEIQTITIREYYKCL YANKLEYLEEMDKFLDITYTLQ RLNQEKVESLHRPITGSEIAIIN SLPT/KKSPGPDRTAQFYQRY/ DGMYLKIHRAIYDKPTANIMLN GQKLEAFPLKTGTROGCPRLSL LFNIVLEVLRARVQKEKEINGIH LGKQEVKLSLFDGMMIVYLENP IVSAQNLLKLISKFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTITTTKRKYLGIGLARDVKD LFKENYKPLLNNKIKEDPNKWK NIPCSWIGRINIMKMAILPK
3886	34254	A	3926	1	1203	
3887	34255	A	3927	1	1233	
3888	34256	A	3928	1	951	MKREKNQIDAINKDKGDIITDP TEIQTITIREYYKPLYTNKLENLE EMDKFPDITYTLPRLNQEEVESL NRPTGFIEIA/TNSLPTK*SPGAE GFTAIFYQSVGSSGQGNQARE RNKGYSRKRGTQIVPVCRW DCIFRKLHGLSPKSP*ADKQLQ QSLRIQNQCAKITSIPHQ*QTYR EPNHE*TPIHNCYKENKIPRNTT YKGCERPFQGELOTTAQ*NKRR HKQMEEHSMMLMDRKNQYREN GHATAQGLH*IQCHPHQATNYFL HRIGKNYFKLHMEPNKSLHSQ DNPQKEQSWRHAT*LTQILQ GYSHQNSI
3889	34257	A	3929	1	814	

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3890	34258	A	3930	1	1545	HQLKVFQRIHSIRSSCDGSAWGV VAPTFKTRGARSRRAAIRLGA ADLDEVKSSLVNESENQSSSD SEAERRPQPVRDTTFQKPRDYFA EVRRPQDSAFFKGPPYPGYPFL MIPDLSSPYLSNGPLSPGGARTN SSPAPKETWICARFGGVSLSFLE IGSRVLLGRDVRNRSLLPAQI PIACHFAVDGGNFIRKGAYLL TFDLFGNWGLFFLIEIAVWELS AHSSGQSEDALELSRGTCSSSL QLCWTAKALVGKGLDGGPVC KNSGICSTRKTQEQMSFMEAL YQEGFLRETVVQAVRKVPQTP RKAVLEVLAARAIHQEIKIGQL GKEEVKLSLFADDMTVYLENPI VSAQNLLKLISNFSKVSYGKIN VQKSQAFPYTNNRQTESQIMSE LPFTITTKRIKYLGIQFTKDVKG LFKENYKPLLNEIKEDTNKWK NIPCSWIGRINIVKMAILPKVIY RFNAIPIKLPLTFFTELEKTTLNF IWNQKSRIGKKILSKKNKAGGI
3891	34259	A	3931	693	1464	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFPIPYTKINSRWIKD LNVRPKTMKTLSESLGNTIQDI GIGKDFMTKTPKAMATK/DQKS FCTAKETTIRVNRQPTWEKIF AIYPSDKGLIS

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3892	34260	A	3932	211	2519	ENRKSNCCLCQMA*LYI*KIPSS QPKISLS**ANLAKSQDTKSMC KNHHKHSYTLITDKQRAKS*VNS HSQLQRE*NT*ESNLQGM*RT SSRRTTNHCSTK*KRTQTNGR TFAHG*EESIS*KWPYCPSK/K RTEITNSPSDHSTNKLRLRIKKL TQNHITWKLNNLLNDSWVN NEIKAEIKKFFETNENKKTYY NLWDATAVLRGKFIALNAHI GNLERSKIYTLISQLKEPERQEQ TNPKASRRQETKIRAELEIET QKTLQKINESRSWFFENIKIDRQ LARLIKKKREKNQIDTITNNKG DITTDPIEIQTIREYYKYLYAN KLENLEEMDKFLDYTLPRLNQ EEVESLNTPTTGSEIKAIINSLPT KRSPGDRSTAE/FYHRYKEEL VLFLKLQFSTEKEGGRDITK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIYHDQVGFIPGMQ GWFNICKSINVIFQYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPVLEIRGHK QMEEHSMMLMDRKNQYCENGH TAQGNL*IQCHPHQATNDFLHR IGKEEVKLSLFADDMIVYLENPI ISAQNLLKLISNFSKVSAYKINV QKSQAFRYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYRPLLNEIKEDTNKWKNI PCSWVGRINIVIMAILSKVIYRF
3893	34261	A	3933	2	1304	
3894	34262	B	3934	141	2008	

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3895	34263	A	3935	1	1845	MVISVDAEKTENKIQQPFTLKT LNKLGIDGSYLKIIRAIYDQPTA NIILNGQKLEAFPLKTGRRQGC PLSPLLFNIVLEVLAIRIQEEI KGILQKGEEVKLSLFADEMIVY LENPIVSVQNLLKPIRNFESVLG YKINVQKSQAFLYTINRHTESQI MSELPTIATKRMKYLGIQVTR YVKDLFKENYKPLLNEVKEDT NKWKNIPCPWIGRINILKMAIL P/KELEKTTLKFIVNQKACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSDIIPIHYNHLIFDKPDKNK KWGMGSLFNKWCWENWLAIC RKLLKLDPLTPYTKINSRWIKD LNVRPKTIKLEENLGNTIQDID MGKDFMSKTPKAMATKAKIDK WDLTKLRSFCTAKETTIRVNRQ PKEWEKIFAIYSSDKGLISRIYK ELNFRKINNPIKKWAKDMNR YF*KEDIYAANRHMCKSSSLA IREMQIKTTMR/YHLTPVRMAII KKSNNRTRENYFKIHMESKKS QNSQGNRKEKEQSWRHATRL QTIVQGYTVAKTACYWYKNRP TDQSNRTENQEIRLHTYNHLIF DKPDKSNGEITTPYSINGARITG
3896	34264	A	3936	1	700	
3897	34265	A	3937	1	3489	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAIYLVG LSGSASLKLAVPLRCEGDKD AGHPLETQTALCERGRGARS LV GNTIMTSQVPVNETIIVLPSNVIN FSQAEKPEPTNQGGDSLKKHLH AEIKVIGVNLQNVLERGWGKC QEMIYVVLGLDICRPFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRS

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3898	34266	A	3938	120	1331	TSLGPIYCAVRHTSSCRKVGSSR CQIIGCQLSVRLQLDQAHHKQL PWLAPKNAVVPKSLEDPQGRK EGVTALTPEAPRSGPPKRLQLFP PSLCPNCSKQGAFFSPFVGTAT LLATPFSSRSRVLVLPGRMRYA DKWRVSKMKRCCIEQWNSSEK THSARASHSLQRQGGPRVGGG SLQAGCHIVISAALSKEEALWV ASFCRQIVQSYLRPLLCSGADP GAFMDLRLGEELRSLLESLSYTP PSNEFKISMKLEAQDPRNTTST CIATVVGLTGARLRLRLDGSND KNDFWRLVDSAEIQIGNCEKN GGMLQPPLGDSFHCDDVRVSILD LFCFLLELPFTIDTKRIKYLGIQ LTKDVKDLFKENYKPLLNE/IK/ EDTNKWKNI PRSRIG*INIVKMA ILPKDFG
3899	34267	A	3939	1	1421	MDSMSGGGQYRKINGNPTSVK CPLLLLPAILTPEPVNRWRQSC KAFARHSPLAFRVTISTSTFFDG LLVTGLYTSTSVQASQSIGGSSA FGFVLEVLARAIRQEKEIKGIQL GKEEIKLSLFAQDMIVYLENPV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGHQLTRDVKDL FKLENYKPLLKEIKEDTNKWK IPCSWVGRINIVKMAILPKNWK KLKFIWNQKRAHIAKSILSQKN KAGGITLPDFKLYYEATVTKTA WYWYRNRRDIDQWNTTPESEIM PHIYNLIFDKPEKNKWKGD LFNKWCWESWLAICRKLKLD FLTPYTKINSRWIKDLNVRPKTI KTLLENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQTTKWEKI FATYSSDKGLISRICNELKQYK KKTNNPIKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 5,410,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3900	34268	A	3940	3	1566	IQTTIGEEYKHLTYTNKLENLEE MDKFLDITYTLPRLNQEEGESLK RPMAGSEIEAIINSLPTKNSPGP DRFTAIFYQRYKEELLISNFSK VS/VIQNQWEKITSPIHQ*QTNR EPNHE*TPIHNCFKENKILGIQL TRDVKDLFKENYKPLLSEIKED TNKWKNIPCSWIGRTNIVKMAI LPKDKTSKYIDVDENEGSHCGK RKYKYGMEKALEILARAIQEK EIKGIQLGKEEVKLSLFADDMI VHLENPIISAQNLLKLISNFSKV SGHKINVQKSQTFLYTNNRQTE SQIMSGLPFKIATKRIKYI.GIQL TRDVRDLFKENYKPLLNETKED TNKWKNILSSWIGRINIVKMA ILPKVIYRFNAILINLPMFTFTEL EKTTLKFIWNQKRACIAKTILSQ RNKAGGITLRDFKPYKATETK TASEMKYYLENKIPFKVLHVM YNVPTHPFFIGDLHPNTKVVS LPNITSLIEPMNQGVISAFKDCY LRKTFVQAVATPEGETEMTVM QFWKDYNT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3901	34269	A	3941	1	2580	MVKGSIQQEELTLNRYAPNTG APRSIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTRQKVSKDI QELNSVLHQADLDIYRTLHPK STECTFFSAPHRTYSKIDHIVGS KALLSKYKRTEIITNCCSDHSAT KLELRINKLTQNRSTTWKLNLL LLNDYWWHNEMKAQIKMFET NENKDTAYQNLWDTFKAMCR GKFIALNAHKRKQERSKIDTLT SRLKELEKQEQLHSKDSRRQE INAEKAFDKIQPFMLKLTNLT DIDETYLKIIRAIYDKPTVNIILN GQKLEVFPLKTGTQGCRLSPL LFNIMLEVLAIRIQEKEIKGIQ LGKEEVKLSLFADDMIVYLENP IISAQNLKLLISNFSKVSQYKIN VQESQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVI YRFNAISNKLPMFTFFTELEKTTL KFI*KQKRACIASKLSQKNKA GGITLPDFKLYYYYKAIVTKTA WYWYQNRDIDQWNRTEPSEIIP HIYNHLIFDKDPKNNKWGNDS LFNKRWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLHVRPKT IKTLEENLGNTIQDIGMGKDFM TKTPKAMATKS/KIDKWDLIK KSFCTAKETTIRVNRQPTIEWK KIFTIYPSDKGLISRIYKEPKQIY

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3902	34270	A	3943	5	2130	QRLRRQHRLEQKTRSTTCHMR QSTTRSAERADTRIESMPT*ITP *HTDDVP/SHCTNSTHTATTSPS TIHHQQLTRVANVAQIRRTDI SSIAATEWISTINTHNYACRTRA VSQRRYVSDFEKERPTSNTP PRFRLVVSPTPLVGTTCGTYP PPARSISIASHLPLPLSLPSSL DLDGRLTACSSVSQFSGSRGS PSSYIVATTRVISDVYDMTTY YNSTITPIS/PSARS*QORSVHLL LSSHRTYRHLVSRHTSQEHSL GGPLHRH*YNPVGSRAAAWAS KSALV/SVSEALVVSALI*LVA TRQRLVGICRTTPIRARSSVVR* VTRYQPNQRAPLIHATYHLLDR GQHPQSMQTIHWTTPPCWCL VCGKKSSLPCCSTSSMSTRNQ YDTLSLTSSWVL*SSIFWLAFIL LPRTSLPWPTVS*LAANA\SSGS TPVNSSFRT/SVRRSKLVVPANE IETPSFVVVTKFSRSASSYDCSIE YASTYAINITIVNSYVFA/PTHTT REHTISYALTSPGQPQNKTRIPE LQWAF*AVRPSTQ/PSTVIYHAP TSQAIASCALHSLGCLLGSAT APLPPTWTTPPPPPQLRTT*STG SLPHPPSC*TRP*PLAPRN*PFTG MSSQHCIPT*PQLASHSIALRG/S RARPTTSQTSIAS/SHSHS*LSHV Q*RPLSDQRSPLDHAHSHSILYA RASRISCLRVCV
3903	34271	A	3944	254	884	MTPNYTSRLFLHMGVLFYPFYR RLT*HIRTHINLKGWK/NRHFM QMDTKNAEKALDKIQHRFMK TLKISIQGTHFKIKAIYKGSTT NTILNGEKLKAFPLRTGIKQGC LLPLPFNIVLELLARAIHQEKEIK GIQIGKEEVKLTFLFADDMIHYLE NSKDSSRKLPELIKEFSKVSRYK VNLHKSIALLYTNSDQAEQIK NSTSFTI
3904	34272	B	3945	52	843	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
3905	34273	A	3946	1	831	MEMLYCLIAEAGHISRMATNT ANSAGLKPTCVCVALPLPPGRS APHRSCSQAGRELPGQGPRYYR HLPQLSILHSIGEGQCGFWSER SFKGYPERPAGAAGVCRLQGC GRRGRGAPFRTTDFSSRPRGAA ERADQGPRAAGSPWPRTTSGAQ RGRAQQGHTARRRGNNSNPGP SRARQASRRRRPATSGPPRGSP RPDRPRRRSPFYKSSSRETSRPP EGPRRPRAPALSAPAPGQPARP RPREPVPCGAVFTARDRLRPPA ATSHAPFSAANPRR*HRPGGPG ARRLGDAQLSRRST/SGAPRCS QTRSR*PTCVCVALPLPPGRSAP HRSCSQAGRELPGQGPRYYRHL PQLSILHSIGEGQCGFWSERSF KGYPERPAGAAGVCRLQGCGR RGRGAPFRTTDFSSRPRGAAER ADQGPRAAGSPWPRTTSGAQRG RAQQGHTARRRGNNSNPGPSR ARQASRRRRPATSGPPRGSPRP DRPRRRSPFYKSSSRETSRPPG PRRPRAPALSAPAPGQPARPRP REPVPAGVFTARDRLRPPAAT SHAPFSAANPRR
3906	34274	B	3947	250	281	
3907	34275	A	3948	3	639	DHTRCLRQLRLRLVLGVGPVPG AGPAG*KGCYGGRSANHHGAP ASCHLARSSCGPRLPGRYSAQQ PRARCAASGLCGWTAADPV PSEVLASQEVQLLCAGE*SGSC GPTHADLQPSGGTGEDGAAR AKRDLPGSVGERAAAPASGRL RACPGRPAGAGPGRARPPGGTA ALAQPPRPQGAARPPSGIGWP GNNNSAQSKGRALMEQAAG

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3908	34276	A	3949	161	2377	SLFHGKVCHEFLHEPLPLVYLSL CTGYQLFKPSLISWLEEEELST LPRVLQEWKMCLKTGKPAIW QDNFCLKTLNGIQLARNQNGEE LYDCKQCEDVFCKHPCLKTNM STQNRGNTSECIQYAKDLLSLY NKTSTIRKVSFVKHGKSFRL/F *MFRSRESVHKINPLK/CTDYGK AFIYQSYLEAHRKTQSGEKLE WKQCGEAFTHSTSHAVNVETH IINKNPYECKECKGDFRYPTHLN NHMQTHIGIKPYCKKHCGKTF VPSGFLEHVRTHTEGKPYGCKE CGKAFGTSAGLIEHIRCHAREK TFKCDHCGKAFISYPSLFGHLR VHNGEKPYEHKEYGKAFGTSS GVIEDRRSNTGQKRFDCDQCG KVFVSFSSLFAHLRTHTEGKPF KCYKCGKPFSSACLRIHMRT TEERLYQCKKCGKAFKCSYLT KHLRTHAGEKPYECMKCGKAF TERSYLTKHLRRHSGEKPYECK KCGKAFTERSDLTKHLRRHTG DKPYEYKDCGKAFVVSSSLVD HLRTHTGYPYKCNACEKAYS RSCVLTQHLKTHAAEKTSECN ACGNSFRNSMCFHDLRLTLTKI KPYKCKDCGKAFCHSDLTNH VRIHTGEKPYKCKECKGAFRTS SGRIQHLRTHMGKPFECDCQCG KAFVFSQVLVHI*KHTREKPCG CEECGKTFVVSSSLTEHVKIHR
3909	34277	A	3950	6	455	GLLHERQAEARCSICLDYLRHP MTTDCRHYI*SARIHQCW*ELQ DISPCPVCLQHCPDKNLKRNFO LCHMTDIAKQLLTARRKRKL QGEPEVCRKSDVALFCEKDP LCHQYRVSLDH*DH/SPMPIEQ AAAKHRKQFSEYIEPLEKQV

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3910	34278	A	3951	2	1009	WNGHRMN*MQSSNGLEWN/QS SNGKEWNHRIESNGIIIAWN/Q WYQHQTTEKNGIFEWNRRSSN GPEWNHVMWNG/DNPWTRM QSSSNGIEWNHRMDSNGIIFQW NGNGNHRIGIEWNYDQ/SNEWV QWNQHQTTEKNGIIKWNRRESS NGPEWNHLMWVN/ENNPWTR MQSSSNGIEWNRMESNGLEW NNH*TESNGSVSSDGNR/QS SSNGIAWNHHKMESNGINIKW NQMESWN/WN*MNRMELSSNG IEWNQHQTEKNGIIEWNRRESS NGPEWNHLMWVN/ENNPWTR MQSSS/NWNRMESSNGLEWNN/ QLNGIEWNHHRMEMNGIIIEW NRJELWN
3911	34279	A	3952	1	1494	MASLLGAPRLAGWASGAGALS RGWAIRPADTGGNLPVPRVPL PPDPVLRTARWAPGVNSGSQFSC HCQAPILEMGHGSSPGLGDAE VRAITVQCIRPIDGPQPQGGGS AGRRLTIPASTQEWALPLVGRV LANVLTGGDTGNQPIQRSLC RPQPCSHAETWGEVEAQVPAQ SNREQPAAAPGCGPGRGETGA RPETTFSPRRAPPNPYDEEGVR WSLEFMLCGTDGPVQPVQHGE GPAARLQLIRGGSLILESEGTLR G/SPVLQTDQPASHLLHTQGFW A/AALSAVCL/HQNIHSGSALL APATRAAWEQIQRSSEGTACL LRRLEGYFSNVARNVQWYTLQ PFVIVTTNMILAVDIFDKFNFTG ARVPWFDAIHEAFPRELESSISF PANFFKPPEEKEGLVVRPASK TTPQTTRPGPTEREAPISR*KR HPDDTG*FTFTLGIVYCTPGQLP PEPYDPNRRSLWLPHWPIINTS MVSALVYSEGAPLPSPL
3912	34280	A	3953	1	681	MGQLLDKNTPSHGARTREECG RERLCVSPSQGTDPRTSAAYLC VGGPAWSPLSESRPAGSSGCPW IKPPDPYRSPIGLCSLLTTEMMS RQPRDLRGQTNPAAPSAVPVL SCSQNLVWPSLMAGTTWHSPL LSPSCFWHSPGHN*H*CCVSKD *KSLFEWPTA/YSPLL PSTSP/SS KSMQPPKPRSNADSSVQASLIP RAMSSPTVSPWIMGNQSQGF HIAVSMWDD

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3913	34281	A	3954	136	420	RESRNLSRGESEDPAPPSIRNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPSPAPPPEHTHTGSPRPPSGRSR IRAYLH
3914	34282	A	3955	1	1782	
3915	34283	B	3956	1	3070	
3916	34284	A	3957	104	279	STTHPSVHE/QEEEEEEEEEEEE EEEEEEEEEEEEEEEEERKKKEC SKAQCKHPLSEVL
3917	34285	A	3958	1	252	MTVCIHASEDLPVGRDVEVED SDIHDRDPGLGDKSETPSE/EKK EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE NFLQHYLHL
3918	34286	A	3959	2	368	
3919	34287	A	3960	239	432	CLWLQEEEEEEEEEEEE*EEE EEE/EEEEEEEEEEEEEEEE EEEEEEEEEEKIFLGHVRGI
3920	34288	A	3961	1	577	MQIPSLHLKKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE/EKKKKKEKKKKEE EEFERRRKKKKERKEEEEE/G KEEEEEEGEEEEEEEEERRK EEEEEEEEEEEEEEEEESCLMGP MCVHIHPDKDLYSLGPPAQRF TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3921	34289	A	3962	327	559	PKGRTPSPSCIHRYPCQTPRPHE P*GCHCPEEK/PRPRVWGPSRC MPLGVSQEKRPCAPGGVQGSF RVSPMLMLTRL
3922	34290	A	3963	1	577	MQIPSLHLKKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE/EKKKKKEKKKKEE EEERRRRKKKKERKEEEEE/G KEEEEEEGEEEEEEEEERRK EEEEEEEEEEEEEEEEESCLMGP MCVHIHPDKDLYSLGPPAQRF TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3923	34291	A	3964	157	272	WCNGSLPSYGW*LVGMESLGR MHKDLWTRQPNQDQLQ
3924	34292	B	3965	1	3723	
3925	34293	B	3966	1	573	

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3926	34294	A	3967	3	424	AGGQALQGPGQGRGSGVVG/ PGTGSSGAQHLGKHYPVLSGGS ERSWGRSHTPAGAGC*VRGRR AGGRPGTGHSRPPGGSCLSPAP PNSARWLGLGAPWQAGAGLR DPGDWRRGQGGPGWAWCPGQ PPAQHTCPPNSTARY
3927	34295	A	3968	3	1238	RGAERRAWSRGPACTRRGPAD WAAAGAGRPCPQRRGVCCTAA VPGAARLSCPIGPGDGPGRRS LTGQGS*GLGAAGGGWTGALP SWHS*SQGWQTDVPR*VRGTE RDICTGL*QCPPPGGLQTGSGG LEHSLPWPBGIGIQA*GNHPCR LPRS*ALSAGGSGGQALQGP QGRGSGVVG/PGTGSSGAQH HCCPPYTPG*HPISLLALGPQ SLQPEWAHSGTASGEQHSAGE HGMGTGGH*LPLGCSRCLVGLK HYPVLSGGSERSWGRSHTPAG AGC*VRGRRAGGRPGTGHSRPP GGSCSPAPNSARWLGLGAP WQAGAGLRDPGDWRRGQGGP GWAWCPGQPPAQ*HTCPCPAGS LPGAAPGVLCAL*GPAAGV*A GPGPGGSR*TRGSPGAPRPA
3928	34296	A	3969	3	415	ETGRHRSQSVSSPPVQPRGKR AMYHSAELVSRGFP RPVPQAP AEPAGAAEGVHSQPASRQEA/G S/TEVRGQAHRFVSPNAAAGAG DG/PDPQSLAPTNRPCPPGGISP ARSEVPAPAGRAAP*CFPDLP LAPPLC
3929	34297	B	3970	1	657	
3930	34298	A	3971	125	524	EAEALENQSQPCDTG/PQSAFSP PGSTQHPRSQLSQCKQRYQDLQ EKLLSEATVFAQANELEK*RV ILSIGEPLLKQDSKQVQVDLQD LGYETCGQSKNEAQEETTSPE HEEHSSRKEMVLVEGLCSEQG
3931	34299	A	3972	1	648	MGQVWGLVHFTLEVHTGDDEE EQEYSEVTEDVTEHVYLP KVAKEEEAGIQQARQEGDLEA WQFPVRIHPPDQENITATFEPF PFKLLKELKQAINQYGPSPFV MGLLKNVTYSSQMIPTDGDPLT RACLTPAQFLQFKTWWADEAS IQAARNAWAQPIQINITADQLLG VGGWAGLDAQFVMQDDAIEQ LRGVCIAREKII*CGEQYPSF

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3932	34300	A	3973	350	1078	GSNRRSNRAEQLRGVCIRAW KUTSGEEQYPSFSIVKQGP TDFIAWLQESLKKVIADSA IVLWLLAFDNANPDCQAAL RGKAHLVDYIKACDGIRG RLSWLSLQGRPAGAACTSS DWKAQLAPGPHAGPLRCP ARQPRLPAVLSAGAAFRDC CVQALLGGSAGPGDRLPG ALVALSLPFVKEATMNRW HRSAFFLFSANAHGAEGV VASR
3933	34301	A	3974	2	630	WDNCGLWFIPSWNLFTLM KESLMK*QKK*QSRFVC /PAKEGEVYPYPSAPPYF WPDPPDLSFLEDAGQKVI VQAAPQAIALSSIQAGIQ EGDLEAWQFPRIHPPDQ ATFEPFPFKLLKESQAIN QYQGSGSPFMELLKNVAV SSQMIPDWDALAQACLT LTQFLQFKTLWADEVSI QAACNA
3934	34302	A	3975	264	634	WSSRCQHSSRPQASESW FPG*G PSFWPRIQGDEK TGAGGHP*LG C*PGMT QGQFSTKCQHTCLMW GSHWAQEAEPENAPGTSC PGSSG SWVLRSSLQRQK SAWSPG/ASM PAPKMP FLTSPSSGFS
3935	34303	A	3976	3	410	KKKVWREEKERLLKMT LEERRKEYLRDYIPLNS LSWKKEEMKG QGPK* EENTQETSQVKKSLTEK VSLYRGDI/*VDAIVNA ANASL LGGGGVDCIHRA AGPCLLAE CRNLNGCDT GHAKITCGYDLP AKCEYN
3936	34304	A	3977	74	432	MLHNLRPRTLTRTRCP STPTT*ATPPTTHGSAG PRAAHLRTGTRRWRA PRRARSCTRSSPR RARA ASTPPLAPARELSASP SPSCEQSAAPPSSGRNG GNFPESIFVKTINSN

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3937	34305	A	3978	2	894	WGGYGMRTGPRTLTTTRCPSTPS*TTT*ATPPTTHGSAGPRA RTCAAQRTSGSHPSQRRSSAA PGV*RVNVPWAH*MKRV*TT LENLTA/PEMAMPAPHVIFAT DDWAAMVHPSARVPGLDGTG ALLVPTGVCAPGCKCPLTSSS VTHTRLKTTLSVPPSARQTGRC RSPDLRCSYPPDEQPVCVVKC GSPWVSVLVAVIQSESALVDP HPQHPYLYPVDMMQNLTLNLGE PQARALAAKLLGRPSSSQSGS RVPAVWAQAGNATYITVHTLC SHNTHMSPVRVKRFTHLG
3938	34306	A	3979	157	570	
3939	34307	A	3980	1	936	
3940	34308	B	3981	257	3934	
3941	34309	A	3982	210	4286	MPLKTRTALSDDPDSSSTSLGN MLELPGTSSSSTSQELPFCQPKK KSTPLKYEVDGLIWAQFKRRP WWPCRICSDPLINTHSKMKVSN RRPYRQYVVEAFGDPSESAWV AGKAIVMFEGRHQFEELPVLRR RGKQKEGYRHKVPQKILSKW EASVGLAEQYDVPKGSKNRCKI PGSILKLDSEEDMPFEDCTNDPE SEHDLNLLNGCLKSLAFDSEHSA DEKEKPCA\KSRARKSSDNPKR T*L*KRATYNFEAH
3942	34310	C	3983	163	309	
3943	34311	A	3984	72	424	RNCGTARSOHEPLGSWLQDTP QPP*TELAGNLPD/F*PGPGK EQGMFVCHPIRQPLPRPLPGSSH QSMPTAQPLSSSSALLPALPAG FPVTTGGQWTKLQVQAPAPFHL PPQVEAV*AFYQKQMLVPCSL* SMPTAQPLSSSSALLPALPAGF PVTGGQWTKLQVQAPAPFHL PQVEAV
3944	34312	A	3985	1	347	KWQRFVLTGIDTYSRYEAYPA CHASTKTTIHGLMEFLIHHGIP HSIASDQGTMLMAKEVQRWAH AHGIHWSYHVPHHPEVAGLIER WNEIGLLKSQLQHLVNLRLRE LQCWL
3945	34313	A	3986	1	1716	

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3946	34314	A	3987	1	737	MSSVLLRLIYQLTKQTASFEGG PEQKALQQIAAVQAALPLGPY DPANPMVLEVSADRDVTVWSL WQVPIGESQLGFWSKALPSSAD NYSPPERQLLACYWALVET EY LTMGHEVTMLPELPIMTWVLS DPSSYKPAPMASWGVYPYQLT EEEKTRAWFTDGSARYTETTR KWTAVAIQPLSRTSLKDSNEGK SSHQQA KNGITVLAGVIDPDYQ DEISL/LTPQWRCHPGSSVWRAS SLGISHPP
3947	34315	A	3988	2	384	CGRSGYWHSSVATKITRLRML RPREGRKLP PGDIMIPLN*KLRL PPGS/FLLLSHQAKKGVMTLAG VTDPDYQDEISLLHNGGTGKS PHISDTFYGSKVASCQNTGPEK QDETQAQETAVYKSQIFGS
3948	34316	A	3989	3	1273	
3949	34317	A	3990	3	341	GLGRRQPAGSWPERRPGPSA/R RSTAPRRCGQAES*TERGSQPH QVQGGQGRWGVCMKIPSHSGKS PDVSEVSKSRNSIISTAVTHAVV APEGLKRNGGGSHLRSSRGHR AVIF
3950	34318	A	3991	44	243	
3951	34319	A	3992	40	558	LGSIQVMQAVRNAGSRFLRSW TWPQTAG*QMTAPSSPPPPGL CSYSCPLSHP/SLPVTVRWPSPS FSSQQGRGQNA/APGPSAQALD SSKTLRPSRKLNRTLPA TPSSG EPHLDQPSGDPQLTLARHPPE EPVNFQLCHLLSVGPYANKSEP QPSHLKMRIMLREVVRIT
3952	34320	A	3993	335	581	RRHLFLQWGQRAWRLQVAAA GTTRPTSAMGIRCSEGAARAT AARA*TAGPEPLE/PAANPPPL TASALRAPPSFVLPOCTR

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3953	34321	A	3994	216	1159	SWHGPPGANTVAAAAPPEEK AALKLRPTHGWVPRATDVHVDV ILKASGESEWRGGSRAHQMS VAMATALGEGVPVRGPAAAGSL RLLPGSSAPLGRDAISSCNGVN GLETTGGRCRHNAPNKRHGD LLEGAAAR/AQAARA*TAGPEP LE/PAANPPPPLTASALRAPP VLPQCTAAPRDPASAAGAN*G KAQSRNC*NEPFA YGGGTHGT GAGAAVTVAADGN*LGSIQVM QAVRNAGSRFLRSWTWPQTAG PWPSPSF/VFPAGSWPERRGPS AQALDSSKTLRPSRKLNRTLR ATPSSAFTLPFQERRAL
3954	34322	A	3995	1	738	MTKRGHGTAWAVASKSASP WQLPHSVFPGTEKSRIE VWE LPRFQRMYGNTWMSGSSLLQG NQNLHAERYCNSTLERNDTPIE SLPKPRESEDLGEHNGSTMEE VGAETRVQRHWVRVSMTELAL ASDAHMWGSNPGQRTVGMV GECGTMLGDTQVLLSNPCGDR ARRAYSTAPDYAVCGNGGKVK LNEQRFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGDS*AI PVVTE LGERIAQLLIMLYVVKWGKSEIK RT/G/GFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGDS
3955	34323	C	3996	87	329	
3956	34324	A	3997	3	122	
3957	34325	A	3998	1	156	
3958	34326	A	3999	1	353	
3959	34327	A	4000	1	201	
3960	34328	A	4001	56	207	EEKKEKEKEKEKE/EEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE
3961	34329	A	4002	1	174	MNRC*RIHYSNEVH*KEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE
3962	34330	A	4003	1	278	MTSYKFTEPKNGIWQLHEAAQ LDTTYKNKLNKKEEEEE/EEEE EEEEEEEEEGEGEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEGVIL
3963	34331	A	4004	144	429	DLPREYALPAGPRRRCRH RYEPNPEFGAKHSCPA*HRAA PATSDTQE*HRSNAFEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEETLFSNM

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3964	34332	A	4005	3	122	TEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
3965	34333	B	4006	1	300	
3966	34334	A	4007	1	1226	MPSSKGVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGIIDSNFEPELVLEFFFEALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYILNQDAQNKSP SAVMSHESDAHSDSARSSSSK LELSPDVNKKIRSEAMVKEKKK ADKKGEKSARSPSLSDNDFS KQDGNITRQEMSPAGVPLGGM QLNEVKPKKDRQNVQQNEDAT QYEEISILTKLIVESYEGEKVRGL YEGEGFAAFQGGCTYRVSCPFE NLQEGEEGRLEECPEPRRVH VAGRSMYEGEVVNGMRNGFG MFKCSTQPVSYIGHWCNGKRH GKVGVEATWRAEKKKKEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEKIRP
3967	34335	A	4008	453	705	LLSIVQAEAVSENHPILPRVSR SGWGQKEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE SCYSITPELSCKLGHR
3968	34336	A	4009	93	705	ESSTQTCSGFWTGCTALHRWR GMPERCPPESRDS*TRFPQSSLP GHKT/SEKEEEENRKEEEEEKE KEK/EEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEQEEEDDEE EEEEKSCSVNLSIELPWPDKA YSRLAPLSSQGPVAVKVPTHEL AKLEDVCVGFTYLTVEKRWAR AVTGAQELGVDYPRNECKPH NNGYDND
3969	34337	A	4010	1	3189	
3970	34338	A	4011	1	5127	
3971	34339	A	4012	209	3816	QGRPTFRFRKYREHHKDTPRE QLQDT*SSDSPKLR*KKC*GQ PERKVKLPTKGSPD*KRISRQ/ KTLQARRQSWFFEKINKIDRP ARLIKKREKNQIDTIKNDKGD ITTDPTIEIQTIREYYKHYANK LENLEEMDKFLDTYTLPRLNQ EVESVNRNITGSEIAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASH LIPKPGRDTTKGNFRPISLMNI DAKIL

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3972	34340	B	4013	1	3570	
3973	34341	A	4014	1	2347	MELKTKARELHDECTSLSSRF QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQSEIEGILPNSFYEPSII LIAKPGRDITTKENFRPISLMNI NAKILNKM LANIQQHKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIIISIDAEKAF DKIQQHFM LKTLNKLVLVLA RAIRQEK EIKGQLGKEEVKVS L FADDMIVYLENPTVSAQNLLKL IGNFSKVS GYKIN VQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVITKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNLYIFDKPE KNKQWGKDSL FNKWCWENWL AICRKVKLD PFLTPYTKMNSR WIKDLNVRPKTIKLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTW EKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKHKMKKC SSSLAIREMQIKTTMRYHLTPV RMAIHKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSL*RRI/W KRLQRTL SIPVLDAV*PPMF*AS
3974	34342	A	4015	1	5073	
3975	34343	A	4016	1	3297	
3976	34344	A	4017	1	3514	MELKTKARELREECRSLRSRCD QLEERVSA MEDEMNEMKREG KFREKRIKRNEQSLQEIWYDVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIEI QRTPQRYSLRRATPRHIVRFTK VEMKEKMLRAAREKDRSTRQK VNKIDTQELNSALHQADLIDIYR TLHPKSTEYTFPSAPHHTYSKT DHIVGSKALLSKCKREITHTNYL SDHSAIKLELRKLNLTKSRSSTTW KLNNLLNDYW

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3977	34345	A	4018	1	2666	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKAULSKCKRTEIITNYLSDHS AIKLELRRIKNTLQSRSTTWKLN NLLNDYWVHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQIDTIKNDKGDITDPTETIQT TIRESYKHLAYANKLENLEEMDT FLDITYTLPRLNQEEVESLNRPI GSEIVAIHNSLPTKKSFGPDGFTA EFY/PESYL*QTHRQYHTEWAK TASIPFENWIKTGMPSLTTPIQH SVGSSGQGNQPGEGNKGYISIRK RGSQIVPVCRRHDCLSRKPHRL SPKSP*ADKQLQQLRIQNQCT KITSILIHQQQTNREPHE*TPIH NCFKENKIPRNPTYKGCEGPLQ GELQTTAQGNKRGHKQMEEHS MLMGRKNQYRENGHTAQGNL QIQCHPHQATNDFLHRJGKNYF KVHMEPKKSPHRQVNPKPKEQ SWRHHTT*LQTLQGYNSQNSM VLVPKQYRSMQNRALRNNA AYLQLSDL*QT*EKQAMGKGFP I**MVLGKLASHM*KAETGSLP
3978	34346	A	4019	824	3693	AWKGTDDRSTRQKVNKDTQEL NSALHQADLIDYRTLHPKSTE YTFFLAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNLL NDYWVHNEMNAEIKMFFETNE NKDDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
3979	34347	B	4020	1	3765	
3980	34348	A	4021	1	4791	
3981	34349	A	4022	1	3297	

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3982	34350	A	4023	1	3170	MVKGSIQEQEELTILNIYAPNTG APRFIKQVLSDLQRLDSDHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTI.H PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEITNYLSDHS AIKLELRINKLNTQSRSTTWKLN NLLNDYVWHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQKLELEKQEQRHSPSRQEQ ITKMRAELKEIETQ
3983	34351	A	4024	281	3030	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNMEMKREGKF REKRIRKNKQSLQEIWDYVKRP NLRISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIEIQ RTPQRYSSRRATPRIIIVRFKSV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKSKSPGPDGFTAEEY QRYKEELVPFLKLFQSIKEGI LPNSFYEAII
3984	34352	A	4025	1	3290	MGELITPLSTLDRSTRQKVND TOELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRINKLNTQNRSTTWKLN LLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKRE KNQIDTIKNDK
3985	34353	A	4026	1	3573	
3986	34354	B	4027	1	4251	
3987	34355	B	4028	1	3065	
3988	34356	A	4029	965	4089	TWKGTTSTRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTF/LAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRINKLNQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQKLEKQEQTHSKA SRRQEI TKIRAELEIETQKTLQ KINESRSWFFERINKIDRPLARI KKKREENQID

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3989	34357	A	4030	523	3981	
3990	34358	A	4031	1	3429	
3991	34359	A	4032	1	3156	
3992	34360	A	4033	2	4943	
3993	34361	A	4034	1	6747	
3994	34362	A	4035	1	3928	MAAWNLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKGLTTRKDIYTENPSV HHHHQRPKLVDTTKMGKKQN RKTGNSKMQSASPPPKERSSP ATEQSWMENDEELREEGFRRS NYSELREDIQTGKKEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRLSRCDQLEER VSAMEDEMNMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
3995	34363	A	4036	1	3638	
3996	34364	A	4037	3	3585	SNSHITILTLNVNGLNAPIKRHR LANWIKSQDPSVCCIQTHTLC RDTHRIKIKGWREIYQANGKQK KAGVAILVSDKTDFKPTKIKRD KEGHYMMVKSGSIQEEELTTLN YAPNTGAPRFIKQVLRDLQRDL DSHTLIMGDFNTPSLTLDRSTR QKYNKDIQDLNSALHQVDLIDI YRTLHPKSTEYTFSSALHHIYSK IDHIVGSKALLSKYKTTEITNC LSDHSAIKLELRIKKLTQNRSTT WKLNNLLLN
3997	34365	B	4038	877	8907	
3998	34366	A	4039	1	450	QGSPSGSRE*NSQSAGPQCALP PAMA*VPLSWRSMGKWWKRT SCTSDST*PPSERRHWSRKS SPSAMPASFRCSASAREMLP*KKG RCAAGSGIAPPPETWGRGTGGC PGKQATCGVSGPNANGEPVL/K YPSSSSEAHGGPGRNGRSD
3999	34367	A	4040	2	522	
4000	34368	B	4041	102	186	
4001	34369	A	4042	2	5417	

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4002	34370	A	4043	45	1585	KQPSGLLKFGNLIKCHPPSLTH MLSQPCAIEAPTPDPNWELA\LY IHPSSGIMSATVSFWSIGTA\YLE AQGIWEPFRRRLSFEASNPPFD VGRPFDLRRIVGISSEGNLNTLS CDPGHSRGFCGAGGSSSRPSAG SHKQ*GPSGHPHSSHSNRNSAD VDDVRAVNSGRTSSMTSAQAA SSQPANKTRPLVLDNSTGAQGH SAGRKSKGAKQSQHSQHHAH SPLEQHQPPLPPVPQPQEPQP ERLSPAPLAHPSPERASSARHS SESDITSLIEAMDKDFDHHDSP ALEVFTEQPPSPLPKSKGSTEGG PASTFTQAVDGGIQFFTDWCWE GPSSLLAVAREVQLALCIHELL IHGFSQLQVSGGPGAMPDPAAH LPFFYGSISRAEAEIILKLAGM ADGLFLVRQCLRSLGGYRQLN GTYAAGGAHCGPAELCEFYS RDPDGLPCNLKPCIPPSGLEPQ PGSSTACETPWARPSRPSARP RRWRSSLLRRTTSGCGPTTAA
4003	34371	A	4044	1	1773	
4004	34372	A	4045	1	663	MALWTLRPTLLVTCMLICAPG VMGAVVAPLTILGGPLLIRAAW YTAGIVGGLSTVAMCAPSEKFL NMGAPLGVGLGLVFVSSLVDQ MGRWFVAGGAAVGLGALCY GLGLSNEIGAIEKAVEYWFNSF VCHSNQONACSHELHDERLLG DMGLPILHAMLLRRLPSVDSQN ALSSIMLLHTALP*QSAERLFS* TS**EALG*YGFAYPACNASAK TTIRGLTECLIQHIVTPHSIASD QGTHFTAKEVQQWAHAHGIH WPYHVPHHPEAAGL
4005	34373	B	4046	147	330	

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4006	34374	A	4047	485	1568	GEGYKADLAAATVECPICQQQ RLTLSPQYSHIPQGDQPTTW*Q VDCIGPLPSWEGQRFVLTGIDT YFRYGFAYPACNASVKTTIHGL TECLVHHHGVPHGVASVQGTH FMA*EVQQWAAHGHHSYH VPHHLEAAGLIEQWNGLLMSQ LQHQLGDNTLQGWGKVLQKG VYALNQCSIYGTVSPRIHJGSR NQGVEVAPLKITPSDPLAKCLL PFPKALHSACLEVLVPEGGTLP PGDTTTIPLNWKLRLLPRHFL LLPLSQKAKKGATVLAGVIDPD YQDEISLLLHIGGKEEYAWNTG DPLGRLLVFPCHVIKVNGLQKQ PNPGKTANDPDPGSMKV*VTPP GKKNPRPAEVLAEKG
4007	34375	B	4048	182	662	
4008	34376	A	4049	1	2250	
4009	34377	A	4050	1	1326	
4010	34378	A	4051	1	1614	
4011	34379	A	4052	1	2586	
4012	34380	B	4053	1	1954	
4013	34381	A	4054	1	705	
4014	34382	A	4055	1	1833	
4015	34383	A	4056	1585	4128	
4016	34384	A	4057	1	1425	MARG/NAITLPV/CGRVAKFT/L EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLTGQQT PAFGRRVSGVIEIADGSRRRKA AALTESDYRVVLVGLDDEQMA ALSRLGNDYRPTSAYERGQRY ASRLQNEFAGNISALADAENIS HKAHKYFVEANTGTETGYQG EESLFNKAYYGGGTNFRKESQ KLQQSAAKKRDAELANGALGIIIE LNNDYTLKKVMKPLITSNVTVD EIERANVFKMNGKWDFAFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKITL APNTQTASPRALADSLMQLAR QVSRLESQQSSQKKAIAITAI RKNKEANAVLARLNSELQQQL KGFADFREPPIKQDFRLLGQTS VDRLLQLSQGQAITELCGAKRV GYFGPTQFYIALKLIAAASGLP VRIESIKCGNSYDHDYEFELGTL VLPRLSEGFALSNCGEHYWL

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4017	34385	A	4058	1461	2496	NKRNHQSVCHAFIRIPAAAPMV DSLIARVGV MARGNAILTPVCG RDVKFTLEVLRGDSVEKTSRV WSGNERDQELLTEDALDDLIPS FLLTGQQTAFGRRVSGVIEIAD GSRRRKAALTESEGTPAFGRR VSGVIEFADGSRRRKAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSA YERGQRYASRLQN EFAGNISALADAENISRKIIITRCI NTAKLPKSVVALFSPHGELSAR SGDALQKAFDKEELLKQAS NLHEQKKAGVIFAEAEVITLLTS VLKTSASRTSLSSRHQFAPGA TVLYKGDKMVLNLDRSRVPTE CIEKIEAILKELEKPAP
4018	34386	A	4059	340	2067	
4019	34387	A	4060	1	1959	
4020	34388	A	4061	1	2319	
4021	34389	A	4062	1	1587	
4022	34390	A	4063	964	1757	GYSGSKPDVITLLEQKEPCVV ARDVTRRQCPAAPMVDSLIAR VGV MARGNAILTPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSA YERGQ RYASRLQNEFAGNISALADANN ISRKNITRCINTAKLPKSVVALF SHPG/ELSARAASQRQCQGYHK LHDKQRLLRG*KGNICAKLLNE
4023	34391	A	4064	1	1554	
4024	34392	B	4065	1	1599	
4025	34393	A	4066	1	682	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGV MARG NAILTPVCGRDVKFTLEVLRGD SVEKTSRVWSGNERDQELLTE DALDDLIPSFLLTGQQTAFGR RVSGVIEIADGSRRRKAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQKHTKKRT ASLILHAMICCRSLNSSKTKNT KCLNSINQRLKILSLQKDL MCG TAGRCKTLTEQ
4026	34394	A	4067	1	2448	
4027	34395	A	4068	1	2541	
4028	34396	A	4069	1	828	
4029	34397	A	4070	1	1899	
4030	34398	B	4071	1	1686	
4031	34399	A	4072	1	1437	

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4032	34400	A	4073	1	3417	
4033	34401	A	4074	1	3826	
4034	34402	A	4075	812	2578	FIRDFADFGTTIKQDFRLLGQTS VDRLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGHNGN GQVSPHFHQTSSSTIRSCSCHLLT LNFLTLQLNTSDIAVFHSTPKLL LVTSTITHMGLNTSQAQSVPI NSVAGSLAALQPVQFSQQLHSP HQQPLMQQSPGSHMAQQPFMA AVTOLQNSHKFSHRSHGPGQS NDACSEPTNKKMRRNRFKWGP ASQILYQAYDRQKNPSKEERE ALVEECNRVWQARRLGAFGKE DVHVSFAARRGAKFRHQTLLG RRSSIPAAPMVDLIA RVGVMA RGNAITLPVCGRDVKFTLEVL GDSVEKTSRVWSGNERDQELL TEDALDDLIPSFLLTQQTPAFG RRVSGVIEIADGSRRRKAAALT ESDYRVLVGELDDQMAALSR LGNDYRPTSAYERGQRYASRL QNEFAGNISALADAENISRKIIT RCINTAKLPKSVVALFSPHGELS ARSGDALQKAFDKEELLKQQ ACKLHEQKKAGVGDNDSIDSW KNAGR VFKDSKFDANDPILK DQTQEWSGSATFTSDGKIRFIL

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4035	34403	A	4076	1474	3367	REEGANSECLGRHGFKKMLYV KRDEVGKGQIRLETVEQAIDQ RFSTDTSLSIPAAPMVDSLIA GVMAAGNAITLPCVGRDVKFT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDIPSPLLTGH KTPAFGQRVSGVIEIADGSR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGKCMVPTESAPH VTVLGCQCGLGLENGLKEY LGRSTLDMEAWQPLQEFYLN LITGQMFEIAVTQNNKINSSP TTEQSWMENDFDELTEVGFR SVITNFSELKEHVLTHRKEAK LEKSDGENTKLENTFQDIQE NFPNLARQVNIQIEIQKTPQ SSRRATPGHIIVRFTKVEMKE VLRAAREKASLAPENLNSKIR PVVILFHYGESWNLRLADQRL FAKSWPRASRYQQGHQDLFIL SDLPSQVFIRDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYVTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
4036	34404	A	4077	794	4235	RVSRGRKWFIFIALKRMAMP AMNLFGLSNVRTVHPEGFTV YISTHISFPLSGYRTGLRSFGLV KQKKSPIRMPVCYVNTLTCQYR KPDGSGIVSLKIDWIIERYQLPQ SYQRMPDFRRRFLQVCVNEINS RTPMRLSYIEKKKGRQTTHIDL ALKGLRVLLVEGNDPQGTASM YHGWWPDLHIHAEDTLLPFYLG EKDDVITYAIKPTCWPGLDIIPSC LALHRIETELMGKFDEGKLPTD PHLMRLAIETVA
4037	34405	A	4078	1	2574	
4038	34406	A	4079	1	536	

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4039	34407	A	4080	368	1449	LKSTNLITLRLFLVPMPLAYM KFTPSGLVAACAPWLQRQRRVV QLGQIAFSAP/YLSQMVRQEMY NRYGESAYEDGYRJTITRKV QQAQAQAVRNVLVDYDMRHG YRGPANVLWKVGESAWDNNK ITDTLKALPTYGPLPAAVTSA NPQQATAMLADGSTVALSMEG VRWAPYRSDTQGGPTPRKVT DVLQTGGQIWRQVGDAWWL AQVPEVNSALVSINPQNGAVM ALALLNNARPWYLGAPRDSTI IFCQFGAHLPLDPKTQPVGCRN AARKSCAEIRLVDPARANSGL VRRYRKYRRQYHKSRSRHOPL RQQQPVRLDWRNVNDQYALT TRFLYQSLQRHAQLNVPLFHVLT
4040	34408	A	4081	1420	1842	
4041	34409	A	4082	407	1347	GRIRVHIHKDGRADGGSQPGVT AIQQQLPFAFAFPN*SY*TESAW AQSIK/GPWWRDQVDGPAGR LAALPQR/SLINAVSTRMEGIG AFNTANPACST*FLCSLLILPSLF STALPNFRLSAMVSDCTISNMV WST/SAVTDWCTPLD*ERKHR GTARLTTGKGVMGMDRDKQVST LFLGFCYAHLQWNEDVFIARH VHLHIALFLDQRAQTASYLQYH IFFARFVPHRTGVFATVARLK HNDNRTIAPCFTRLWTLRLWR HLLFEVAFVVLQQRQQRVLHI LCIGRIEVHHQTLFKPGDRRKG KQLRFYVLL
4042	34410	A	4083	1	649	MRHGYPARANVLVKVGESAW DNNKDYRYAKALPTYGPLLPA AVTS/ANPQQATAMLADGSTV A/LSMEGVRWAPYRSDT/QQG PTPRKVTVDVLQTGGQ/QIWRQV GDAWWLAQV/PEVNSALVSINP QNGAV/MALVGGDFNQSKFN RATQALRQAGAHLPAHSQSGH HQQTAR*KSNFCARM*TPDQLS W**KNCPFRLSPT*QRQWSLRR YRPVSQRTSF

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4043	34411	A	4084	2	551	WRAAGPEPCPTGRQLRP/AGDL ACSAAGPGEFPTAPLALAGR SKCGAAEPATQNSRWPMSPH LSLHASPQAEAGAGSGL/VPAPR AAAG*RAPQMRP/VVGAEEAE APGP*EPCRHAPHASQHRVGC HPS/AEEPCHRPAPHASQHRVY CHPSGLNPAGTQHPMPASTGTA AIHRG*TLAPSSP
4044	34412	B	4085	1	1029	
4045	34413	A	4086	1	2157	
4046	34414	A	4087	1258	1838	TQVVFITSAWGLGEMVVQGA NPDEFYVHKPTLAANRPAIVRR TMGSKKIRMVYAPTQEHGKQV KIEDVPQEQRDIFSLTNEEVQ LAQQAQVQIEKHVYGSMD/IEW/ AKDG/HTGNGHVQALRNRCPE ARQHRMRIPGRILPRPIGRMAG PKTRIEHTSVTVISNRKKIKTEN RGHKGYEDRKLHEDQLRHQS
4047	34415	A	4088	2806	3540	
4048	34416	B	4089	1	1251	
4049	34417	A	4090	341	946	GLSSVGQSVNDHLPWT*GLSSV GQSVNDHLPWT*GLSSVGQSV NDHLPWT*GLSSVGQSVNDHLP WA*VLSSVRQSIDDHLPWT*VL SSVRQSIDDHLPWT*GLSSVGQ SVDDHLPWT*GLSSVGQSVDDH LPWT*VLSSVRQSIDDHLPWT* GLSSVGQSVDDHLP*M*GLSSV RQ*VT*AKVNPKISAVTRNRGS VESPHLEGRSLKQVFIQVED MSWGPPWLWVEGESWT
4050	34418	A	4091	426	706	VLGGGSEKAPLWWSGPMVLP GAHSMKT*LPHTHVEFGFACLA SAGAQDVGMEGPRHTTENSVT GSPSHFPPRASQHRGICRPHAG RATADF
4051	34419	A	4092	596	905	GLSSVGQSVNDHLPWT*VLSSV RQSIDDHLPWT*GLSSVGQSV DHLPT*GLSSVGQSVDDHLP WT*GLSSVGQSVDDHLPWS*G LSSVGQSVDDHLPWT*GLSSVG QSIDDHLPWA*VLSSVRQSIDD HLPWT*VLSSVRQSIDD/HSSMD VRSV*CRTISR*PSSMDVRAV*C RTINR*PSSMDVASV*CKTINR* PSSMDVRSV*CRTISR*PSIP*T* GLSMSLIPSQCLGSAVTPFSAV TRNRGS/ENHPILKAAASRSKSS FPRLKT

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4052	34420	A	4093	3	1194	SLGPRSHSCCRSDYRSGTTVPL VLLPVCVGPALLVFALLSPLCV VCSALCGGLLPVLRASLFLWCV AFLAGLVFVFGFAFFGSLVRGR FLVVVPFFLLFALCRLFLVCW LRSFGACPVSVCVAGFACFAGL FLVLVSLSSGFGRLSFSCVVG SLCLPGFAFRAFCLFFLPCVGPA LLAFPGFCGPSSPSLSYGGLFAP WSCALLGFFGCLGWSAPGLSS FGLSVRVLSPCASGLRSLSGC ALVPGLFLPWVFSRSLRPLVSF GCLLCFSVSHNMDWIKESAG KVIQGN*WLPVILFFGSVPLTS KAATAKPLMRMG/RALTVSQL T/AVASFAAVYGLFILPT*PTLV GAVQMDDTGTTTRIGKLVSNHP FFIRVLLGVALTVCFGFVLGSF
4053	34421	C	4094	70	1950	
4054	34422	B	4095	262	4347	
4055	34423	A	4096	2	458	
4056	34424	A	4097	2	445	QPTERGLCASLKPSRAAIKSQSS KVISFDSMSHIQGTVVQGVGSQ GLEQQYRSGVAVFRLHSFSHRL LSACEFSRCRVQAVSRSIILGSG RWQPPSHSSTREWPSGHTVWG LQPHISPLHCPSKDLS*GLCLCN KLPPENLGFSYVL

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4057	34425	A	4098	1	2589	MVWFLKNVNHGTHINAKEYN DVENKERTGWKVGSTYELLCA RPLRKGNVGLSGDVFLTVFVM KTGHSSSLPSTTTSDSTAQEGY ESRGGMLDWKHLLDSPDSTDP LGAVSSHNHQDKKAMLDGEE RPFNEPGVFHLLADHQLTQKV ASIPGSAVCAYDMLDIASVFTG RFKEQKSPDSTWTPVPDERVPK PRPGCCAGSSSLERYATSNEFPD DTLNFIKTHPLMDEAVPSIFNRP WFLRTMVRYRLTKIAVDTAAG PYQNHTVVFLGSEKGIILKFLAR IGNSGFLNDSLFLEEMSVYNSE KKWSTAKPVRVTIILNPGQASF CITLRETVC*RRKHWCPPYRC TLQ*HFCPC*HCLSGKETLCRVT GGMKVKADRDESLPYAAMLA AQDMAQRCKELGITALHIKHR ATGGNRTKTPGPGA\SRPSSPCP LGCLK/WQTLFPRRLRWPGGG RRKRSQLEAQRVIRESYLKGHD QLVPVTLIAIVIAFVVMGAVF SGITVYCVCDHRRKDVAVVQR KEKELTHSRGSMSSVTKLSGL FGDTQSKDKPEAILTPLMHNG KLATPGNTAKMLIKADQHHLD LTALPTPESTPTLQQRKPSRGS REWERNQNLINACTKDMPPMG SPVIPTDLPLRASPSHIPSVVVL ITQGGYQHEYYVDQPKMSEVAQ MALEDQAATLEYKTIKEHLSSK
4058	34426	B	4099	1	1299	
4059	34427	A	4100	95	502	FPEIPQSCREGAPGPAKPGGPRA REPCPNRTAASWGVHCEDEGGS TVRTGGPL*GRGVHREDGASSP QHPPRRGRGLGHLGPRPL*GGQ DAAAAPGHRGKS/GGKGFLPAL RVQRGERGRVSRRAVCMWTS CASVPS
4060	34428	A	4101	2	653	DSFGMSVLKINPRTLFGGKPY VCRECGRGTWKSNIHQRT SGEKPYVCKDCGRGFTWKSNI FTHQRTSHGLKLYVCKECCGQSF SLKSNLITHQRAHTGEKPYVCR ECGRGRQHSNLRHHRKTHSG EKPYICRECEQGFSSQKSHIRHL RTHTEKPYVCTECGRHFSWK SNL.KTHQRTSHGVKPYVCLC GQCFSKSNLKNHQ\RSHTGEK

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4061	34429	A	4102	8	389	LPASASQSVGTTGVISFENTCNI CHFFFLLLFFSSSSFFFLPFSFS FRVSLF*IQPLKTTASTVQGRQH SGGYRASPERRADQRAHTGEK P/YVCRECGRGFRQHSLLQLSV YPHSFWTQDKRSNH
4062	34430	A	4103	1	740	EGKGRGPRFRPRAHPFPHELQS RLCILKLPHHPTPSSCPSS*TPVA PLPSHPCAPH/SARSCPVSDEAA LP*SMALWARAGLLEAPTLL PAADASSPA/MPFSRKLPPPLP L/CPEPLGPSAAPSPPAPPGPNA AARPP/PPSPSAAPGPRRPGAIR PVGPSRGPG/PRNSRSLRAPDVH TAPMRCLPSVRPPLPVLAL/PD PLPRPPSFVPSLSP/PSSGPSCPP TSAPPGSPRPGFVRLPCLLFWGS
4063	34431	B	4104	48	272	
4064	34432	A	4105	2	622	CPLSPLLFNIVLELLARAIKEK */LKGIGIEEEVKLSLFGDDLIV YLENPKYSSKKLLELVNEFNKV SGYKIYVHKSVALLYTNSDQAE NQIKNSTPFTTATSSSSSSSSSP QGIFLTKRLKNF*RGKFKTLVK KNQGDPKKGKNPPGPKMGKN NFGKTPFWAKKI*KFHSNPKKT PPFFQKLLKKTGVKFFWAPKGP KGFLSKK
4065	34433	A	4106	39	1043	QKQPVVQRCREIGTLGYCGWK WTLDIHGRGHRILSGGVEIPGP WTEGFIQGRDVGELQEPGLSGR ESIH*GKSYEYECSEDEGEVFRV RASLTNHQVIHTAEKPYKCTEC GKVFSRNSHLVEHWRIHTGQK PYKCECDKVFNRNSNLARHQ RIHTGEKPHKCNECGKAFRECS GLTTHLVIHTGEKPYKCNECGK NFRHKFSLTNHQRSHTAEKPYK CNECGKVFSLLSYLARHQIHHST EKPYKCNECGRAFHKRPGMLMA HLLIHTGEKPYKCNECDKVFGR KFNLTNHQRIHTGERPYKCNA CGKVFNQNPHLRHRKIHAGE NSLRTIQME

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4066	34434	A	4107	3	941	QQHQQQQHFGVQVAIQQQQQ QGPVQVTNQLGPKPQGLMPP SSHQDLLVQQVSPRPQGPQG MVGPAQVGVLIQIQLHGALGP QGLH*QVFMPQSRVFSSPQLA QQGQGLMGHRLVTAQQQQQQ QQHQQQGSMAGLSHLQQLMS HSGQPKLSAQPMCSLLQLLQ QQLS*QQHLQQQQQQQLQQQ QQL*QPQLHQQQQQQLQQQ PQQLQQQHQQQLQPQINSQ/HL FSPRRPPNHMGLLTHSPNLTA LRLTSTHKAALGPGLQAALGHP KDGLLWKTGLTWRARGLICTG GIISYFTQHSWEVKVFRTL
4067	34435	A	4108	1	2255	MEKNKVVKREAEANSINLSVY EPFKVRKAEDKLEKNSDNVLE NRVLGKLSSEKNDTCLPGTAP SKTKSSSKLSSCSAIMALSAKK AASDSCKEPVANSRESSPLPKE VNDSQARAPLQSTVMTNAVSP AELTPKQVTIKPVA TAFLPVSA VNEMKTAGSRVINLKLANTTT VKATVISAASVQSASSAIK AAN AIQQQTVVVPAPSRANAKLVK TVHLANINLLPQGAQATSELQ VLTKAQQIKQAIINAASQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPTNAG ITLPTRGYKCLECGDSFAVEKS LTQHYDRQSMRIEVTCHNGTK NLIFYNKCSLLSHARGHKEKGV AADTRGQKTCTICQMLLPNQC YASHQRIHQHKSLEYTCPEGAI CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGSCHCEVFKPICPMACKSAP STHSHTYTQHPGKIGEPETIYKC SMCDTVFTLQTLRYRHFQDHI NQKLSVFKCPDCYLLYAQKQL MMDHIKSMHGTLKSIEGPPNGL INLPLSIKPATQNSANQNKEDT KSMNGKEKLEKSPSPVKKSV ETKQVAPGWTCWECDRLEFIQ RDVYISHVRKEQGMKKHPC RHLQCHNRKHKIRKVVYACSH CPDSRRFTTKRLMLEKHVQLM
4068	34436	B	4109	1	411	
4069	34437	C	4110	54	146	
4070	34438	A	4111	1	1937	

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4071	34439	A	4112	1	1830	MCIEVTCNHCTKNLIVYNKCNL LSQARGHKEKGVVMQCSYSIL KPVSAAGHIVPSSNSSSSSTLQ SPVGTGIHTVTKIQSGITGTVISA PSSTPSTTAMPLDEDPKLCRHH NLKCLKCNEIFQDKRSLATHFQ QAADMSGQKTCCTICQMLLPNQ/ CQRHGHKSPYTCPECRAICRK KRTQIHEWERETGKEISISFEKK SMETKKVASPGWTCWECDFHLF MQRDVYISHLRKEHGKQMKK HPCRQCDKPFSSSHRLCWHNRI KHKGIRKVVACSHCPDSTGTFT KGLMLEKHVH*CMASRTLTK K*QTTPMRRKQK*K*TSRAVP SGVVERTGSGVQASQRSNNSTT EKAENQCF*GSQAPLCCTQVKG TSASAQAKWGWR*PTGEQTQ PRGRISQWVMSDRCKVCAKT FETKAALNTHMQTHGHAEGCL KQPCRSLLSQPRIKTEARNLIRN ADFLNSILRNGEGYSKEKKNGT GFLGRSARLALGAQGGKSWRF LFWVLLPNVLRVGMHDVN HRLINAAGCVQLAVTLSTEPH GISSAISRVPRHCHPSGENSMAT SLNVNRSISRLAAGSGVLAMD PIPAGHRAIETGLGTEDTEQ
4072	34440	C	4113	217	510	
4073	34441	A	4114	210	281	
4074	34442	A	4115	1	675	
4075	34443	C	4116	126	434	
4076	34444	A	4117	804	2061	WERREAGGEDEGINIH*VEE EMKKHESNNVGLLENLTNGVT AGNGDNGLIPQRKSRTPENQQF PDNESEEYHSLGDKSKTSFQNS NNNNNKQEQQQQNPTFSNTR KLTKLYKAPIPPSIILSGCPNIND SNWQEIHEHGMQTAGLPTRPLSH GLQQKGAAFRCLGCKCEPFTG SLILQKAKTNTQKWQATYPKS QNEQLVPSVGKSYRCSTPAQP MKTAVGHKPKCATGAELPKAL GAQPLHPCALDVGGQFKGNF GAVGLNGLLGLFHVGSVGLL VGPDGGLISEGVVREDLMCG VWSAGTWSVGTAERCLEKPGA LHVIEGPLDSWDGVPVMPNGPV KSRQSSCLDGPGRCCSEILTGQS HGNNKPARASSKSSQINDRPL AVLTNQYQCEQLASERQPSNS

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4077	34445	A	4118	1	357	GKLMPLGSTRKPQVPVDRKMG HEGVFVWQAGLRARPGSLPFS HGLTLHLHWPLALPV/GATSSP CEAGDLGVPLAAGTWCPWEA *RQEEAGWQAPGRAGPARVG WGGTGLTSAEVIIT
4078	34446	A	4119	1	771	MLISHKQLSPQLLSLTPLSE GK AGWAGECPNPPSKDSPVQIGG/ GPPPGYQKCR*DTASMLTMAP CHGPVCPHPGWRPRSGSRVIL PAPPGHHPWP*GPRARNGLGT QGCTGWQVQETCFPGPGWLG DRHLVGPAATGARCLPAARGP/ DGALHPAVPTGKLGQPGPGA RHQRTYD*LPRPCGAAGLGSP A*HPISEETENQWGLHGPPQPA WARPDHGC/APILSPSLKRRK PGRVTAGGPMPCFSTSSVPTT
4079	34447	A	4120	1	402	MLISHKQLSPQLLSLTPLSE GK AGWAGECPNPPSKDSPVQIGG/ LHQLPKMQIRYSIHADDGVS PRAAHKGRLRKRRLTKTISL PRQESAFPFHGGQDGPVVP GSSFLHP LGTTGPGQPRARNGLGPSRAA PPAGRGVAGGSPSGVPAATGA RCLPAARGPVGPYTOQQORAS *KGS LGPGARHQR TYD*LPRPCG AAGLGSPPA*HPISEETENQWG LHGPPQPAWARPDHGRQPLRC HPP*RGSGGPGKAAVSQQIPR AGQEGTH*DPTEWGPDPDQDQ GPRESCRGLQGGRGQCLCDWS PNTSEI*YPHA*NGD*KAG/PPM DTKSQLQVSTPKSPASHGEDVA RLEEPEASGD/RSPV/GLPGASLI PIWRPPFSRISVRTFLPSFWNLL RDCGLGLTSLASSSGRVTA
4080	34448	C	4121	111	218	
4081	34449	A	4122	2	453	WWPVLSPPECLPGRLPSPG*V RGPAPWWPEPASQDKSQLSSR GFGPKVSLGKGMAFSP LQTAP* KWLGLSPPLSSTENTASRGHTS PSSRNGFDSQPRDSRTGREGQA TQLPAQHSHAEVLHFGGAMSG QLSLVGPQDSKRTARLTDSQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4082	34450	A	4123	1146	1775	KGWLEGAPEA*ERYPGVPPCVV CSLSDAPWVGHPAPSLGVV*EP NPP*SRGESQGTSSICRQSSGD LG*KLESPIHTVIPRHTSQARQG HTAPFPFFQVFS*LLV*LKAVSL APAEAP*PASGLHAPWVAPRV TCAI/PAKGTTPVAPGAELRPVS PPILLP/PDSRSSAFFPSRKGPASP YEICSPPTS*/EVPS*TYKSMGP GIRLPALPASPRVPSEGPLSEH PEGPPALPPAIPFS/SPSWFKQCS FSIRPGWLLHGAPOQKGWVQA SWVGKGT*PEKRGSPRGPESHA LNLRVALPGVAV/*EGPACVGV GGPPQPPGAICEATAPPSI/VPL SLPAPFFGTLP/PPTPAASP/PPAL PPLLRRGRPRPCAALALPALSSL FS/PPVFSLLSLQLPADRVVRQVH PVLRAFGPPFRPPKQIPSSSGDL PPPSLPGR/PVL*LEKWLPPAPK ASPPSSVNLILLVVVKLNTFRCG PLVKNLVPPSVVCPSPCSYKYL *ILIYIHTLHMGGQPPSPSSAGNQ SLCYPCGGLVAQPTKRTLVPPTI QLQSVPPPV/KPPCHARPVDSPQ PPSLPPPTKHGGAVQAQVWPDS FYPVLLSLG
4083	34451	A	4124	146	1701	TFLGYLETAHGPSAQQCPTGLF AFRSLGRGLLLTSLPKQPARSP REDVPRSTTQEMTRPRHPPRKP AQPGLGARRRGAPV/RGLSKSR ELNSGNTSDSGNSFTPPHPRTR GPCWRISPPPGAESQGDAMLL ARMQMPSLGLMSRTFFHSSST GKARGFQSPCLECAEVKKSSLV PSTARSSPMKGCSRSSSYASTRS SSHSSQSPNPRASPRVRTIITCIL *TRKRPRETKSSAKVTTHYYSK SGKRSPSPSSSRSSPSYSRYS PSSPNSPADIPQNSHPQPSASTD RPHIQSPQFLPTHQGLRNIHVLT PAAPALL*CPPANADTPAQAPQ PPLRY*QPSQTLTAAPSSSLRSP LRQRADPIP*PSGGAGSQI/WK DSQQRERERARRRRSYSPMR KRRRDSPSHLEARRITSARKRPI PYRYRSPSSSGSLSSSTSSWYSSSS SRASRSYSRSTRSRSRRRSRT RTSSSSSRSPSPGSRSRSRSR SRSRSRQSRSYSSADSYSTRR

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4084	34452	A	4125	1	1068	MLLLELNAPEHVLETINFQTLT AFCNTFHILRPTKAPGFVYAWL ELISHRIFIARMLAHTPQQKGW PMYAQLLIDLFKYLAPFLRNVE LTKPMQILYKGTLRVLLVLLHD FPEFLCDYHYGFCDVIPNCIQL RNLILSAFPRNMRLPDPFTPNLK VDMLEINIAPRILTNFTGVMPP QFKKDLDSYLKTRSPVTFLSDL RSNLQVSNFPGNRYNLQLINA LVLYVGTQAIHHHNGSTPSM STITHSAHMDIFQNLAVDLDE GRYLFNAIANQLRYPNSHTH YFSCMTLYLFGRRANSRPFQ EQITRVLLERLIVNRPHPWGLLI TFIELKKNPAFKFWNHEFVHCAP
4085	34453	A	4126	1	984	MQANLEMGAGNVTSMGMEPL AIPHIYCCSEGTNFSNTENHCL RAALSMLLNGTPFAFVIDLAAL ASRREYLKLDKWLTDKIREHGP SVHGLFPSRVLSPALPGGAFPG RHNGGSCVAPQSGLPGVHPVEL PWSISKFLRLRSPANFSDVLGSR SKVLLLMCTLK YCGMQLGADA TRVDMLTFLPTLGFIRNNDYTD DTKASELTELSHNLHAYDSVTG VPGDETECSKTVSTWAYTAESL QGYMAAKLLGRNLTVPSTRYLF LNAIANQLRYPNSHTHYFSCTM LYLFAEANTEAIQEQT/RLVRE RI*S*ANAYWHSEKFYQFTCEL
4086	34454	C	4127	1	399	
4087	34455	A	4128	1	868	MANVCNPSTLGGRRGJRTRRPE DPGSPVYSVPASYPHPKRWLGA QPATVVTGPNVTLRCRAPQP AWRFGLFKPGEIAPLLFRDVSS ELAEFFLEEVTPAQGGIYRCY RRPDWGPVWSQPSDVLELLV TEELPRPSLVALPGPVVGPAGAN VSLRCAGRLRNMSFVLYREGV AAPLQYRHSAPWADFLLGA RAPGTYSYCYHTPSAPYVLSQR SEVLVISWEITLAPPTPGGT*S AWGWPGWSSSPWARWSLLTG AVRTALLFPQVPHRATTWPVT SYDWVWLP
4088	34456	A	4129	1	270	
4089	34457	B	4130	39	919	

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4090	34458	A	4131	3	466	GRALCPPRLLAAGRVLPGRRS PGPGPGVP/GG*R*GGAEP APRGRVLPSSAGSQFSAATPA QNGLPALRGPSRPGIRSKAVR PVPLGRVGVYFRDALRASGQS GRKLCGIGNTLSPTSFSVGKEVP RKHETNQKHEKGILCMEAVKP
4091	34459	A	4132	1	1647	MWRWLYAGARMTVRDKQPLE QMLAGCTHASLVPTQLWRLLV NRSSVSLKAVLLGGAAIPVELT EQARDMGIRCFCGYGLTEFAST VCAKEADGLADVGSPLPGREV KIVNNEVWLRAASMAEGYWR NGQLVSLVNDEGWYATDRRRE MHNGKLTIVGRLDNLFFSGGEG IQPEEVERVIAAHPAVLQVFIVP VADKEFCHRPVAVMEYDHEVS DLSEWVKDKLARFQHLVRWLT LPAEPKNGGKIFHVSAKRVGAL TTRMEAAQQHADDKIRQMIN EQRLSEGFENLANRFEHSNRR VDEQNRQSI: NSLLSPLREQLDG FRRQFRTASLMKVAGWDYLM NSLYANSSALVNRVRYKWIA AFEGGFTGIVATLDTRGPVPM AFRVDMDALDLSSEQDVSHRP YRDGFASCNAGMMHACGHDG HTAIGLGLAHTLKQFESGLHGV IKLIFQPAEEVVRVARGRWSMQ VS*MMLIILLPCTLALAYLRALL CAAVIILWQPPNLTTRTSPVPLT QAQNKQKTVTMPCWRHTSHSCT ACNRPAQRSSFOS
4092	34460	A	4133	864	1128	TGRSTIRKQRREPRRKAATLRF DRNGCRARCTPPGRKEQRYQQ TADGDKGAEFYRRPEGVEIVA VMEQRDEVIQADKLAGECHKRI DAL
4093	34461	A	4134	618	1102	HSNAAPTARSSFFVQNTPS CGY SRRAWRISSEETDRTSYRNIQ CGNHPPVPARLPAGQTGDGDI PRPRWQSPQAPRKPDP/LIR KNKIPMFRSATTQPLGTGIAK ASSSEVKAIIGARVKMTRSENF GIQSSLNILIMSATSWEPPQP TRLGP

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4094	34462	A	4135	2400	3201	VGGGRNRSPGVACWVEDGNG DAVRDQWALDADWQASQAM RRKQQPEYWQHDAATADADR QMNMPLVLRALVAGRAQEM NGAQGKTLKGVWDEASARRG TKTEDVFCEEDTRDDAMIAWM PR*PGVLPRAAWANVLNHGV GWKKAQLKSTWMPQVQQ*W RGDKAANSNAVAHTVVLN SGGDATQTAAPFISPLSV/EEV CVTMVIA*FWMWDSGSGGVVL CSSSGRSLTSWSATKVRG/SGH KGRWCSRQGVTCQVRHGGHV APH
4095	34463	A	4136	118	1008	
4096	34464	A	4137	3	1140	KHTYMLSILKPVRTSALPPPAP AQTLCQTLSRVSSRL*DHPSR WGLR/PSTGMSQARACSPGSLG WMQSSFTPGAGVRVHIPNSA GSTRRPACGSRSAAPVPRCRR TR*G/RSSVVERFMTALSLACR ALPGP*AAPGPSITRRFTISAEK DTRL/PREHVPLVCTHAIAVPD RGAAVRPTRRRDAAPPSPLVG DVTLQCPQSQ*RGSNAPDQVRLP CVG*RPSSLRQSGLSVFSADGS TSGPEPASGRKDAGWPARVLR GTLRGAPEAGADWGPYSPGSP GAAASGAPWLGQPQALQGAG GQLVGSSENGERTGKPRVSVS VAYGEIALPADTSSWSSRAGAA VLLGLSRSTGGEGPGNMHGGG QSQMLTLEVL
4097	34465	A	4138	10	585	PLEMELNLISIEVWGERLGISTG TEKMPTLKHRTW/PVECSKASSL EGDLRLS/S*LEVISAFSADPASA DDSPGCWKKKDDCSMVHLHR QEWQQQCCQ*K*RKQPPGER RNKCGSHPVCGTVLWQP*QTH/ QISSCPTVGCPPSHSSFSILDGAN AGQEQSQSTTEPEPALFLLPPSRG AFGPFGLLSDLRRQL
4098	34466	A	4139	1	474	
4099	34467	A	4140	458	612	ASCMASVDISVLTCMWRCETIEQ SSSFLCLLTPLWE*SWCHVTRIC PFISLG

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4100	34468	A	4141	1	829	MGRPDLILSSILGLRWLLLPQSS RAGRRAIREASDAEQVTFSGG TVPARTSSGREWRSLGPDMET TSLFCIDTKTTLFVYRYGDHIP LVPEQSGLEPLLIWADPGLFHV RLFHILLTIDDNFCGLDMNAPLG VSDMVRGIPVFTEDRDRMTSVI AYVYKNHSLAFVGTKSGKLLK /VRSSAAP*VWDQTPRSLGQQ GAQRQP/ILRQCVYTFQLN*RC PHSTARRELRTGGFIPTRSHQD GLRSAARCTQGTQ*ASWSCV HVCASVRAMCSYC
4101	34469	A	4142	5	237	NFGAMTRIR/DLPWEINPLSSCS SLCEKDPPTTSSPQTN*PKEHHT NFQSETGDEFYPWTQNFSTGHG LGKTVFPWCL
4102	34470	A	4143	1125	1190	
4103	34471	A	4144	306	573	RNFGAMTRIR/DLPWEINPLSSC SLLREKDPPTTSGPQTNQPKKH LTNFKSGKRPLLTLFNLSHCP TTFPPFFNLSELLISIPFIW
4104	34472	A	4145	1	329	ASHSWQTLQHSGRYSRSSG/SA GSPRDCAARAPTISPGCMAWL NLDSISPSQSKASPLSQLTCPET SYTGCP*SAPHSPPPWPQERC ACKGHCLHHRDGC CGYGYN
4105	34473	A	4146	2	336	SILTRKCKYGM EIPT/NIPGLGA AGPTGMFFGSAPSPMGGISPAM TPWNQGA TPAYGAWSPSVGSG MTPGAAGFSPPKA/PTYSPTSPG YSPTSPTYSLTSPAISPDSDDE
4106	34474	B	4147	1	1260	
4107	34475	A	4148	150	335	SFQQSAPW*ASGQSCASDPAPP ATARGRFGPHQSQAFHSRHSPIP DPLPPCSCGGWGHRSRW
4108	34476	B	4149	1	3267	

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4109	34477	A	4150	1528	2973	GKQIFSLIIPGHINCIRTHSTHPD DEDSGPYKHHISPGDTKTVINNW LLIEGHTIGIGDSIADSKTYQDIQ NTIKKAKQDVIEVIEKAHNNEL EPTPGNTLRQTFENQVIAVVGQ QNVEGKRIP*LPPPL*WGAGRR EGVG*CGRFSEHSRSSAAGYRG GRPCC/PSWEDDP/GAPPDPAS AQIPAPTRSGCVRCSARPSGPPP AECAAGPSHWYNQSGTSSQKP CWKA*AYPGSGTQSRGSQLAR SHP**SEAESGA*SQMESACPRR SAVQRQQ*PDSQTSAAECSLG WAPAHCCVPSR*PLLRPAWPS* *CSECPGKS*NQWSPQCQ*YD PNPQSTVVAEDQEWVNVYYE MPDFDVARISPWLLRVELDRK HMTDRKLTMEQIAEKINAGFG DDLNCIFNDDNAEKLVLRLIRM NSDENKMQEVVMGVLEVSVSHV
4110	34478	A	4151	459	940	HLPGGGVPGREGGSPDQHVAP GAYSGGAGGGSTRGRGSRRRR PGRPRPGPRQPRRGAIPGGEHG LRASARCAARAQQRDGP/TPSC SSWACPTPRRPWAPAASSLRR PPRGPACATPPPCRPPARRTCTG RCPPSCCLCGSPITWRRPPPTG GALESPKRR
4111	34479	A	4152	264	1386	SSRCQPVCESGHPGYGQSPA/YT TAGRTESGGTGST/GDNHPLWP CI/GGAPCAQNTPHLRVC*RSH ALALDSAGSSPESPH*RASIPH TTLGQKRRSWAGTAHS/PMAPC AAASISTST*LSHHHSPAAQSVC PSSHTTSPFCPIQKFHCFR/SPQR NTS*VVLCPGG*LRVG*WPSSG HDRSWYHTREPSVGN*HRSHQ RR*RGTAAPAGPSARLQCPARG SRSSHSAPASSRRRPFPGSTPAG LGFP SARFPVGPV VPAALMNR PTRGERRFAYWAPGWFFFPVR RATADCPSP/SW*ESCSKRSTL VCPSRRKSLMVVPKSAKSPVL AK/YGYPVGHHDGTEHDVVLGE VQKRPVAPMTMGTPKHKA VHP RAPH
4112	34480	B	4153	52	363	

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4113	34481	A	4154	321	802	HLPGGGVPGREGGSPDQHVP GAVSGGAGGGSTRGRSRRRR PGRPRPGRPQRGALPGGEHG LRASARCAARAQQRDGP/TPSC SSWACPTPRRPWAPAASSRLRR PPRGACATPPPGRPPARRTCTG RCPPSCCLCGSPITWRRPPPTG GALESPKRR
4114	34482	A	4155	15	263	CGRFSEHSRSSAAGYRGGRPCC VPSWEDDP/GAPDPAPASAIQAP TRSGCVRC SARSPGPPECAA GPSHWYNQSGTWKCKG
4115	34483	A	4156	3	518	SPSVGSGMTPGAAGFSPSAASD ASGFSFGYSPAWSKPGVPGVP QVPSKPLKSLHPGGVVRHL.SGQ VCFHSSG*VCPLLIHFVGCFT GGAMSPSYSPSPA\VEPRSPGG YTPQSPSYSPSPSYSPSYSP TSPNYSPTSPSYSPSYSPSYSP SYSPSYSPSYSP
4116	34484	B	4157	620	6763	
4117	34485	C	4158	430	870	
4118	34486	A	4159	1	3039	MDSETRRTAKVRLMTVLRLDQ DRVSGVQAHPQFQQAICPLCG VSLTRSGTTFGSPSEIYSLGESR ASSGLPRRDGRLIGEEPPEKKFS RSPKGD/LSSGGQRIDYRVCVPT KFNL*VLSF*PRGQAGGQSPG FSVRRLLVLVWSSGTFV*NGK* QKLL*TLCEVHD*GVQGPASG SPVCSSATAKATEFEKDPSPGFSS SSLPLTPYISFSRVTAASSAPGLG SALTPTQLKRGRI*AICL*VVE TPKVR
4119	34487	A	4160	1	772	MVARAFLWSQVIRRLGRKGGL SQDGRGCNTALAEGRDPLDT RGHPALCLPRRAPRPAEVRRE GEAEQPEAGQPPGAAPRRARD NGAAAAAAGRLLQSVRPVV CPHPGPQASYGLRYIAKVLKNS IHEKFPDA TEDELLKIVGNLLY YRYMNPAPIVAPDGFDIIDMTA GGQNNSDQRKNLRSTAKVLQH AASNKLFEGENEHLSSMNNYLS ETYQEFRFKNVTFDIIATEDVGI FDVRSKFLGVEMEKVQLNIQ
4120	34488	A	4161	174	444	YHRHDSWRNTRR*IKLDGKGE PKGAEESEATSKYTAALKHEK GVLLDIDDLQTNQNAVNDFSV GPQDEVIVEDITNCYLCEIFKRY EWVT

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4121	34489	A	4162	379	520	GTSHRGASQRRCCPPLSKTGPK TPCGKGAPSA*QGGLDVQGEP GGKIGDSSGECVGGNVACLHK GGGTRADSQVPGGMRGGRMS YGG/HLTAEGPMGRSGPR/GAV PSLYPPGFSRGCSRQYSGAHM PILTGHVGVWSESLDPPRAGQD RFLGTARP*GTSHRGASQRRCC PPLSKTGPKTPCGKGAPSAFIP AGPTFDHKALM
4122	34490	A	4163	455	798	
4123	34491	A	4164	32	2109	WIGGCPGSPQDATAIMGWTLA PHSSRCHRCCHYRCHRCCLCP AEMTVGRPEGAPGGAEGSRQIF PPESFADTEAGEELSGDGLVLP RASKLDEVLSPQEEIDPTSDSTG SIYHTLLDLAQGRWLSVWSLS FSLTQRVMKTSKMRKTWRVS SKTRTGGWCRSSARRL*GVAPQ GAA/DSLNNLPSNIPRQTPPP GSRPPSQHRVSVWASSITVPRP FRMTLREARKKAEWLGSPASF EQERQRAQRQGEFEAECHRQF RAQPVPAAHVYLPYQEIMERSE ARRQAGIQKRKELLSSLKPFSF LEKEEQLEAAARQDLAATAE AKISKQKATRRIPKSILEPALGD KLQEAELFRKIRIQMRALDMLQ MASSPIASSNRANQPRTATRT QQEKLGFLLHTNFRFQPRVNPVV PDYEGLYKAFQRAAKRRETQ EATRNKPFLLRTANLRHPQRPC DAATTGRRQDSPQPATPLPRS RSLSGLASLANTLPVHITDATR KRESAVRSALEKKNKADESIQ WLEIHKKSQAMSKSVTLRAK AMDPHKSLEEVFKAKLKENRN NDRKRAKEYKKEEEMKQRIQ TRPYLFEQVAKDLAKKEAFQW YLDTLKQAGRRKTL*ETRVKA PGLFKRRPKSRIFPGSKKLQNS ASEIQSR/RLEGSLEQPASPRKV LEELSHQSPENLVSLA
4124	34492	A	4165	251	637	

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4125	34493	A	4166	1	1344	PGRTRTSMADVFLSAPIPRG ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEEE EEEEDAVLVAEAEAAAGWM LNFLCLSLCRAFREGRSDFRRT RNSAEAIHGLCSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKEHDKLHE EIQNLIKIAIIVCMENGNFKG AEEVFERIFGDPNSHMPFKSKL LMIIISQKDTFHSFF/QHFSYNHM MEKIKSYVNVVLSEKSTFLM KAAAKVVESKRTRTITSQDKPS GNDVEMETEANLGYKKK*LT NSLR*LNQVRVQYPY*GSHKNL FLSKLQHGTQQQDLNKKERRV GTFQSTKKKKESRRATESRIPVS KSQPVTPKHKRARKRQAWLWE EDKNLRSQVRKYGEGNWSKIL LHYKFNNRSTVMLKDRWRTM KKLKLISDSED
4126	34494	A	4167	1	1345	IPGSTISCLKGQYPSEFPNMAED VSSAAPSPRGACADGRDADPTEF QMAETERNDEEQFERQELLE QVQVGAPEEEEEEEEDAGLV AEAEAAAGWMLDFLCLSLCR AFRDGRSEDFRRTNRNSAEAIH LSSLTACQLRTIYICQFLTRIAA GKTLDAQFENDERITPLESALMI WGSIEKEHDKLHEEIQNLIKIA IIVCMENGNFKEAEEVFERIFG DPNSHMPFKSKLLMIIISQKDTF HSFFQHFSYNHMMMEKIKSYVN YVLSEKSTFLMKAAAKVVES KRTRTITSQDKPSGNDVEMETE ANLDTKRSHKNLFLSKLQH GTQQQDLNKKERRVGTQSTKK KKESRRATESRIPVSKSQPVTP KHKRARKRQAWLWEEDKNLRS QVRKYGEGNWSKILLHYKFNN R/TSVMLKARWRTMKKLLIS DSEDWIVFVKL
4127	34495	A	4168	3	378	LTSGSRADQEGQEAGGGR ASSSSSSSPRGQHPHLHGDP AEHRPGHPLCSPDPLTVAYQM PEVPAEDM/SDPSFCARQGGQ RGLDSGPAPWSSSHSPHSRQ EASHGACAGWRWCRQEEL

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4128	34496	A	4169	1	1044	SGQE VNKEDGQADVQDHHH DEDGVGDLARQPHLHHLRL CRQCGLLPRLILGPRIQQPSSLS LAGLGPGLFGDDGLGLQLGG GLACRLGASERGGQLRGGRG RGRGLGP/GPRARAGPQRVGA RAAWCAQHSCGSPGKAPPPAP A/TGAGGACRASMAMRSVAGR AGLRRPAPSDGVTDRLPSPLGS PFQAP/EAQQA/VLGHGPGPLG LRGRPGR*RGATLGPRLT/PRA AAGSRGA/VGGPLRRRPRGGA PAGSPSPGSPAAGASDIPDLA GRSPEPAPWPKECQWT/PGWQ PGRPVPLQLWPWRGLSIGSGM PLGEGLEDGSDPMTSPCLPGT
4129	34497	A	4170	1	732	SLTQAGTVSLGLDAEGQEVFP FSAVLPMPVAPNDLVFDGWDISS LNLAEAMRRAKVLWDGLQEQ LWPHMEALRPRPSVYIPEFIAA NQSARADNLIPIGSRQAQLEQIR RDIRDFRSSAGLDKVIIVLWTAN TERFCEVIGLNDTAENLLRTIE LGLVSPSTLFAVASII.GGLCLS FNGSPQNTLVPGALELAWQHR VFVGGDDFKSGQTKVKSVD FLIGFRLQRP/VSIVSYNHLGNN
4130	34498	A	4171	1	908	MEKAPPQTQHEGLKSKEHLPE QTDEGKTEYRRVPSLRAVVLFR QRSNIENILRACVGLPPQNHML LEHKMERPGPSLKRVPQVAAT YPMLNKKGPLVWEVSPATLFA VASILEGCAFLNGSPQNTLVPG ALELAWQHRVFVGGDDFKSGQ TKVKSVDLFLIGSGLKTMSIV SYNHLG/NNNDGENLSAPLQFRS KEV/SRSNNVDDMVA/INP/ML YTPGEEDPHCRMGRNLPE*GSS
4131	34499	A	4172	85	529	ECGARPGSSTRPPARLSPLFCFS AIRAALKTRPAPALACTWRTG* RASLPTTRCAGSLGTCTAEGS EGCSPHPLGTGTG/RQEACPGT APAGSPSCLHPRGRPRPCPPGTL APRMSCPWPRSPPLTRYLPSGE NLQSKLESNTSEKF
4132	34500	C	4173	215	324	

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4133	34501	A	4174	2	505	YKCEVCDKVFNQ*FLVCHNR CHTGKKPYSCYECGKTFSQTSS FTCYRRLHTGGKPYKSEHNK TFG*NSALVIHKAHTGENPCKC NECGKVFNQKAHLARHRLHT REKPYKCECEKVFSRKSHLER/ HKLKRGGVAL/C*ECPTVYQN TSLRSLSCSYPMSLNG
4134	34502	A	4175	1	6192	
4135	34503	A	4176	2	3389	
4136	34504	A	4177	3	875	GEEAALSCMIHSTDDATRLGA RDTEPLWHVPAQ/ARLSAIAGS SGNKHPSR/QDAAGKDSNPRHS KVGSKPSAGSLRLSSREGEDRTA WTGPRGAVEQEVTGPDLC*GR GQQGLLVGWT**EQKRGQKGP QYSSSHSSNTLSSN/ASSSHSDD RWFDPDPL/EPEQDPLS/KGCM SLAK/APRPAKPHKPPGSMGLC/ GGGREAAGRSHHADR/REVSP APAVAGQSKGYR/PKLYSSGSS TPTGLAGG/SRDPPRPQSTLWH RTWYL/YHTASAAVHRGLCRE LEQADQIPPSWYGRPMGNS
4137	34505	B	4178	108	318	
4138	34506	A	4179	103	540	RRGCESHKTLRRGTSWGDLAR GGGPGPGQVSAGRDGAEVWLS TCDRGHALSGSVEELLFLQN/G ARTER*EGPGEWPRPPPPGLASP ALWRFWAEQVGGSFQNESSPS CRTARGSSRTWGSILQNSSWLF QDLGLHLAEGCFLETP
4139	34507	A	4180	33	896	KITRHTAPGKIRIVPKESQEST PQDQAGPGRATSCSARWSPR SWKSHELFCMEPQVLEEPRA VLQDQAGPGRATSCSARKGR GPEKPVQGLPN/GSVRAHSGGR AAPQSPRGHGPGRG*TAAPLP HLCPLTPVLLQG*GPD*WPLGW ATMRPLPLRAQAPPPPHWML LTSPAPPPGTGKPGQGRGQTSG SCVPATDPHCLRSAPSPGKLGPP CDFLEPP*QRTTNWGSSEAGSP KSRCPRGHVPSGGSKGGIFLSL HFGAPQSLFFPGSQPHGLIGAS
4140	34508	B	4181	1	625	

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4141	34509	A	4182	160	1149	FASERMKVEPWRAGPGRRAWS EGAGQAPQKRARAGAEPQLPA TPALPGGKMVARRTKLA\RGTR RTY\PEPTVYAAIPIKFSEKQQA SHVLYVRAHGVROGKTSTWPQ KRTLFVLNVPPYCTEESLSRLLS TCGLVQSVLELQEKPD\LAESPKE SRSKFFHFKPVPGFQVAYVVFQ KPSGVSAAALALKGPLL\STESH PVKSGIHKWISDYADSVDPPEA LRVEVDTFMEAYDQKIAEEEE KAKEEEGV\PEEGWVKVTRRG RR\LCSPGLRQPA\CGCWGRD SAA\KRAAQLLRLAASREQDGA SSAA\RK\FEEDKQRIELLRAQR KFRPY
4142	34510	A	4183	2	361	GTMVARRTKLA\RGTRRTGIPS PPC*AA\AIMCSEKQQA\SHYLY GRAHGIQGTSTWPHKRTIFA FNGPPYCSEQESLSCLQSTCGL VQSVKLKEKLELGWESRSKFFH PKPVPVTEEQ
4143	34511	A	4184	917	1128	
4144	34512	A	4185	1	660	MAWQMMQLLLLLVTAAGSA QPR SARARTDLLNVCMNAKYH KTQPSPEDELYGQ/C\SWRKNA/ CSFTSTTQEAHKN/TSHLYGFN WNHCGEMVPACKRHFIQDTCL YE*PPNLGPW\IRRYAWLPGIQE LAELNFP\GVSAGSNPSSSIQ WVPGILEPEPFFSTKISQVDQSW RKEWVLNVPLCKEDCEQ\WWE DCRTSYTCKSNHGKGWNWTSG SNKCQVAAA
4145	34513	A	4186	216	781	MDMAWQMMQLLLLLVTA GSAQPRISARA\RTDLLNVCMN AKHHKTQPSPEDEAVWDP/W MCKGSCRKTKSWNI\HRKSKCE VG\LA/WEACVSAGTGRGPGC GRWVGAPQGP/CPRKCSSG*PT W/VQRSQNMEEMAV\VNQSWR KERILNVPLCKEDCERW\WEDC RTSYTCKSNWHKGWNWTSAPS AVCDPLL

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4146	34514	A	4187	3	625	QCRPWKRKNACCSTNTSQEAHK DVSYLRYFNWNHCGKMAPDC KRHFHPTGTPALYE/CAPHNLGA WDPAGWIQSWRKERVNLNVPLC KEDCEQWWECDRTSYTCKSN WHKGWNWTSGFNK/CAVGAA CPTF/HFYFPTPTVLCNEIWTHS YKVSNSYRSGRGIQMWFDAS PGATPIEEV\ARFYVAAMSGAG PWAAPWFLSLALMLLWLS
4147	34515	A	4188	1	268	EQGRH/GSSTPVGPRGPRGAE HAPKHQCGDRAGPQVGMQ RRRDPPRAPAPRPWCQQRRAA LSSLGGSHLCDDA*VQPSAGLG KVLKF
4148	34516	A	4189	2	1632	WKRCPLPRAAATFPSSGSGAG GARREAGGRAPTPGPASPTAR GHARNSPAPARTAGRTGSAGA WQTPCPAPLFPMSAGLPAACH WNPV*LRALKTG/LEGVLGSSA DTQHNRTVDGSLAPN/AACVYT PKINGNRHPNTCKMFIVSLDA KGKKWKQPTVHIQQRKRETCG LHPRKCLQYTPS*WSTTTGILPS RTPRISCVQFVKKGLGQAGLLG HPGACLLCTL*PAGVGTFLFP RGC*GVVH*LEHTTCG
4149	34517	A	4190	2	87	
4150	34518	A	4191	3	291	
4151	34519	A	4192	112	286	AWLLWLTSLPWGSLYALALLA NKPAL*SLLLRYTLPLPHHQ EKVPRWNEPQPTLFP
4152	34520	A	4193	1	933	
4153	34521	B	4194	1	999	
4154	34522	A	4195	135	1160	VVALVRSTLELFTDDEEEGE YDEVTEEVTEQVYLPAAKVA QEEEVHPYSPAPHYFEEKEW PDPPDLSFLEDTGKVVAPVTE QHLERLLSVLFQRQFSLDERD DAVEQLRGVCIRAWEKITSGGE QYPSFSAVKQGPKELYADFIW NLLRQESLKKVISDSAAQDIVL QLLAFGNVNLDCQAALRPIRGK AHLVDYIKACDGIKQDSERF AFTIPVNNLQPAKHFYFTDG SSNGKASYSGSKGQNGQPIWIL SRHLKPYHEPDAKEEIPGG/CPR TPWLQPCRD*C*GGP*/PVSNT R*TQPPTWGQIKKLSQMVEENL RKAGQLVTMTVYWN

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4155	34523	A	4196	502	578	LV*EDCIAERAELVRNESYGIID WSP*GMFSLNCTSQSACHGHT MFSW
4156	34524	A	4197	2	408	
4157	34525	A	4198	3	853	LLKVMSAKIFTKKENSTERL CGDGEKRGPDFRTERS VWLLR LEEA VAMVQQRGSRAPE SRVVA QVLTL LDGASGDREV VVVGAT NRPDALDPALRRPGRFDREVVI GTPTLKQRKEILQVITSKMPISS HVDLGLLAEMTVGYVGADLTA LCREAA MHALLHSEKNQDNPV IDEIDFLEAFKNIQPS/LVFEASL GLMGIKPVDWEEIGGLE DVKPE VKTAH/WSLRQKSGHC/RSCAR LPTGLLATLGSGSGSGRATEAV SGPAG*KRASIGSSQRP RRFPPT
4158	34526	A	4199	266	370	AERINSITVFSETLKRFLQASGK *FHRDIHNSRN
4159	34527	A	4200	1	1780	MGDVNQS VASDFILVGLFSHSG SRQLLFSLVAVMFVIGLLGNTV LLFLIRVDSRLHTPMYFLLSQLS LFDIGCPMVTIPKMASDFLRGE GATSYGGGAAQIFFLTMGVA EGVLLVLMYSYDRYVAVCQPLQ YPVLMRRQVCLLMGSSWVW GVLNASIQTSITLHFPYCASRIV DHFFCEVPALLKLSADTCAEY MALSTSGVLILMLPLSLIATSYG HVLQAVLSMRSEEARHKAVTT CSSHITVVGIFYGAAVFMYMV PCAYHSPQQDNVVSIFYSLVTP TLNPLIYSLRNPEERSHRGVKL NECNQCFKVFSTKSNLTQHKRI HTGEKPYDCSQCGKSFSSRSYL TIHKRIHNGEKP YECNHCGKAF SDPSSLRLHLRIHTGEKPYECNQ CFHVFR TSCNLKSHKRIHTGEN HHIECNQCGKAFSTRSSLTGHN IHTGEKPYECHDCGKTFRKSSY LTQHVRTHTEKPYECNECGK SFSSSFLTVHKRIHTGEKPYEC SDCGKAFNNLSAVKKHLRTH TEKPYECNHCGKSFTSNSYLSV HKRIHNRWI*/YYGRNFWRKAL IDLSSLR*FERAHTGYISYLLQH
4160	34528	C	4201	18	182	
4161	34529	A	4202	1	389	
4162	34530	C	4203	114	548	

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4163	34531	A	4204	122	735	LRAQQQH*N*VLT.LHKPACT.LST TS*K*LHKIRK*L.WHLRDRAPFI FTSEMEYFITEGGK/NPQH/QDF VELCCRAYNIIRKHSQ.LLLN.LLE MNSYNGYVGLLHNILQLEREG LATKEELQONFPPLSVSLPFDQS INQISEHRSLIFNGQYPYGSCWF RQAVCKLIQKYAGEWGIATA ELRAEIDLNVLFKFTIQVLSWKV QASLQ
4164	34532	A	4205	139	4496	KMAYSWQTDPNPNSEHEKQYE HQEFLFVNQPHSSSQVSLGFDQI VDEISGKIPHYESEIDENTFFVPT APKWDSTGHSLNEAHQISLNEF TSKSRELSWHQVSKAPAIGFSPS VLPKPQNTNKECSWGSPIGKHH GADDSRFSILAPSFSTLSDKINLE KELENNHNYHIGFESSIPPTNS SFSSDFMPKEENKRSRGHVNIVE PSMLLLKGSLOPGMWESTWQK NIESIGCSIQLVFVPQSSNTSLAS FCNKVKK
4165	34533	A	4206	1	3150	MEKPRPLEAPSAWPQDDVQCG VTVMGDGAAVRANKTPWPQD LEQTKWIEIKKSFTWSSQLSL NRGFLTCKDENNNAGLLRVSS YSSREDQLKNIASDSLFLPFGG LCQSPGTGSHCSNQMETQGGGS PGGAVRGDKALGPEKARQCGG MNGSGKYCKFRVLAIQGKPEC LATLMQPDLDGDSPLREMNIV EHLRASFPVEQWYWRGGQRGE AEGARSSKAENNTSLICNFRLD YAPIEKQWDLHFADYFAEDLK
4166	34534	A	4207	1	1203	

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4167	34535	A	4208	1	1470	MLHSRGFLAEVFGILARHNISV DLITTSSEVSVALTLDITGSTSTG DTLLTQSLLMELSALCRVEVEE GLALVALIGNDLKACGVGKE VFGVLEPFNIRMICYGASSHNL CFLVPGEDAEQDGTGTSIGGAQ KKKMYANNGAIDRKLLFEATF VTIEKCCDTNQKDDTHALGQ PIRGHDKSLAGSCFYACRSEEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNIAGDLTAVIAPDGS RNGTQYDAWGKAVRTTQGGAL TRSVIEYDAAAGRVIRLTSENGS HTTFRYDVLDRLIQETGFDGRT QRYHHDLTGKLIRSEDEGLVTH WHYDEADRLTHRTVKGETAER WQYDERGWLTDISHISEGHRV AVHYRYDEKGRLTGERQTVHH PQTEALLWQHETRHAYNAQGL ANRCIPDSLPVAVELTYGSGYL AGMKLGDTPLVEYTRDRDLHRE TLRSFGRYELTTAYTPAGQLQS QHLNSLLTYRHANFAL
4168	34536	A	4209	757	907	RRYCRITVRWQSM/WADNRRIA VDAHYPYR*CRS/GRVTEKND/ LIPKGVIRTDDETRHYHYDSQ HRLVHYTRTQYAEPLVESRYL YDPLGRRVAKRVVRRERDLTG WMSLSRKQVVTWYGWDGDRLL TTIQNDRITRIQTIYQPGSFTPLIR VETATAVMDRILKDHQIVVDIP HGEAWLRDDEERPMILIAAGTG FSYARSILLTALARNPNRDITII WGGREEQHLYDLCELEALSLK HPGLQVVPVVEQPEAGWRGRT GTVLTAVLQDHGTLAEHDIYIA GRFEMAKIARDLFCSEARNARE RLFGDAFAFI
4169	34537	B	4210	1	3258	

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4170	34538	A	4211	281	1571	CQCPGAACPTTSCRVPVHWA/Y DEADRLT/HRTVNIGETAERWQ YDER/GWLTDISHISEGHRVA/V HYRYDEKGRLTGERQT/VIIHQ TEALLWQHETRH/AYNAQGLA NRCIPDSL/PAVEWLTGYSGYL AGMK/LGDT/PAANLDIRIPYAT DPA/GNRLPDPDLHPDSTLSM/W ADNRJARDAHYLYRY/DRHGRL TEKTDLIPEGV/RTDDERTHRY HYDSQ/HRLVHYTRTQYAEPLV E/SRYLYDPLGRRVAKRK/DRTR IQTMYPGSGFTPL/IRVETATGE QAKTQR/RQLADTLQQSDGED GGSVVFP/PVLIVQMLADR/LESE SSADRVRSFISLANQSKCVEHA Y*RWQCHLGVCWWSSHQIPAV PLTGSVTRWHCHLASSSEAGSV AWLPHLSEGHNSRTSSPELLRS RMCAWHTLSAQSVHVLVSLYL EILALMNSINSL
4171	34539	A	4212	311	788	
4172	34540	A	4213	29	395	RIFHSVIGVAAHKGGVYKTSVS VHLAQDVAEIT/LLEGNDPQGT VS*YQPGRTLIPLEAALRNIAH LSIPPPKIFAAPILRHYFALFFC GHSLFAPHIELLEAGTVLQLPQ GPWSSPTSF
4173	34541	A	4214	1	1033	MKMPEAIATKEKIDKWDLIKIK SFFSTPKETNVRNRHHTEWEDI SAIHLSDKGPISYIYKNLRFTR KKQPHYKVGKGNEQTRILESHP HLLKGLASTPFDSEGVRTERRD IHKDILTQWLLTSYSARKLGLK STGHAGGIHNWRIAGQGLSFEQ MLKEMGTGLVVPGTAEARSC IRAYFYDIHETLCRQEEMALSV VDDHVREKLIWLRQHEDMTI LLSEVSAACLHCEKTLQDDCR VVLAKQEITRLLETQKQQQF TEVADHIQLDASIPVFTTKDNR VHIGPKMEIRVVTLGIGMGAG KNLLSLF*V*NRVEFHGSPFPTI WFLTWEIVGFLK
4174	34542	B	4215	414	1022	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
4175	34543	A	4216	896	1626	NATTIRYEHQVRVLKAAQYLHQ QGITRCNSSTLTSAAPGRVDSP PTSMIVAPALIIRFACFTASISEL CVPPSEKESGVTLRIPITHLMRE LTCRLIRDKSATVTGSHTLVVA RHCCYAAPGGCCLLANWLKPG LFGPIGVLSRRGTSVILPIGGFY QWNPIMICPNGVPMQHG*RRG LAQERPLEEWLPVCRDMLNAF FLPDAETEAAMTLIEQQWQAI AEGGLAQYGDVPLSLLRDEL AQRLDQERISQRFAGPVNICTL MPMRSIPFKVVCLLGMNDGVY PRQLAPLGFDLMSQKPKRGDRS RRDDDRYLFLEALISAQQLYI SYIGRSIQDNSERFPSVLVQELI DYIGQSHYLPGEALNCDESEA RVKAHLTCLHTRMPFDPQNYQ PGERQSYAREWLPAASQAGKA HSEFVQPLPFTLPETVPLKRYN DSVRAPTCAESRAIFTSRNNTL QLFFNANFRPWARGLATNVN DRRASVDHQIRMFHRIYQVRM RATIRKGIRRDVEDPHYSSDAG TYLSPNSRQISNGNWQSHIGRSP SLLL CRTWGLLFTGKLVETRFI WPNRGVIPTGNERYIAHRRFLP MEPDDMPQWRCPHATWLAEA KMFDSLAKAGKYLGAACKLMI GMPDYDNYVEHMRVNHDPQT PMTYEEFFRERQDARYGKGG
4176	34544	A	4217	838	1575	CFFLSPSPSPSPNRSQTTEE TKRQE/ERERKREEEEEKGRR KETKKRRNRQEGKQHRKEEKE GEKQTKQRTETERETKRRRENE QAKAHKGTRKRKEEQKKAKA ARRRTHKRQNP SRGREGTHPK QRQGKEE/VNRQNEEAKQKR EEAGRTRR/EDRGRKDDKKERR QQQTEKKAKPKAEHQERTDT TTKKARQREGRPSERRRRERE/ MSKHDPQNRAEKTNEEKEEGR QHER*TKSSSTGI

SFQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of last codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4177	34545	A	4218	1	692	MNALHAEALEMTSQFDQELAA KFEADHEMALLMKNKDFDRDRE EQRRLEAQARREHEERIKREAA EQARRDAEAKHKAIEIAAARR EAEEKARAELEAERQRIEAQRA EREKKETEERARREKEEAVAAE RRRQEEAEAAALVEEQKAE EARRAADKEHRRRTVNR/GLRR SDCSGHPRRIRTESSAGDRWRQ SAGRAHQILRQT*THSLITAS KNGAGLSSNSPTRKRS
4178	34546	A	4219	3	1120	
4179	34547	A	4220	1	831	MVKARKIMETPPQPAWEMRVRI CTVDWSKLNPIPDDFSLIKSEK KYDHPELIVDESRLRVVYAPSR YFASEPKADVSLILRNPKAMDS ARNQALLEGYFSFTA TEDQLEQ AKSWYNQMM/D/SPEKGKAFEH GNMPA\QMLLQVPYFLRE\ERE H*IIITPILHMRKQEQSG*/RNL KAAQLSMMQDLQTLMAASY CSELGHVATQFGMLACTRNP NSWDRNSETSGKAE GFIP\QLG DVADPSVRCSSVSL WGHSSPK LLRSVCMANRICVKLQRWT
4180	34548	A	4221	1	1503	
4181	34549	A	4222	1	1113	
4182	34550	B	4223	1	760	
4183	34551	B	4224	1	1755	
4184	34552	C	4225	1	4215	
4185	34553	A	4226	1	3240	
4186	34554	A	4227	1989	2144	
4187	34555	A	4228	1	1203	
4188	34556	A	4229	1	4767	
4189	34557	A	4230	31	512	EYRKSPDIRPVIQHGEEAEITH HFR*QELADKTLIFEITHREMQR FQPVGTGDIREPVFVFFRWRLT NPFNILEHGEPEGIRVDAAVPR AVIGGLEDHIGVAVQKLQHKTF RYFPFIQMVKDGVPVPEGRPAF VHHLSLFLRIKILAHLTHTNQDF
4190	34558	A	4231	369	918	RPGMSNPWRDLFRGTGVDPTND RLSALVEI/YRMMRPGEPPTREA AE/SLFENLFFSEDRYDLSA/VG RMKFNRSLREEIE/GSGILSKD DIIDVMKKL/IDIRNG/KGEVDDI DHLG/NNRIRSVGEMAENQFRV /GLVRCTGTVPFLHQQKCEYH L/PQRPVASTLSRYF*HFRLLNF SMPRANEIKKGMV

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4191	34559	A	4232	3	1012	SVVLKIVERVDGYFSPPLFLGA AFGSHVRSRALPDCVLFVRVTI YLCVLAASVARTFSPLLPVSRKK HITPLGGFQLHETHLCLQDCRTI ILRPRLGEFGNKFSQLVDTIDLH INQHGLAHL*KESARGQYSLLL LGMVSLCALILILWRVYRSVT CPLADQTQALHRLLDGDIVSPF PETAGVRELDITIGRLMDAFRSN VHALNRHREQLAAQVKARTAE LQELVIEHRQARAEAEKASQAK SAFLAAMSHEIRTPLYGILGTA QLLADNPALNAQRDDLRITDS GESLLTILNDILDYSAIEAGGK NVSVQSYVARLEPVAASGWHK YPWLN
4192	34560	A	4233	1	502	
4193	34561	A	4234	1	653	
4194	34562	A	4235	2	300	YALATPLPSV/INQWQLALDKG QLPTE/VAGLAPQHPQYAAHME SYWPYSALR/EILQRTGMLDGG PKITL/PGDDTPTDAVVSPSAVT NSHGR*VPTLGGVWGL
4195	34563	C	4236	40	105	
4196	34564	A	4237	355	526	
4197	34565	A	4238	116	949	RPGTGRCSAVQLPVLLLRGPHS SHTVGTHMVLDLSGQLCVYP GNSDESMPAATQARERLLADT AKKKAQIAELQSFVSRFSANA* KSRQATSRARQIDKIKLEEVKA SSRQNPFIREFQDKKLFNALE VEGLTKGFDNGPLFKTLNLVLA EVGENLPVLGTNGVGKSTL/LK TLVGDLPDPSGTVKWSENARI GYAAQDHEYEFENDLPVFEWM SQWKQEGDDEQAVRSILGRLLF SQGDIKKPAKVLSGGEKGRML FGKLMMQKPNILMDPEPTHP
4198	34566	A	4239	1	319	MVKKMARAPMNLVALANPEPEI LACRHGRKEVRPDAIIC/TPGRS DYPNQSETNVL/CFPANVHRIPQ AASHLRAHQSRIPISLMSISAKIL TYLLANQIQFLVKQH
4199	34567	B	4240	263	1390	
4200	34568	A	4241	1	323	
4201	34569	A	4242	3	1855	

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4202	34570	A	4243	2	964	LLKHGVSLEYIQDKEGLSALDLV MKDRPTHVVFKNTPDPTDVYTW GDNTNFTLGHGSQNSKHHPEL VDLFSRSGIYIKQVVLCKFHVSF LSQKGQVYTWGHGPGGRIGT WEMNRHAWVPRLVGRD*MVII VSPSWPAKDHDTVVLTEGCV YTFGLNIFHQLGIIPPPSSCNVPR QGLHNRQNRPPVPGSAGPTS MEPSKIRPTGLKFSLTTQQSEI DLGCSSLCWDYRREPLRLAYW FIKKDIAKDTDEETRRHGVSLYI QDKFGLSALDLV MKDRPTHVV FKNTGSLQFQSIPSCRESQILSEK QGDLFREEPMFGS
4203	34571	A	4244	1	725	FRVDPVRKHFGLFYAMGIVL MMEGVLSAC*HVCNYSNFQF DTSFMYMAGLCMLKLYQTRH PDINASAYSAYSAFVVMVTV LGVVFGKNDVWFVVFSAIHV LASLALSTQIYYMGRFKIDLGF RRAAMVYFTDCIQQCSRLPYM DRMVLLVVGNLVNWSFALFGL IYRPRDFASYMLGIFCNLLLYL AFYIIMKLRSS*KVLPVPLFCIV ATAGMWACALYFFQNLSSW
4204	34572	A	4245	1	833	MKPVWVATLLWMLLVPRLG AARKGSPEEASFYYGTFLPGFS WGVGSSAYQTGEAWDQDGKG PSIWDVFTHSKGKVLGNETA DVACDGYKKVQEDIIILRELHV NHYRFSLSWPRLLPTGIRAEQV NKKGIEFYSLDIALSSNITPIV TLHHWDLQQLQVKYGGWQN VSMANYFRDYANLCFEAFGDR VKHWITFSDPRMAEKGYETG HHAPGLKLRGTGLYKAAHHII/ KAHTL*VCFHAADKGPETEEK RRLNWTYSSTWLGFRFHHHGRG
4205	34573	A	4246	1	672	GTQNAVNG/VIIFLSWGDVKS FWIYRGGRKREGPLFAH*Q/FLI YTIHRAVGSINYVIANYKLFPI TPGVDFICTSLIAGILTIKLFLLI NQFEKQIQKGRDITSARIMSRI IKITIIVGLVLLYGEHFGMSLSG LLTFGGIGGLAVGMAGKDILSN FFSGIMLYFDRPFSIGDWIRSPD RNIEGTVAEIGWRITKITTFDNR PLYVPNSLFSSISVENPG

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4206	34574	A	4247	1	347	PLRPVGGQPGPGGAGT/RALRAPPLPSSSELICYGPGQPGRWPRCPQFPSLPPHSS*LLHTGHWPCITLGYCFIPILRAAPPLPCKCASPVL/SC TYPLPAAPSLPVLVHTSIKCFCHLQ
4207	34575	A	4248	43	446	VLPVAVPRPGQ/PPCVPAVPVQAPPPRPSPGWSQATGSPGPAGAAPSWRIGLPAVPGHITAGVLGPGPPGQRQPGPGGAGTQLCGPHFLRLNLNVAYGPGQPAL/RNVPLQTAPALTPSPQHLLCPFLSTHLLNASVFIC
4208	34576	A	4249	1	1521	RIPESRLPTIAFVQAPWARSGLLRWEKHAGQQVGVWARGPGVGRGRQAAGGGAAALICRGGAGSAVRSACAGPLSLASGAGCR LHPSYSFGFKVGS/PTVPAALSS*STS/RGREHGGVTVPVMTQNPRS'PDGPARVEDCEAIA*GTGWLQQGIGTRPPGTGLGRAR/GAPAVQWNPVKSCQGP GHPNR LPSHGPPSGEAGRGW/RGLQITPQL/PEVTHRRVLPGDHPATEA/GGFGTG*PGLPGRVPGPGVGTYQAKALTPLGPVGLLAPASCAQLQOSADGPGATGHL*ELAESQRRQPTG'PPGQLAVSGWATVPGVPAAPRPFPAQQPA/SVPTPSYWA/GSPGAAAWPESHRR*ACDWAW**VLPVAVPRPGQ/PPCVPA PVQ/PQSHRGPADHGARLY*GLPQAEQLHPGGGLPAVPGHITAGVLGPGPPGQRQPGPGGAGTQLCGPHILFLCLNVAYGPGQPGRWPRCPQFPFLPPLSWNIFVGTQKKKKKNQSLFKKKKKK
4209	34577	A	4250	167	582	RSLGLAVTEMVPVWRTMGQKLKQRLRLDVGREICRQYPLFCFLLLLCLSAASLLLN*RRSAEPGRRL/SL/LK VQTPGPCCLTVRRPRSCTGTDQWGERAPQRSGLGEHGGASRPEAQAGGVGLIASFPEASSPELPFSHP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4210	34578	A	4251	402	1465	DLILSHPTAWFTIKYKPKQLGL QELFPQGHSCAVCGKVKCKRH RPSLLLENYQPWLDLKISSKVE\ ESLSKDLELVLENFVYPWYRD VTDDES FVDEL RITL RFFASVLI RRIHKVDIPSIYNQETIKSSNESI *KWIVKARQKVKNTTEFLQQA LEEYGP ELHVALRSRRDELHYL RKLTELLFPYILPPKATDCRSLT LLIREILSGSVFLPSLDFLADPDT VNHLLIIFIDDSPAEKATEPASTL VPFLQKFAEPRNKKPSVLKLEL KQIREQQDLLFRFMNFKQEGA VHVL/QFCLTVEEFNDRILRPEL SNG*NAVSS/WKNCRRFIKHTV WMKVLTKDLIPSLVEEIPR
4211	34579	A	4252	1	1232	FPGRFRFLVVRLRGAEEASERQ VYSVTMKLLLLHPAFQSCLLLT LLGLWRTTPEAHASSPGAPAI AASF*DLIHYRGEGDSLTLQQ LKALLNHL DVG VGRGNVSQHV QGHNRNPTTCFSGGDLTAHNF\S EQLRIGSSLEHFCPTILQQDLS RACTSENQENEENEQTEEGRPS AVEVWGFGLSVSLINLASLLG VLVLPCTEKAFFSRVLTYFIALS IGTLLSNALFQLIPERSYKNKAQ VDSLPTFLAQAGMLLWRVRIR RRVVDPIRESWMLPFTKIPLWG YGLLCVTVISLCSLLGASVVPF MKKTfYKRLLLYFIALAIGTLY SNALFQLIPENRRKWWQPVHN TFGGSTA WHTDKSIEQSIDLFD EVKKESEKETPSLQIGDLGPQES LKTfNNTNSPHH
4212	34580	A	4253	3	924	VGACTAAARPLPIPQLPIHHR GEKSQ LWAHSGSSWGFLAVAA VPPSHLCPLQSRGWKRPP/PLA SAGVLPGCCCCACLVSPSLAQP AGVLGPKPAAPLGPGPWVSVAP CSRPGPCGTRSPA/P*GHPAMG R/GVHEPRVGPAPPEKAIITETG AGLAERRGQGLGGSSFRSAEP QGCRLSGPQSPGGDPAHTILRPP SQNGDCAEMHACRLHPAILGT HGTGGLAAQSHAPRALLPSCPS SQQPADGWCSLHLCLPGLLLAP RIHGPSTREGGPGHGTGPPTNP ASSGATRGTRRVRPSPRSPTL

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4213	34581	A	4254	1	318	VADPVGAARAGGQPLAGRVW PRAGGGHSPRVLGAAGPGPHV CTLRLPGTAIRTEPGAPLACAR AWPGSSPAG/PECLPTSC*E*EG QEPSSHVASLPWGPVGGETQ
4214	34582	A	4255	1	718	FFFFFFFLCHLYWVSPTPGPHG KLANMANWAPWPS*GLSKLVG KHSCPAG*LPGHARAQASGAP G/ISPDSSAREA*ECT/PCGP APSTRGECPPSSRPHS/SQQDP GRCSFAPAVPQDAGGQGHWC APATGHSAPRGCPPARAAPTGS ATPAPPPAACASSLSMVSAPS R*TTGIASSGTSIPETKHQGT TAPAGT/GPGGSTGPKA/PGPAP AHPTRLAGTSGHTAPPTCPPAV
4215	34583	A	4256	702	1026	RSGRTQRAAGVSGSALHQVQS WPHLKISADQRAGLLF*EHPFP PSASSGCLDVSISSYPVGSDFIN GMARANGRWKFTFTGLHSGKPL GFSDAFCQHNLILLCWKWTW
4216	34584	A	4257	170	1049	RSGGCSAELVPSSRWPRGSRAG AAAGTETPG*PRVYVPAGNGE AGGPGAAWARRAALPGTAA GPPRPAARPGAAPARGGPAPGA PAQALPR/TPTWPAAR*AQRAP SPPSWGSAQPGHPGDLAAGVG RGAGGGHSRRGRHHVVRSLAD LLQLPGAEGAGDRGHLPGPD/ GERS*AASSFSAAGRAAGTASC CSAGGTPPSPCTILSTSSSLAH VASSS/RRRAEGDTKVS/RGRAE GQDSETGREPGVLHRSGRQT RAAGVSGS/RSAPSPVVATTSS LLTSVQGCFSENILSP
4217	34585	A	4258	178	556	QSPQEHFHPECGRRDILCQVRQ EIRWPNPGEVHHILGLEICPVWI LQLHLALRTRAPEHPLQVHRPG GGAV*RGVPPPLRLI.QACDGPE VPAAGRPRPARSSPGQWPP*/PA AVAPPVTERPPTPSAA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
4218	34586	A	4259	5	1044	TGRILDGWHWAKELRLDCPLG DSRRPPFSRVSTEGSPAFLALRL PNVTAGS*EVSMLASTETPLVIT RPSPG/GHDPGAPRGAAASPA GSPAP*QKSPRLSAAAPLLAS DPAPPRAAAPADTESSVQPPA APHAGPWT/PSAPGLDVHSPPP VPSRGPFVQSSAEPHNRPSGAT RPRP/PPRGAAASPAGSPAP*QK SPRLSAAAPLLASDPAPPRAA APPADTESSVQPPAAPHAGPWT LERSWAP*RLTPIPVADPLCR APLSHRYP*GDCQRSGLCHTSP GRASHLPGPGAHKRTPHACWL PLECHRRSPHP*THPSG*PGPSP QSFFPEFLGSGP
4219	34587	A	4260	2	576	CLVNSTRRSFQLRLVPVPKFQ PPHMTVR*LFNFGRLTATTFS/ LRKSYAVREAYELQNCPPPPF QNGYMINSDYSVGQSVSFECYP GYILIGHPVLTQHGIRNWNWY PFPRCDAPCGYNVTSQNGTIYS PGFDEYPILKDCIWLITVPPGH GVYINFLLHTEAVNDHIAVW YENLSSQNICDCDQOF
4220	34588	A	4261	1	837	MWAGNAWRAALSGVP CGRSA QSVLAQLRGILEGELEGIRGAG TWKSERVITSRQGPPIHVDGVS GGILNLTSVRFIRGTQSIHKNLE AKIARFHQREDAILYPSCCDAN AGLFEVLLRPEDAVLSDELNCA SIHGICLCKAHKYHYCHLDVA YLETQLQEAQKHRLFLVATDG AFSMDGDIVLQKICRLASRYG ALVFVDECHATGFLGLTGQGT DELLGVMGQVTINSTLGKALG GASGGYTTGPGPLVSL/RAQP YLFNSLPPAVVGCTSKAL

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4221	34589	A	4262	1	2142	MIILIDA EKAFDKIQQPFMLKTL NKLGDGTYLKITRAIYDKPTA NIILNGQKLEAFPLK1GTRQGCP LSPLLFNIVLEVLAAQAIHQKEI KGIGLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSISVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNTWTQEGEHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSISNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNI CSRGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTASEVTSHIYNH LIFYKPDKNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPT KIHSRWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVILKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELQIYRKK/TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
4222	34590	A	4263	1	1989	
4223	34591	A	4264	1	1104	
4224	34592	A	4265	1	879	
4225	34593	A	4266	1	1659	
4226	34594	B	4267	1	1500	
4227	34595	B	4268	1	1962	
4228	34596	B	4269	1	1716	
4229	34597	A	4270	1	1152	
4230	34598	A	4271	1	4752	
4231	34599	A	4272	1	2790	
4232	34600	A	4273	1	3477	

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4233	34601	A	4274	1	1007	MLDASCHRTSDSKFFSFGVQTG FLTPELAHLVGPCDRDHNSSPA REQNWTENEFDELTEVGFRKW VITNSSELKEHVLTSQKEAKNL EKRAIKQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVSAQNL LKLISKFSKVSGYKINVQKSQA LLYTNNRSQIMSELPTTIAMKR IKYLGILTRDVKDLFKDNYKP LLKEIREDTNKWKNIPCSWLGR INIMKMAILPKAIYRFNAIPKLL *TFFTELEKTTLNFIIWNQKRARI AKTILSKKNKAGGITLPDFKLY HKATVTKTAWYWYQNRVIDQ WNRTEASEITPHIYNHLIFDKPE
4234	34602	A	4275	737	2460	RIKYLRIQLTRDVKDLFKENYK SLLNEIKEDTNKWNIPCSWIG RMNIIKMAILPKVIYRFNVIPIK LPMTFFSELEKSTLKFIIWNQKR ARIAKTILSQKNKAGGIMLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTEPSEMTPHIYNHLIFD KPDKNKQWGDLSLFNKWCWE NWLAIQRQLKLDPLTPYTKIN SRWIKDLNVRPKTIKLEENLG NTIQDISMGKDFMSKTPKAMA TKAKMDKWDLIKLSFCTAKE TTIRVNRQPTWEKNFAIYSSD KGLISRIYKQLKQIYKKKTNNPI KKWAKDMNRHFSKEDVYAAN RHMKKCSSSLAIREMQIKTIMIY HLTPVTMAIIKSGNNRCWRG CGEMGTLLYCWWDCKL VQPL WKTLLWQFLRDLELGIPFPAIP LLGIYPKDYKSCCYKDTCTPKL ARDDQIHILQHRRKELETRQK QYRAWYEINPFHSVWPVTAGK SPRHQLPVWVHNPTSPYLQL QTRDGEESNENNFSGTILASDFF AEIDKLSILQIHMEMEGTQNSQ NNLDKKKTKMEDLHFSISKLLH SYSIQDNVISA
4235	34603	A	4276	3	355	RQPVHLVHEL PQQSWGICLNSS EQHGALQHSSLHL/RMCSEPW SADPQ*R*TCRNL*LPVRGPPRR TDLFSVSSKSTLKEWPLLLMIL AELGSYLILSGRREESYFTSLVL ISIGDC
4236	34604	B	4277	78	791	

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4237	34605	A	4278	1	3395	MIISIDTENAFEKIQQPFMLKTL NKLIGDGYLKKIIRAIYDKPTAN IILNGQKLEAFPLKTGTGRQGCPL SPLLFIIVLEVMA RVIRQEKEIK GIQLGKEEVKLSLFVDDMIVYL ENPIVSAQNLLKLISNLSKVSGY KINVQKSQAFSYTNNRQTESI MNGLPFTTASRKIKYLGILQTR DVKELFKENYKPLLNEKKVDT NKWKNIPCSWIGRINILKMAIL P/KELEKTTLKFIWNQKRACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEI/PHIYNHLIFDKPDKN KKWGMGSLFNKWCWENWLAI CRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKLEENLGNTIQDI DMGKDFMSKTPKAMATKAKID KWDLTCLRSTAKETTIRVNR QPKWEKIFAIYSSDKGLISRIY KELKRIYK/KKNNPIKKWAKD MNRYF*KEDIYAANRHMKKCS SSLAIEMQIKTTMR/YHLTPVR MAIIKSGNNRWEMNNENTWT QEGEHTLG/HC/WWKARRSR CLTWMAAGKKRMKRLQMT
4238	34606	B	4279	1	2011	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 5,400,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
4239	34607	A	4280	1	2661	MTMNFVADSHITGRNPLASAA AKTGLRPLPRPCGARVWNPPD AGGGGVGSLKSTPLGPLSAAN SPVHQGSVPQTRARGGGTLFQE VVTSRTLAFRNSLSAFTEVTS TVSGRKGGRSTHLAGRRVSGG EGSRKAAAAALAAVAAAPGPV RRCSSQSCFSSSGSSHYARTSP VRVRPRRSLSSRAAGNRAEAT ESAMEKTLTVPLERKKREKEQ FRKLFIGGLSFETTESLRNYYE QWGKLTDCCVVMRDPASKRSRG FGFVTFSSMAEVDAAAMAARPH SIDGRVVEPKRAVAREESGKPG AHVTVKLFFVGKIKEDTEHHHL RDYFEEYKIDTIEIITDRQSGK KRGGFGVTFDDHDPVDKIVLQK YHTINGHNAEVRKALSQEMQ EVQSSRSRGDGYGSGRGFGD GYNQYGGGPGGNGFGSPGYG GGRGGYGGGPGYGNQGGGY GGGYDNYGGGNYGSGNYNDF GNYNQPSNYGPMKSGNFGGS RNMGGPYGGGIWKNTSITERK KSRKLDLIQSKKGSRTKEAPQP PVASLCMHLGHWSRLMVSPGA QLTGKNSHGLSVSSVRKSNVGP RRLCAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTD RPHPLSRPKPPTQISLVLPKT DGALERMPQQL/HAASS/GAKVP NPSTQTPPVLLAFFYPNLP* N
4240	34608	A	4281	1	908	MRKVKGKNRQSFKCLPPPSGA LQAHGAAPHGSLTLHLHLV PVSSAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTD RPHPLSWPTWISLALLLKT ALERMPPQLPSLHPSQGTQSIH PDPSTSTFLLFPQPTLKRAAF CPSPSIVNPAVWDTSTPSVAEHH TPIRITLKEPTQLFSQKQYPIPQA ALVGLQPIIHLASHLLRPDTS PFNTPLPVKKPNGTYRLVQDL RLINQAVLPLVQE/DYSVLLVLP LNVTPGLPPATAFSYPPSPGPVA RARLASRLHSHAA

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4241	34609	A	4282	1	915	MPNYVTFDTDKQLISDTPNNQV PMNRASMAFDKCLTGC RFDD AIVQFDMITYWPF TVVNDAGR KVQVEYERDKLLPIGGVFGS DKDEGNCKSLPWEDCYQCET SQNVQDFLFDVTPLSLDIKTA DGVMAVLKCDATIPTRQTQTF TTYSDKPSM/LIAKDKNLLRKFE LTGVPPAHHGAHQIEVTFDINA KGILNV/TLTDDKGHLSKEDI MVQETEKYKADEKQRDKVSS KNSLDPYVFNMKATAEDEKLQ VKINNEHKQILSKCHEINWL DKNQTAEEKEFEHAQQUELEKSS
4242	34610	A	4283	1	994	MHQTCKGNQWHFGMKAHIGV DAKSGLTHSLVTRPNEHDLNQ LGNLLHGEQFVSADAGYQGA PQREELAEVDVDWLIAERPGK VRTLKQHPRKNTAINIEMKA SIRARVEHPFRJIKRQFGVVKAR YKGLLKNDNQLAMLFTLANLF RADQMIHCTRGEGLITTKIPKAP DNGSYCLPSKNDSEEDPEMS PMVVTKMKEIAEAYLGKTVTN AVLTVPAYFNDSQRQAT/KKDA RTIAGLNGLRISNEPTAAIAYG LNQKVGTERNVLIFDLGGSITPR IRTPETGSDDAIKSILEQAKKEIE SQKGECDCPCRQSLRPPGPAAN
4243	34611	A	4284	3	677	
4244	34612	A	4285	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKQORLLARAEEK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLVCRKMGVP YCIHKGKARGLRVHRKTCTTV AFTQVN
4245	34613	A	4286	3	432	NSRVDDFVAAQDAKGGKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ/QRLLARAEEKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIADHVDPIELV VFLPALCRKMGVPYCIHKGKAR LGLRVHRKTCTTVAF
4246	34614	C	4287	62	217	

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4247	34615	A	4288	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRILYKRLKVPAINQFTQAL DRQTATQLLKLAKHVRPETKQ EKKQRLARAEKKAAGKGDVP TKRPPVLRAVNTVTTLVENK KAQLVVAHDVDPIELVVFLPA L\CRKMGVPYCIKKGKARLGR VHRKCTTVAFTQVNSDKG/ ALAKLVEAIRTNNDRYDEIRR HWGGNDLRPK\SVARIAKLEKA KAKELATKLG
4248	34616	B	4289	1	273	
4249	34617	A	4290	1	441	
4250	34618	B	4291	47	482	
4251	34619	A	4292	1	762	
4252	34620	A	4293	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLSHFQWGTLDTCVV MRDPNTKRSRGFGVTYATVE EVDAAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYKGIE VIFIMTDRGSGKKRGFAVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSQGRGS GSGNFGGGRGGGFGGNDNFR GGNFGSGRGFGGSHGGGGYGG SGDGYNGFGNDGSGNFGGGGSY NDFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSYGSGRRF
4253	34621	A	4294	1	1674	
4254	34622	A	4295	1	506	KYHTVNGHNCVVRKALSKQEI ASASCSQGRSGSGNFGGDRG GGFGGNDNFRGGNFGSHGGF GGSCCGGGYGGSGDGYNGFGN DASNFGGGGS/YNEFG/YNNQ SSHFGPLS/GGNFGGRSS/SPLGG APASTYVKGPNSQRTQNEGWF EG*APWRGDDGGARGNKGGGA

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4255	34623	A	4296	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCGWIEEER DESRKSETIFKDLFKVPVLEKETI YYKFYGPVPYQIETVYFMAISP PKSKQFDKTKQNNNNKKTHQF VIVFFKTDHLSARGRRRSIVK VSLLPVAVIGLKSFLKPKDQLR KLFI\GG\LSFETT\DESLEEFSSR QWQKRYTDSVVMRDPNTKRSR GVGFVITYATVVEVDAAWMNA RPHKVEWKELLEPKRA\VSRED SQRP\GCPH*LVKKIFVGGIKEDT VEHHRLRDYFEQYGGKIEVIEIMT DARGSGKKRGFAFVTFDDHD\VS VDKIVIQKYHTVNGHN\CEV* KSPVSKSKKMASASSKPKEGRS FWETFGGGSWEVGGGNDNF GRG\GNFSWSV\AFGGSRG\GG GYG\GSGDG\YNGFGNDG\SNF G\GGG\SYNDFG\NYNNQ\SSNF GPMKGG\NFG\GRSSGPY\GGG QYFAKPR\NQGQYGGSS\SN
4256	34624	A	4297	1	920	DPGDTPTNTASAPNCRSGKGRSS SPEHIPPLEKLEDSMQTNPSTNP EPGRLEAWLDPEERQQSLQFGL QEATSIGKGGQYIKGTPHGTK ESEQQPSALDLPSDRAYPNEKE PENQLWRLVIKLIKEAPEKGAY LNVIKAVYDKPTNGEKLRAFPL RTGTHKRCPLSPLLFNILLEVLA RAIRQEKEIKSIQIGKEEVKLSLF ADDDIHYLESPKYSSRKLQELIKE FSKVSRYEINVHKSVALLYTNS NQAENQIKNSASFTIAAKNKIK YLGYYLTAKADGKYKENYKTL MKEIIDDKNKQKYIP
4257	34625	A	4298	1	1194	
4258	34626	A	4299	3	1834	
4259	34627	A	4300	285	502	
4260	34628	B	4301	77	1306	
4261	34629	A	4302	1	354	
4262	34630	A	4303	1	1182	
4263	34631	B	4304	1	1995	
4264	34632	B	4305	1	1518	

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4265	34633	A	4306	1	918	MCPVGPWTHPPVVISPVSECIVGI DILGSWQNLHIGSLTDITMVHYI DDMMLIGSSEQEVANSLDLLV RHLHARGCKINPTKIQGTSTSV KFLEFQWCGVCQDIPSKWVLE QKALQQVQAQVQAALPLEPYD PADPMVLEVSADGVAVWSL WQAPIARIHGSRNQGVEVEVSP LTNIPSDPLAKFLFPAPSTLCSA GLELLVPEGGTLPGNTTMIPL NWKLRLVPGYFGLLLALSPQA KNGVTVLAVIDPDYQDEITLL FHNGGGEEYARNTGDPRLHLL VLPSPMIKVNGK/LQHPNPGRT
4266	34634	B	4307	1	1599	
4267	34635	B	4308	1	1569	
4268	34636	A	4309	3	422	
4269	34637	A	4310	1	1089	
4270	34638	A	4311	2	549	LKMTAMQRPMEKRMMNREIIL KERLSLTGIDIKILKKRSIMKVE SHRGEQISVSLSALQRIKYLGIQI TRDVKDLFKENYKPLLNKLKE DTNKWRNVPCPRVGRISIVKM AILPK/ILKKKTTLKFIWNQKRA HIAKTILSKKNKAGGITLPDFKL YYKAT/KTAWCWYQNRDTDQ WNRTPKPEI

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4271	34639	A	4312	371	3036	LIAYQPKKVVQDQMSQPNSTR VLEVLARAIRQEKEIKGIQLGK/ EEVKLSMFADDITAYLENPIVS APNLLKLISNFSK/VSGYKINVQ KSQAFLYTNKRQTE/QIMSELPF TVASKRIKYLGIKLRRDVKDLF KENYKPLLNEIKEDTNKWNIP CSWIGRINIVKMTILPKVIYRFN AIIKLPMTFFAELEKTTLKFIW NQKRAHIAKTILSQKNKAGGIM LPDFKLYKATVTKTAWYVY QNRDIDQWNRJEPSEIIPHICKH LIFDKPKDNKKWGDLSLFNKW CWENWLAICRKLHLDPLTPYT KINSRWIKDLNVRHKTIKTLLE NLGNTIQDIGMGKDFMTKTPK AMATKAKIDKWDLIKLSFCT AKETTIRVNRQPTWEKIFATY SSDKGLISRIYNELKQIYKKTN NPIKKWAKDMNRHFSKEDIYA AKKHHMKCSSSLAIRETYNDR RIGKLTQTCDEATFQPHVCTISR PMLSSPYRSSLTEKWSQDFSKP PYPFLFHKGYNPREQDKEVLT RAIRQEKERKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNPK VVSNFSKVSGYKISVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLRQLTRDVKDLFKENCKP LLNEIEEDTNKWNIPCSWIGRI NIVKMAILPKVIYRFNAIPIKLP MTFTFVLEKTTLKFIWNQKRAH
4272	34640	B	4313	1	1995	
4273	34641	A	4314	3	549	
4274	34642	A	4315	3	614	EAYGQTECTGGCTFTLPGDWT SGQFINILEMCLELSPCKSFSAD SARYVLGHVGVPLACNYVKLE DVADMMNYFTVNNEGEVCIKGT NVFKGYLKDPEKTQEALDSDG WLHTGDIGRWLPDIENHNRLIV CTLTNTSWRSHKIIVLKYQKA DDTKTPKETTFQNMNLFLEKE RATAVLIRGGVGETSDLSKKK PAKLLANF
4275	34643	A	4316	1	478	MKLDLHLSPYTKINSRWIKDLN LRPETIKILEDIIRKTLDDIGLGK DFMIKNPKVNATKTKINKWDLI KLKWNCTAKEISSREIREPTEW EKIFANSASDKGLISRIYKELKQ IRSTLQLLFGISELPASLFLGFGA IMSKSKASLNTSTAILRQLIW

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4276	34644	A	4317	1	1125	MCHGIGAQIIPSHQT VQLDITAF LKT VKK NKHKFYPAFIHILARL MNAHPFERMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYYTQGDVLMPL LAIGGPLES PDRDGGPLESTNR DASPESWSCRKSTPRLVAVVS AAKVFI RDKLMERRNRRTGRT EKARIWEVTDRTVRTWIGEA V AAAAADGGGFRVDLARRSIRK DRNARSQNPVHTEGDMNMNIK KIVKQATVLTFTTAF LAGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYVQPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQVKGVDN SIDSWKNAGR VF
4277	34645	B	4318	1	1374	
4278	34646	A	4319	1	1293	
4279	34647	A	4320	1	1278	
4280	34648	A	4321	1	1254	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVS KDDTLKINGV/N GYYCEESL FNKA/Y YGGGTNFF RKESQKLQQA KKRDAELANG ALGIELNNDYTLKKVMKLITS NTVTDEIERANVFKMNGKWWL FTDSRGSKMTIDGINSNDIYML GYVSNLTGPYKPLNKTGLVLQ MGLDPNDVTFTYSHFAVPQAK GNNVVITSYMTNRGF FEDKKA TFAPSLMNIKGNKTSVVKNLSL EQGQLTVN
4281	34649	A	4322	1	726	
4282	34650	A	4323	1	1050	

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4283	34651	A	4324	1	1185	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNISDSWKNAGRKFVSDSD KFDANDPILKDQQTQEWGSA TFTSDGKIRLFYTDYSGKH YKGQS LTTAQVNVSKSDDTL KINGVED HKTIFDGDGKTYQ NVQQFIDEG NYTSGDNITL RDPHYVEDKGH KYLVFEANT GTENG YQGEESLF NKAYY GGGTNFFRKESQKLQQ SAKKRDAELANGALGHI ELNND YTLKKVMKPLITS N/TVPQAKG NNVVITSY MTNRGFFEDKKATF APSLFNMNIKNKTSV VKNLSILE QGQLTVN
4284	34652	B	4325	1	867	
4285	34653	A	4326	1	495	
4286	34654	A	4327	3	1394	GDMNMNIKKIVKQATVLTFTT A/LLAGGATQAFAKENNQKAY KETYGVSHTIRHDMLQIPKQQ QNEKYQVPQFDQSTIKNIESAK GLDVWDSWPLQNAADGTVAEY NNGYHVVFALAGSPKDADDT SIYMFYQKVGDNISDSWKNAGR FVKDSDFDANDPILKDQQTQ EWSGSATFTSDGKIRLFYTD YSGKH YGKQSLTTAQVNV SKSDDTLKI NGVEDHKTIF DGDGKTYQNVQ QFIDEGNY TGDPLEAETA VINH KKRKNS PRIVQSNDLTEAAYSLSR DQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFP FWFIKRAH SPSRGLYSVH NPYLPPIFFIGLQN RFTQ FRLSETKEITNPYAMRLY ESLCQYRKPDGSGIVSLKID WIIERYQLPQSYQRTPD FRRRLQV CVNEING
4287	34655	B	4328	9	1004	
4288	34656	A	4329	1	768	
4289	34657	A	4330	1	1308	
4290	34658	B	4331	58	753	
4291	34659	B	4332	1	409	
4292	34660	B	4333	1	921	
4293	34661	A	4334	1	1026	
4294	34662	B	4335	1	945	

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4295	34663	A	4336	1	528	MNMNIKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDDTSIYMFY/Q KDQTQEWSGSATFTSDGKIRLF YTDYSGKHYGKQSLDTA\Q*NV VKSG
4296	34664	A	4337	1	1701	
4297	34665	B	4338	97	1449	
4298	34666	A	4339	1	1581	
4299	34667	B	4340	1	1539	
4300	34668	A	4341	87	1078	SLPNLDNAAICSSSSPTRTR*SL SEGATQ\AFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKADDDTSIYMFY QKVGDNIDSIDSWKNAGRVFKDS DKFDANDPILKDDQTEWSSGA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTL KINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSGLTLQGFPAPAWLALAH VHPLKHKSGGNSRLSAAIWGIK RKPAR
4301	34669	A	4342	1	1344	
4302	34670	A	4343	1	1713	
4303	34671	A	4344	3	1918	
4304	34672	A	4345	254	1118	RPPAFAKK*PKAYKET/YGVSHI TRHDMLQIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVFALA GSPKADDDTSIYMFYQKVGDN SIDSWKNAGRVFKDSKFDAN DPILKDDQTEWSSSATFTSDGK IRLFYTDYSGKHYGKQSLTTAQ VNVSKSDDTL KINGVEDHKTIF DGDGKTYQNVQQFIDEGNYTS GDNHTRDPHYVGGTSEWPGV FSVSCVFFGQQEGV/HG*DEFDLD FSYWFQGG*ICLYQKAS*QNTT SYKRYTGS

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4305	34673	A	4346	1	1952	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDS WKNAGR VF KDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDS WKNAGR VF KDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKH YGKQS LTTAQVNVSKSDDTLKINGVED HKTFIDGDKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL VFQDHTGTEEHPQPQ ERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIA YLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKE LASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHSRSA YKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHL PDLCSPSQDAQTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYM TNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQQQLTV
4306	34674	A	4347	1	1029	
4307	34675	A	4348	276	1248	CVWLGRGYYPKAYKET YGV SHITRHDMLQIPKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNIDS WKNAGR VF KDSDKF DANDPILKDQTQEWSGSATF TS DGKIRLFYTDYSGKH YGKQSLT TAQQLQLVQFQEVDTDFDFPE EDKKEFEFEECLEKFFSTGPARPP TKEKVKRRVLIEPGMPLNHIEY CNHEIMGKNVY YKHRWVAEH YFLLMQYDELQKICYNEFVPSV IFLRYKSPGEAAGTCHLKQRRW VMPEAAAPVGTGSRYP LTGQL
4308	34676	A	4349	1	242	MNSIQIPKQQQNEKYQVPQFDQ STIKYIESPKELDVWDSWPLQN ADGTVAEYNGYHVAFALAG/S PKDADDTSIYMFYQKI
4309	34677	B	4350	1	2198	

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4310	34678	A	4351	1	2796	
4311	34679	A	4352	2047	3531	
4312	34680	A	4353	1	3336	
4313	34681	A	4354	1	1409	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDLSLIARVGVGMARG NAITLPVCGRDVFKFTLEVLRGD SVEKTSRVWSGNFRDQELLTE DALDDLIPSFLLTGQQTAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQK\AYKETY GVSHITRIIDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWSKNAGR VFKDSD KFDANDPILKDQTQEWGSGATF TSDGKIRLFYTDYSGKHGKQS LTTAQVNVSKSDDTLKINGVED HKTFDGDGKTYQNVQQFIDGY LLEPDGGALQNFQRYTGIQHVH RIGMAERMWCDNRERHTYSS SGGNRLPNPGPDRSVRHFPDPR FLCPSCATVTPLHELIANKYLSG KIGAKKLRKLLIKHVD
4314	34682	A	4355	1	2316	
4315	34683	A	4356	93	924	AQTDAAEKSVSIAQLFQACLSIF SSGDV/AGGATQAFAKENNQK AYKETYGVSHTIRHDMQLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDA DDT IYMFYQKVGDNIDSWSKNAGR VFKDSDFDANDPILKDQTQE WSGSAFTSDGKIRLFYTDYSG KHYGKQLTTAQVNVSKSNDT LKINGVGKYKTIFDGDGKTYQT VQQFIDEKNYTSGGHHTLKDP SYNPLDLSGNSGYQSQET

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4316	34684	A	4357	1	3118	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNISDSWKNAGR VFKDSD KFDANDPILKDQTQEWGSA TFTSDGKIRLFYTDYSGKH YKQSLTTAQNVSKSDDTL KINGVEDHKTIFDGDGKTY QNVQQFIDEGNYTSGDNHT LARDPHYVENKGGHKYLG FETNTGTENG YQGEESL FNKAYYGGGTNFFRKESQ KLQQSAAKRRDAELANGAL GIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKM NGKWYLFDTDSRGSKMT IDGINSNDIYMLGSD ESPNDFGNRHLHKERLA VYRWHA SFCSGNTMPIVLVDWSD IREQKRLMVLRA SYALHGRSVTLYEKAF PLSEQCSKKAHDQFLAD LASILPSNTTPLIVSDAG FKVPWYKSV EKLGWYWLSRVRGKVQY ADLGAENWKPI SNLHDMSSSHSKTL GYKRLTKSNPISCO JILLYKSRSGRKNQR STRTHCHHPSPKIY SA SAKEPWV LATNLP EIRTPKQL VNIYSKRMQIEET FRDLKSPAY GLGLRHSRTSS SERFDMILLIAL MLQLTCWLAGV HAQKQ
4317	34685	A	4358	1	1326	
4318	34686	A	4359	2140	4390	
4319	34687	B	4360	1	7271	
4320	34688	A	4361	1	1729	
4321	34689	A	4362	5118	5687	
4322	34690	B	4363	1	4726	
4323	34691	B	4364	1	3688	
4324	34692	A	4365	1	1401	
4325	34693	A	4366	1	1932	
4326	34694	A	4367	1	1407	
4327	34695	A	4368	1	1491	
4328	34696	B	4369	1	855	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
4329	34697	A	4370	137	1014	ASEGKQMLRDFVTTRSAKELL KRALNMARNNQYQLQKHAK L*RPSML*RCIN*QPGRD/TN KKENFRPISLMNIDAKILNKILA NRIQQHIKKLIHNDQVGFIPGM QGWFIHKSINIIHHIKRTNDKN HMIISIDAEKAFNKIQQPFMLKT LNKLGIDGTYLKIIRAIYDRPTA NVILNGQKLEAFPFGTGRQGC PLSPLLFNIVLKVLAIRIQETEI KGIQLAKEEVKLSLFADDMIVY LENPIISAQNLKLIISFSK/VSG YKINVQKSQAFLYTINRQTESQI
4330	34698	A	4371	3	1234	
4331	34699	A	4372	1	2850	MGMGPAKPGMGGNLLVCWLQ RPWEKRSIWAEEVYRSSRYSHS WLPLSRKKGCDPFGTCRQTL TQPLRQWGLEGIKKPNSWIISEE SVSNGGPPLIPRQTASGVDLQ QTPTDLQLRVLTVRRTKNKQK GIATSTKRTSTPKPHLYVTIHK DQSYIKPQRWGKNIAEKLKILKI RVALSQRNAAPHQQWNKAG RRMSLMSSQKKASEVIESQMN EIKGEEKFREKRVKRNEQSLQEI WDYVVRPDLRLIGVDP
4332	34700	B	4373	16	701	
4333	34701	B	4374	1	3743	
4334	34702	A	4375	227	686	KVMLAEYPVFAQLTLTLPFSSA SWEPSRGPGRGIRGSCPEWLA SGPGKAAAPGAGVPPPAASFDP PPRLRAPALAVSRGLRRELPSG LDWTHCLRTLPSLIVILQQA LLGLPPAYSQQLQRAGQLHFYS GLIKISLVLTTRLSFWGTTE
4335	34703	A	4376	216	644	VTYSKEKEGCEVADSVAKTAL EKDGAPRTGDPRLNADPPRS LVSSAGPQAVRPVKPARQFP PPRYSQGPARAAGEEGRGMRPP GAGRRLPGPPLPGPEASHSGQL PLM/PPGPGPRLGSQEPVSL LQTOARMPGPRP

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4336	34704	A	4377	18	1023	QIQHSPLVSLPLSLPPQPLVAEE EPPVA/PWPRRLPATSTSH/PSH PLTEPVPTSGRGCLWTKRQ QKMCRTITYTSVGRK/CTFPIDS GALRLSDGEMRALQITPGPQST VEGHTHLQSL/PHHDRVATPG TEPLRAAGNRRIYPGP/VT SQ VQPQLLCGYGNASRTPAALTPG PAPPTQASLPNGICPHLQMG PTSPC/PPEGHPSSSLYISLSPPP PSAPALRLPPPLP/SAPTAPAL/P/ PAAPSAPALRLRLPCCSFRPR PAAPSAPAPRLPPLLVCSEFRPC PAAPSAPAGLLLPPLLCCSGLSP RLCCPHSSCSDPPRLQRKADSS
4337	34705	B	4378	1	984	
4338	34706	A	4379	332	847	VKLLQDKEICILCQKTVYPME CLVADKQNFHKSCFRCHHCNS KLSLGNYASLHGQIYCKPHFKP TFQNPKGNYDEGFGHKAHKD RWNVQKPKADSVDIPNEEPN MCKNIAENTLVPGRNEHLDA GNSEGQRNDLRKLGERGKLKV IWPPSEIKPKTLPFEEELKMSK
4339	34707	A	4380	305	505	GNLERMLNLGMVKQKQLPAIM KTQVLMML*AINVPAKPLFPQSG GAVRTTHGGSRLKETGATSD TE
4340	34708	A	4381	56	260	IVKTQSIDG/MGNLRITEKGLKL EGDS/EFLLQPLYAKEIQSRPGLG TQEQSCQTLSSCSSRQGOQHAE
4341	34709	A	4382	137	920	
4342	34710	A	4383	532	1680	LLTTRTSFRSENHRHVGLLVM TDNTRDKEYFGDESKRENEKT VEKSIGEKQATLTTHANIITIRH CVKPEPDFSDHLNLLGRADIT GEEMAAQRSSVEKLANGNIAL VDSLRSRSLEEGSDPHKRLSG AQDIKTTVVEVIADVVEIARELE LEVEPEDVTEFLQAHEKTLTDV ELFLINEQIKWFLEMKSTPRED AVIIAETITKVEYDINLVTKQ QGMRLTLPILKEVLLVWKCHQ TALHATEKPFKGRINPCGKIHT CLNLRNCGQLIREEEEEEDKEE EEQYEEKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEDKE DEEEDKEKEEEDNKEEEEEED KEKEEEEEEDKEKEDEEEEEEDK

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4343	34711	A	4384	3	495	EDTGTFRIFYESAGAVKKARGF LEFVEDFIQVSKNLIGKVGKNG KVIQEIVDKSDMPVVRIEGDSE NKLPRDEKDDRSRHRQDRSR CPGGRCSRVSRRGRGGPRGG KSSISSVPKDPDSNPYSVLN/T ESDQTADTDASKSHHSTNRHTR SRRRTDEDAVL
4344	34712	A	4385	1	550	TESERKDELSDWLAGEDDRDS RHQRDSRRRPPGGRGSRVSGGR GRGGPRGGKSSISSVLKDPDSN PYSLLDNTESDQTADTDASESH HSTNRRRRSRRRTDEDAVLM DGMTESDTASVNEGLAKDV IEEHGPSEKAINGPTSASGDDIS KLQRTPGERKRLIP*KKENTQE AAVLNGVS
4345	34713	A	4386	1	2063	MAELTVEVRGSGAFYKGF DVHEDSLTVVFENNWQPERQV PFNEVRLPPPPDIKKEISEGDEV EVYSRANDQPCGWWLAKVR MMKGEFYVIEYAACDATYNEI VTFERLRPVNQNTVKKNFTFK CTVDVPEDLREACANENAHKD FKKAVGACRIFYHPETTQLML SASEATVKRVNLSMDHLRSIR TKLMLMSRNEEATKHLECTQ LAAAFHEEFVREDLMLAIGT HGSNIQQARKVPGVTAIELDED TGTFRIFYESADAVKKARGFLE FVEDFIQVPRNLVGKVGKNGK VQEIQVSKGVVRVRIEGRNEN KLPRDEGMVPFVFGTKESIGN VQVLLLEYHIAYLKEVEQLRME RLQIDEQLRQIGMGFRPSSTRGP EKEKGYATDESTVSSVQGSRSY SGRGRGRRGPNYTSGYGTNSEL SNPSETESERKDELSDWLAG DDRDSRHRQDSRRRPPGGRGSR VSGGRGGRGGPRGGKSSISSVQY RSNIHNCSTLKRIFLADSMNIVL KDPDSNPYSLLDNTESDQTADT DASESHHSTNRRRRSRRRTDE DAVLMDGMTESDTASVNEGL DDSEKKPQRRNRSSRRRRFRGQ AEVDRQPAIDFIYKEVEKVVSL WQAKDVIEEHGPSEKAINGPTS ASGDDISKLQRTPGEEKINTLKE

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4346	34714	A	4387	1	1882	CGSNMADVTVVEVRGNGAFYK GFIKDVHEDSLTVVFENNWQPE RQVPFNEVRLPPPPDIKKEISEG DEVEVYSRANDQEPGCGWLA KVRMMKGFEYVIEYAACDATY NEIVTFERLPRVNQNKTVKKNT FFKCTVDVPEDLREACANENA HKDFKKA V GACRIFYHPETTQL MILSASEATVKRVNLSMDHLR SIRTKLMLMSRNEEATKHLECT KQLAAAFHEEFVVREDLMGLA IGTHGSNIQQA R K VPGVT AIEL DEDTGTFRIGESADAVKKAR GFLEFVEDFIQVPRNLVGKVIG KNGKVIQEI VDKSGVVRVRIEG DNEKNLPREDGMVPFVFGTK ESIGNVQV LLEYHIA YLKEVEQ LRMERLQIDEQLRQIGRSYSG RGRGRRGPNYTS GYG T NSELSN PSETESERKDELS DWSLAGEDN RDSRHQRDSRRRPGGRGRSVSG GRGRGGPRGGKSSISSVLKDPD SNPYSLLDNTESDQTADTDASE SHHSTNRRRR/SIRRRRTDIEDA VLMNGMTESDTASVNGELVT VADYISRAESQSRQRNLPRETL AKNKKEMAKDVIEEHGPSEKAI NGPTSASGDDISKLRTPGEEKI NTLKEENTQEA AVLNGVS
4347	34715	A	4388	2	421	PRVRSDTDEDDSEAEHFESFIHP TAMMFTSTINLLQTLCLSGVH AEIMQSEATKLCGLLAKSSPNR LVYREQHRSWCTLGFVQSIALT LQVCGALSSLQWITLLMKVVE GHAPFTATSLQRQILA V HLLQA VLP S WDK
4348	34716	A	4389	269	417	DLNCKVGSCFEVYSS*KQGIN*1 KLGD SKT*P*LSGPTSEN LKNSS LAE
4349	34717	A	4390	1	516	
4350	34718	C	4391	1	1527	

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4351	34719	A	4392	200	1267	TFSKASRGGNPHSMTKAPSDFR KARQTGIPGCSQLGSRYSLEPE QSALRLVCIQKLQESSSTTCEDFF CPLCGRAWAVSTPLTDSPSPGH QPAVK*LGLVPFSDTHHPLPFQ VLSTDDTSSSSSCSSSCASSSSP /SLLLLLLFLLLLLLLMLLLKL FLLLLLFL/RPPASPPLLPAL PPL/HCSSSPSPAPSPPPAPPPPP APPPSPPPAPSPSPAPSPAPPPA PASPPFSCSSSCSSSCSSSFSSC SSLSSSAQAEGSLRAPRESSPSL DPSAPQRVKVPVQAGSGIIRA GGALENRPRGKKPWLHFRPGL RSRLPARSLRSRPAPTRWRLRSS GRFTGAATATATART
4352	34720	A	4393	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAQSGQCSRN ARHQAQKARSMPLQDQHLALAIL LELAVQRTLSQMLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLQTFQSIICSKDTPPSEGN MHLLSGPLSPSEFLRESFTVQ NCRNNEEVTICKADLENHNK DGGFWIVIDEKVYDIKDFQTS LTGNSILAQFAGENPVVALEAA FEFEVTRSMHAFVGVQYLEVR LYALSDAEDGRGTL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTAPASKSR/CSIIRWALG DHSQAFLOAIADNNIQDHNKVT HQEQGRSYKEVCTPVIERLRFL SNELRPAVGNDSLHSEFKLLSSL PRWRIAQKIIRERRKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPPIAKSPKTITSEN LGPSLGSIPQARFLLMMLSLT LQHSANNLDDLNSGTALALQT ALRLIGPSCDNVEEDMNASQ GVSATVLEATRKETAPVHLVPS GPELAATMKIGTRVMRGVDW KWDGQDGPPLGLRVIGELGE DGWIRVQWGTGSTNSYRMKG EGKYDLKLAELPAAQPSAEDS DTEDDASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFAASL QRQRWVAVSLPHALVKSQGTVP

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4353	34721	A	4394	266	1110	WARGGCARNALASGNAIQGGK CNPGLFPPSPNRLVYREQHRWS CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFAASL QRQLCPE/HTSCPVLKDFCKSVI TDVACSSLISTLLVFWGGGLLHT HKEASESWREAKSTSYVAAAR ENEEDAKAEPPTGPKPSDLVRL IHYQENSMGETAPMIQIISHWV PPTTHGIYGSTIQDEIRVGVSY GHTDARGFQLLLVSGDFSIPYW SLSSAYTSVNSSFVESLQSNLLK GILLPATIMTDPRTTGHQ
4354	34722	A	4395	1	734	MVQLSGKRILNSPYLELRCHQN MDHLGWVVKSLNRSEVSWVP GLEFPWGPKEPREVIAGPLLRN NGQSLESSLESHVGVYFSAH WCPPCRSLTRVLVESYRKIKEA GQNFEEIIFVSADRSEESFKQYFS EMPWLA VPYTDEARRSLNRL YGIQAHFLTANAEDFDTTVQV NKIILITYRQENSLSSLKGTGET EAQGRQLQGSFNSVRGHDPRH AIPLSVNRWNPSKSSPSAVWS
4355	34723	A	4396	195	1071	LHEFDSSRDLTSLGGARTHR LGGPSDAPRGLPAPPPAPVVRPG /PRSPGFSAGTAR/DAPRPSVQM RAQRPARGSTKDLIETCCAAGQ QWAIDNDECLIPESGTEDNVC RTAQRHCCVSYLQEKSCMAGV LGAKEGETCGAEDNDSGISLY KASLTCGLQGRCLNPQQASMG LFSYDVQSSKKINRSIQEKLGG HGVCAATPGGGMNRNCGRLRRS GQRRGGTDRCEAVLTGLFTRA LIREQMGDPHPLDHTGQLAKPL EVEKTPARWKYLDTNGEKEEP ELRTQCPSLYED
4356	34724	A	4397	1	520	MMGEKAEKPDTEKKKPKAKK ADAGGKRNCRYSRSAMYSRKT TSRKKYSAASKVEKKKKFLA TVTKPVGVGDKNSGTQVVKLHK MPRYYPTEDEVPLKLLSHG/KKK PFSQHR/RRVVFLKQLV/SGTGP LVLNQVPLRRTHQKFVIATSTKI GSSNVKIAKRLTGAYFKKVKWK PKHQE
4357	34725	C	4398	67	243	

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4358	34726	A	4399	1	333	QRSCIENILRAC/VGLPPQNHML LEHKMDAKRVGPVAATYPML NKKGPVPAATNGCTGDANGHL QEEPPMPTT*GPGH TVSRLFLPA APHDP TLKAPTNNNSAATQPSKN KKK
4359	34727	A	4400	587	1013	GAASAGRGPGRAPGLWGRGP AAAGASLVPTD HVHLSYNHLG NNDGENLSAP/SQFRSKEVSKS NVVDD/MVQSNPVLYTPGEPPD HATRCWPHPSAGPSAADRAVP ARPA GAPATEPHAPGTQNGAP GPSLKR VGPVAATYPI
4360	34728	A	4401	2	334	
4361	34729	B	4402	257	975	
4362	34730	A	4403	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRL LARA EKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLVCRKMGVP YCIK GKARLGR LVHRKTCTTV AFTQVN
4363	34731	C	4404	62	217	
4364	34732	A	4405	2	69	
4365	34733	A	4406	1	951	GTRPKMPKGK KAKGKKVAPAP AVVKKQEGFRKKW*IPWFEKR P\KNFGIGQDIQPKRPPPLL*K WPRQYQACSGQRAILYKRILKV PPAMKPVSPRALD\ RQTATQLA *AVAHKVQTORQKQEKKQRL\ LARADEEGCLAKGDVPNERDP PVPSSQEFNPVSPPLVKEQEKLK LVVNWH TDVDPHPSLVCLPC/ LC PAPVS*KMG GPFTCIHQKRA RLWDR LVPQERPCTTCPPFTQV N\SEDKVRL LAKAGLEAIQGPY N*PDTMEIRPSLG VGNVLGPKS VARIAKARNRHKAKETATHTG LNVTL SFLYYKNN

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4366	34734	A	4407	1	1392	MPDVSEEQKESVCTGSMRMREE ESSRKGVRTAGAKSSSSDRVP RLNQEEVESLNRPITGAIEVAIIN SLPTKKSPAPDGFATAEFYQRIRI QQPIIRIQQPIKKLIQHDKVGFI GMQGWFNICKSINVIQHNRK EKNHMIISIDAEPDKIQQCFM LKTNLKLGIDGTYLKIIRAIYHK PTANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIHQE KEIKGIQLGKEEVKLSLFADDM IYILENPTVSAQNLLKLSNFSK VSGYKINVQKSQAFLYTNNRQ TFEQIMSELPFTIASKRIKHLGIQ LTRDVKDLFKENYKPLLNEIKE DTKKWKNIPCSWAGRISIMKM AIPKVIYRFNAIPKLPMTFFTE LEKTTLKFIHQKRAHIAKSILS QKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQCTRTQP SEITPHIYNILIF
4367	34735	A	4408	1	1947	MALRLRLSHDVSGALLANGES TGNSSGSSGSSPSSGATSSGSQ TSISGDVVEACCSVLMSVCA VPYKVVYAALQCMMLVLTEDPS SHFTRMRRRLM/AYADEVEIAE AIQLGVEDTLDGQDQSF/CRHL FPTTIWKPQRTVP/LECTIHLEKT GKGLCATKLSASSEDISERLASI SVGPSSSTTTTTTEQPKPMVQ TKGRPHSQCLNSSPLSHHSQML FPALSTPSSSTPSVPAGTATDVS KHRLQGFIQCRIPASPTQKRF SLQFHRCNPENKDSKLSPVFT QSRPLPSSNIHRPKPSRPTPGNTS KQGDPSKNSMTLDLNSSSKCD DSFGCSSNS/CCYTSDETFT PVEEKCRDLVNTLNSSIEDLLE ASMPSSDTTIVTFKSEVAVLSPE KAENDDTYKDDVNHQKCKE KMEAEELAAIAMAAMSASQD ALPIVPQLQVENGEDIIIIQQDM TFRHIIPPIQWIYKKESANLLID STGQRLRIADFGAAARLASKGT GAGEFQGLLTGTAFMAPEVLR GQQYGRSCDVWSVGCAIEMA CAKPPWNAEKHSNHLALIFKLL LDFANTACDGDKESEVEDVET DSGNPDELKKEIMIGLQYQAEI PPYLGEDGNEKDSPPQKKMT GVQNAKEVLST

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4368	34736	A	4409	1	4485	
4369	34737	A	4410	2	927	IDHMIGHKASLNKFKKIEIISSTL SGHNGIKLEINSKRDLQNHANT RKVLNNLLNEHWVKNEIKMEI LKFFELNDHNDTTYQNLWDTA KATFLLRGKFTALNAYIKKTER AQTDILRSHVKELEKQEQTQPK PSRRKEITKIREELNEMETNKK KIQKINETKSRRFEQINKIDRSLA RLAKKRREKIQITSIRNKTGDTT TDTTEIQKIIQGYEHLIAHKLE NLEEMDKFLEYNPPSLNQEEL DTLNRITTSNKIEMVIKKLPTKK KSPGPNGTAEFYQTFFK/EEELVP ILSILVHKTEKEGTLT
4370	34738	A	4411	405	517	
4371	34739	A	4412	1	1197	MEISELNAKLSRSEKEKQNEIHK LQLEKLQHFQEEKNKEIALRN TIRDLEQRLSVGKDSHLKRENE QLKISADLIKEKLSHEQEYKN NIAKLVSSEMIKEEGYKKEISK LYQDMQRKGRIKVTCEWTCSE RKTEGREPGVPREPTGRSQSAE NEGSKTLAEINTKGTQSPAERIN KIDRLAARLTNRREKVQISSIR NKTGDIRTDTTEKQKFMQGYH EHLVYMHKLENLKEMDKFLEIY SPRLKREDIETLSRPITSDIEM KNLKIPPKLPKLINKFSKVSRYK INVHKLVALLYANSQTDNDQIK NSTHTIVAKKLYLGIYLTQDM KDLHKENSK/PLLKEIIDDTIKW KHIIPCSWMSTTNIVKMTILPKTI YKFNAIIKIPPSFFAERKKQS
4372	34740	A	4413	1	190	MIQRKRASIGAPCAWVRKKEE EEEEEEEEEEEEEEEEEEEEK KKKKKKKERTTWLWGNPLT
4373	34741	A	4414	303	429	
4374	34742	A	4415	123	252	
4375	34743	A	4416	1	156	
4376	34744	A	4417	3	351	EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEE/KEEEEEEEEEEEEEEEE LGRLHGGSGKVRGLGFTENQQ GSTNRQHQREDNRKSKQKKIN NTKPEATESLIYNGITITAPA
4377	34745	A	4418	1	192	
4378	34746	A	4419	3	259	
4379	34747	A	4420	1	279	
4380	34748	B	4421	1	708	
4381	34749	A	4422	3	269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4382	34750	A	4423	1	322	MAGKQGRSEGAASWRLSSVLQ LNSQYFLQGAQQCTFLAATAW KKRKKEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKKKKKKKK KKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKK KKKKKKKENPFSCF
4383	34751	B	4424	327	674	
4384	34752	A	4425	494	960	TRFYDHALHLHRRKGSTTVRSP PPLYFIGESKASALLAISLRWSG RSQPRSSVNQIRKAWGFRPKKG TEE/DERSGCPSDALESDDPMA YIHFTAEGEVTFKSILFVPTSAP RGLFDEYGSKKSDYIKLYVRRV FITDDFHDMMPKYLNFFVKGVV
4385	34753	A	4426	1	2539	VGGPRGWRCEDPNPVGVGGGGG SCDRRLGLETFRPHAMRALWVL GLCCVLLTFGSVRADDEVVDV GTVEEDLGKREGSRTDDEVV QREEEAIQLDGLNASQIRELRE KSEKFAFQAEVNRMMKLIINSL YKNKEIFLRELISNASDALDKIR LISLTDENALSGNEELTVKIKCD KEKNLLHVTDGTGVGMTREELV KNLGTIAKSGTSEFLNKMTEAQ EDGQSTSELIGQFGVGFYSAFL VADKVVITSKHNNDTQHIWES DSNEFSVIADPRGNTLGRGTTIT LVLKEEASDYLELDTIKNLVKK YSQFINFPIYVWSSKTETVEEPM EEEEAAKEEKEESDDEAAVEEE EEEEKPKTKKVEKTVWDWEL MNDIKPIWQRPSEVEEEDYKA FYKFSKESDDPMAYIHFTAEG EVTFKISILFVPTSAPRGLFDDY GSKKSDYIKLYVRRVFTIDDF HDMMPKYLNFVKGVDSDDL PLNVSRETLLQHKLLKVRKKL VP*NRWDMIKK/SLDDKYNDT FWKEFGYQHSSLVVIEGPLRIR TRLAKLLR/QSSHHPTDNTSLD QYVERMKEKQDKIYFMAGSSK KEAESSPFVERLLKKGYEVYIL TEPVDEYCIQALPEFDGKRFQN VAKGVKFDESEKTESREAVE KEFEPLLNWMKDKALKDKIEK AVVSQRLTESPCALVASQYGV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4386	34754	A	4427	2	622	PARAALGILTSHQSGFLKTSTSK ITSTAWKNKIDITMQSTKQYAC LHDLTNKGIGEEIDNEHPWTKP VSSENFSTSPYVWMLDAEDLA DIEDTVEWRIIRNVESLCVMET ASNFSCSVTSGCFKDIVGLRTS\ ACWQQHCASPAFAYCGHGFCC TGTALRTMSSLPRESSAMW*KKP ARTRLPRGKDLIYFGSEKSDQE TGTLPLPVSS
4387	34755	A	4428	2	1421	QHCSQKDTAELLRGLSLWNHA EERQKFFKYSVDEKSDKEAEVS EHSTGITHLPPEVMLSIFSYLENP QELCRCQVSMKWSQLTKTGS LWKHLYPVHWARGDWYSGPA TELDTPEPDEWVKNRKDESR AFHEWDEDADIDEESEAEESI AISIAQMEKRLLHGLIHNVLPY VGTSVKTLVLA YSSAVSSKMV RQILELCPNLEHLDLTQTDISDS AFDSWSVLGCCQSLRHLDLSG CEKITDVALEKISRALGNSGHL HQSGFLKSTSTSKITSTAWKNKD ITMQSTKQYACLHDLTNKGIGE EIDNEHPWTKPVSSSENFSTSPYV WMLDAEDLADIEDTVEWRHR NVESLCVMETASNFSCSTSGCF NHRPWSQNEYELNYAKQLKE RLEAFTRDFLPHMKEEEEVFQP MLMEYFTYEELDKIKKKVIAQ HCSQKDTAELLRGLSLWNHAE ERQKFFKYSVDEKSDKEAEVS
4388	34756	B	4429	70	348	
4389	34757	A	4430	2	371	
4390	34758	A	4431	1	907	MGHRINIVCKIDAPCARQTRTF HPVVKTVEDCGRYPVIEFGKY EIQTWYSSPYQEYARNLAKEG KMGEREMSFVQQLPQMSGRCS LFRELSSCTYLLNTQPP/AVSIH FLAVWIILLVDGNMSKIYQCNL CLLAKLFLDHKTLYYDVPEPLF YVLTKNDEKGCHLVGYFSKWT VLQGGWQVQGIHAFSRALTYLI CFSFPQEKLCQQKYNVSCIMIM PQHQRQGGFRFLIDFISFRLTIG ASFTQLRKQSMNSTEIPLLGD NGKSSPTFWQSLTSSPNAHFS LEAQLSILGHLFQSP

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4391	34759	A	4432	1	3468	MGKKQNRKTGNSKNQASPPP KERSSSPATEQSWMENDFDEL EEGFRLSNYSLEPDIQTGKKE VENFEKNLEECITRITNKRNF TKIKRDKEGHYIMVKGSIQQUE LTIILNIYAPTGA PRFIQVLS QRDLDFHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHKSSTEYRFFSAPH HTYSKIDHLLGSKAFLSKCKRT EIITNYLSDHSAIKLELRKLNLTQ NRSTTWKLNN
4392	34760	A	4433	3	1900	FNKCMTLKFRLNKFSRINKIDTP LARLIKKKREKNRIDTIKNDKG DITSNPTIEQSTIREYYKHLVTN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTGSEIMAIINSLPT KKSPGPDGFTAKFYQRYKEELV PFLKLFQSIKEGILPNSFYEAS IILIPKGRDTTKNENFRPISLMN IDAKILNKILANRIQQHKKLIH HDQVGFIPGMQGWFNIRKSINV IQHISRTKDKNHHIISDAEKAF DKIQQPFMLKTLNKLGIKYLGI QLTRDVKDLFKERS/YEPLLEI KEDTNKWKNPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRALIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITLHIYNYLIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLD PFLTPYTKINSRWIKDL NVRPKTIKLEENLGITIQDIGM GKDYMSKTPKAMATKAKIDK WDLIKLKSFACTETIRVNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKHKMKCSP SLAIREMQIKTMRYHLTPVRM AIIKKS GNN
4393	34761	A	4434	2	1932	

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4394	34762	A	4435	1	2571	MKAEIKMFFETNENKDDTTYQN LWNTFKAMCRGKFIALNAHKR KQERSNTDTLTSQKELKKQEQ THSKPSRRQEITKIRAEMKEIET QKTLQKIKESRTWFEKINKIDR LLARLTKKRKNQIDAINKDK GDITTDPTIEIQTIREYYKHLYA NKLLENLEMDKFLDITYLPRLN QEEVESLNRPTGSEIEAIIINSLP T/KKCPGPDGFTAIFYRRKRGU LPNSFYEASIIIPKPGTDTTKKE NFRPISLMNIDVKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSIHIIQHINRAKDKNH MIISIDAEKAADFQIQCFMLKTL NKLGDGTYLKIIIRAIYDKPTAN IILNGQKLEVFPLKTGTGRQGCPL SPLLFNIVLEVLAIRAIQKEIK GIQLGNEEVKLSLFADDMIVYL ENPIISAPNLLKLINNSFKGSAY KIKVQKSQAFLYTNNRQTESQI MSELPTFIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAILIKLPMFTFFTELEKST LKFIWNQKRARIKSIKSNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNGTEPSEIM PHIYNYLIFDKPEKNQWGWKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLHVRPKTI KTLLENLNTIQDIGMGKDFMSK

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4395	34763	A	4436	1	1965	MTLESEQTFVYAVTATQTGAK EGTRMSKSNVAGQQGDSEKA LQKTYQKILREKESALEAKYQA MERAATFEHNRDKVKRQFKIF RETKENEIQDLLRAKRELESKL QRLQAQGIQVDFPDGESDDNC TDVTAAGTQCEYWTGGALGSE PSIGSMIQLQQSFRGPEFAHSSID VEGPFANVNRDDWDIAVASLL QVTPLFSLWSNTRCYLIYT DETQPEMDLFLKDYSPKLKRM CETMGYFFHAVYFPIDVENQYL TVRKWEIEKSSLVILFIHLTLPRI KYLGIQLTRDVKDLFKENYKPL LNEIKEDTNKWKNILCSWTGR NNVMKMATLPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR AHIAKTILSEKNKAGGIMLPDF KLYFKATVTKAAWYWCQNRD IDQWNRTEASEITPHIYNHLIFD KPDKNKKWGKDSLFWKWCWE NWLAIKRLKLDPFLLPYTKIN SRWKDLNVRPKTKITLEENLG NAIQDIGMGKDFMTKTPKAMA TKAKIDKWDLIKLSFCMAKET PIGVNRQLTEWEKIFAIYPSDKG LISRIYKELQTYKKKTNNPIEK LAKEMNRHLSKEDIYAANRHK KKCSSLVIREMQIKTT/MRYHL TPVRMAIIKKSGNNRCWRGCG
4396	34764	A	4437	300	476	PDLSLWLPITFFPSQLW*IQQL CVLELLFSRSIFVAFSVPFEFES WPALLGWGSSPG

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4397	34765	A	4438	413	1689	OKLYKPERIKYLGILQTRDVKD LFKENY/KLNEIKEDTNKRKNIP CSWVGRINILKMAILQKVIYRF NAIPIELPITFFTKLEKTTLRFIW NKKRVHIAKSIPSKKNKAGGIM LPDFKLYYKATTTKTAWYLYQ NRDIDQWNRTEALGITPHIYNH LIFDKPDKNKQRGKDSLFNKW CWENWLVICRKLKDAFLTPY TKINSRWIKDLNIRPKTIKTLLE NLGNTIQIGMGKDFMTKTPK AMATKAKIDKRDLIKLSFCTA KETNIRVNRQPIEWKIFAIYRS DKGLISRIYKELKQIYKKKTNN SIKKWAKDMNRHFSKEDIYAA NRHEKKWSPSLVTREMQIKTIM RYHLTPVRIMTIKMSGNNRCW RGYGEIGMLLHCWWECKLVQ ALWKTVWRFLKDLEIIPFDPV IPLGLIYPKDYT
4398	34766	A	4439	3	2404	
4399	34767	A	4440	1	1572	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKMSMA RELHDTCTSFNSRFDQVEERS AIEDQTNEINNGENGTKLENTL QDIIQENFPNLAQANIQIEIRR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKVLEVLAIRAI SQEKEIKCTQLGKEEVKLSLFA DDMIVCLENPVVSDHNVKLKLS NFSKVSVYKINVQKSHAFLYTN NRQTESQIMSELPFTITTKRIKY LGIQLTRAVKDFFEKQYKPLL EIKKDTNKWKNIPSCIGRINIM KMAIVPKVIYGFNAIPKLPRTF FTELEKTTLKFIWKKKGAKTILS IKNKAGGIMLPDFKLYYKATVT KIAWYQYQNRINQNRNRTETS EITSHIYNHL/IFDKPDKNKKWG KDSLNFNKCWENWL
4400	34768	B	4441	1	1558	

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4401	34769	A	4442	837	4329	TWKGTTDRSTRQKVNKDTQEL NSALHQADLIDYRTLHPKST YTFE/LAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNLL NDYVWHNEMNAEIKMFFETNE NKDDTTYQNLWDFAKAVCRGK FIALNAHKRKQERSKIDTLTSQ KELEKQEQTHSKASRRQETKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
4402	34770	A	4443	1	816	MRRDYPVKAFTSRKREQHVQK VPSKKSQRQVQRTERRFLETPD LLYQKEKDLLLISSSKKQPRPGI ERHYMMTQGSIHQEDVAILK/V YTSNKRASKYIQQ/TLEIKGKI/ AHPQIVGDFNTPSTIDRTIRQQI/ SIEFYDTIKOWDLTDCRTGHPI TEYIFCSGAHLTFTKINHIQGP RILKRFRKRIEIECVLVKGCQA KNRKKEEDLQTY/WMLNIYGP YRSGSYAAIHRQETICSGQLSQ ALRDRFAMNAKLLLSLAHLW VIKLDPM
4403	34771	A	4444	87	307	
4404	34772	A	4445	1	534	MEESRGAKPPALLPGDATALPP GSLGARHPPEP/RPVGP/PPHQ TCPGPSACSSRPPEPRSSPGSPA RAPPAPPPAAPRCEPPLWLL LRVPCPGRSGWSWMTT*/I/SERP VQKRARSQGPRLPCLPLSPP TAPDRATAVATPPVLGPMSSW SPRRAGGPTRPCTALQALSIPA
4405	34773	A	4446	164	660	YPSGRRLREPADVADWDGME ESRGAKPPALLPGDATALPP/AP SGQLGTRPSPPSSRPSPHQTC PSACSSRRPEPRSSPGSPARAPP APPPAAPAPRA/SPRRPLAPRS ASVPAFSAAPPQWPEVGPSPCA LRRAMPRGPGPPPEPLVAEPG EDAAPTAGR
4406	34774	A	4447	1	417	

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4407	34775	A	4448	1	1802	MSYPADDYSEAAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIVEIKNFQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVVEIQDIYENSWTKLTERFFK NTPWPEAAEAIAPQVGNDVFLI LYKELYRHIYAKVSGGPSLEQ RFESYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSLVNLVHLSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLRLHSL GDYYQAIKVENIELNKKSMYS RVPECQVTITYYVGFAYLMMR RYQDAIRVFANILLYIQRTKSM FQRTTYKYEMINKQNEQMHAL LAIALTMYPMRIDESIHLQREK YGDKMLRMQKGDPOVVEELF SYSCPKFLSPVVPNYDNVHPN YHKE\PFLO\QLKGVF**SSSQ AQLS/TPIRSFLKLYT/TMP/VAK LAGFPGPSQSQEF/RIPGFFVFKQ QDERTSVVWTVRFSPAGW*NF SQASEVDFYIDKDMIHADTK VA\RRYGDFFIRQ\HKF/EELNR TLKEGWGQRPMIFHTHFREP GFECIGQGSVFC

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4408	34776	A	4449	1	1722	MNIKAKILNKILANRIQQHIKKL IHHDHVSFIPRMQGWFIHKKPIN VIHHINRTNDKNNHIIISIDA EKA FDKIQHPFTLKTNLKDDMTVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPTFIASKRIKYLGLQTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINVVKMAILP KVYIRFNAIPKLPMTFFTELEK TTLKFIWNQKRARIKSI LQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTEIPSEI MPHIYNHLTFDKPDKNKQWGK DSLFNKWCWENWLAI CRKLKL DPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNVTQDIGMCKD FMTKTPKAMATKAKIDK WDLI KLKSFCTSKETIIRVNRQPTWE KMFAYIPSEGLISRICKE/LFKQ IYKKKNHPKWKADMN RHFS KEDIYVANKHMKSSSLVIRE MQIKTTMRHHLTPVRMTI IKKS GNNRFWRGCGETGMLLHCWW ECKLVQPL*KIVW*FLKDL ESEI PSDSAIPLGGIHPKAYKSFYY
4409	34777	A	4450	1050	1147	PGEWHGQGSFRCWR*PLPQRC GHLLSCRWRT
4410	34778	A	4451	1	614	MEELVDEGLVKALGVSNFSHF QIEKLLNKPLKYKPVTNQNSL GTMQNRAGFPRDEDCLLQVE CHPYLTQEKLIQYCHSKGITVT AYSPLGSPDRPAWKPEDPSLLE DPKIKEIAAKHKKTAAQVLI RF HIQRNVVIVPKSVTPARIVENIQN TEHYKCYGLCVGPNLEKNLYP VDRM/WKNSCGQFVL*ISSHLE DYPFNAEY
4411	34779	A	4452	2	240	WMELESLSHFQIEKLLN/KPGL KYKPVNTQVNSIQFGSILEEGI VNMGGDSSMHVSAPEPPVGQ DVEAEDSDTDDPDPV
4412	34780	A	4453	1	1019	
4413	34781	A	4454	1	2028	

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4414	34782	A	4455	3	1045	DFTSENFSAAWYLIENHSNTSF EQLKMAVTNLKRQANKKSEGS LAYVKGGLSTFLEAQDALSAIH QKLEADGTEKVEGSMITQKLEN VLNRASNTADTLFQ/EKVLGRK DKADSTRNALNVLQRFKFLFN LPLNIERNIQKGDYDVVINDYE KAKSLFGKTEVQVF/KKYYAE VIEPRVEALRELLADKLETPST LHDQKRYIRYLSDLHASGDPA WQCIGAQHKWILQLMHSCKEG YVKDLKKGDFSSNVFQSGSAL RRVPDTRVRLDSQFSRSALRSV PDTVQVLDQFSGSALRRVPDT VRVLDGQFSRSALRSVPDTRV LDKCHCSPAkvVMNAVITFTG
4415	34783	A	4456	1	440	MQRNLARAFSPGIKKIKMMCL GNSEKDWPKFRGVGEDAGLLA ARECGALLVIRHLINAVRAIVP NKSNNIILVLQHFDCVNDK/TV QAFMEGSASEVLKEWTVTGKK KLLQGEELARLPFITGGSGSC YSSSTLAVEECRVLA
4416	34784	A	4457	1	276	MEDEMEGLTEAGFRRWVTTNS AELKEHVLVTQCKEAKNLDKRL EELLSRITSLERDISDQME/RELC EAYTSINSQINQAEERISEFEDH LAEI
4417	34785	A	4458	3	361	EMVHRKKKAVHRTATADDDK LQFSLKKLEVNNVSGIEEVNMF TNQGTVIHFNAEMPANSFTITG HAETKQLMEMLPSILNQLGAH CLTSLRRLAEALPKQSVNGKAP LATGEDDDDEVPA
4418	34786	A	4459	1	475	EDSGGGGKFPGARQGGTGQR RRRKAMRRTGAPAQADSRGRG RARGGCPGGEATLSQPPRGGT RGQEPQMKETIMNQEKTRHTC RAQVIRIGGKGTARRKKKV VH RGAAS/ADDKKLQFSLKK/LGV NNISGIEEVNMF/FTNIQGTSGST FNNP*KFGQISWPANTFHHLQ HAEDKGS*QEMLAQHLKPSLG ADSLTSLRRLAEALPKQSV DVGK APLATGEDDDDEV/VDLV/ENF* *RLPRNEANLNSQLLKIKP
4419	34787	A	4460	57	820	
4420	34788	A	4461	1	1527	

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4421	34789	A	4462	8	327	LIWQLTFTKTIKS/CEEYGVKIVST KAILDKNTNQCKGMCKGIRTL KSCLCYLINGSIVVQKRLAY AGTLEPSLVHQVYSELSYYKLP GTQVVRHAEVLRMQDSSE
4422	34790	A	4463	2	573	WMEGREKWRGRRKDGRRKEGR KEGRKERREREKGRERK/GKE RKGGKRGKGRKGRKGRER KGTEGKGTEGKGKRGKGEKG GKERKGRKGRKGRKGEKG KEQKGKGRKGRKGRKGRKGRK ERKGRKGRKGRKGRKGRKGRK GKGRERKKGEGGKEGRKERR KEGRKEGKKFSNNGMVEMEQ
4423	34791	B	4464	1	1344	
4424	34792	A	4465	3	373	
4425	34793	A	4466	1	3864	MQWEEAEKDPSGSCVFQRPVP ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHPOP CESRPPVPPEYEVTVLRSGQTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLKGFSDN
4426	34794	A	4467	3	415	
4427	34795	A	4468	396	676	LCFFPYAERPDLQFLC*DLCARSP YLLQAQKYLQEF*AIPHLDDQT EPPDPSSVSFYLLDCTLNCTAQH KTC*KKSIGL*EQNQQTLSIPY SHT
4428	34796	A	4469	1	858	MEWEDNPLELGRVAKLLSD HSQTPGLIQMFLFSLSRKSP VCLSYLFNFRFTLESEVQHLG AITLTAWPKIFLGIREAKSPRS ENTRLATILEAGHRHLGTSVSK DHPVTFWRPRRDQLQSDLKQIKI DLGKFSNPDGYIDVLQELGQS FDLTWRDIMLLNQTLPNERS ATTAAAREFGDLWYISQVVAAV AGLVSEAVKIIQGLTVWT/SHD VNGILTAKGDLWLSDNHLLKY QALLLEGVPLRLRTCATLPAT FLPDNEEKIEHNCQQVIAQTYA
4429	34797	A	4470	918	1939	

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4430	34798	A	4471	3	2693	PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGVLGQ PVTRYFFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAIL HLNIGEGTPICRLLFEEGISPEV WATEGQYGGAKNAHFVQVKL KDSTSPYQRYPLRPEAQORL QKIVKDLKAQGLVKPYSSPCNT PILGVQKPKRQWRLVQDLRIIN EAVFPLYPAIPSPYLLSQIPEEA EWFTVLDLKDAFFCIPVHPDSQ FLFAFEDPSNPTSLTWTVLPO GFRDSPHLFGQALAQDLSQFSY LDPVLQCMDDLLAARSETLC HQATQALLNFLTTCGYKVKP KAQLCSQQVKCLGLKLSKVTR ALSEERIQPIAYPPYKTLKQLR GFLGITGFCRIWIPRYGKIARPL YTLIKETQKANTHLVRWTPEAE AAFHALKKALMQAPVLSLLTG QDFSSYVTKNKQTKKKK*IA LRVLALV*GTSLQPVAYLSKKT DVAAGWPHCLWVMAAIAVLI SKAVKMIQ*RDLTWVWTHSDVN GILTAKGDLWSDNHLKYQA LLEGPMLRLCTCAALNLDLFL PHNEEKIEHNQQVIAQTYATR GDHLEVPLTDPNPNLYTDGRSF VEKGLQKVGYA VVSDNGILES NPLTPGTSQAQLAELIALTWALE LGEGRVNIYDTSKYAYLVLH AHAVIWREREFLTSEGTPIKHQ
4431	34799	C	4472	11	1639	
4432	34800	A	4473	95	2539	
4433	34801	A	4474	345	768	PRGARSTRCLPVERR/CDGLQD CGDGSDEAGCPDLACGRRLGSF YGSFASPDLFGAARGPSDIHCT WLVDTQDSRRVLLQLELRLGY DDYVQVYEGLGERGDRLLQTL SYRSNHRPVSLEAAQGRLTVA YHARARSHPLMNE
4434	34802	A	4475	47	563	RLRFVFTGAFHALSFLSFVV LCCTYLKGLKVARFHCKRIDV/ MHHADARAAGGPAPQCAGTLS IEEQKRRQRATKKISTFIGTFL VCFAPYVITRLVELFSTVPIGSH WGVLSKCLAYSKAASDPFVYS LLRHQYRKSCKEILNRLHRRSI HSSGLTGDSHSQNLVPSE

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4435	34803	A	4476	1	332	ERGRQEMSAKLRPPAEPCCVPA RISP*RPS*RQ*MERRCPPWRCS PMP/CFREHALQVRCGPTSA DCGRDPLFSHPKPLPHVPVDIG WVATAGAQRSSPVPSLFW
4436	34804	A	4477	297	943	TGSWGGGGADQLRALTTALM PPDNRFGENTPAAPANGHCAP EPDITLVQDHSSELPIGAAATMA HEIGHSLGLSHDPDGGCCVEAAA ESGGCVMAAAT/GVRGHFFPRV FS/SCSRQLRAFFRKGCGACLS NAPD/TRTPGAAALCGNGFVEA GEECYCVS/GQECRDLCFAHN CSLRPGAQCAHGDCVRLVR/ CMEGSGSHQLPRLVPGGDSAEI LM
4437	34805	A	4478	1	836	MGPLTRFDVKIEFSLEEWQCLD TAPGNLYRDMLENYRNLVFL VMCSHFAQDVWPEHSIKDSFQ KVILRTYGYGHENLQLRKDH KSVDAKVVYKGGYNGLNQCLT TTDSKIFQCDKYVKVFHKFPNV NRNKIRHTGKKPFCKNRKGSF CMLSQTLQHKKIHTREYSYKCE ECGKAFNWSSTLTKHKIHTGE KPYKCEECGKAFNRSSNLTKH KIIHTGEKPYKCEECGKAFNRS STLTKHKRIHTEEPYKCEECG KAFNQFSILNKHKRIHMGR
4438	34806	A	4479	1	588	MLGKVQQEQTIKADLVVTKY KMGCGT/DIANRVLRLSVEASS SGGQDYILKEGDLVKIDLGVH VDGFIANVTHTFVVDVAQGTQ VTGRKGDVIKAAQLCVEAALC LVKPGNQNIQVREAWSKVALS FNCMPIEGMLSHQLKQHVIDGE KNIQNPTDQKKDHEKAEFEV HEVYAADVLYSSGEGKAKDAG
4439	34807	A	4480	85	561	LSHCLPLQTTEVGGFGNLLGY WIACSIGCVLSTGMLSHQLKQH VIDGEKTIQNPTDQKKDHEK AEFEVHEVYADVLYSSGEGK VRRVPELAKRGD*ECSPDQMLL KLLFQAKDAGQRTTIYKRDPSK QYGLKMKTSRAFFSEVERRFD AMPFLRY

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4440	34808	A	4481	1	1408	GTSAPQPARSALLALACLPA LARAFAARPLEDRGSDHSLW LGRETEAAAAQKRGCSGGS KMSGDEQQEQTIVD/DSLVT KYKMGGDIANRVLRLSVEASS GVSVLSLCEKGDAMIMETGKI FKKEKEMKKGIAPTSIS/VNNC VCHFSP/L*KSDQDYILKEGDLV KIDLVGHVVDGFIANVAHTFVV DVAQGTQVTGRKADVIKAAH L\CAEAALRLVKPGNQNTQVT EAWNKVAHSFNCTP\EGMLSH SLKQHVIDGEKP*FQNPTDKQK RAHEKADFEVHDVYAVEGLV KPQERARPKDAGQRTTIYKRDP SKQYGLKMKTSRAFFSEVERRF DAMPFTLRAFEDEKKARMGV VECAKHEL/VWQPFNVLYSGRE GDFVCPVLNFTVL\MPNGPML ITSGPFEPDLYKSQMEVQ\DAEL KALLQSSASRKTQKKKKKKAS KTAENATSGETLEENEAGD
4441	34809	A	4482	3	190	
4442	34810	B	4483	1	588	
4443	34811	A	4484	1	1312	MSSKGSVVLAYSGGLDTSCILV WLKEQGYDVIAYLANIGQKED FEEARKKALKGAKKVFIEDVS REFVEEFIWPAIQSSALYEDRYL LGTFFARPCIAKQVEIAQREG AKYVSHGATGKGNQVRFELS CYS LAP\QIKVIAPWRMPFYNR FKGRNDLMEYAK\QHGIPVTP KNPWSMDENLMHISYEAGILE NPNQAPPGLYTKTQDPAKAP NTPDILEIEFKKGVPVEGGPTF KDG\TTHQTFL\ELFMYLNEVA GKHGVGPYLTWENRFHWELK SRGILRRPQAG\TILYHAHLDE AFTMGGDRAQIPNQGLGFEFVE LGVYRFSGTAPCELVGPCLRQ SPQERVEGKSAGVPSLKGPRCT SLQPEVPHCSLYNEIELVKHGT CQGDYE\PN*LPPGIQTSLKA EGNYHRLPRAKVTAQIRPRVQ
4444	34812	B	4485	47	482	

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4445	34813	A	4486	2328	3435	KTTTLEDNLGNTIQDIGPKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKRNVKHDESLRS HYE*WGMLTDCVVMRDPNTK RSRGC GFV TYATVEEVDAA'TN ARPHKVDGKVVEPKRTVSRED SQRPGAHLTVKKIFVGGIKEDT GGFAFVTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQGRSGRGGGFGGNENFG CGGNFSGHGGFGGSHDGGGGYG GSGDGYNGFGNDGGYPGGPG YSGGSRGYGSGGQCGNQDSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSYNDFGNYNQY SNFGPMKGGNF/GRRRSGP*GD GGQYFAKPPNHSGYGSSSSSS
4446	34814	A	4487	1	762	
4447	34815	A	4488	3	333	
4448	34816	A	4489	1	1676	MRDPNTKRSRGFGV TYATVE EVDAA MNTTPHKVDGRVVEPK RAVSREDSQRPGAHLTVKKIFV GGIKEDTEEHLRDYFEQYVKI EVIEIMTDRSGSKRGFAFVTF DDHDSVDKIVIQKYHTVKGHN CEVRKALPKQEMASASSSQRG RRGSGNFGGRGDGFGGNDNF GRGNGFSGRGGFGGSCGGGY GSGDGYNGFGNDGSNF*G/GG SYNDSGNYNQSSKFEPMKGG NFGGRSSGPYGGGQYFAKPQ NQAARCVAAARWLFRTAARLVF LQKFPWPVAVVEVTVVIVAAPA AATATTRDGGGCSRNCNPEVF PELLGCPNRRGPPGVREKQQQ TNSKSTRRQEIKTIAELKEIETR KTLQKINESRSWFYEKINKVDR LLDRLIKKKREKSQIDA KNDIG DIVTDP AEIQT TIKEYKRLYAN ELENLEEMDKFLATYSLHSLNQ EEVESLNKPVTSSEVAVTNSL PTKSPGPDGFTVLLEVLA PAIR QEKEIKHIPGREEVKLSLFADD VIVYLENPIVSAQNLLKLSNFS

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4449	34817	A	4490	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCGEWIEER DESRKSETIFKDLFKVPVLKETI YYKFYGGPPVYQIETVYFMALSP PKSKQFDKTKQNNNNKKTQF VIVFFKTDEHLSARGRRRSIVK VSLLPVAVIGLKSFLKPKDQLR KLFVIGGLSFETTDESLRSHFEQ WGTLDTCVVMRDPTNKRSGF GFVTYATVVEEVDAAAMNAPH KVDIGRVVVEPKRAVSREDSQRP GAHI/TLVKKIFVGGIKEDTEEI HLRDDYFEEIILNSMEKIEVIEI MTDRGSGKKRGFAFVTFDDH DSVDKIVIQKYHT/VGNHNC VRKALSKQEDG*VLHPAQRGA RSGSGKLLVVGRGRWFSVGM NFGVRGGNFSWSVAFGGTRGA GGGYGVQWGMAYNGFGNDGA SNFGGGGYSYNDFG\NYNNQISS NFGPMKGGNFG/GRSSGPYVG GGQYFAKPR\NQGQYGGSSSS\
4450	34818	A	4491	134	612	TVLNSMSVILASTLLKITTGELL QSFQDGLLWNLVIGIRGIDGLSP KVRKVLQLRLRQIFN/GTFVK LIKVTVNMLRTVEPYIAWGPVN LKSVNELIYKHGYGKISKKRRIA LTDNVLIARSLGKYGIICMEDLI YEIYTVGKRFRKEANNFLWPFKL
4451	34819	A	4492	1	1983	
4452	34820	A	4493	1	1527	
4453	34821	B	4494	1	2211	
4454	34822	A	4495	1	2478	
4455	34823	A	4496	2	1544	
4456	34824	B	4497	1	2151	
4457	34825	A	4498	1	744	
4458	34826	B	4499	1	2172	

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4459	34827	A	4500	1	2535	MKSGHPEKEQDNDSDVQETREIT IRGLLCTALMRHSTGAIAIYLGVL LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAFAFDKIQQHF MLKTL SKLGDGTYLKIIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPSPLLFNIVLEVLAIRIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPVSDQNLKLSNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRKIYLG QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELEKTTLKF1WYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNLYFFDNPDKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLLTPYTKINSRWIKDL NIRPKTIKLEENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLKSFCGTGKETTIRVNRQPT
4460	34828	B	4501	1	1785	
4461	34829	A	4502	1	1415	
4462	34830	B	4503	1	3262	
4463	34831	A	4504	1	278	

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4464	34832	A	4505	3	2528	ENKDDTTYQNLWDAFKAIVCRG KFIALNAHKRKQEKSKIDTLTSL QLKELEKQEQTTHSKASRRQEIT KIRAELEKIDTQKTLQKINESRS WFFERINKIDRPLARLIKKKREK NQDITKKNCKGDITDPTETIQTT IREYYKHLYANKLENLEEMDK FLNTYTLPRLNQEEVESLNRPT GAEIVAIHSSLP/T/K/KSPGPDGFT AEFYQRYKEE/LEKEGILPNSFY EASIIIPKPGRDATKKENFRPIS LMNIDAKILNKILAKRIQQHIKK LIHHDQVGFIPGMQGWFNIRKSI INVIQHINRTKDKNHMIIIDAEK KAFDKIQQRFLKLTNLKLGIDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTROGCPPLSPLFNIV LEVLAIRAIQKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLSINFSKVSQYKINVQKS QAFLYTNNTQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLEKIKDDTNKWNIPCS WVGRINIVKMAILPKLPMTFTFT ELEKVTTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNR EPSEIMPPYNYLIFDKPEKNKQ WGDLSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTEENLGITIQDIGL GKDFMSKTPKAMATKAKIDK
4465	34833	B	4506	1	5401	
4466	34834	A	4507	1	5271	MNIDAKILNKILPNQIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIIIDAEK SFDKIQQPFMLKLTNLKLGIDGT YFKIIRAIYDKPTANIILNGQKLE VFTLKTGTROGCPPLSPLFNIVL EVLAIRAIQKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKQISNFSKISQYKINVQKSQA FLYTNNRQTESQIMSEIPFTIAL KRIKYLGIQLTRDVKDLFKENY
4467	34835	B	4508	924	3423	
4468	34836	A	4509	525	673	RDSWGTCPSVSGAGKVDWPPSS *HHR*HQWCCGMPHQLSTKE NISIKDHLTEKKRKGAV*RII

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4469	34837	A	4510	25	1766	GTCQFAAMNVVFAVKQYISKM IEDSGPGMKVLLMDKETTGI MVYVTSQSEILQKEVYLFERID NREIMKHLKAICFLRPTEKENV YIIQELRRPKYTIYFIYFSNVISK SDVEVIGLKLIEQEVVAEVQEF YGDYIAVNPFLFSI.NILGCCQG RNWDPAQLSRTTQGLTALLLSL KKCPMIRYQLSSEAAKRLAECV KQVITKEYELFEFRRTTEVPPLLL ILDRLDDAITPLLNQWTYQAM VHELLGINNNRIDLSRVPGISKD LREVVLSAENDEFYANNMYLN FAEIGSNIKNL.MEDFQKKPKPE QQKLESIGSMKA\FVENYPQFK KMSGTVSKHVTVVGELSRLVS ERNLLEVSEVEQELACQNDHSS ALQNIKRLLQNPKVTEFDAARL VMLYALHYERHSSNSLPGLM MDLRNKGVSSEYKRLVSAVVE YGGKRVGSDLFSPKDAVAITK QFLKGLKGVGNYVYTLQPPFL HETLDHLIKGRLENL.YPYLGP STLDRPQDIIVFVIGGATYEEA LTVYNLNRITPGVRIVLGGTTV HNTKSFLEEVLASGLHSRSKES
4470	34838	A	4511	1	1335	MAPVTMMGYRSGMKGILADV QLQVGPWPWLHLVVIAPVPEC ITGIGIFSSWGSPDVGPPLYDIR AIMWGLAPAEWTWILGNNHR RFLAQLKPRVIMQDFSNVISKS DVKSIAEADEQEVVAEVQQVI TKEYELFEFRRTTEVPPLLLILDR CDDAITPLLNQWTYQAMVHEL LGINNNRIDLSRVPGISKDLREV VSSAEIDEFYANNMYLNFAEIG SNIKNL.MEDFQKKPKPEQQKL ESIADMKAFVENYPQFKKMSG TVSKHVTVVGELSRLVVSERN LAGRFSEVEARNWACQNDHS SALQNIKRLLQNPKVTEFDAAR LVMLYALHYERHSSNSLPGL MMDLRNKGVSFWRKYSKARVL AVVEYGGKRVGSDLFSPKDA VAITKQFLKGLKQGEIVNCVLA AANVYIKQLPLSIQPSASLNGCI SLEKKPLVSTQRN
4471	34839	A	4512	1	816	
4472	34840	A	4513	26	257	
4473	34841	A	4514	56	236	

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4474	34842	A	4515	170	373	HSPRGSTASF/CEVSETKNPPID IPATREAEGLRSRLAVYSTRDS PCVACSGSYTQAQGLGRKFQ DP
4475	34843	A	4516	262	358	
4476	34844	A	4517	2298	2556	NHKNPRRKPRQYHSGHRHGG LHD*NTKSNGTSGNGKSNQ* QWDLINLKSFCTAKETTIRVNR QPTWEKIFTIYPSDKGLISRI
4477	34845	A	4518	801	944	DQEPINSRHILATQMGSPITKQ SNPGV**KECGFSCSPRVRYL VS
4478	34846	B	4519	85	660	
4479	34847	A	4520	693	827	
4480	34848	A	4521	272	339	
4481	34849	C	4522	532	2754	
4482	34850	B	4523	1	519	
4483	34851	B	4524	266	935	
4484	34852	A	4525	1	1584	
4485	34853	A	4526	1	723	GALPNGDRGRRKSRFALYKRP KANGVKPSTVHVISTPQASKAI SCKGGHSISYTLNRNQTVVVEY THDKDMDMFQVGRSTESPIDFV VTDITISGSQNTDEAQITQSTISR FACRIVCDRNEPYTARIFAAGF DSSKNIFLGEKAAGWKNPDGH MDGLTTNGVLVMHPRGGFTTE SQPGVWREISVCGDVYTLRETR SAQQRGKLGGLQTGDMAENT/T VHALPSNCMVWRRSQTRQQIS
4486	34854	A	4527	1	335	
4487	34855	A	4528	328	871	DCGGGRARTAFAGAAARAADN KKCAGARRALGRARGCSATAR PRRRRRRPRGLAPPRPARPPG GMSYKPNLAHMPAAALNAA GSVHSPSTSMATSSQYRQLLSD YGPPLSGYTQGTGNSQVPQSKY AELLAIIEELGKEIRPTYAGSKSS MERLVRGIIHARGLVRECLAE TERNARS
4488	34856	A	4529	1	653	MAGPAESSPQGAHPNSPFALQH HSSLTVKPLHRQNVIIHQVAG QENRRGHQAGSSTSPQPLEALK RPNLRAPFHSQSRRLIPAGNP TPGAAAPADPSTQRRDRWGCA LPMPRVAAAGSAHHQAGPTAA AQHRTPVALFSPPLSLVYQQQ RKESETPIVPTPPARARGWTET GVEHVPAYNRTRAPEKCDI/SV PSPHSSFDAETSHPRHISPCPG

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4489	34857	A	4530	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQQRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVIAHDVDPIELV VFLPALCRKMGVPYCIK GKAR LGRVLVHRKTCTTVAFT
4490	34858	A	4531	1	2073	MKPCAHSWNAELSRNIHRHSFN LVMVAASQVAVSQLLGSYEILL LVSIELMFCFGLGYFFIPMQEW PNTYGERVFDVDESSVFKWNH KCLHKTEAERDYTEKKRLKLCG HKPGNAVGGQKLEEARNRFFT RAPGGSAAALPTLRFQPSDTRF LLASRTILTFETKNPSELAERLR SVCNGQSNAYARLLEYRLNAL RGLWNAQRQLALEEQHERESS GDEETLALLKRGQLLQQPEQAP FTSRMGLLLVFLIQSQSRDTPS LCNITAIEVLLNCLRDCQPLSLT KEPADCLNGIETLLCSWLEETS DTGRHIFPHKQKENAAALVAL ACARGFVYCRNEEPEPGWVAF GSGSLLHRPVSFDNPKHSLFQVI DQNTLQVCQVPMANHLPIG STMSTVHLSDDGTIFYFIWSPA SLNEKTPKGHSVFMDFELVTL KGKKAKGKKVAPAPAVVKKQ EAKKVNSLFEKR/DIQPKRELT YFVKW/PRYVRLQQQRILYKQ LKVPAINQFTQALNCQTVTQL LKLAKHYRPETKQKKQRLLA QAEKKAAGKGGVPTKRPPALR AGVNTITTLVENKKAQLVIAH DVDSIELVFLPALCKMGVPY CIK GKARLGRVLVHRKTCTTVA FTQVNLEDKGALEKLEVGIRTN DNDRYDEICCHWGGNIGPKS VACIAKLEKAKELATKLG
4491	34859	A	4532	1	2565	
4492	34860	A	4533	1	644	MPKGKKAKÉKKVAPAPAVVK KQEAKKVVNPLFEKRPNFNGT GQDIQPKRDLTHFVKWPCYIRL QQQRTILYKWLKVPPEINQFTQ APDSQTATLLKLAH/KYRPET NQEKKQRLLARAKKAAGKG DIP/TSKPPVLRAGVNTITTLVE NKKKAQLVIAHDVDPIKLVFL PVLCHK/MGVPYCIK GKARLG HLVHRKTCTTVTFTQVNSDK

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4493	34861	A	4534	1	931	KSIQKGLKMLCSSLLPPSKMP KGKKAKGKKVAPAPAVVKKQ EAKKVVNPLFEKRPKNFGIGQ DIQPKRDFTRFVKWPRLSGC MRKRAILYKAG*KLPPAINQF HPGPWDPANKLLQLL*AWAHK YRPMETKAKRKKQRL/LARA/E KKAAGKGDVPNERDPPV/LRA/ GVNTVTHLWWRNKKAPAVVV IATRRWIPFEL/VVFLPALCREK WGSFYCIKGKARLGR/LVHRR PCTVTGFFTR*NSKDKRLLA* AGLEAIRTQFTIDQIRWSGRH/ WGGNVLGPKSVARIRQASKR QRLKELATKLG
4494	34862	A	4535	3	227	
4495	34863	A	4536	1	338	
4496	34864	A	4537	1	352	
4497	34865	A	4538	2	368	
4498	34866	A	4539	3	468	
4499	34867	A	4540	2	790	PRGRNRRRKTQERRMTLNESP EKIGKWIECYGHPASKLVEIYI HTVFVEDKLSICRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PDVVSLLQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELDLCSLPRDTTLVHYI DDIMLIGSSVQEVENKDLLLVK DKLLHLAPPTTKEEVQHMVGL FGFWRQHPIHLGVHLQPIYRVI RKAA/SFEWGPQEKAQQVQ A/VGGKQSENNLGHQKSPGLW
4500	34868	B	4541	179	1219	
4501	34869	A	4542	1706	2517	THLLVPGMQPLTWQMPSPFLS ISPTRSNLPSAAIPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLATVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGIPHSIA SDQARIHRSRNQEVVEVAPLT ITPSDPLAKFLLSVPTLRSAGL EVLVPGEGLPMPGNTRTIPLNW KLRLPPGHFGLLLTSLQEAENG VTVLAVGIDLDYQDEISLLHN GGKKEYARNTGDPGLGRLLVLP CPVIKINGKLQQPNPGGTTNGS DPSGMKV

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4502	34870	A	4543	3	367	DLWPFTRVTVH/WGKANDQTF QGLLDGTGSELTLPYGPKRHCC PPVKVRVYGGQTGDSWRMTV GYHKLNQVVTPIAAVDPDVVS LLEQINTTPAIKVVVHSSIPSSN GSGVYVIRLEQVLKAQ
4503	34871	A	4544	2	541	
4504	34872	B	4545	1	681	
4505	34873	A	4546	2	1091	PRGRNRRRTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAAIAAI PDVVSLEQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELD CFSLPDITLVHYI DDIMLIGSIKFLGVQWCGACRD IPSKDPADPMVLEVSADRDV WSIWQALIDESQQRPLGFWSKS LPSSADNYSFERQLLAYWAL VETERSTMGHQVTMLPELPVM NWVLSDPSSHK/ANGLAGWSG TGKKHDWKIGDKIWRGGMW MDLSEWSK/DVKIFVSHVSAH QRVTSAAEEFNQVDRMTRSM DTTQPLYPPTPVIAQWAHE
4506	34874	A	4547	1	1236	
4507	34875	A	4548	1	1467	GEKGNQDQTFERKLLDTGSELMLI PLRVVPIPTSLFNSPIWPVQKTD GSGRMRVDYHKLNQVMTPTA AAVDPVVSLEFINTFLGTWYA AIDLANALFSIPVCKAHQKQFA FSWQGGQYTFTVLPRYINCLA LCHNLIQRDLDHFLLPQGITLV HYIDSGPFK*PEAASFEGPEQ EKALQQVQAQAAALSIGPYD PADPMVLEVSADGDVWWSL WQAPKGESQWRPLGFWSKALP SSTDNYSSTDVQLYTDSWAVA SSLAG*SGTWKHKHWKIGDKEI WGRGMWMDLSEWSKTGKIFV SHVNAHQLVTSAEEDFNQVD RMTRSDTTQPLSPATPVVAAQ WAHEQSGHGRNEGYAWTQQ HGLPLTKADLTATAECPIQQ QRPTLRPRYGTTSQGDQATC WQVDYIEPLPSWKQRFLITGI NTHSGYGFAYPNCASAKTTH GLIACLIHCHGIPHSIASLYRER GTHFTDKEVQQWAHAH

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4508	34876	A	4549	2	1602	NLSPILPQDLWPFTRVTVHWGK GNDQTFQGLQDTGSELMIPGD PKRHCSPPVKVGSYGGVINGV LAQVRLTVGTVGPRTHPVVIS VPECIHDIDLNSWQNP HIDS LTG RVKAIMVGKAKWKPFEP L LPIK IVNQKQYRIPGGIAEISATIKDL KDAGVVIPITLPFNSPFWPVKKT DGSWRMKVYCKLNQVVTPII AAVPDV/VVSLLEQINTSPGTW YAAIDLANAIFSI PVHKAHQKQ FAFSWQGHQNTFTVFTILLHIH KVGHAQQHSIIKWKWYIHDGA RAGSEGTSKI.NEEVPQMPMVT TSAALPSLPRPAPMASWGVLV DQLTEEEKTRAWFTDGSARYA GTTQKWTAAALQPLSRTSLKG SGEGKSSQWAE LQAVHLVVHF SWKDKWPDVRLYIDSWAVAN GLAGWSGTWKKIIDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISA EEDFN NQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
4509	34877	A	4550	1	1891	MLSSTQNAAGGSYQVRVGA.LDT QEWWKGEVSPRTLNV.DGRAL VSVANTHGTDRPAYTLNPQSR DQRSGVITLGYKRPLEREDLFE LKESDSFCTACPIFEKQWRKEV LRNQERQKV.KALNKLDEALCP GIII.TQSTD.SNANLFQKQPHRHT QTSGRWQIIIFCEHSSDFGWNG YGYAVALLVVVFLQTLILQQY QRFNMLTSAKVKTAVNGLIYK KLGWSGKVS.WLILHDVGHGIM EGYIAWKGSDVRITWEKKST EMRTRPAQKMALLSNVSRQK FSTGEIINLMSATHGLDSKPQSP LVCPSFNPNGRISPLARAGLAD HYRVTHLQILKLYAWEPSYKN KIIKIRDQEFQKSARYLTVFS MLTLTCIPFLT.KISLGRLEDFLN TEELLPQSIETNYTGDHAIGFTD ASFSWDKTGMPVLKESIRIRIEQ VLNQSLSFETVDYPGSVAYVSQ QAWIQNCILQENILFGSIMKKKEF YEQVLEACALLPDLEQLPKGD QTEIGERAVNISGGQQRHVSLA RAVYSGADVLLDDPLSAIDV HVGKQLFEKVIGSLGLLKNRTH ILVTHNLTLPLQMNLIIVVMKSG RIAQMGIYQELLCKTKNLTN/FT KSSVNNKKVGEWEESGRGS
4510	34878	A	4551	2	542	LTSAKVKTAVNGLIYKKVSLAT LCVYFLLDERJILAPKVFTSMS LFNILRIPLFELPSVISAVVQTKI SLGRLEDFLNTEELLPQSIETNY TGDHAIGFTDASFSWDKTGMP VLNRGSEAYVSQAWIQNCIL QENILFGSIMKKKEFYEQVLEAC ALLPDLEQLPKGDQTEIGERV
4511	34879	A	4552	1	667	IETNYTGDHAIGFTDASFSWDK TGMPVLKESVAYVSQAWIQ NCILQENILFGSIMKKKEFYEQVL EACALLPDLEQLPKGDQTEIGE R/GKETAVNISGGQQRHVSLAR AVYSGADVLLDDPLSAIDVH VGKQLFEKVIGSLGLLKNRTSH SVCHYTLLAVPHLLEVLQTLTGN FIQSLGFNYHEYANNNSNAYIVN LDLFPFGQTCVYKLLSPIRCLIC
4512	34880	A	4553	201	336	QQTPGKAVHAPFIADQSLT*EL VSVFPQQLFPYRR*DSHSGKS
4513	34881	A	4554	3	515	

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4514	34882	A	4555	1	852	MPCTTSGLDKVPSTSKKALTRY GYGSLTLDFSGSIIPCKMCLSPS TRIVRPSQPRGTEDPDETDGTEF VNSDESFLLEGTASPPVAVASP PRPMLPSAFPPLSEDINPVLPEA TVLASPEVVAKQTHVDSPRKPL STFLFASRPVTKLSRQTPGGE VDSVTCEEKTDGPWRKTVDYC KLNQVVTPIAALVPDMVSLLV QINTSSDTSYAAIDLAKAFFSIP VYKAHQKQFIFSWQAQYVTF VLPQGYIISPALCHNLIR/DLD HFLLPQDITLVHYIDDRL
4515	34883	B	4556	288	327	
4516	34884	A	4557	51	598	LFGGCHTSGGLAVRVPMPRG SRSRTRMAPSASRAPLK*ELE PRQAQVAQPPAAAPSAVGS AAAPRQPG/LFMAQMATTAG VAIVGCCGGHTLGHGVTGGLS VGGKLI*ALRRP*HQFNQGSF RGTOAKHKSQPALPLLWRIKT SFREVVPPEPRVTIQGFCGFP RLLETVPDL
4517	34885	A	4558	1	10434	MTVIRSGIAYILHLKSYDVNIQT GSNACNQPTHNGDCSHFCFPV PNFQVCGCPYGMRLASNHLT CEGDPTNEPPTQCGLFSFPCK NGRCVPNNYLCDGVDCHDNS DEQLCGTLNNTCSSAFTCGHG ECIPAHWRCDKRNDKVDGSD HNCPTHAPASCLDTQYTCDNH QCISKNWVCDTDNDCGDSDE KNCILNCTASQFKCASGDKCIG VTNRCDGVFDCSDNSDEAGCP TRPPGMCHSDEFQCCQEDG
4518	34886	A	4559	24	849	ATGRCCCGLAPGFLCWVLYP GGRGSA/CEPHVLRGTGSPLORE QRTNGRTDLSSLNPNLNFDSPP RCKHKNQLAITLRKIRKLATS LFSSTIFRISGTSV/IISAPGAGLPL PALFPTRCQPKFSRSIDPTGKAV QTADIRLSARATLWLGGSIEESP VLCSTLRLRLRPPLTW/TS RPTQPTCAQTQTNSVSGIAAPS AIRVIYPESVVLNAVIVLPGDPE VSGLPRAFKRFSVEVRLDCGT FKLLLVYCTHPGDKKVNTCKT GALVAF
4519	34887	C	4560	192	449	
4520	34888	A	4561	1	786	
4521	34889	A	4562	3	14073	

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4522	34890	B	4563	58	1282	
4523	34891	B	4564	1	684	
4524	34892	A	4565	1	1356	MGRKYTLKWEFEEGFTEKKEL KKVTS EGYITPVEIYDYRQYCY ALQRPIATTQIDVDVRDGHTRRL AKLEKQEQT HSKASRRQEIIKIR AEPKEIETQKTLQKINESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDKGDITNPTEIQTITRE YYKHL YANKLENLEEMDKFLH TYILPRLNQEEVESLNRPI TGSEI EAIINSI.PTKKSPGPDGFTADFY QMLEVLARAIMQEKEIKGIQL GKEEVKLSLFADYMI VYLENAI ISAQNLLKLI/SNFSK VSGYKINV QKSQAFLYINN RQTESQIMSER PFTIASKRKYLGIQLTRDVKNL FKENYKPLLNEIKEDTNKWKKI PCSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI WNQKRACITKSILSQKNKAGGI MLPEFKLY/YQGSSTQTAWYW
4525	34893	A	4566	1	1102	MANCDINRKDEKGGKEKKDRS KSKSLMDTLKRQLSAKQKPKG KAGKPSGSSADETFSSSSAPIV FKAVRAQRPIR/STLSRSHCSP MPWPLRPTNSEETCIKMEIPSP LNGVRKDFHDLQSETACQEQE NSLKSSASQNGDLYLR LDEHVP VVIGLLPQDIQYTVPLDEGMC PLEGSSSYCLDSSSTMEVSVPVS QVGGRSFPEDSQADQNLVVA PEIFVDQSMNGLLTGTTGVMLQ SPRVGPHHVPLSPLPPMQNN QIQRNFSGLTGT EAHMAESMLC HLNFDNFNSAPGARVYVVSQSS GPMVVTSLTEELKR/LAKQGWL WPPLKSRRCLVARRSLYTKQL NQEEGT ELLNGSSCLLC
4526	34894	A	4567	364	661	PFHFTCFCKVYFADPGSAARS VPGSPSAVCAQCILCTGHCAVC PGLGEHHSSGRTL MKTKLHSH KLKPCYLLC*SKN*KTQGGSPK S*NVNKYLVTLI
4527	34895	A	4568	53	470	CISIIILPGPSAKT LSPVLSLSPY TASFQPTFVR TFSHQTTYLSLGS VPYAQLKCSAGQQRGELLCCR GVWGSWISVSHFETIATLP AAC LEDGE\DFNLGGILDSSKYL*SIQ KTNTHRIVDGVVSETNIH\DL

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4528	34896	A	4569	1	1635	MGWTCILFLVAAATGAHFLV QLVQSGAEVKKPGASVKVSCK ASGYTFYCYLHWREPVSFIGG RCILLTLGLGDCLWGEAWTQ GDVLQPSDRASFLAMGVNTTG QQVGDLSGDFPNSVGKACKCR EFHTLPLAHTSSTTHETFPGMS HIALELSQGSSLLQCLEAQQTG QRQELTVSANEQPESRGHGCYL LCETQSEKGSVRAQAQTSLKGS QKRLGGARTLCTGLSPGQRKQ ERSKIDTLTSQLKELEKQEQTYS KASRRQEITKIRAEKIEITQKT LQKINESRSWFFEKIYKIDRPLA RLIKKKREKNQIDAKNGKGD TTDPTEIQTTLRQYYKHL YANK LENLEGMCKFLDAYTL PRLNQ EEVESLNRPITGPEIEAII/STPT KKSPGPDRETAEFYQ/RSDVLA RAIRQKKEIKQLGKEEVKLSL FADDMIVYLEIPIISAQNLLKLI NFSKVSQYKISVQKSAFLYT NRQTESQIMSELPTIASRIK Y LGIQLTKVDKDLFKDNCKPLLN EIKEDTNK WKNIPCS
4529	34897	B	4570	1	429	
4530	34898	A	4571	1	897	MDLNYTLEQMDLTDIYRTFHPT TTEYTFYSTGHGTFKTDVVIG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLNECWVKNMKMEIKKLF ELNDNDTTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKKNHMIISIDAEKAFDKIQH PFMIKTLKISIRGTYLNLIKDIY DKPTANIMLNGEKLKAFTLRTG TRMNQGCPLPSLLFN/VLEVL ARAIQKEKEIKGIQIGKEEVKVS LFADYVIVYFENPTDSSRKLEL IKEFSSFWIQD
4531	34899	A	4572	1	1461	
4532	34900	A	4573	49	365	
4533	34901	A	4574	45	534	VCHLEPGERCPSRGCRVGV QTEKMQTAGALFISPALIRCT RGLIRPVSAFLNSPVNSKQPS YSNFPQLVARREFQTSVVSRI DTAAKFIGVAGSATVGVADSGA GIGAVFGSLIIVYARKLSLKQQL LFYAILGPAALSEGMI/GLFCLMV AFLILFAM

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4534	34902	A	4575	98	624	DWYSRSHPKELWEGSKKKSIN HSACSLQAHGGPISTSLNPHSKP RGRVSPPPGKRQQECRAPGRS PELAGPPANVQETSQKNACAS RLSEPPGEGPEPAAHPPQPIIRGS SSGPCSRGGYRQPLFPQPAASG VPASGSVRSRIPGAPQGVAlAR RGPQGSPPAPRFFPATERQS
4535	34903	B	4576	1	604	
4536	34904	A	4577	3	331	LAPAPSAAWRTGLKALTSPST WMLCASEHHVSGSCVGDHLLA GCRQEKTLPCQRVCVFCRRRR ARSLQAQCGLSLTPALELLPVPF LKLCPGPPRRRRICRILPGAGL
4537	34905	A	4578	1	871	
4538	34906	A	4579	3	510	GPSPRVDDFVAAAAA AVAPVV LYACPRHSPIPPWSIRGRRVVVT GFGPFGEHTVNANWIAVQELE KLGGLGDSVDLHVYEIPVEYQTV QRLIPALWEKHSPQLVVHVGV SGMATTVTLEKCGHNKGYKGL DNCRCFPGSQCCVEDGPEISDSI IDMDAVCKRVTTLGQCI
4539	34907	A	4580	1	285	MAPGALPALGEEEGPGASGLSA ELGHLASAGSRAFRETSDVSALD TPFPAGTFRLEFKLRQTESGR RKDWKPKCKVQPERRKQKCL TCVKLEC
4540	34908	B	4581	1	228	
4541	34909	A	4582	1	697	MGLERPVDYVMWLPALWNS AVVSAPVGEWALAGTGNQGL QDIQGMHCPEEGISQIHGRDHR NAKDSHTGVWCSCITGLIITIIIR PKCRFSIDRSDSDYLPSTSSCRRD PGGAEPQCDRPRVEQLCSVLAN RSGPLAKCHWYESPVS YTVQC VSDLCQYGTGNRMLCTMLEAY VQLCALRCALPARVASQPGMQ LRVACPANSYYDSCGPPFPATC ASLNSSAPCTLQCTVSCFCLEGF ALEAGSSVPHACCGCHLQGRY I/APGPWPSATGMRAPCPTRRC VSLTSASMARATACCAPCWRP TSNSAPCAARCLPAWRASLGCS YVWRVQPTATMTPVGHPSRPP VLASTPPRPAPSSAQ
4542	34910	B	4583	1	208	
4543	34911	A	4584	2	230	

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4544	34912	A	4585	106	669	GCGCVLLPGGVGAPGHSPEGP VPPRDARQLRTCLAGTLHLST SCGHPTGAWRGALGSQWNGH NPVQDHLQEAQPWFLEFDRG* RCFWRMATSFPRYPTWDDY*R LPCCRCLPQCKKPAETTGCLPIS GEKTHGGVGDLLGEAPARLRQ WASQRQPATDLP*ASRGRPA* GKDTHRACVAGEAAQDA
4545	34913	A	4586	2	597	TPKGGIRLGLAKLGCPTAWINP YGRGMPLAHSVLSSGARVLVV DPDLRESLEEILPKLQAEINRCF YLSHTSPTPGVGALGAALDAAP SHPVPADLRAGITWRSALFIYT SGTTGLPKPAILTHERVLQMSK MLALSATADDVVVYTEVLP.Y HVMGLVVGILGCLDLGTSLAS YGLRVYFYLWSVLGSPRRTLCL
4546	34914	A	4587	9	573	EEEEERKKKKKKKEEEEEEEE GGMGEEKKKKEEEEEEEEE KEREKER\EKERKKKKEERKEK ERERKKKERKKKEKERKEG EGERERKSTECTSSSYI\IKKLVV KQPQAAPSGEIPEEGIAVLGGDS SMPVIVPEDLPVGQDVEVEDSD INDPDSLILVSSQAGGGGVITAY CNLEHLGSSDPPT
4547	34915	A	4588	1	297	
4548	34916	A	4589	114	752	DGSAAPRATSDSFITYVCVSEF PVDDFMELGRSIPDTQL/DAVIE SQKANQCAVLIYT/SGTTGIPKG VMLSHDNITWIAGAVTKDFK/P TDKHETVVSYLPLSHI/AAQMM DIW\PIKIGAL\IFYAQADALKV RLSKDLGSDFILLGSPVGLRPST KRLPVLSKLGHTYRRVVVVEE SSGPHITISNQNNYRLQGPMMK LKRHFVAQYKKQIDHMYH
4549	34917	A	4590	1	837	MVTQKLPNAQENLKHAEQAA GCCPGRSHIFQHVGPAGESLR GEGCSTHPEAQGAQERCEQWK KDQHWCLASHTDVTQQWGRH IVQEGGTHRGPSAVLSLRTALD EG/ARGGCSPITAQLPLQLRHL PRPPAPAR\PSAPPAATSPTTP PPAPAR\SSAPPAATSPTASSG ACAALPQLPLQLRHLPRPPAP AR\SSAPPAAMSPPARPPAPAR RLRRSTACATLRPGERGSAAA QPGARSETSFCRLG/AAAAVL PAFISSQALACPVVGV

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4550	34918	A	4591	3	377	
4551	34919	B	4592	1	1632	
4552	34920	A	4593	1	1224	MDGTNRFYLYVWETERQQDV EHVARCILCYDKCRPDPECPAG TPGPQEVVDVLVFFVVDSSYGV DADVYRGSLSLADAALEDLEV AEQPGASHRGARVALVTHHTP NFGRGFHLTTYGNRKQMRH VREASARPLQGTAPPGHALEW TLENVLLAAPRPRKAQVLFAlV ASETSSWDREKLWLSLEAKC KGITLFLVALGPGVGTHELAE AELVSAPSEQHLLRLQGVSEPE VNYAQGFTRAFNLNLKSEQSPG TGAPWVVEWGEGETPEGIWACR WTNQYPPPELTEECGGLHRGD TVLQLVTPVNRPFMYAAKENS LKRKTKANFHLEVELEDESIFR AYYEGTLYEVSALPLQRSNELL QKWSLFHGSNGRRVSGSHPEV ALQGGGTGLPAVLVWQLWRQ
4553	34921	A	4594	266	556	HKVQQICYRLRLVSQILFSINQT LAERQIVFTFVYPDTERDRETR NLADLKQIKIDLKGFSDNPDGY IDILRGLRQSFDLTWADIMLLL NQTLPAN
4554	34922	B	4595	1	735	
4555	34923	A	4596	70	624	PTAMVEEGIAAGGVMDVNTAV QEVLTALIHDLGARGIREAAK ALDKYVYQSQCGLQPDQKL ATQGGKGMGVHGVKRSKSM ASVLPGNLRKRRAHLCLVLAS NCDEPMYVKLVEALCAEHQIN LIKVDNKKLGEWVGLCKIDR EGKPRKVVGCSCVVVKDYGKE SQAQDVIEEYFKCKK
4556	34924	A	4597	145	682	SWRNRTVSNGSVSASSVHLCF AECKALCGERILTDGSDVSRPTI AAGGVTDVNTALQEVILKTALI HDGLARIGISRTWPKALDKRQ AHLCLVLAASNCDEPMYVKLAV EALCAEHQINLIKVDNQET* EKWVGLCKNDREGKPRE*WL VGS*CSSLRTIGKESQAQDVIEE YFKCKK
4557	34925	A	4598	252	590	RSLDLVWQLSGGLAGSAKPK PCTPVKQSTVMSFSPHKEQYFL MDGKKK/YDKSEKEYSILEKH LNLSAKKKESHQENSSGPSVS TKLINLFSKRLLCFLPAQLTPY SFCS

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4558	34926	A	4599	1	1662	
4559	34927	A	4600	4430	4904	LIKGRCLGRPSFAYSRSNI*A *S*/P/EGTSAQLAELLALTALALE LGNGKRINVTDSKYAYLILHD HAAIWKERAFLTSGGTPIKYHK EIMELLHTVQKPKEVAVLHCQS HQKESSPLEDTTTAGPLLHPYP AGSSPERSSPSSQQLLGD LFRGII
4560	34928	A	4601	1	2630	MEQANHPVRLINVVCKD TLKKI VQQETSCPLTHVHYAEAITGR TAPEDKGS LDQKPTDPTGCP WQVPAHVITLTETWVCLTIEGQ EIDFLDTG VQKPNGQWRLVQ DLIPIKEA VIPLYPVVPNYTLIS QIPEKAEWFMALDLKDAFFCIS LHSDSQFLFAFEDPTNHTSKITR TVLPQGFDRDSP LFGQALAQDL GHFSSPGTL VFQYVDDLILATSS EASCCQATLDLLN FLANQGV VPNLWGKLP LNTRKSWSYCT QCKNPRRWQSYTAKAIKKQLA EAGPVTAILLLIFGPIFNLLIK FVSSRIEAIMLQMVLMQEPQMS STNNFYQGPLDRCTDPLSGLES SPRCSEAPCLMSQWTGDI EYDL LLPPIPHQTTLCDLQNLKGIFSR YHRKWYGEIALLTPTANVCG HSQVPHACSIYHDPVTWNPQ LLPKSLYGVTKWGDKEHFEWG SQQQRAFYELKVKKLMSAPALG LPDLTKLFTLHVSDREKKMAV RVLTQTMGPWLG PVAYLSKQL DGVSKSWPPCLRALAATALLA REVDKLT LGQNLNIKAPHAVV TLMNTKGHHWLMNARITRYQS LLCDKPHITIEVCNTLNPTLL VSESPVEHNCVEVLDSVYSSRP NLRDHPWTSVDWELYVDGSSF INPQGESVWGIIQGRPIKLWG KRRKVSARDLAIIGGSVEAPKL
4561	34929	A	4602	1	506	FLALTSRFLFVLLNEETRSHLEK SLCWKVSPHIKMDLLQWISQK AQSDGSTLQQGSLEFFSCLYEIQ EEEFIQALSHFQVIVVSNIAASK MEHVMVSSFLCKRCRQAQVLHL YGATYSADGEDRARCAGAHT LLVQLPERTVLLDAYSEHLAAA LCTNPNLIELSLYR
4562	34930	A	4603	3	381	
4563	34931	A	4604	3	483	
4564	34932	A	4605	3	410	

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4565	34933	A	4606	2	249	SADAPMFDMGVNHKEYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSILFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
4566	34934	A	4607	2	481	LAPLVKEIHDNFGMGEGLMTT GHAITATHKTAADGPSGLWRD GRGAHQNIIPASTGAAKAVGK VMPELNGKLTGVAFRVPTANV SVVDLTCRRQKPAKYDDIGKV VRQAPEGPLKGILGYTEHQVVS SDFNSDTHSSTFDAGAGIALND HFATLSPPPH
4567	34935	B	4608	79	278	
4568	34936	A	4609	2	1201	PSTACRNSARACSTVSRIFFCVA SRATSLRTPMGKVGVGNVFG RIGRLVTRAFAFNSGKVDIVAIN DPFIDLNYMVYMFQYDSTHGK FHGTVKAENGKLVINGNPITIFQ ER/YPSKINWG/DAGA EYVLEST GAFTTMENAGAHLQGGAKRVI ISAPSA/DAPMFVGMVNHKEY DNSLKIISNAISCTTNCLAPLA KVIHDNFGVVEGLMTTVHAI ATQKTVDGPSGLWALMGPR GFFQEHQSLPFTGGC/ARVVGQ GSSPELERGKLTWAWAFRCQ LPKRVNGWDLTCRLUEKPCPK YD*HQGRVVKAGRRKGPLQGA ILGLQLSNPGSGPSGLSTSDNPL LPFFDAWGLAFALQRTFCSKL IFLGIDNGILGYSNQGGWDLHG PPWPTWAFQGS
4569	34937	A	4610	61	226	WRIMPTKKVMITMGRRTQRRM LES/SQQFWPCHLH*KLVPSCLQ LGCLVFHFRER
4570	34938	A	4611	153	495	QHAAECKAHAGLPGLPLPARK LASRHGAPRWQSGVGPQGGKV ENYGRRLVPGTRIHPQSLSHKP AKKIDVARVTFDLYKLNPDQFI GCLNMKATFYDYSLSYDLHC CGAKRIMK
4571	34939	A	4612	1	643	
4572	34940	A	4613	286	698	ESDNNLTQGTISI*QGTIRHPQSLF PLSPAKKI*CGPVLTLTCYKLN PQGLSLGCLNIEGRFFMDYVIPF PIDLALLLGAKRIMKGTLHWA LFSMQTTGPRA/VFTSCYLQQL LDATEDGHPPKKGKASSLIPTCL KILQ
4573	34941	A	4614	59	294	
4574	34942	A	4615	1	2253	

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4575	34943	A	4616	2	197	LARSGMGFYRRGLLGEVKGGRV EGNRMWHVVRTSPNHRYTFT LKTHPSVVPGSIAFSLPQ/RPWS
4576	34944	A	4617	302	441	
4577	34945	A	4618	944	1257	RLPFSRPSRVGPTPQAPRLLCNG WRQLPTTFFTELEKTTLKFIWN QKRALIAKT/LKPKNKAGGITL PDFKLYYKATVTKTARFLLYK VSQIDNTDLDFPVKIKFE
4578	34946	A	4619	1	1370	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSM NVIQHINRTKDKNHMISIDAEEK AFDKIQQPFMLNTLNKLGIDGM YLKIIIRAIYDKPTANIILNGQKL EAFPSKHGTRQGCPPLSPLLFNIV LEVLAIRAIRQEIKGIQLGKEE VKLSLFADDMIYLENPIVSAQN LLKLIGNFSKVSEYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SIRIKYLG1*LTRGVKDLFRENY KPLLNNKIKEDTNKWNIPCSWV GRN/NIMKMAILPKVIYRFNAIP IKLPMTFFTELEK/TTLKFIWNQ KRARIAKSILRQKNKAGGITLP DFKLYYKATVTKGAWFQHHK HTLIKEPLLDVFSFNPDPDHGK KQDKQPQTKNIANASADSKNT QQMNGFVTGAATSFIPKDRITAS SLCGCTGRRRQSVAKYLRIIRPHI NVPSFTYYK
4579	34947	A	4620	2	671	WHQNLALTRASGSFHS/WEEG KGGADMSHEICVANLQVYVRS TDFDRTLMSAEANLAGLFPNE VQHFNPNISWQPIPVHTVPITED RLLKFPLGPCPRYEQLQNETRQ TPEYQNRSIQNAQFLNMVANET GLTNVTLETIWNVYDITLSCEAP SPPWGRKPPLERLWPRPRELTC PLRYTVQTHGLLPPWASPQT VQRLSQLKDFSLFLFGIHEQVQ KARLQG

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4580	34948	A	4621	1	1923	DSVAFEDVAVNFTQEEWALLG PCQKNLYEDVMQETIRNLDCG HETEFVEYENLRDPMNMLPH TDGPHKCKICGKGFDPCSSLKS HERHTHTGEKLYECKQCGKALS HSSSRFRHMTMHTGDGPHKCK ICGKAFVYPSVFQRHEKHTAE KPYKCKQCGKAYRISSSLRRHE THTTGEKPYKCKCGKAFIDFYS FQNHKTTHAGEKPYECKECGK AFSCFQYLSQHRRHTTGEKPYE CNTCKAFSHFGNLKVHERIHS GEKPYECKECGKAFSWLTCFLR HERIHMREKPYEQCGKAF HSRFLQGHRIHTGFKPYECKE CRKAFSWLTCLLQHERIHTREK PYEGKQCGKAFTHSRFLQGHE RTHAKKLCECLSTVSARKSVD LIASVPLFLNLFSTPKTLRNCYS RRHERMHTGEKPYECKQCSKA LPDSSSYIRHERIHTGKPYTCK QCGKAFSVSSSLRRHETTHSAE KPYECKQCGKTFHHLGSFQIHM KRHTGDRPHKCKICGKGFDPRPT LVRYHERISTGEKPHCKQCGK AFDHLGSFORHMRHTRDGP KCKICGKGFDCSSTLQSHERTH TGEKKLYECKQCGKALSHSSSF RRHMTMHTGDGPHKCKICGK
4581	34949	A	4622	1	256	MKGGSFKYAWALYKQKAEECE RGVTIDTSLWKFETSKCYVTIK DFIKNIITGTSQQGQTASVAAFC ILSSCPASWKNQVSHRLGG
4582	34950	A	4623	173	717	SINAVASTRRRTIEKFEKAAEM GKGSFKYAWVLDKLKAERERG ITIDISLWKFETSKYVVTIDAPG HRDFIKNMITGTSQADCAVLIV AAGVGEFEAISICQNGIQTREH ALLAYTLGVKQQLICRVNKMMD STEPFYSQKRYEEIVKEVSTYIK KIGYNPDTRAFVPIISGLNGDH MLEPKC
4583	34951	A	4624	3	525	GCPSPGPHRCVAGHGAPGAVC RHVPTAWPGYSRCSPPGPRGV EAVGHQRHRAPEHSTPAADR HRRGLPGSKSDSAMEPSPSPAP QAQPPKVPKPRTVFGGLSGPA TTQRPGLSPALGGPGVSRSPES PRPPPLPTSSEQSALNTVEMM PNSIFYGLDSRGAQAQAQDK

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4584	34952	A	4625	2	448	RRAHACARRRRKKEMLGVNVLTSHSSQERMKLTFFKKAVNFA DAAAAQGPLLPA MVNPTMFFH IAVDGEPLGCVSF EVRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFYKGSFCFHIIPGFTCQSGDFTRTPA
4585	34953	A	4626	1	751	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSEVVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQCLLFLRILPL FADKVPKTAGV*FFFKQKIFRA LSTGIEKGFYKGFPAFHRIPG FMCQGW*LSHRHNGTGWQVH LMGRNFEDNFILKAYGVLGS LSMAKCLDPTKIGSPVFPSC TA KTVEWL/DGQALWCFGK/VKKG LNIVEAMERFVGSRNKGTSSK I TIADCGQLE
4586	34954	A	4627	3	615	PECIIGIDILSSGQNP HIGSLTGR VRAIMVGAKRRKPLELPLPRKI LNQKQYRIAGGIEEISATJKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPIISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGP AIFCR* LLSF*ETALGLLGF GGN*TFDY
4587	34955	A	4628	3	354	DSWA/VANGLA/GWS/GTWKK HDWKINDNEIWGK/SMWIDL S EWSKTVKIFVSHESAHHIT*KSS AEEDFNNQVDRMIHVSVDTRPL SPATPVIAQWTHEQSGHGGRD GGYTWAQQHGL

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4588	34956	A	4629	281	1529	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLAMGVI GSHGARGQVVALNRQQRGDL QPFTRVTVHWGKG/NMQIFGGL LDTGSELTLPDGPDKHHCPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKQYHIL GGTVEISATIKDLKDTEA VTPIT SPFNSPIWPVQKTDGWSRMTV DYCKLNQVVTPIAAAVPDVVS LLEQINTSPGTWFEWSPKIKAL QQVQAAVQAALPFGPYDPADP MVLEVSVADRDAIWSLWNAAI GESQRRPLGFWSKALLSSADNY SPFERQLASYWALVETERLTV GHQVTLRPELPIMNWVLSDPSS HKVSGAQQRSIIKLKWIHDW
4589	34957	A	4630	453	719	ARGSKHTGLIAQWAHEQSGHG GRAGGYAWAQHQHGLPLTKAD LPVAMATAECPIQQQRPTLSPR YGTIPW/WAWDAPGGRGCWRL QKAGE
4590	34958	C	4631	122	325	
4591	34959	A	4632	1	346	MAGEKVEKPDTEKKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAASKIEKKKEK VLATVTKPVGGDKNGGTQVF QIITYSSYTQKVQLPKSTLKQRQ GPCPQAL
4592	34960	A	4633	115	905	EAFQTLHFCCGLRQGTKRMA GEKVEKPDTEKKKPEAKKVDA IGGKVKKGNIKA/KKPKKG/RPH ICSRNPVLCSEGFGRYSRSVAMY SRKAIYQEGSTFSPLKSKVEKK KKEKVLATVTKPVGGDKNGGT RVVKLRKMPRYYPTEVDPRKL LSHGKK/PFSQ/HVRKLRASITP GTILHILTGRHRGKRVVFLKQL AKLAYLLC/LGPLVLNRVPLRR THQKFCHLPLSTKIDISNVKIPK HLTDAYFKKKLKRPRHQEGEI
4593	34961	A	4634	2	350	FVALAAVLCRQCLPRAWVCCR AGQGSGRHYRAAICAEKKPLT IEEVAP/DPVGPHEVRVDVHFC GVNFGDILICRDQYQERPHLPFT PGPVADSRKGLPIRSCCPPYNL WHCDFCS

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4594	34962	A	4635	1	556	MGLKLNTHMDQTRGSLSGDTL EGSPSKRAKILKRGGFRGILGG VGQERRTGQRPALPCHDLRR AEVVPDHRRGGRPVGPPIEDL WQIPEKVSLEAAVLPITYGTE SFALEHRARTQPGFIVLVTAAA GATGLAVMWQIQSSGQGNIAA AGSDEKCKLAMEKGAQSSVN YSQGLKDSATDQ
4595	34963	A	4636	1	142	
4596	34964	A	4637	2	368	
4597	34965	A	4638	2	504	HKVGHAQHHSFITWKWYTRD WSRAGPEGTVGPYDQLTEEEK TRAWFTDGSARYAGTIRRWTA AALQPLSRTSLKESGEGKSSQW AEVRAVHLVVHFTWKEK*PDV RLYTDSWAVANGLAGWSGTW KKHDWKIDDNEIWGRGMWIDL SEWSKTVKIFVSHESAHHIT
4598	34966	A	4639	182	840	RTAVKGNLPTTPVLSQWAHEQ SGHGGRDSGYTWAQQHGLLIT KADLAMTTAECLISQQQRPLS LQYSSIPWGNQPATWVQIDYIR PLPSWKGSQSDSRNRNQGV KVKVAPLTITPSDTTAKFLLHV PAALHSAGVDVLVPEGGMPLP GGTTTIPLNWKRLPPGHFGLLI PLSQAKKRVTVLAVGVIDLDC QDEISLLLYNRDAKELYRYTAH
4599	34967	A	4640	3	283	SRVSCSPPLSPPPPLSPPPPLSPP PLLSPPPPLSPPPSPPPVSLPPP PPVFSFPSSCP/PPFPPLLPPLPPP PPLSPPPPPPPVSPSPPI
4600	34968	A	4641	1	531	MGSSHCTQPGMLAAAVGQAVP GTDTGADSVLSASCCHQHAH CAQAIRAKGHLQAHTLPSAPT QPFPSCARQCCKSGDGLGGRELY NNHEIRSGKHIGVCISFANNRLF VVSIPKSKTKEQILEEFKVTGS YVWLGLSDFDKWPV/GQCCQ SFHGRLRATPARRAERRDARSE AL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 95/40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
4601	34969	A	4642	115	2405	ATAEGSGSGVKGKRGAGIRKAE RRRTEASGGGGGRRRRSWRR AGAEGVSEADARGGKGKREG KGGSRGGARAHREARRRVEL DRVCCQRRELPPFYNSSSTRAG HREQRARVSRNPISDRISPPQP NGEISGNMATEHVNGNGTEEP MDTTSAVIHSENFQTL DAGLP QKVAEKLDEIYVAGLVAHSDL DERAIEALKEFNEDGALAVLQQ FKDSDL SHVQNKSAFLCGVMK TYRQREKQGTKVADSSKGPDE AKIKALLERTGYTL DVTTGQRK YGGPPDSVYSGQQPSVGT EIF VGKIPRDLFEDEL VPLFEKAGPI WDLRLMMDPLTGLNRYAFV TFCTKEAAQEAVKLYNNHEIRS GKHIGVCISVANNRL FVGSIPK SKTKEQILEEFKVT EGLTDVIL YHQPD DKKNRGFCFLEYEDH KTAAQARRRFN*VGKVQGF GNVGTVEWADPIEDPDEVMA KVKVLFVRNLANTVT EILEK AFSQF\GKLERVKKLKDYAFIHF DERDGA VKAMEEMNGKDLEG ENIEIVFAKFPDQKRKERKAQR QAAKNQMYDDYYYYY GPPHMP PPTRGRGRGGRGGYGYPPDYY GYEDYYDYYGYDYHNYRGGY EDPYGYEDFQVGARGRGGRG ARGAAPSRGRGAAPPRGRAGY SQRGGPGSARGVRGARGGAQQ
4602	34970	A	4643	2	369	
4603	34971	A	4644	1	1002	MNAGCGQTHDCAYRQKRPE VNEEGRL EQRNRKRQDEWGPR DKPASSGYKAGTLDVENWNRA GEGLKHAHQGLKVDSSA FCT CSLIRTVLMPLSPYY SAGQQA SKNLKESVVPPTAS IENKKQER EDKNWPILPPPVAETSVP PPSVA GIETPIQRILRSAAIAGEPSGPCA FPISVRPDSNNPQQFIHEHTPLEF KLLNELKTSVVNIGVQSPFTLG LPESAFGAMRLLPFDVKHWAR TCLSASAYLTWNLNGQEMCTD QVRQNRRAAGHG DIAEDMLLGN GP/YFRPGTSGTKRAWATIPEE GVPVQSFLPFMEGSQEPSAQFL ARLREAV
4604	34972	B	4645	1	575	

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4605	34973	A	4646	1	776	VVLNRNLSMSGTIFSMLANISML GSLVIIQYITQEIPDPSRVPLVA SWKTYPLFFGTAFSFSIGVDL PLENEMKNARHFPPILTGMP VTTLDIGMAALGYLRFGDVDTK GSIILSLPICWYLIHLSGEGPSQ SFSERETQAQVIVPRSEVNVPRR PVSEHSGRGEQLCGLSCLRYQS VKLLYIAGILCTYALQFYVPAEI IIPFAISRVSSTRWALPLDSLRLV MVCLTSAPMTRSTPFCKYSTRG RRRWLEIPV
4606	34974	A	4647	1	1294	MKGDFMSKTPKAMATKTKIDK WDLIKRKSFACTAKETIIVNRQP TEWEKIFATYSSHKELISRIYTE LKQIYKKKTNNPINKWAKDMN RHFSKEDIYASKKHKMKCSSSL AIREMQIKTTMYHLTPVRMEII KKSNNRQPIVGPCDNSVILLY KILANRIQQHIKKLIHHDQVGF PGMQGWENTCKSINVQIHINRT KDKNHMIIISIDAFAFDKIQQPF MLKTLNKLIGDGMYLKIIIAIDY RPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRQ EKEIKGSQLGKEEVNLSLFADN MIVYLENPIISAQNLPKLINNF KVSVCINQVQPAFLYTNNR QTESQIMSLEPFTIASRIKYLVI QLTRDVKDLFKENYKPLLEI/ K/EDTNKWNIPCSWVGRINIV KMAILSK
4607	34975	A	4648	2	711	WNRPRPCIAKTL/SQKNKAGGI TLPDFKVYCKSTVKTAWYWY QNRHIDRWSRTETSEITHIYNH QIVDKPHKNQWGWKDLLFSKW CWENWVAICRKLKLNLFTRY TKINSRWIKLHEKLTIKTLEE NLGNTIQDIGIGDFMTKMPKA IATKAKIDKWDI.KLSFACTAK ETIIRVKNQPTWENISAIYPSD RSLISRIYKELKNYKRLDAVA HTCNPITLKGQGRWIT
4608	34976	A	4649	1	576	
4609	34977	A	4650	1	771	

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4610	34978	A	4651	1	887	FPEDSEPIISHGNYTKQYPVFV GHKPGRNNTQRHRLDIQMIMIM NGTLYIAARDHIYTVDIDTSHTF EIYCSKKTAWELDPRMVATCR MKGKHKDECHNFIKVLKKK DDALFVCGTNAFNPSCRNYKM DTLEPFGEFSGMARCPYDAK HANVALFADGKLYSATVTDLF AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDIYIFF FREIAVEYNTMGKLLGLHHELL RRTQDYGHKAGCPESCLLSVRR CPPPQSKAHRESVEELIKGCR HAGFCAAGHIT
4611	34979	A	4652	1	2890	MVLLKVDPLWGSRLVLLKA DPYPGTQAHAEHRHGRALAGGL GVGEQSQSLDLLRMSHTYGA FLPRAAVSSWCASVRIRKIKKSP LLDGAPLLYEPDTWLGKWS WTLVFTHPFSAALTHSALTARS DTGSLTSPDGKLYSATVTDLF AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDIYIFF FREIAVEYNTMGKVVFPRVAQ VCKNDMGGSQRVLEKQWTSFL KARLNCSPGDSHFYFNI
4612	34980	A	4653	1	480	MEGVEEKVPVAVPETLKKKQ GNFAELKIKPKMAFVLRIGVS GVSPKVRKVLQLLRLHQIFSGT FVKLN/KASVNMLRIVEPYIAW GYPNLKS VNELIYKRGYKINK KRIALTDNTLIVPSLGKYGILCM EDLHIEITYVGKHFKEANNLLW PFLSSP
4613	34981	A	4654	3	279	
4614	34982	B	4655	119	177	
4615	34983	A	4656	157	359	HQRCRK**TKLEG*TCRKIEVN TDYIKP**EFWMIYISYILTSI CSSICNENILQLENREKSRNT

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4616	34984	A	4657	65	900	GLAAPPILQKESPHCLWILFTSP VALSTRPPCVISSAALCPRRHG FLPPRLLAPLAAAFPCPRCFLP LPRLFAAPVDFCPRRCGLPL PPRVFAVSCPRRGLLPPLLFAP SAAAFCGFLAPSPWLF AAFGTR CRGFLGLLVPA A A A A F P R R L R F FLPRLFSPA A A V T F C H P C F L P P P PRLSVPA A A S F C R R G F Q Q E I R T V EIRGSGTRVGLQHQTGHLPRGP SSLP A E L H A * A R V S P L E A S P P S C TR/WMQQPEDLGPALTLGRICG VGACWEL
4617	34985	A	4658	927	1157	ARRSTAPV DCK* LQ P* AQAAL WVLVVDHEAARQPEGVVQPA PGLWPSSRRWRKFQAPGSSGV CHPGALQACPEELS
4618	34986	A	4659	1	563	MKLVAVFDKQDLHHGGDDISA SSMHTQSPERF T S A S E L G T N N V SAFSVYQAASEIEVTSSVLHAS SQKGLSSQHLGFGAPQAGGGSF RHLAPQRKEVLEEYFKYDPEH KLIFRFVRTLFKAMRLTAFAIE ITHGGRDVERATGLV N K I H R Q G CGDSFCNIGGNAPYVCCGKE YVSSSKHQNGIAI
4619	34987	A	4660	1	681	MGKYAEALRSQQKAVLMSVR VMGIEHPNTIQENMHLALHCFT SRQLSLALSL L QGAHYLM/LLV LGE/DHPEVA/LLDNIRRVLHRV MEYDLSLCFLONALAVSTKYQ GPKALKVALGHHLITSVYESKA EFVSALQHQKEGLAAH/TSLGE DQEKTKESSEYLKCLTQLAVAL RRAMHEIYRNGSSNNIPPLNFT APSMASVLEQFKGNGILFIPLS QKDLES L K A E V A Q
4620	34988	A	4661	2	443	VWQSGGDSITSKTNITVCNVCY LYTCIDSSFNQYHSILIVRARQD IWL P V A L H R P W E S S P F I H V I N N I LQKILKRSTQFIFTLAIIMGLIA VTVIAATAGVALRQSIQT V H F V DKWQKNSTRMWS/QRIDQKL ANQINDLRQTVIW
4621	34989	A	4662	2	377	FAFTWTDPDTHQAQQITWALL PQGFADSPHYFSQAQISSSITY LGIILHENTRALPADHV* LISQT PISSTKQQLLSFLGMVRYFCLWI PSFTILT K P L Y * F T K A N L A D P T D PKSFPHSSFRSL

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4622	34990	A	4663	1	1095	MAKAVLSKKNK TGSTTLPDFKI YYKDIVTEEPGIELRHITSSTKF SKGLPSRESFSEKQNKTTTHLH PGEINSFIAHTKPA WRS LHTDA HEI WCRDSDQVNSPGRSIPCPA LCSMRKIHLRPLVLRPASPRNIS PILNPLHLIAALLPNKPPFRPPL VSPDLNPQVKDISTPSWATDHV HLTVSLKPYHPYPAQCQYPIQ HALKGLKPVITRLLQHGLLKPI NSPYNSHILPVLKPKDPYRLVV QDLRLINIHVLLPIHPMVPNPYT LLSSIPASTTHYSVLDLKHAFET IPLHPSSQLFAFTWTDPTHQA QQIT*AVQPQSFTDSPHYLNQA QISSSSVTYLGIILIKAHVLSLPIV
4623	34991	A	4664	655	2417	KKRESMNIDAKILNKILANRIQ QHKKLIHHDQVGFI PRQGW NICKSINVIQHINRAKDKNIHMI SIDAEKAFDKIQFLMLKTLNK LGIDGTYFKIIRAIYDKPTANIL NGKKLEAFPLKTGTGRQCPLSP LLFNIVLEVLARAIQEKEIGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDANKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRAHITKAILSQKNKA RGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTPQSEITP HIYNYLIFDKPDKNKQWGKGS LFNKWCWENWLAICRKLKLD FLTPYTKINSRWIKDLNVRPKT TKTLEENLGITQDIGMGDMFM SKTPKAMATKDKIDKWDLIK KSFCTAKETIRVNRQPTKWEK VFSQPTHLTG*YPESTMNSNKF TRKKQTTPSKSGRRWNEQTLLK RGHLCSQKTHEKMLTITGHQR NANQNHNEIPSHTC

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4624	34992	A	4665	1	234	MQNQEKFGELISEWAPYGRPRP QIAVGDHHISVYDGEVNW RMS SLQASAAAGKDYANRGTEWGEE PSQMLRIIHELLSGEMCVSRNRG QPLANSERRSEALSPVTPKKLIP ADGHKSDPGRTWMKLETHLSK LTQEQTCKHHMFSLISG*FAEN DGFQLHPCPSGSLWPSAGISF FGVTGLRASDLLSLARGCPRF LDTHISPLSSS
4625	34993	B	4666	1	2553	
4626	34994	A	4667	33	272	
4627	34995	A	4668	1	3045	
4628	34996	A	4669	1	334	
4629	34997	A	4670	159	245	FPIVASPWLLC*LMSFAGTWVK LETHLSKLSHGQKTKHRMFSLI DTVVVGSDDFLLRVPGCCASS LNAHTSVNIKLELT
4630	34998	A	4671	122	359	TANLKNRGRKFL*PIHLTKG*YPE STKNVKNKFRKKQTPSKSGQK I*INTSQKKTQMPTGT*KNH HHWSSECKSKP
4631	34999	A	4672	2	66	RLVYADTCFSTIKLKAEDASTS ENMRCLVFCACDSLRLMIVSSF IRVPTKDMYSSFFMAA*YLLQY HQVKSRRRCFYE
4632	35000	A	4673	519	899	SALVCHTCSNWQVHLGDSVFY RSEEQPLEPLPFSYLSLFPGLHP DPVSSGSQQPS*MPHTDASVTS SHGLGGLAGRNSCIYPCCAPAL CADYLWGSPDLFLLLSFQHKG NVGVGLAHSPPQFQQN
4633	35001	A	4674	1	278	
4634	35002	A	4675	158	592	GYYWRPSFQSLRENNECQRKS NSVNAGCLNCDHCVLGIYQQH *QNYFSFDIHYFLSETGRKVS I/VYFTIGETEALSGKVVPYWQQ AAGQGCTLHLLLPQTRLFPKGK RRQPGLLREF
4635	35003	A	4676	302	721	
4636	35004	B	4677	1	871	
4637	35005	B	4678	1	559	

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4638	35006	A	4679	3	2386	RVATMAPHRPAPALLCALSLAL CALSLPVRRAATASRGASQAGAP QGRVPEARPNSMVVEHPEFLK AGKEPGLQIWRVEKFDLVPVPT NL YG D F F T G D A Y V I L K T V Q L R N G N L Q Y D L H Y W L G N E C S Q D E S G A A A I F T V Q L D D Y L N G R A V Q H R E V Q G F E L A P F L G Y F K S G L K I Y K K G G V A S G F K H V \ P N E V V V Q R L F Q V K G R R V R A T E V P V S W E S F N N G D C F I L I D L G N \ N I H Q W C G S \ N S N R Y E R L K A T Q V S K G I R Y N E R S G R A \ R V H V S E E G T E P E A \ M L Q V L G P R I V A L P A G T E D T A K E D A A N \ R K L A K L Y K V S N G A G T M \ Y V S L W A D \ E N E F T Q G A \ L K S E D C F I L D H G K D G K I F V W K I G K H A N T E E R K A A L K T A S G F H S P R W D Y P K Q I Q V S V P F L E G G \ E T P L F K Q V F K N W R D P D Q T D G L G L S Y L S S H I A N V E R V P F D A A T L H T S T A M A A Q H G M D D D G T G Q K Q I W R I E G S N K V P V D P A T Y G Q F Y G G D S V I I L Y N Y R H G G R Q G Q I I Y N W Q G A Q S T Q D E V A A S A I L T A Q L D E L G G T P V Q S R V V Q G K E P A H L M S L F G G K P M I I Y K G G T S R E G G Q T A P A S T R L F Q V R A N S A G A T R A V E V L P K A G A L N S N D A F V L K T P S A A Y L W V G T G A S E A E K T G A Q E L L R V L R A Q P V Q V A E G S E P D G F W E A L G G K A A Y R T S P R L K D K K M D A H P P R L
4639	35007	A	4680	1894	2161	MFGLPNARAATSTAPFASHSLC LCFRILLLLGPGINLANPRNHLY LHQKFSILGRHFSLATETEEPCISL ALAPSKRWECNSSS*RYENN
4640	35008	A	4681	1	1803	
4641	35009	A	4682	1	501	MTFQCVVNTHYLTYPRPQRF YL V V V R P S C A S W I M F V L I D R G Y V F S Y F P Q S Y G G F G S R I L S K P I E V Q V G G R S V V A Q M W S N K C G Q Y S D L A S L G C I S R Y S A G S V Y Y P S Y H H Q H \ N P V Q V Q K L Q K E L Q R Y L T R \ K I G F E A V M R I R C T K A K P T R H R H Y G E L E I S I T I R A I G K
4642	35010	A	4683	350	623	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4643	35011	A	4684	1	3252	PPGPERSRLGLGVSLHQRSCP CIAVFTRVSEPRIQFPASRILPSS NTSKDFDPVSGQSNYGGSQGS GQTLNRPPVASNPVTPSLHSGP APRMPLPASQNPATTPMPSSSF LPEANLPPPLNWQYNYPSTASQ TNHCPRASQPTVSGNTSLTTN HQYVSSGYPSLQNSFIKSGPSVP PLVNPPLPTTFQPGAPHGPPAG GPPPVRALTPLTSSYRDVPQPLF NSAVNQEGITSTNTNNGSMVVH SSYDEIEGGG
4644	35012	B	4685	51	236	
4645	35013	A	4686	1004	1405	
4646	35014	A	4687	1	771	
4647	35015	A	4688	1	405	SENVDDVSVMMG/TPANKALL DTTGFWHD/DFNNA/TPNDICVA IRSE/AADAGIAQAIMQQLAEA/ LKQQA/LDRNLNVMMFSDNVT LE/DEIQLK/TRAREKGLLV/MG PDCGTSMIAGTPLAFA/NVMPE GNIGVIGASGTGFRR
4648	35016	B	4689	1	1656	
4649	35017	A	4690	1657	2259	LPQPQPATPWPSAPTPrFASPAA AMATLWSGTCRIRLWSGSSRA TRTAPAALIFPITALGSGQGAW TTRCAAGTCGRAASCSSMTSA/ AQIFSPCHCPNQDWLAVGMES NVEILHVKGPEKYQLHLHESCV LSLKFAPCGRWFVSTGKDNLL NAWRTPYGASIFQSKESSSVLS CDISRNKYYVTGSGDKKATVY EVVY

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4650	35018	A	4691	62	1371	QNQSTISVMLRSAMTTTMAAD LITAI/MGQRKQHIDTGFWHDD FNNATPNDICVAIRSEAADAGI AQAIMQQLEELKQLAQSGS SQALTQVRRWDSACQKLPDAN LALISVAGEYAAELANQALDR NLNVMMFSDNVLTLEDEIQKKT RAREKGLLVMGPDCTSMIAG TPLAFANVMPEGNIGVIGASGT GIQELCSQIALAGEGITHAIGLG GRDLSREVGGISALTALEMLSA DEKSEVLAFVSKPPAEAVRLKI VNAMKATGKPTVALFLGYTPA VARDEN/VWFGSSSLDEA/SLAG CFSVRARSPLTRIDGMMILGMF GGCFAASLWANNVKLRMPRSR IRIMQAIIGGHIAGFGARLAMGC NLAAFFTGIQFSLHAWFFANP LLIGQTTLEDPHEIDYLDKEFPL YQLVECVVSLNYSYHWECTEI
4651	35019	A	4692	1	1125	MEAEVDKLELMFQKAESDLDY IQYRLYEIKTNHPDSASEKNPV TLCLKELSVKSYQYTLYARFKP VAVEQKETKSRICAGMTKTMN VIQKLQKQTDLDLSPLTKEEKT AAEQFKSHSFGMWPCCLKYRQ NKKKKKKLSQNRSTTWKLNLL LLNDYWIQNEKAEIKMFFET NENKDTTYQNLDWTFKAVCRG KFIALNAHKKRQERSKIDTLAL QLKELEEQEQTHSKASRRQEIT KIRAEKKEIETQKNLQKINESRS CFFEEKINKMDRLLARLIKKKRE KNQIDAIKNDKGGITNDPTEIQT TIREYYKHYANKLENLEEMD KFLDTYNLPRLNQEEVESLNRPI TGSEIEARINSLPTKKSPGPDGF
4652	35020	A	4693	2	421	GRVGGRVGKIRT*LN*IETKKY KR*NETKSWFFEKIKMDRPLAR LTKKRRIEQITSLRNETGNIIDT TTEIHKIIQG*SSSSSSSSSSSSSS SS/SSSSSSSSSSSSSDTFKRPI GIKIEMVF*KLPTKKSRISL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4653	35021	A	4694	1	654	MEYYAAIKNNTFMSFAATWM KLEAIILSKLTKEQKTKRHMFSL VSTLELGALTALVRCGRWRRQ CDDEAMACVTQGRPLARLTKK RREKIQTSLRNETGDITDTTEI QKIIQGYDEHTYAHKVENLEG MDKLLLEKYNPPRLNQEELGTL NRPITSYEMEMIIKKL/PNEKSP GPDGFTAIFYQTFFKEELVPILLA LFHKTEKEGILPNSFYEAISIL
4654	35022	A	4695	1	786	MPPSLAYKKNRPQQADTQVA/T MSRGVHWRRKKMQAAGRPEDY KRSTQAEHTDRHQHTSRVHQL LLMRIFEMGWKKPSPFQESIP ALSGRDILARAKNGTGKSSAHD IPLLKRLDLKKDTIQTIVIVPTG GPALQVSQICQVSKHMGVVK VVMTTGGTNSGDDVLRLLDDTV HNVIAAPGRILNLIKKGVAKLE ETYL RHIGRPGHFGHFGLA INLI TYGDHFNKLGIEQLGKEIKPIP SNIDKSLHVAEFHSAVENEKP
4655	35023	B	4696	1	501	
4656	35024	A	4697	2	573	YSACFFLFSIAMGILLTVPPSFWI PTSFS AFLGFFSSFSLLVLHQPD FSFVLGLWRIISLLVLKIVEGSS NQGMQMASRSWEWPSSSRKM ATSVRTLPEP/GPSGCRAPSAFPF RKEAGADPSGCPGGRQVPLVAI GRGGALEPQRWELRAPGSAGR LPREGGRTPGAQSPAGAQSPA GKQSPGAQSPLH
4657	35025	A	4698	2	346	PPINISVPHC*PFGG/EPLEILIPAP ERSSHVLVSQSPPVTHSSAVHQ VGASLNCGDQKPPNPFSGSKIFF LIYHLMTGQVGRGSSVLCHPNT GIOKEGGTVNEIPAIIEKRKKHA
4658	35026	B	4699	1	468	
4659	35027	A	4700	2	284	ETGEFTQLKELNIQGCNWLTL PELGNLYLTGGKKVCKVENS WVTPIAGQFQLDVSCVSECVCS ETYEYLYGQHMQANP/EPKPKH NNHKSGKD
4660	35028	A	4701	5	189	
4661	35029	A	4702	38	190	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4662	35030	A	4703	2	882	WPSVSSG/PSSAVSFSSFDPGVA SCTSSASGIQRPMASEVPCASG IPIKIGHRGVDSSGETTYRKTT SSALKCAIQLCITHTVGSLDPTP ERHVLIEPLIELSSSGADGSLH VSIHDEFIITVQHKQAEFLQKL IPGYHIDLNQNSWTLTPKFYGL CCVKAGGKNTQIAVMKNLLLR LNSEGERILLCIGITDILQSYRFV KKLEHSWKALVCDGDTVSVHR PGFYTERFQCFMONTAFKKIPA RTLTTNPAGKDVEQQLSSLLM GMRSGTATVEDSLVVS YKTKH
4663	35031	A	4704	2	410	
4664	35032	A	4705	2	728	
4665	35033	A	4706	1	1208	MKMEKVNTSWLLPPSSISVLIR RGAGSMVLLQLSQRQYIFYEYDS SDRLLAVTMPVS VARHSMSTHTS IGYIRNIYNPPESNASVIFDYSD DGRILKTSFLGTGRQVFYKYGK LSKLSEIVYDSTAVTFGYDETT GVLKMYNLQSGGFSCITIRYRKI GPLVDKQIYRFSEEGMVNARFD YTYHDNSFRJASIKPVISETPLPV DLRYRYDEISGKVEHFUITAEM TLSKHFDTHGRIKEVLA/YEMF RSLMYWMTVQYDSMGRVIKR ELKLGYPANTTKYTYDYDGGG QLQSVACNDRPTWRYSYELNG NLHLLNPGNSVRLMPLRYDLR DRITRLGDVQY/KIDDDGYLCQ RGSDIFEYNFNAGPTKTLSSQAS GILQSLQGLHEVHRNPACSDFA
4666	35034	A	4707	1	663	MMLLLLALLGAGLLGASLLTS WHAPARNKIPRAQKWREPD DPKPILEPLAELAQQLRTEELS LESILCSYLKQALKVHQEVNCL MDFLGECHEELQALKKLLKKE RGLLYGVPM SLKDTYDSMFLE KPATKDGVMKVLKAQGAIPFV KTNIPLTLRLSLKRASWALNAA TPIYQGMLSPNLNKKTCGGSS/G GDHGGWPHGPGRGEPAVPCK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
4667	35035	A	4708	2	624	SDARLHKDDTDICFSKTLNSCK VPQIRYASVERLLERLTDLRFLS IDFLNTFLHTYRIFTTAAVVLGK LSDIYKRPFITSPVRRARKLSLT SPLNSKIGALDLTSSSPPTTTQ SPAASPPPHGTGQIPLDLRGLSS PEQSPGTQPEVSGSSPHSTAQSK IWSLVWKQYWLMAPSHAKT CHAARLARTFVTSSSATKVHCA ISLK
4668	35036	A	4709	1	195	
4669	35037	A	4710	1	1845	MAEAEPRGPRGERGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPDKKEIVICDRASVKE FKEEISRFRKAQQDQLVLISGK ILKDGDTLNQHGIKDGTLVHLV IKTPQKAQDPAATASSPSTPDP ASAPSTTPASPTTTPQSTSDSA SSDAGSGSRSSGGGSPGTGE GSPSATA SILSGFGILGLGSLG LGSANFMELQQQMQRQLMSNP EMLLQIMENPLVQDMMSNPDL MRHMIIAKPQMQLMERNPEIS HMLNPNELMRQTMELARNPAV MQEMMRNQDRALSNLEIPGG YNALRRMYTDIQEPMFSAARE QFGNPFSSLAGNSDSSSSQPLR TENREPLRNP/WSPSPPTSQAPG SGGEGTGGSGTSQP/GSGMFNS PEMQALLQIQISENPQLMQNVIS APYMRSMMQTLAQNPDFAAQ MMVNVNPLFAGNPQLQEQLRLQ LPVFLQQMQNPESLSILTNPRA MQALLQIQQLQLQTEAPGL VPVSLVSGMSRTPAPSAGSNAG STPEAPTSSPATPATSSPTGASST QQQLMQMIQLLAGSGNSQVQ TSEVRFQQQLEQLNSMGFINRE ANLQALATGGDINAAIERLLGS
4670	35038	C	4711	59	464	

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4671	35039	A	4712	1	1902	MAEAEPRGRPGERGGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPKDKKEIVICDRASVKE FKEEISRRFKAQQDQLVLIISGK ILKDGDTLNQHGKIDGLTVHLV IKTPQKAQDPAATASSPSTPD ASAPSTTPASPPTPTQPSTSDSA SSDAGSGSRRSSGGGPGTGE GSPSATA SILSGFGILGLGSLG LGSANFMELQQMQRQLMSNP EMLLQIMENPLVQDMMNSPDL MRHMIIAKPQMQLMEERNPEIS HMLNPNELMRQTMELARNPAV MQEMMRNQDRALSNLEIPGG YNALRRMYTDIQEPMFSAARE QFGNNPFSSLAGNSDSSSSQPLR TENREPLPNPWSPSPPTSQAPGS GGEGTGGSGTSQVHPTVLNPF INAASLRSGMFNSPEMQALLQQ ISENPQLMQNVISAPYMRSM QTLAQNPDFAAQMMVNVPLFA G/NPQLQEQLRLQLPVFLQQMQ NPESLSILTNPRAMQALLQIQ GLQTLQTEAPGLVPSLVSF GMS RTPAPSAGSNAGVYPPRPPLPH P ATPSHIFSNRG/SPAPQQQLMQ MIQLLAGSGNSQVQTPEVRFQ Q/QLLEQLNSMGFINREANLQALI ATGGDINAAIERLLGSQLS
4672	35040	B	4713	309	527	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
4673	35041	A	4714	1111	2506	KKDQRETRNQKGLGFLDRDPQ WVSGMKMQECLQ/HWNAMAI NNHRAVAIFPKRRRHGREDGLLS NLPTFGSYAPLRRVSNFIASAV QRILLERRALPHGNCKLGGGLTP QFMNRKNALVLEVLARAIHQE KEIKGIQLGKEEVKLSLFADDM IVYLENPVSAQNLKLIISNFSK VSGYKINVQKSAFLYTNNRQ TESQIMSELPTIASKRKYLGIG LTRDVKDLFKENYKPLLNEIKE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTFTTE LEKTTLKFIWNQKRARIASILS QKNKAGGITLPDFKLHYKATV TKTAWYWFQNTDIDQWNRTEP SEIMPHIYNLYIFDNPEKNKQW GTDLFNKCWENWLAICRKL KLDPFLLTPYTIKSRWIKDINVR PKTIKALEENLGNTIQDIGMGK DFMSETPKAMTTKVVIDKWDL IKLKSF
4674	35042	A	4715	3	372	SVGVLRPWKRE/RAASERRSS SGGGGGGGGGGGGGGGSGS GQ/HAPAAAGGIEAVNMAAS YHISNLLGLAALAVTQALP YPSAVAGSFSAPKSPAHRSAGL PIPAEPLSSPLLQPPPP
4675	35043	A	4716	1	1008	
4676	35044	A	4717	1	2619	
4677	35045	A	4718	449	801	VLLSSMSRRKCQSLYVDLLM KKETE*SMEKEKLTMHPLSCTH I*PRPQAPADKQMR*TEEQN CRMMWQKKEKHLNAKRLA GSGWRDQPLDGKAPGEDHLP SPFQLPHPI
4678	35046	A	4719	1	1255	
4679	35047	A	4720	2	843	CLHGFYGRIRDSELQKIHRAAV KGDAAGVERCLARRSGDDLAL NK/TAQIAGAQPREEACTVILLE HGTNPNLKDIIYRNTALHYAVY SESTSLAEKLFHGANIEALDK VLSISFLSKILMSSLKTCGRDAE DYTISHHLTKIQQJILRKKKIL KKEKRGKASEFLNSLGGPTL DKKIRNVEISDESAVSILHEL CV DSLPALEDVLSVATKCVPEKV SEPLCRPSHEKGNRIVNGKGE SEECLCPAAHRLRCGERLYLPP RLGCERLCLATIPSEK
4680	35048	A	4721	295	1050	

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4681	35049	B	4722	306	554	
4682	35050	A	4723	2	7973	
4683	35051	A	4724	2	316	
4684	35052	A	4725	81	228	DPPLCLGLL/LHRAISIVQKRIYF QDEGSLTKKLCEQGKTLKHSQ QMFFK
4685	35053	A	4726	1	1043	MELEWKVNVKVNQSDTNHHG SLQLARGEAAVKFGRMSKKQ RDSLYAEVQKHQRLQEQRQQ QSGEAEALARVYSSISNGLSN LNNETSGTYANGHVIDLPKSEG YYNVDSGQSPDQSGLDMTGI KQIKQEPYDLTSVPNLFYSSF NNVQLAPGITMTEIEIVAAEF PLIYKQSFLLTVLSFGGGGSVIC GPTFAKVSSRRFIHHGDKIQPS INALGWTFMEETPQIFKCRNT HGKELEHDLPEHSSGQGSTRRK SSCLRRDNNPMLLSGGRFYEKI HNFTGTFDVRKMEHAEGKTS LVHVGFQAIKMPSSLKQEA SNGLIKLEEASGARMKTGHK
4686	35054	A	4727	467	584	
4687	35055	A	4728	1	1794	
4688	35056	A	4729	110	1797	PSQPEPGSGTSLRYCWAQTL PSVTMKLVWSALLMAWFGVLS CVQAEFFTSIGHMTDLIYAEKE LVQSLKEYILVEEAKLSKISW ANKMEALTSKSAADAEGYLAH PVNAYKLVKRLNTDWPALDEL VLQDSAAGFIANLSVQRQFFPT DEDEIGAALKMRLQDTYRLD PGTISRGLPGTKYQAMLSVDD CFGMGRSAYNEGDIYHTVLW MEQVLKQLDAGEEATTTKSQV LDYLSYAVFQLGDLHRALELTR RLLSLDPSHERAGGN/LCRYFE QLLEEREKTLTNQTEAELTTP EGIYERPVDYLPEDVYESLCR GEGVKLTPRRQKRLFCRYHHG NRAPQLLIAPFKEEDEDSPHI VRYDDVMSDEEIERIKEAPK LARATVRDPKTGVLTVASRV SKSSWLEEDDPVVARVNRRM QHITGLTVKTAELLQVANYGV GGQYEPHDFSRNDRDITFKHL GTGNRVATFLNYMSDVEAGGA TVFPDLGAAIWPKKGTAVFWY NLLRSGEGDYRTHAACPVLV GCKWVSNKWFHERGQEFRLPC
4689	35057	B	4730	1	2433	

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4690	35058	A	4731	425	1079	PMGTSFLYECANFQSVSLGDPQ EPSCLCGGPPQGAAGSSGSED ALLCLWDLQARKWKFEMSYTS GNIRGSSFCQFKSSFLVYFKALL KFRELFAQFKSFMGEKKLSLAP PMSDSSGDIIRKIDYASCKRSG SSIRALPKTYQQP/EVLNDTWV SFPSWSEDSTFVSSKKTPEEQL HRCEDERFEEMKTAGFASFGER SKTGVPNLRVTDWYRLVAC
4691	35059	A	4732	3	425	GASSEEAEAGASEP/GAPGGWG APGSQAQEGGDLQEAEESEQE GGDPRKPRSPRKVERHRKAGA PGRDLGRPSLTVLLNHCVLQR LRKIYHSSIKPLEQSYKYNELRQ HEITGQRCPCCEPKPQHQUERA LFVVVSENRI
4692	35060	B	4733	1	1056	
4693	35061	A	4734	171	511	LLSVRHVVVNTQETANDVQVW /LDREGGSKI/NTGVCFLDHMLD QIATAVSRMEINVKGDLYIDD HHTVVEDTGLALGEALKIAPGD KPGICRFQFVLP/MDCELAACAL DISGGPH
4694	35062	A	4735	563	763	
4695	35063	A	4736	365	1644	RTSQMSSSAWRQNRARPSAI LPSSLSLGHAPLPQFSQRMPAT ASQLPGMVGVLEGYGGTAASP GSVSSCPACSSCCLGCWWPSS WPSCRLHPHLGRPIAHCLPE/VL TTTTTTTITTSQAAGTPKGQOE SGVSPSPQSTCGLLSGPRGFFS SPNPYPDPYPNTHCVWHIQTAT DHAIQLKIEALSIESVASCLFDR LELSPPEGLLRVCGRVPPPTL NTNASHLLVVFVSDSSVEGFGF HAWYQAMAPGRGSCAHDEFR CDQLICLLPDSVCDGFANCADG SDETNCSAKFSGCCGNLTGLQG TFSTPSYLQYYPHQLLCTWHIS VPAGHSIELQFHNFSLAQDEC KFDYVEVYETSSSGAFSLGRF CGAEPHPHLVSSHHLAVLFRT DHGSSGGFSATYLAFNATERL CLVESTSS
4696	35064	A	4737	1	154	

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4697	35065	A	4738	1	700	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVILRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTALGGILKKKGHHE AEIKPRGTVSNA TKHKIPVKVT WRSSPECINQVLQSKHPGDFGA IDAQGAMKQGP GSCFRKDNWP PTYKELGLSRAKPLAGFPTPNPS WAPGFKRERGLISV
4698	35066	A	4739	1	154	
4699	35067	A	4740	1	617	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVILRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTALGGILKKKGHHE AEIKPRGTVSNA TKHKIPVKVT WRSSPECINQVLQSKHPGDFGA IDAQGAMNKALELFRKDMAS NYKELGFQ
4700	35068	C	4741	46	522	
4701	35069	A	4742	78	617	TKELLHSKRNC HQSEQATYKM GENFCNLLI*QSANIQLQRT*T NLQEK NKQPHQKVGE GYEQTL LNRRSLCSQKTHEKILIITGHQR NANQNHNEIPSHTS*NGNH*KV RKQQVSYKLL*MRPRTRQVT Q*RREPETSLAKETPGNPTNTN AKFKTRGARISHYSSNGERLP RTVC
4702	35070	B	4743	1	6477	
4703	35071	A	4744	1	623	MSSDISEVEDKNEFLTEQLSKP QIKFNTLKDKFLKTRDTLARKKS LALETVHNLSQTQQQIKEMK EMYENAEAKENNSTGKWSCVE ERICQLQHENPCIEQQLDDVHQ KECLPSRKEKFKSEPPAFLSGN QVKSSSCSLQTLFPDDLILYLE NPKDSTKKLLELINKFRVTGYK IKLQKSVAF LNDKNEQSKEENQ ECNPIYNNYK
4704	35072	A	4745	2	3272	
4705	35073	A	4746	1	579	
4706	35074	A	4747	3	510	

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4707	35075	A	4748	1	1261	MEAVDTFLVFNALNFLTSQTT GCSSSCDPGHGLGQSGNRFPI AAASARTAEAAKWWFSNNDYS NVLQLDPKKT EYHIHEKRFSD SRILCYYPEFGKVEEILTAMKH DWFGRHKKDDKIEKTKGIQIE SFTSEEEIRIMKQEQERIQAKTR EFREIRQARERDYAEIQDFHRTF GCDDLMYGGVSSYEGSMALN ARQSPREGHMMDA/LYAQVK KPRNSKSPVPSKGVVLGEADP VYPRRNPTEGNASSLPVSFSE SPPVRAAFAGYHYVAFPLQK LMSGTSGKDPEKADLARVVT LRVVTLRITHVKTLAFTAALL QQLACIDVGMDKQNDVYTYN KILLSFKRKEILTHTTTRMSLED IILSEINQWQEDKYRFGLYEVA QVVKLIETESKVVVSRDGGRG
4708	35076	A	4749	10	2051	
4709	35077	A	4750	2	2118	
4710	35078	A	4751	1	658	MWNSKTLAAFRPCPKDPLNFE LERDNLAYLAEEIPKQSIQYIT WMILKAFSHMHLQRDNLKLEL MFKRKAKHKGLKNLHPDHVIE KKNLFSAEKFKPAEIIYISNEEP NVNSQDNGKKCLQGMSEIFAA APAITDNTSDKTTLIKVSSWPVI ADRRCLPLVNVTRDSPSPDPVF LRTLKGQDWFGEKALQGWGL\
4711	35079	B	4752	1	471	KGIHHVSAQEPVCLLLPFMTPR
4712	35080	A	4753	315	407	
4713	35081	A	4754	411	1042	
4714	35082	A	4755	1	423	
4715	35083	C	4756	202	321	
4716	35084	A	4757	5	413	CGFFFFFETESHFVTQAGVQWR DLGSLQSPPPGFTFPS/SQPPKE PGPQAPATTGQSFAFLVEMGF HHVSQEVSSIS*PRDPPASASQS AGTTGVSHRAWTFCLRQSLA LSPDWSA VARSQLTATSASVV QVSR
4717	35085	C	4758	150	491	

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4718	35086	A	4759	1	548	GIAFLNLIKTLKLPNFKSCVIL LGLLLLVDV/FFVFITPFITKNGE SIMVELAAGPFGNNEKNDGNL VEATGQPSAPHEKL/PVIRVVPK LIYFSVMVCLMPVSILGFGDII VPGLLIAYCRRFDVQTGSSYIY YVSVTAAYAIGMLTFVVLVLM KKGQPALLYLPCTLITASVVA
4719	35087	B	4760	642	1985	
4720	35088	A	4761	39	252	
4721	35089	A	4762	1	783	
4722	35090	C	4763	218	358	
4723	35091	B	4764	372	374	
4724	35092	B	4765	129	1036	
4725	35093	A	4766	1211	1983	SQSLILQEDFAPAGEQEAQ HQEDILALLRASLQGCQRQP GTRLHGSAWPWGEAQNRSRLP GDSPSLDRYRG/SDAVGKSRSG DIGSSLRVEAGDKRTQASPERQ PHCGAHDADISGGREIFKPRQ LPGSAIWSIKVGHGSGFPKRR PRGAGLSGRGGRGRSKLKSIGI AVVLPGVSTADISSNKDDENS VLDMMVVLFSSSDKFTLN/QVCG SFGQGAEGRLACSCQCGQCYH PYCVSIKMDACSSSELKY
4726	35094	A	4767	1	603	MANFNDVCVLDKEKVCIAAKFIT HAPAGEFNEVFSDIRLLCNDS LLRERAARAFAHYNMDQFTPV KMEGCEQTHIACIESHECQPKN FWNGRWRSEWKFTITPTPAQV VGVLKIQVHYEYEDGSVQLVSH KDVQDSLTVSNDAQTAKFIKII ENAENEYQTAISENCQTMDSDTT FKVLRQLPVTRTKIDWNKILS YNI
4727	35095	A	4768	1	867	MADFDDRVSDEEKVRIAAKFIT HAPPGFNEVFNDRLLNND NLREGAAHAFAYQNMDFH AVKIEGYEDQVLITEHG/DLGN SRVLDPRNKISFKFDHLRKEAS DPQPEEADGGLKSWRESCDSA LRAYVKDHYSNGFCTVYAKTI DGQQTIIACIESHQFQPKNFWN GRWRSEWKVPITPPSAQVVG VLKIQVHYEYEDGNVQLVSHKD VQDSLTVSNEAQTAKEFIKII NAENEYQTAICGNQTMDSDTT FKALRRQLPVTRTKIDWNKILS YKIGKEMQNA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4728	35096	A	4769	2	690	WPSGSASRPHRLRAPEPV/GKA GKNKGAGLTPA/AGTSGCAGR AESRGPPTGSHGSEPSRGSKGL CGRGTRSLPERGAELPHLPAQ TSPQLGSQGAWP/RHPRKPRFP AARAGTQPPGFVPSTPALLKVL YRSAHTQHSGRAAPEPSRLALG PTLQKQRHMGHRRNLTFSTY NKKCGFGWAVEMRFSALLDVT TTPSRVAFWGSRGPLGMRQL QLLSGYS PDGWLSTSM
4729	35097	A	4770	1	590	MDTRIGTDTGTGYGKVEGARR MRLKKLPHEYAYYYLDDEICTS NPCEFPGYGIERYPCETSGPLE LTVQEDQGEFPQREELTRKKT KVCRGSPLAWATGVKPKLKKK RRRRKEERRKKKEEGEGEGEEEE EEEEEEEEEEEEEEEEEEEEEEEE EE/EEEEEEEEEEEEEEEEEEEE EEEEESDPCTSWNTSQP
4730	35098	A	4771	1	288	
4731	35099	A	4772	1	237	MRSSVIGPRSHIPSRQKSGIQEE EEEEEFQEEEEEEEEEEEEEEEE EEEEEEEEEEKGLDQEAARHLV LPAATQCKPKM
4732	35100	A	4773	1	794	MASHSSPMGSGYQYYGFGPD AMHALNTVVSEKDLTDLGL VARNKRCGPHYSYLNTHLLHA CLRLPTQRENTTLKTFIPQGW HTDQVEREAECQPGRLKICVHD TAQELPLASTARNALLGRNLCP FRQSTTQMPDEIPISLDDRM PSLKKKK/VVGEEEEEEEEKEK EEEEEE/DEGEEEEEEEEEEEE EEEEEEEEEGGGGGVGE EEGEGEGGGGGEDEEE*EEEE EQKKKEKKKKEQEEGGGEGG
4733	35101	A	4774	115	341	
4734	35102	A	4775	1	651	
4735	35103	A	4776	189	618	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAEISGNNSISPHHE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEDLLYNFI YHFSKMPTKVPSLWDSKLGAE QAAPEENNKKEQEEYQGKSF SFLNLTECWP
4736	35104	A	4777	1	414	

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4737	35105	A	4778	189	692	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAEISGNNISIFHHE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEDLLYNF IYIIFSKMPTKAMSISSMFKFAT KIRMTVTNPKCCWIPVFPAYL STSKAAKCMHHTAHHGQEKSD HCISPSPIAP
4738	35106	A	4779	2	3815	
4739	35107	A	4780	957	1493	KNNRYNKLRLPQCNPTRTQD* ETHSKPLNYMETEQSP*LLG T*RNEGRHKAVL*NQ*EKRHNI PESLGH/AKQCVEGNL*H*MPT RESRKDLKLT*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQELVF*KDQ QN**TASKTNKEEKREESNRN KKC
4740	35108	A	4781	1	4962	
4741	35109	A	4782	2421	3011	NQACQPGQAGAAARAGQCFPRV AQRPGPGPAGMALAHPDLYL HSAGDQCR*DEEADPPQGAPT HFQVHPAGGLHLLDRLAAPH QAGTQGGQPGRRH*PAARSS PVEPPSTGSPSRPTTMMWPSCSR RQGGGLGGL*CVQQPHLLDAP GTLPLVGLVCRLOPWRLCL GGGGGVGGSQRPVGGGGGNG GRNWG
4742	35110	A	4783	1	932	MRTPKSSIKPSLGEKENYRGS LKETAAPSLQKEWAEQSSKSQET VGKVGITRHFQVSTLLERREDR KSKEPPLLIPTQVSGVDLQQT TDLQLSVLTVRRKTNKQKQHP HQKPICTSPSSNTKVNLEKQL DEWLTRITNAEKSSKDRMELKT KARELHDECTSLSSRCDQLEER VSVTEDEMNMKRGEKFKREKR IKRNEQSLQEIWDYVKRPNLCL IGVPESDGENGTLENTLQDIIQ ENFPNLARQANIQEI/RENAT KILLEKSNSKTHNCQIHQS*NEG KNVKGSRERSGYPQREAHQT
4743	35111	A	4784	477	638	LLCCGFELPLLARRSLIV*SLLS THQSHSPSFVPLLVRSCIPLEEE RRSDF
4744	35112	B	4785	1	1509	

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4745	35113	A	4786	3	832	ERHHPPQAGPHPPRRRKERT HRQPTPQPHGA/WKISVPQT TNGISSITSTQRNPQATTVEKA HNESTRTPPEPKGAVRGTR*KK KKTSRDTPQT*EKSSSATRNK AGGKSDSKRERKATEDQTTPS KRRKLHPMAKKLTLKKN*MN G*LE*PMQSP*RT*WS*KPRHE NYVMNAQASVTDAINWKKGPP PRPTTNDKIVTRPTHPTCSHH RPPRKPPRTHPTPTQNKISQ* NGYTPPRGKRVREDRCKPPQAP TSAPRAAKQRQS
4746	35114	B	4787	1580	4673	
4747	35115	A	4788	1	462	MKLEHQAQRSGQGREKRR WPEGKAGPGCEGAWILCPESQ DDSKQEGDNNMIVVSRNAVRS VKAEFQGDNLNWECSAEIIV QGRDNGVPHKAHGLGTEEGT VLKISERQNWLDLVDFILLGGD LFHENKPSRKTLHTCLELLRKY CMGDRPVQFEILDQSVNFGFR KLNRKDIHTKNPSVRHHQRP KVDETIKMGKTQSRKTRNSKN QSTSPPPKERSSPAIEQSWMEN DFDELKEEGFRRSNYSELKEEV RTNGKEVKNLEKLDKWITRIT NAEKSLKDLMLKTLIAQLRDE CTSLSNQCDQLEERSVSMEDQ MNMKREEKFREKRIKRNESQ LQEIWDYVVRPNLCLIGVPESD GENGTKLENTLQDIQVNFNL ARQANIQIEIQRMPQYSLRR ETPRHIVRFTKVEMKEMLR AREKLECSGAGLAHCKLWLL GPSDPPDCSSVSPVLRVHLVPS SLPHSVGTPLGVSVPSPVPRFP DRVHFPYPYTHYCDNLKTCHT SHGSVMAETAVINHKKRKNP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRL YSVINPYLIPFFIGLQNRFTQFR LSEKTEITNPYAMRLYESLCQY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
4748	35116	A	4789	1314	2221	KNRNYNKLRLRPQCNPTRTQD* ETHSKPLNYMETEQSPSE*LLG T*RNENGRHKA VL*NQ*EK RHNI PESLGHI/AKQCVENGL*H*MPT RESRKDLKLT*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQLVF*KDQ QN**TASKT/IQRRKERRIK*TO* KMLKEDITDPTIEIKTHREYYK HLYAHNLENLEEMDKFLDTYT LPRLNQEEAESLNRPITNSEIET VINSLKEKAQDQKDLQLNSTRA LFTIAKAWNQPKCPSMTDEIK/I NVEHIIHGILCSHQKE
4749	35117	A	4790	2	2260	TKDKNHHMISIDGGKAFDKIQQ PFMLKTLNKLIGDGYTLKRIRAI FDKPTANIILNGQKLEAFPLKGT TRQGCPLSPLLFNIVLEVLARVI RQEKEIKGIQFGKEEVKLSLFA DDMTVYLENPIFSAQNLLKLIS NFSNVSGYKINQVKSQAFLYTN NSQIMSELPTIATKRITYLGQL ARDVKDLFKENYKPLLNEIKED TNKWKNIPCSQIGRILWPYCP QEDENFNSLLQNGDILNSSTEE KFKAHDKKDFNLPEYDLNVEE RLVLEIKSVDSTATADDT HKLD HINMNLNKLITNDTFQPEIMERS KTQDIVLGTSFLSINSKEETEL ENGKNYPNLESVNVKVNHGSEE TSQSPNRTEPHSDSCSVDLGISK STEDLSQKSGPVGSVVKSHSIT NMEIGGLKIYDILSDNGPQPST TVKITSADV DGNIVRSKSATLL YDQPLQVFTGSSSSSDISGTKA IFKFDSNNHNPEEPNIIRGPTSGPQ SAPQIVYGPQYNIQYSSAAVK DTLWHISKQNPQIDHASFPQPLL PRSESTENQSYAKHSANMNFN HNNVRANTAYHLHQRLGPARRH GEMWAISPNDRLIPAVTRSTIQ QSSVSSTASVNLGDPGSTRRAQ IPEGDYLSYREFHSAGRTPPMM PGSQRPLSARTYSIDGPNASRPQ SARPSINEIPERTMSVSDFNYSR TSPSKRPNARVGSEHSLDPPG
4750	35118	A	4791	1516	1729	ILAPHSLACRVSAERSAVSPM GFPLWVTQPFSLAALN/DFLHF NFG/RJ*QLCVLELLFSRSIVVAF SEFP

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4751	35119	A	4792	3	1426	RRYDELQNSSGRDGKPRAMAV TRSTSSTSSGSNSVLVPVSWK RPQYSQKRAKEKL VHVLSLCC QEVGLSKNPSVIFSSCGDLDLLE HQTSLVSSSEDGAREQENMDDT NSEQQFRVFRDFFDL DVELEDG EELQGESMDNFNWGVRRRSLD SLDKCDMQILEERQLSGSTPSL NKMHHEDFDESSEEDLTASQI LEHSDLIMTLSPSEETNPMELLT TACDSTPPEPHSFNTRMSSFDAS LPDMNNLQISEGSKAEAVREE EDTTVHEDDLSSINELPAAFEC SDSFSLDMTEGEEKGNRALDQF TLASFGEGRGVSPPPSPFFSAI LAAFQPAACDDAEAWRSHIN QLMCDSDGSCAVYTFHVSSLF KNIQKRFCFLTCDAASYLGDNL RGIGSKFVSSSQMLTSCSLDKL KFSVLELQEYLDYNNRKEATL SWLANCKATFAGGSRDGVITC QPGDSEEEKVIKAC
4752	35120	C	4793	60	164	
4753	35121	B	4794	44	2547	
4754	35122	A	4795	401	9546	PRADITTCDDRITPGTCRPLPV LPASLYAADMASQQDSGFFEISI KYLLKSWSNTPVPGNGYIKPPV PPASGTHREKGPPTMLPINVDP DSKPGEYVLKSLFVNFTTQAE KIRIIMAEPLKPLTKSLQRGED PQFDQVISSMSSLSEYCLPSILRT LFDWYKRQNGIEDESHEYRPT SNKSKSDEQQRDYL MERRDLAI DFIFSLVLEVLKQPLHPVIDSLI HDVINLAFKHFKYKEGYLGPN TGNMHI
4755	35123	A	4796	2	6107	GERKPKIDLFRTCVAAIPRLLPD GMSKLEIDLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNLLREVNDMHHTLL DSSKLKLLQLLTQWKLVIQTQG KVVEQANKIRNSEARDELDV GVDVDVGVDVDADVDVDVDL GVDVDVGVDVDADVDVDVD MGVDVDVDRIYGFCKCGCDR DVDRVVDVDVDIDVDVDVDM DVNIDVDVGLGAGVDVDMDV HIDMDMDVDIGSDNQLQSALRR

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4756	35124	A	4797	3	565	MLPGHLFLAKAGKEEQEEKG QHTRKTITPQNIPGGAHITATH RGRCTVATKFSGGGLCKEPNRLT WY/GPPLKGAHGGGR/GPSSRVPS FPAAGQPPIGGALHGAGSRGLA RTRAQLGGPPGGELRGTSNGG DGQGGPDGDSRKSGLRPSHL/P DPAAVAGAPVSGHLQTPGHHA GRRQQAGPRGAGLP
4757	35125	A	4798	1	417	
4758	35126	A	4799	1	1069	MPRPVPPANALGARGEAVRLG LQGEELRLQEVSVRLHQINYL SDRISLHRRLLPVRWNPLCKEKK YDYDNLPRTSVTKAFYNEAWS TLRLTVYSVLETSPIILLEEVIL VDDYSREHLKERLANELSGLP KVRLIRANKREG/LVRARLLGA SAARGDVLTFLDCHCECHGW LEPLLQRIHEEESAVVCPVTDVI DWNTEYLGNSGEPQIGGFDW RLVFRWHTVPERERIRMQSPV DVIRSPTMAGGLFAVSKKYFEY LGSYDTGMEVWGGENLEFSFRI WQCGGVLETHPCSHVGHVFPK QAPYSRNKALANSVRAAEVW MDEFKELYHYHRNPRARLGLAC DECSIKAGWWL
4759	35127	A	4800	1	1152	MHNSDGIEVMRQQAIEIGRVG GLEGIQLGVTEIVNGARMLES YNCKAELGATGLVNYQISVKC SNQFKLEVYLLNAENKVVNDQ AGTQGGQLKVLGTNLWWPYLM HEHPAYLYSWEGRPDGAQAVG ALTPGTLAIVEVWLTAQKSLGP/ SDFYTLPVGLRTVAVTESQFLIS GKPFYFHGVNKHEDADIQGGK FNWPLLKDFNLLCWLANTF CTSHYPYTEMLQICYRYGIVVI DECPAPSGHTGPSVPSLLARW QLFNNVSMHHHMWVVEEPVL RDKNHPAMVMWSLAKEPASFL ESAGYSFKSLTMEQTRVLDLDD TGEAVLQYRSRPRGAHKTLGK KRKISSYNVDLTSCQLAKEKCL KGPSSFLQSRQERMNSLRDN
4760	35128	A	4801	293	535	
4761	35129	A	4802	94	686	
4762	35130	B	4803	1	2187	

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4763	35131	A	4804	596	1789	MFHVIERPYECKECGKNFRSGY QLTLHQRFHTGDIHKGKGPYEC KECKKTFTLYRNLTRHQNIHTG EKLFECKQCGKTYTTGSKLFQH QKTHTEKPYECKECGKAFTSL YGYLKQHQKIHTGMKHFECKE CKKTFTLYRNLTRHQNIHTGKK LFECQECGKAYSTGSNLJQHRK THTGEKPYKCECGKTFSLHG YLNQHQKIHTGVKPYECKKIHT GGKPYECKECGKAFTSRASNLV QHERIHTGEKPYVCKQCGKTFR YGSALKAHQRIHRSIKVNQWL DSPRHKSINCDPMSPRTRKTRE RSHVSGRSLCQRLLGQGAQLRE FKQPPNRFRRCVGLVARNTFP RGLRGRASRRNAASRLEDA VAELLKARCSALGSGSGLPEGLS
4764	35132	A	4805	2	489	CQEGAKWEQGMTGRRVWVG PPASSTPPHS/HFWLLVLSRGLV GIGEASYSTIAPTIGDLFTKNTR TLMLSVVFYFAIPLGSGGLGYITGS SVKQAAAGDWHCALRESFLQLV RLLKVTHLLQQLQLLYPTNGK RQDTNHTRSQCAHYLPHLDFQ VALCAYAVLQC
4765	35133	A	4806	1	327	
4766	35134	A	4807	899	1219	ANRKASTMRWYVRPFCSGLST LSREKLYPLRLMRRASTGPLS GALGMYSTASPRLMFSGCSISS AR*LFRSSAVTMPAAWMSFTI WAVRLPL*KAWAPSMASVS
4767	35135	A	4808	2152	2633	SRLDCGQGLVNGSCDYHHGCT GDTPRRPEWHRS LAHCMSPVD SLPGCAVSGSSDPWEVSWLWQ QVDRCDNREE/VMW*QRLGFP SPTVSFPQRAVSASKPLQ*APS WISLHSTLSQCRASDLRGHRTV PEVVVYWSPCALPTHREHPNAI MEGWPPPQAWWA
4768	35136	A	4809	2	387	SNASVILEGEDLRFSCSVMAG RLQGRFSVIWQLVDRQNRKSDI MWLDR/DGTVQPGSSYWERSSE GSVQMEQVQPNFSFLGIFNSRK EDEGQYECHVTEWVRVVDGE WQIVGERRASTPISIALGE

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4769	35137	A	4810	46	3753	EIRSWEKRRRLVLCLEAADM KCFFPVLSCLAVLGVVSAQRQV TVQEGPLYRTEGSHITIWCNV GYQGQPSQNFQWSIYLPSSPER EVQIVSTMDSSFPIYITQRVR GGKIFIERVQGNSTLLHITDLQA RDAGEYECHTPSTDKQYFGSYS AKMNLVVIPDSLQTTAMPQTL HRVEQDPLELTCEVASETIQHS HLSVAWLRQKVGEKPVEVISLS RDFMLHSSSEYAQRQSLGEVRL DKLGRITTFRLTIFH
4770	35138	A	4811	1	3728	MKCFPPVLSCLAVLGVVSAQR QVTVQEGPLYRTEGSHITIWCN VSGYQGQPSQNFQWSIYLPSSP EREVQIVSTMDSSFPIYITQR VRGGKIFIERVQGNSTLLHITDL QARDAGEYECHTPSTDKQYFG SYSAKMNLVVIPDSLQTTAMPQ TLHRVEQDPLELTCEVASETIQ HSHLSVAWLRQKVGEKPVEVIS LSRDFMLHSSSEYAQRQSLGEV RLDKLGRITTFRLTIFHLQPSDQ GEFYCEAAEWIQDP
4771	35139	A	4812	897	1217	ANRKASTMRWYVRPFCSGLST LSREKLYPLRMLRMRASTGPLS GALGMYSTASPRLMFSGCSISS AR*LFRSSAVTMPAAWMSFTI WAVRLPL*KAWAPSMASVS

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4772	35140	A	4813	1	1507	MWNSKINHDIIDDOFLKTYTVL ESSISVGVASNASVILEGDDDLRF SCSVRMAGRPOGRFSVIWQLV DRQNCRSNIMWLDNRDGTVQPG SSYWERSFFGSVQMEQVQPNF SLGIFNSRKEDEGQYECHEVTEW VRVVDGEWQIVGERRASTPISII ALEMGFAVTAISRTPGVTVSDS FDLQCIKPHYPAQVPVSVTWR FQPVGTVEFHDLVTFTRDGGV QWGDRESSFRTRATEKAESSN NVRLLIIRASDTEAGKYQCVAE LWKNYNTWTQLAERTSNL LVIRVLQPDRLMGVSARALRGE SPSQMPQACCHGNTGALVIGIN EPESLPCLTQVTKLVQVSKSKRT LTLVENKPIQLNCVSKSQTSON SHFAVLWYVHKPSDANGKLL KTHNSAFEYGTYYEEGLRAR LQFERHVSGLDLSLTVQRAEWL LSPNYAWYKLAEVSGRTEVT VKQPGGSLGLGCSVSGWAAEP VCTQGRPCSWNTPLALTAAC
4773	35141	A	4814	1	627	
4774	35142	A	4815	166	435	
4775	35143	B	4816	1	240	
4776	35144	A	4817	1	288	VVPASSPGAASEPRRRRCLQP EKSVPSPGGGHRDPPKARPPR PPSAPKP*RRPFS*LARSLCFPA AGCAYGVGVGGAGGGRAGLR QVPVAE
4777	35145	A	4818	206	1041	VSVGSAPSDMPAAATRW/CNSR COHQRLSAR/PVAGPGT/RTSS FPWLA PRNVVPGSLEMPGTA GPORGSHSSPGSSALLSFS/CV HNVESKEPVCLLLPSMASRLT PRGTCRPVPGCLQHPLSLPPVL VGTQSPSQAPKSARKPSQPQL GWLQLHPGSGSLCLLPAPAGS MECAALESVPSQLGIGAPGPCW AQAGVQGSWNVATSSSPGSA QGQPRAPPCLVCGPAQCGTSGS RSRATGLRPSCLECQVWWSQV CGANPGDTTSSQDAGTRCSKV
4778	35146	A	4819	2	487	

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4779	35147	A	4820	152	758	RGARGPEWDGQLDGPQSGMC GMAAPRLRRSGVRAAAGHPV QQPRLLDGLSLTDESDSCVSFEP PSHPSSSSGPVTALSRGWNFLK AFPLMGETQERER/VLTHFSRR YQCQNPDAQPSDEGHI/TLTCA LMLLNTDLHGHVIGEVGTETN RTDKQQNRTEQSKRQANADKH NEHANNEQQHEHDKDNDTRTR DTEMRHAKRDNA
4780	35148	A	4821	100	220	
4781	35149	A	4822	100	1588	CLKISTGYTGSMFAEEASGNLTI MAEEGEAGTSTHGQSRKRRE KEEVLHPFKQPDVRSYRENS KEEICPHDSVTSQITPPPTLGITI RHEIAASICHVADTAGVAGDA MMRKTDLIPPFIGLTLQGGRA DMGNQKKWRKGSENATLVA MASERFHWQYSGNSTIQPKQK QHGMITRLVTAAPVCPGLVQPSL CAVGLRNIMSLSSHTCALQNTK QAWEGYDDCHSQRVSQGEN MTKLFLNLLNQMPSWGEGKM VPADFGSGCWEGTGTGSPAGSQ VSFLNRHNDGQLAGDSPGLPPP PCPRGLQGAEQRSALRRHKAD VHRDQWLVISFSKKLRTSARK WYEAGPFGVPRVLPAQAQGG TDFPFSPSEEPFQSPFSMVQAH TVRSKPQFHFAAGENCNLRSE LSRNQGLQARVGPLAIMSSDPS GDFVLYTPTILGVGLEVLVSR EGTFLWRYSTCP/LNYKLWLP GYLGLLVPKDQKVRAVFLGM
4782	35150	A	4823	1329	1881	AHLEAAGWSSSVQPGSPRVLG RAEEHQQSGRAKEIGHKIPKE TFDELTALETISSK/CLYLAKK NQVIQELLSMKEVQKCKKL EEVKNILEQEVVNLKTHEKNM VEFGDVEECKLQLEERAGQIE KLEEINLQRACLSAKKVRAEGE LEPRRHHNHLTGFTGFWGLM SVITGAYDLIR
4783	35151	A	4824	176	308	LGNLTSPPFN*KHRSTKGTFTLS TVALLTLGHVGKITSNCHPGY

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4784	35152	A	4825	1467	1890	DWFDeltaETISSKICLYLAK KNQVIQELLSSMKEVQQCKK LEEVNKILEQEVVNLKTHEKN MVEFGDVEEKLQLEFRAGQE EKLEELNQRACLSAKKVRAEG ELEPRRHHNHTLGFTEGPWGL MSVITGAYDLIR
4785	35153	B	4826	1	753	
4786	35154	A	4827	225	410	
4787	35155	A	4828	225	410	
4788	35156	A	4829	225	411	
4789	35157	A	4830	141	1001	GGVRGVQKETCAFKVLESIG KLG/LALSVAGGAENSALYNVD AGHRAVIFDRFRGEQDIVVGE THFLIPWVQK/PIIFDCRSRPRN VPVITGSKDLQNVNITLRIFLRP VASQLPRIFTSIGEDYDERVLP TTENLKSVMVAPFDAGELITQRE LVSRQVSDDLATERAATFGLIL DDVSLTHLTFGKEFTEAVEAKQ VAQQEAQARFVVEKAQEQKK AAIISAEGDSKAAELIANSLATA GDGLIELRKLEAAEDIAVQLSR SRNITYLPTG/QSVLLQLPQ
4790	35158	A	4831	194	453	QPLPELELRPKAL*LTSPQFSA *RLKTAARLPKPWAVLPQGFT DTPPHFSQAQISSSVTYLSIILV KTHVLCSPFHRTGTVV
4791	35159	A	4832	1	86	PCESYLEHL*WSCRLRLRLGSV SLQLLS
4792	35160	C	4833	191	263	
4793	35161	B	4834	1	741	
4794	35162	A	4835	3	96	
4795	35163	A	4836	1	301	QEQQKMNTLQGPVSFKDVAVD FTQEEWRQLDPDEKITYGDVM LENYSHLVSLAYEVATSTCTSEIL KPSNLPKSFSSH*QDMISPSQT SSLSWSRERSG
4796	35164	A	4837	3	273	VLHFISAGNTFAHQEHSRPG PNNLSKRKLLPAVIGPRVFHGE DRHIL/LFSTRKE*ARSLCYVQG GVQAPAAAFCSLLSLGWGAGC AFWC

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4797	35165	A	4838	3062	3688	RSVTRAPPRTSTFPLAQAPSRS HIREPTSPHLGRLGSHRGPPS RPLPPALAAALSLETLQPRLLHP HLHLALHDQGRACVRAYAHPS YLWRCHALGVWVES/ARLRPS ALPPAHSPPLAAPLLSSSVQPPA PALEPPPRPPAAGAAARCLAAQ HHHPSRLGVRQPPLAVGALGST WPPQAPAPPELSALEQDRVGA QPPPPPSQGA
4798	35166	A	4839	1	197	
4799	35167	C	4840	26	358	
4800	35168	A	4841	84	433	PASAPLGLSATVSACFQEQQKM NTLQGPVSFKDVAVDFTQEEW RQLDPDEKITYGDVMLENYSH LVSLAYEVATCTSEILKPSNLP KSFFFSH*QDMISPSQTSLSWS RERSCG
4801	35169	A	4842	1	372	VQWLFMQICLGGKHQQLRHQG VQEKMLPLEGS*VIEAGSPTLIG ETLSLEIINYIIGAGLESVHTHKS RQLGGWTRPGSHFQVQLIPAHT PMNLEPSQLSLEPRLVPAQQSL PSAPTSPKALSQ
4802	35170	B	4843	7	267	
4803	35171	B	4844	213	3895	
4804	35172	C	4845	141	359	

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4805	35173	A	4846	831	3017	RRRLHYSGSTRPWRTRAMLPRL TLSLRPHLSLHLPLPCLLLHLA LPTHLPKPKHQPTVREL/ARRC RLPRACHPAQNLEQQPLRPSH LQRH/LSLLPPLGLSQSGPPG/LA PQPLL*LQTPDHFAGADPCSIHG TSH*HQGTSNPSGRDGYQTPSH ICPSPAPKQSFLEGTQNTSPSSP AAPAASSAPPMFKPIFTAPPKSE KEGTPPGPSVTATAPSSSLPT TTSTTAPTQPVFSSMGPPASVP LPAPFFKQTTPATPTTAPLFL TGLASATSAPITSAASPTDSA SKPAFGFGINSVSSSVSTTTST ATAASQPFLFGAPQASAASTP AMGSIFQFGKPPALPTTTVTTF SQLLHTAVPTATSSAADFSFG GSTLATSAPATSSQPTLTFNNTS TPTFNIPFGSSAKSPLPSYPGAN PQPAFGAAEGQPPGAAPALAP SFGSSFTFGNSAAPATAPTPA PASTIKIVPAHVPTPIQPTFGGAT HSAFGLKATASAFGAPASSQPA FGGSTAVFSFGAATSSGFGATT QTASSGSSSVFGSTTSPFTFG GSAAPAGSGSFGINVATPGSSA TTGAFSFGAGQSGSTATSTPFT GGLGQNALGTTGQSTPFAFNV GSTTESKPVFGGTATPTFGQNT PAPGVGTSGSSLFGASSAPAQ GFVGVPFGNTFAHQQEHSPR KGNPNLSKRKLLPAVRAQGPPR
4806	35174	A	4847	9	935	IPCFCGAMPYQTRRQENDLR TASIAV*RRKQDDH*QKRRW QNIQRKGPRIYIAGNSQSHQ PMIFSMLRKLPKVTCRDVLPPIR AICIEIGCWMQSYSTSLTDSY LKYIGWTLHDKHREVRVKCVK ALKGLYGNRDLTARLELFTGRF KDWVMVSMIMDREYSVAEAV RLILILKNNMEGVLMVDVDCES VYPIV*ASN*ALASAVEGFYLYW KLFYPECEIRTMGGREQRQSPG AQRFTFQLLLSFFVESKSHFVTQ GGSGGQFAHRNCLPGSGNFH VSASRVAGIAGAPHTWLIYVF
4807	35175	A	4848	1	1749	
4808	35176	B	4849	282	1227	

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4809	35177	A	4850	221	907	FEDSFNIRGVKKKAARPLKTPP VAKYPKKGSQAVHRHSRKQSE PPANDIFNAAKAASDMQHRE VRVKCVKALKGLYGNRDLTAR LELFTGRFKDWMVMSIMDRE YSVAVEAVRLILILKNMEGVL MDVDCESVYPIVLKYPECEIRT MGGREQRQSPGAQRTFFQLLS FFVESKLHDHAAAYLVNLDWDC AGTQLKDWEGLTSLLEKQDS TCHMEPGPGTFHLLG
4810	35178	B	4851	1	2361	
4811	35179	B	4852	1	878	
4812	35180	A	4853	1	313	MPHTPRCLFRPQASCLVHFLEQ QNKLLKLETKLQFFQNRCECKSNL EPLFEGYTLRREAECMEANS RLASELNHVQEVLEGYKKKYE EEVALKATAENEFVALKK
4813	35181	A	4854	188	354	
4814	35182	A	4855	405	647	LPLISDQVSYSPLMSKSLASLY QESY*TLARLPLISPFVNSLST DLFILLIGNTSIAIAFEGVSAISL PSCNSLE
4815	35183	A	4856	1	585	MSSGEGKRTWLGLWGGRVVP VPPICGLRVAVTSAAGTSSFLA PKPTRIRGERGKGQGRG/SSGN GGGRGRAGASAGSRGEVVSVA NDGRWRGRGRGVGCPRSSKRE DNRFAKHGRASGKAWEPHPPS QALRALFGPIRRRGRAAETRIV YWKDRQLTNRDSTILELQKVL KTCCAQSMKIFCCLWNFVYKQ
4816	35184	C	4857	12	468	
4817	35185	A	4858	1	1156	MAFRKKIITAGCIDHVLVSVD QQMQANLTQRTEAIRKQTQIA PTFPAHSLPDKYLGALLNRKII GTFLVFNMCNRNHEDKNEAFT VLEKKVFNLEFCTLQNYSEV KEKERQRFSKQTLREFATRKP ALKEMLVQLQRYKERKHIRKR NVKYSADHTTDTANQADPNQ QEPHVPGHAPDNKTIROKQNO HKDNTTRKHNQMTSDTSRTNT KVSQQRPGKQTRRRHERQQA RERQGRHQRK/RDAQTRHTQR QRQARAE/QVIENKREEKRTS ERTNDSTRREGTRRPRTEKGE RQEEGDRATATHRKDHDRQPP HGAPHCSRSSRHGAPTPLYCC SPLPGTPSCTICTVQYGRWLPH MATEQLNMAGPNQDFQDVVW

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4818	35186	A	4859	1	1580	MAPALLLLLASGAAACPLPCV CQNLSESLSTLCAHRLGLFVPP NVDRRITVELRLADNFQALGPP DFRNMGTGLVDLTLSRNAITRIG ARAFGDLESRLSLHLDGNQAG GAGHPRALRGPVNLQHLILSGN QLGRIAPGAFDDFLESLEDLDS YNNLRQVPWAGIGAMPALHTL NLDHNLIDALPPGAFAQLGQLS RLDL.TSNRLATLAPDPLFSRGR DAEASAPLVLSFSGNPLHCNC ELLWLRLARPDDLETASP LAGRYFWAVPEGEFSCEPLIA RHTQRLVWLEGQRLTLRCLRAL GDPAPTMHVVGPDRLVGNSS RARAFPNGLTLEIGVTGAGDAG GYTCIATNPAGEATARVELRVL ALPHGGNSSAEGGRPGPRTSPP PLALLPRYNSSDETLIYRIVPA SSHFLKHLVPGADYDLCLLA LSPAAGPSDLTATRLLGCAHFS TLPASPLCHALQAHVLGGTLTV AVGGVLVAALLVFTVALLVRG RGAGNGRLPLKLSHVQSQTNA
4819	35187	A	4860	2	403	
4820	35188	A	4861	87	442	PVFPWHYPYKQKEESQSVLVI WQKTAGGGWSTW/WLSFSPET EKVVKK/AHVDTL*NEMWDVT K*TAFKIPSC*T*HQHP*SFFRK SESQVIVFAGQGVKIH*YILLHS NVIHYMNEI
4821	35189	A	4862	2	651	EFIKQWDADKFEHIQTLEGHQ EIWCLAVSPSGDYVVSSSHDKS LRLWERTREPLILEEREMERE AEYESVAKEDQPA/VPGIQQ DSYFT*KKTITVK/AERIMEA FELYREETAKMKEHKAICKAA GKEVPLPSNPILMAYGSISPSAY VLEIFKGIKSSELESLLVLPSFY VPDILKLFNEFIQLGSDVELICR CLFLLRIHFGQITS

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4822	35190	A	4863	1	703	MGLTKQYLRVVASAVFGVIGS KQGNVFFVTLRGEKGRVYAVP ACEHVFVWDLRKGEKGLKQEV TCLCSPDGLHLAVGVEDGSIRI FSLLSGEGNVTFNGHKAAITTL KYDQLGRLASGSK/RQPGGIV FTESILAYSSACQDKQNHVWGS SQ*CADFVIQLRQYCCSFCS*F H*NMEQVYTAVYSHNDL*ICTL LILCTW**TGSHRNKAPKTMFP RCTEGLDRGNRPATHS
4823	35191	B	4864	1	2616	
4824	35192	A	4865	3	674	PECTGRTLRSASQHQHDTFYILA CELNSLADDAQRYDVPNSCL YPPDLWPRVPMQAKKKELARR DDIEDGDSMISSATSDTGSAGR KSKKNIRKQRMKILFNVVLEAR EPGSGRRLCDLFMVKPSKKDYP DYIIHLEPMDLKIEHNIRNDKY AGEEGMIEDMKLMFRNARHYN EEGSQVYNDAHILEKLLKEKRR ELGPLDDDDMASPKLKLKA ASHFII
4825	35193	A	4866	3	425	
4826	35194	A	4867	1	1115	LCSVPTLCLASSHLVSNLSTFKQ VTSSFIRHVATLLGLYLALFCF GWYALHFLVQSGISYCIIMHGV ENMHNYCFVFALGYLTVQCVT RVYIFDYGQYSADFSGPMIIT QKITSACEIHDGMFRKDEELT SSQRDLAVRRMPSLLEYLSYNC NFMGILAGPLCSYKDYITFIEGR SYHITQSGENGKEETQYERTEP SPNTAVVQKLLVCGLALLFHLT ICTTLPEYNIIDEHFQATASWPT KIYLYISLLAARPKYYFAWTLG TAPRKWSPCPGPQCIQLRAADP SGPEPLMLSSQERQPKAKPPK EAHADIAGTPREGEKTRTGGPG KAFLRDPGASSVELSRTQLWV LTPPIAKAPCECLQ
4827	35195	B	4868	218	656	
4828	35196	A	4869	1	180	
4829	35197	A	4870	12	199	GLFPLEPGANGI*GC/SGRIRAQ RWLPGRPKFTGESFIR*PPRVAK ESGQLIWFCVPTQISS

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4830	35198	A	4871	1	5058	MKLRGVSLAAGLFLALSLWG QPAEAAACYGCSPGSKCDCSGI KGEKGERGFPGLEGHPLPGFP GPEGPPGRGQKGGDIPGPPG PKGIRGPPGLPGFPGTPGLPGMP GHDGAPGPQGIPEGCNGTKGER GFPGPSGFPGLQGP GPPGIPGM KGEPGSIISSSLPGPKGNPGYPG PPGIQGLPGPTGIPGPIPGPPPG LMGPPGPPGLPGPKGNMGI.NF QGPKGEKGEQGLQGPPPPGQ! SEQKRPI DVEF
4831	35199	A	4872	3	1646	EDEGRAKGHHTWQQTRENEQ AKGETPYKTIRFRETY YHKNSM GETTMIQLSFTGSLPQHVGIM GATIQDKIWVTPGLPGFPPTG LPVKRGFPGPSGFPGLQGPPVIP GPTGIPGPIGPPGPGMLMVTGP PGLPGPKVNMGLNFQGPKEK VKQGLQGPPGPPGQISEQKRPI D VEFQKGDQVIPGDRGPPGPPGI RGPPVTPGGEKGEKGEQGEPE KRVKPGKDGENGQPGIPVMPG DPGYPGEPGRDG/EKGNAVMG PPGPPGFPGERGQKGGDEGPPGIS IPGPPGLDGQFGAPGLPGPPGA GPHIPPENKGDTCFNCIGTGISG PPGQPLPGLPGPPGIPGAPGA PGFPGSKGEPDILTFPGMKGD KGELGSPGAPGLPGLPTPGQD GLPGLPGPKGEPVRITFKGERGP PGNPGLPGLPGNIGPMGPPGFG PPGPVGEKGIQGVAGNPGQPGI PGNKGDPPGTTITQPKPGLPGN PGRDGDVGLPGIPGLPGQPLP GIPGSKGEPGIPGIGLPGPPGPK
4832	35200	A	4873	110	256	CSGT YRCYSF/HSRDPYLWSAPS DPLE/LVVTGPARQY YTKGNLV RIASGL
4833	35201	A	4874	2	2888	LSDPCSSRWDRSLSQRSRSWS YNGYYSDLSTARHSGHHKRR KEKKVKHKKKGKKQKCHRRH KQTKRRILIPSDIESSKSSTR MKSSCDRESRSSSSLSHHSSK RDWSKSDKDVQSSLT HSSRDSY RSKSHSQSYSRGSSRSRTASKSS SHSRSRKSRSSSKSGHRKRAS KSPRKASQSENKPVKTEPLR ATMAQENVVVQPVVAENIPV IPLSDSPPSRWKPGQKPKWPKS YERIQEMKAKTTHL

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4834	35202	A	4875	350	986	LWGGGSARLLRLPRGPCLPPAS PSSPSSSSSELS*SCSLGPSSSSSSSS SSSCSLCPSSSSSSSP*LPSSSS SSSRPLPPSSSSSSSSSSSSSSSS SECLCPSSRPRTTVAGLGAPAG FPSGPVDTCSVWLLRFTSTMW DCSLRL*VPEPPSSSSNSPPSSL HKLAGPPASTPPSFSSLLKKG WAGPMVAGTVPPAVPAPSSSTR TE
4835	35203	A	4876	1	496	SQSYSVRGSSRSRTASKSSSHSRS RSKSRSSSKSAVLASTARCAGS RKQCVPPLPRLCQLQSRSLQPS MVPWRWGLTGPRGIALPPAAR PGPLHEAPRWGPPRRRAPRPWP PGARPGRRRRRAAASPSSCG PRASGAAGGRGAPIGARASA GAAVWTPISTT
4836	35204	A	4877	3	4578	TLAVFVPTLAGFSVALGGPAW GRRRRSVSGVGVLWQQCFLF CSRGPAQAGGQPALAATSVAM GAQDRPQCHFIDIEINREPVGRI MFQLFSDICPKTKNKLCLCSG EKGGLGKTTGKKLCYKGSTFHR VVKNFMIQGGDFSEGNGKGGE SIYGGYFKDENFILKHIDRAFLLS MANRGKHTNGSQFFITTKPAPH LDGVHVVFGLVISGFEVIEQIEN LKTDAASRPYADVVRIDCGVL ATKSIKDVFEKKRKKPT
4837	35205	A	4878	1	1689	

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4838	35206	A	4879	1	1604	MGISCPGSSKMLNSRALPVLKL TQGALRDCRERANYTNFNLYK AVESQKGFVCVLYNGQSQPEY VMIPCTSVPTGQEVPEDRGMR MVMKNKPNKPSKMQSLKSSKH LTNSVIVIAVGIFSVTLQARDP QLDDAIEQLRGVCIRAWKEKITS GGEQYPSFSAIKQGPKEPYIDFI ARLQESLKKMIADSAAQDIVLQ LLAFDNANPDQAAALRPARGKA HLVDCIKACDDIGDSSNGKAS YFGSKSKVFQTSYSAQKAEVL AVIEVLTAFDMPINVISDSYM VYSTQLIENALRFHTDEQLMT LFTQLQTAFRSTMHPFYITHIRA RHPTPLPGPLTEGNQMADCLVA NAISNARHFHNLTHVNASGLK HRYSTITWKEAKNIQRCPTQCM VHSSFRGGVNPRLGEPNSLWQ MDVTHIPLFGLRAYVHKRRIR GGGGGEGEGEGEGEGEEEEEEE EEEEEEEEEEEEEEEEEQEQEQE EQEQEQEQEQEQEQERRRKDTE ELSYSLPLNRTQPCWHPDFGLP
4839	35207	A	4880	1	1146	
4840	35208	A	4881	1	1577	MGQVWALVHSTLETFTHTDEEE GEYNEVTEQVCLPAKAGSAAV DLCCCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQIVTS TSVPWKAKPGDHIAQLLIVPKK FUEGLKEPLQVERQSSCQGLGY/ PFLMAAIVKPPPIPLKWLTDKP IWTEQWPLSKEKLEALEDLITQ QLKKGHIAPTFSPWNSPVFIKK KSAEQDCEWFVFTILAVNNLQL KPAKRFHWKVLPGQPNQPIWI PSRYLKYPHYKPDACEEIPESQ GFPVAAMSRLTLRRTPVTISNT HRTQPPTWGQIEKLQMAEENL RKAGQPVITISNWLPRITKFKPI EGAENVFTDSSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFNHNLTHVNASGLKRRYSIT WKEAKAIHQRCPTQVMLSAAE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPHYKPD GEKISGNGCGRPHPRQLQPCPD

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4841	35209	A	4882	1	420	MTNISTTLKDLKDAGMIDPIKS TFNL/PIWIPQKPDGSWKTANN /R/KLNQATISIAAIVLDVASLPG KARSYHGFSSHAGRVIDSNQK DIEGCTYILNVAGKNMFGIQLR RSVIFPCPNLMYTDNCSSHGPR GPSDYDSDP
4842	35210	A	4883	213	687	PEHILPGAQEGPSC/PLEPELE/V *NMSSWNLTSECKMHGDLKY L.FVITAKDQQ/VSIAAST/*GFC WNQ*VSASPSQAPGMPLVLGR RLWQGSRLGGLSISLDDCHGA HNHSFKRVTTLQVFSWTVPQ AEPAMDCIHTA/DSRQRLP*QA HESVAEVIIT
4843	35211	A	4884	1	648	MSSWNPLPESFKKHIGYLLYLFV ITAKDQQ/VSITASTWGFYWNH SQGKNPEQMEASQKPVAGLWA WWNLISLSAASHGAQNHPFKR VTTLQSQGWNKDLWIMRELL CNRPEQLLQETATIKAPIAPAD PWSQEVIVNFCNAVSSVSCMPF NIHFNISNIPPESSGDWRMQQPC KVEQSILGAQRGGGCRPGSLR ELFPCLLAEPNMEEEVAALRA
4844	35212	A	4885	3	597	GTLEPAEWSVLLGVHSDQGP LDGAHTRAVAAIVVPANYSQV ELGADLALLRLASPASLGPV WPVCLPRASHRFVHGTACWAT GWGDVQEADPLPLPWVLQVEVE LRLLGATCQCLYSQPGPFNL LQILPGMLCAGYPEGRRDTCQP SPEPGPMCIS/SHIQRLRDAVS HTWQRGTPEARLGSWERRQRQ QQQGPV
4845	35213	B	4886	387	552	
4846	35214	A	4887	20	612	
4847	35215	A	4888	792	959	TGLSSSQNPKATKSIPWHNRLL PNVDSQVQQNSQAIHVTN*GNS ESQYPFSKMDT
4848	35216	A	4889	268	500	
4849	35217	A	4890	1	529	
4850	35218	B	4891	259	1672	
4851	35219	A	4892	480	657	
4852	35220	A	4893	2	377	WCDPSSSLHRSVQALRTFCVTL SGAFVRDCTTVLSSTICEPSTD V/CWAMNIVSVLLLYGSEEEA FWLLVALCERMLPDYYNTRV VVIRTYDQRYEQCDVLDGLP TTLFTTDDWHVWPDLTGLP

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4853	35221	A	4894	1	251	TEARKAAAVMPKTAVLAAERPKKAWGVLIIPKSKTKRTPKAFAGGGCW/TKVGVWSKVAKKVPKP EASKPKKAAPKTRRYKSTLTKTK
4854	35222	A	4895	283	427	PSVSKESPLNSPASQAGSATFAT TPLTPPK/PAATSSVAAAALLPALPR
4855	35223	A	4896	111	1095	SRGWSRLPVPCCAPALLSPWAVNGIRRRGAGDGTTRGGSGCAG AHSAGLVASGPESWIPGPVPPG AEPPRRGDSGLARCPAGHPSR ASPQRP AEGFDALAAAPSRVPGD SRQLSRNNTRSRCEGRGGKTTP AWA G VHRHGPPPAAPPGRARV HGHR LRGG LGPGGGKRGLPGC CPRAADPRGRP/GETSRSGERG PGRSAPLSLQPRHRTGLET/RQPSPLARSRPGLGPRPSARRPSRPA PPPPPPELHRGAPQGRVVASQT RPGARARPAADTHSSLKSPASQ AGSAAAFATAPLTQPKQLRAP WQPLHSFRPCRGVTSRLRTAPP
4856	35224	B	4897	243	452	
4857	35225	A	4898	3	353	RRYLSPKYIKMFVLDEADEMLS RGFKDQIYDIFQKLSNNTQVVL SATMPSDVLEVTKKFM RDP IRLVKKEELTLEGIRQFYINVERE EWKLDTLCDLSAMHGDM DQKERD VIMR
4858	35226	A	4899	3	410	NLQEWKLDTLCDLYETLTITQA VIFINTRRKVDWLTEKMHARDFTVSAMVCLPAASLLWVCPSEV SYLKP GFLEPRCLPGLLHICFLF QHGDMDQK ERDVIMREFRSGS SRVLITDILLVSRGN**QRQKG GSKVI
4859	35227	A	4900	1	235	MLSYVLEVTKKFM RDP IWL VKKEELILES IHQFCINVEQEKWKL DTLRDLYETLTITQA VIFINTNR RKCCSKVREI
4860	35228	A	4901	3	48	NSNVEREEWKLDTLCDLYETLTITQA VIFINTRRKVDWLTEKMHARDFTVSAMHGDM DQKERD VIMREFRSGSSRVLITDILLVSRGN**QRGTRGVEAGHTM

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4861	35229	A	4902	2	879	AQFPTRLDLKATQALVLAPTRE LAQHIQKVVMALGDYMGASC HACIGGTNVRAEVQKLQMEAP HIIVGTGPRVDFDMLNRRYLSPK YIKMFVLDEADEMLSRGFKDQI YDIFQKLNSTQVVLLSATMPS DVLEVTKKFMDDPIRILVKKEE LTLEGIQFYINVEREEWKLDL LCDLYETLTITQAVIFINTRRKV DWLTEKMHARDFTVSAMHGD MDQKERDVMREFRSGSSRVLI TTDLLARGIDVQQVSLVINYL PTNRENYIHRJRGGRFGRKGV AINMVTEDDK
4862	35230	A	4903	1	1764	MASLEEGIYSLKINSKRSSYNS MNPQFTAGSEGGNETEEPKNFKQ SRKGRPQDSGSSLSVLQEIQL DDIPKVKEEAVISSQSDLGECPY CGERPARNATIFAPQKEKESAP EMSSSCDKRVTVNPPEKFSEGR PKTQNTLICEKCSQPSNFLDDY NPHVIIQKRLSNQSRVICEKSSP PLNVDPNYSNSHVIQKHKEKM AIERPSSGSDWSDVGGTTVIFSE EKPFSCLCPVVSEPPYYATDYT TFPPHYSFPHDYTSSWFSSTKS SCYPSLGSSNTLQAGKSSCSSS SRSNNNIFQGERSSHQFSLDYS TSFPVSSENTSRLKMTTEGRS KNSSLFYYSRNVAAEAEKERVY QEETLGHYPYGRASSFPPTIW QPEQPGFIDTHCLDLLYSRLPF KGTFTKFRKIYSNTFFKEFQGC SCFCNPQNLSDNLWEDQLKDD LVWGVFGCRPHFAHYNNYQE RSILKALRHPKAVAFGEMGLD YSSKCTTHIPEQQKVFKRLRL AVSLKVKPMMIHCREADEDLLG ILKKYVPSDHKMYQHCFGTGSYP VIKPLLSCFPNLYVGFMAILTYS SAEQARETVKK

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4863	35231	A	4904	125	820	VLAPNYHITFRNLSSVSSPVSTA EPVLQAGQARELSFSSLHPASPL LVPSTPALTLHAFNALVLFPSFP LEKAAKRERPKSKIQTARVGK MRRTWSPHTTISAGGSVNGAST LKNLSLVWEAKPADTINPTPTT HPNPGPTPTNTNRHPPPHHPLT NTPAPPHQPPATTP/SPQTQTPN YCPNTDHTTPTHTDPNPVPPTR RTPPNRTGKRNTNTSQNYRLVSP APKIHWEA
4864	35232	A	4905	407	757	
4865	35233	A	4906	5	426	GKSTKSQNASSPPKDHNSSPA REQN/WIENEFNELTEVGFRIT SLEKNINDLMELKNTARELREA YTSINSQINQVEERISEIEDQLNE IKHEDKIREKRMKRNNQSLQEI WDYVYKRPNLRLIGVPESDIENG TKLENTL
4866	35234	A	4907	1	2267	MTGQFQDQDVVREEARPLPNRIM RLRFNFHATECSWDHLVYVDG DSIYAPLVAAFRCEVENRYQGN PLRGTCYYTLIDYQTFSLSQE DDRYYTAINFVATPDEETPPIRG RQTAAHTGELQLTSGGYPGSMK LPEEGTGERNRITINKDVHTET PSKGHQHQRPVKDKSTKIKKN QRKKAENSKNKNASSPEDHN SSPAREQNWMENEFDELTEVG FRRWVITNSSKLKKHVLTCQKE AKNLEKRLGQLLTRITSLEKNV KELMELKNKAQELCEAYTSINS QIDQAEESISEIEDQLNEIKHED KIREKRIKRNKQSLQEIWDYVK RPNLRLIGVPESDGENGTLEN TLQDIVQDNFPLARQANIQIE ILKTPQRYFSRRATPRNIITFTK VEIKGKMLRAVREKDHSAIKLE LRIKKLTQNCCTMWKLNLL NEYWVHNEIKAEINKFFETNEK KDTTYQDLWDATAKAVFKGKFI ALNAHRRKWERSRIDTLTSQK ELEKQEQTNSKASKRQETKIR AELKEIETQKTLQKINESRSWFF EKINKIDRLRLARPIKKKREKNQI DTIKNDKGDITTEPTQMOTTIRE YYKHLIYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPPTTSE IEAIINSLPTKKSPPDGFTAKL YQRYKEEVVPLLLKLFQTVGK EGPLNSFYWANILIPKGRHT

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4867	35235	C	4908	605	760	
4868	35236	A	4909	94	400	
4869	35237	A	4910	I	1538	MPIQMQYPQYKLVENKTQPPV YQYWPADLQYRPPPEVKYRP QVVCVPVNSTAPYQQPTAVVF NPTAPPSSGGIIAQNTDLVEWF FLPHSTIKTFTLYLDQMATLIGQ ARLRIKLCESDSKIIIVPLNKEQ VRQAFINSGAWQIGLADFVGII DNHYPKTKIFQLKLTWILPKI TRHKPLENALTVFTDGSSNGKA AYTRPKERLIETQYHWAQRAE LVAVITVLQDFNQSINIVSDSA YVVQATKDVETALIKYSIDDQL NQLFNMLQQTVRKRNFYVVT HIRAHTNLPEPLTKANEQVDLL VSSAFLEAQELHALTHVYNTGL KNKFEDITWKQAKNIVQHYTQC QIPHLPTEAGVNPREQHFTGK KNSPHEGKLIWWKDKKNTW EIGKVITWERGFAACVSGENQL PGWIPTRNLKFYNEPLGDAKKS ASAETKNQPLSIIDSPGKAPGCL MPTTQNLWVEVPTVSATSKFT YHMYVPPAPKRQRPARTGHND DGSFVKKGDM
4870	35238	A	4911	I	759	FRMVIRCLPQRELDGDRGNWT ATSaelTGJKWRRYNFGGHGD CGPIISVPAQDDPILLSFIRCLQA NLLCVWRDVP*PDC*ELWIFW WGDEPNLVGVYIMNCRLLWKK DSGKMAFPMNVGRC/FFKAIHN LLERCLMDKNFVRIGKWFVRP YEKDEKPVNKSEHLSCAF/TFFL \HGESNVCTSVIEIAQHQPILIN EEHIIHMAQSSPAPFQVLVSPYG LNGTLTGQAYKMSDPATRKLLIE EWQYFPMVLKKKKK
4871	35239	A	4912	I	539	MRHPCDGNLSLYFDHISYNMLA VMLYYGFGRVSIGKTGLRGVQ RHLWPLPLDASSTKTVSSSHSD KGEIFSPFPCLINCNFEMRNT TKCLMDKNFVRIGKWFVRPYE KDEKPVNKRVTQEIWLDFEY\ GVSLPCFAVERCALLPLCLLPR LMISISSTRQRPQYISRRGLKAKI SWVV
4872	35240	A	4913	198	620	

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4873	35241	A	4914	63	1267	RNRILRMEFFDWFWAFWSWLL NMIRSQNAKDSSNSMENTDSP WCELFRELCINALDVPDLLV RGNEFSASVHNTFDHMMWRTKE RYEAGWLLSSADRMKENEDE LRDSVSWLQKQILSLKSAKIAL SGSLISYRERAEIVEKQTQTLM RVADLQQKGYINSPALCHNLW RDLDFHSFPYDITLFHYIDDIML IGSSEFEVANTLDILKGQRFVLT VIDTYSRYWFASPECNAA/KT TIHGFTECIHYHGPHISIASYQG THFMAEEPWASKNQGEVETPF TITPSDPVATFLLPVPMTLRSAG LEVLPVEGGTLPFGDTTMIPLN WMLRLPPGHFGLLLPLSQQAK KGVTVLAVVIDPDYQDEISLLF HNGAIIISDGNVILIGLLQWFST
4874	35242	A	4915	2	2210	
4875	35243	A	4916	1	2036	MDTFLDTYTLPLRNQEEVESLN RPITGAIEIVAINSLPTKKSPGD GFTAIFYQRYKEELVPFLQLQF QSIEKEGILPNSFYEASIIIPKPG RETTKKENFRPISLMNIDAKIVN KILAKRIQQHIKKLIHHDQVGFI PGMQGWLNTCKSINVIQHINRA KDKNHMIIISIDA EKAFDKIQPF MLKTLKKLGTGDTYFKIVRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPFLFNIVLEVLARAIR QKEIKGIQLGKEEVILSLFADD MIVYLENPVISAQNLKLIISNFS KVSIGYKTNVQKSAFLYTNNI QTGSQIMSDLPFTIASKRIKYL IQLTRDMKDLFKNYKPLITEM/ KTKKWKNNIPCS/WELEKTLTKFI /WNRKRARIAKSILSQKNKAGG ITLPDFKLYYKATVTKTAYWY DQNRDIDQWNRTEPSEITPHIY NYLIFDKPEKNKQWGKESLFN KWCWENWLAICRKLKLDPLFT PYTKINSRWIKDLNLRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATQAKIDKWEIKLKSFCF AKETIIRVNRQPTKWEKIFTTYS SDKGLISRIYNELKQIYKKKKQP HQKDFAYHFTVFVFFYGAFLLLE AAATSLHDLHCNTTITG/HATPE **PV*HKRSSLTITVLCRSG*IIW WCDPHTHS
4876	35244	A	4917	1	1359	

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4877	35245	B	4918	1	948	
4878	35246	A	4919	1	981	
4879	35247	A	4920	1	3747	
4880	35248	A	4921	1	1875	
4881	35249	A	4922	1	2238	
4882	35250	A	4923	1	3924	
4883	35251	A	4924	1	1068	
4884	35252	B	4925	62	389	
4885	35253	B	4926	1	3663	
4886	35254	A	4927	1	1474	MAVSTTVRVDMPCCAVMLYC WGRSGKEQQPDEALKKGFTV CFEGLRFQKPGSYFSLDQIGH VEIQMITPPWRGTTLSTKRGG KRGKTESDREHNLAPPKGRDTP KKEGAHVRRGGLSGTPTTEKK GKARSPRYGDTHRGEGLNKT RAPQNFSESEPTINKIDRPLAR LIKKKREKNQIDTIKNDKGDTT NPTEIQTIREYYKHLIYANKLE NLEETDKFLDTYTLPRLNQEEV ESLNRPIGTGSEIEAIIINSLP(TKKS) PGTDGFTAIFYQRYKEELVPFL LKLFSQIEKEGILPNSFYEAII PKPGRDQTQKENFRPISLMNID AKIVSKILANRIQVHIKKLIHHD QVGFIPGMQGCVGSSARAIGQE KEIKGIQLGKEEAKLSLFADDTI ECLNPIVSAQNLFLKISNFSKV SGYKIHVPKSVSFLYTNNIAES QIKNAIFPTIASKRIKYLGIQLTL EVKELYNKNYKTLKEIRDE
4887	35255	A	4928	419	1002	CYQRWKVLKSSGGLARL/IKK REKNQIDAINKDGDITDPTTEI QTTIREYYKHLIYNKLENLEET DKFLDTYTLPRLNQEEVESLNR PITGSEIEAIIINSLQTKKSPGPG FTAKLYQRYKEELVIYRFNAIPI KLPMFTFFTELEKTTLKFTWNQK RIRIAKSILSQKNKAGGITLPDF KLYYKATVTKTAWYW

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4888	35256	A	4929	1	2502	MFFETNENKDDTTYQNLWDTFK AVCRGKFIALNTHRRKQERSKI DTLTSQLEKEPEKQEQTHSKASR RQEITKIRAEKKEIETQKTLQKIL QKINESRSWFFEEINKIDRLAR LIKKKKREKNQIDAIGNDKGDIT DRTEIQTTIREYYKHLANKLE NLEEMDKFLDTYNLPRLNQEE VESLHRLITGSEIEAIINSLPTKK SPGPDGFTAKFYQRYKEELVPF LLKLFQSEKEGILPNSFYEANI LIPKPGDITTKENFRPISLMNI DVKILNKILANRIQQQIKKLIHH DQVGFIGMGQGFENIHKINVI QHINRTKDKNHMISIDAELKAF DKIQQPFMLKSLNKL VLEVLAR AIRQEKEMKGIQLGKEEVKLSL FADDMIVYLENPIISAQDLLKLI SNFSKVSGYEINVQKSQASLYT NNRQTESQIMSELPFTIASKRIK YLGQITRDVDFKFNKYKPLL NEIKEDTNKWNIPCSWVGRIN IVKMAILPKVIYRFNAILIKLPM TFFTELEKVTTLKFIRNQKRACIA KSILSKKEKAGGIMLPEFKL*Y KATVTKTVWYWCQNRYIDQW NRTEPSEIIPHIYNHLIFDKPDKN KKWGKDSLFNKWCWEHWLAI CRKLLKDPFLTPYTKINSRWIK DLNVPRPKTIKLAGHLGNITRDI GLGKDFMTKTPKAMATKAKID KWDLIKLKSFCTAKETAIKRVNR
4889	35257	A	4930	1	4187	MGDFTNPLSTLDRSMRQKVNK DSQELNSALHQAADLTIDICRTLH PKSTEYTFEAPHHTYSKIDHIV GSKALFSKCKRTEIITNCLSDHS AIKLELRIKKLTQNRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDTFKAVY RGKFIKAVCRGKFIALNAQN RKQERSKIDTLTSQLEKEKQE QTHSKASRRQEITKIRAEKKEI TQKTLQKISESRSWFFETNKI DRPLARLIKKR

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4890	35258	A	4931	1	1818	MSSRGPCTLETLINPSPSVADDI PHLRPKPVYITTTDRDNENIYSTK IPYMAARVVFIKWIVTFLEKK YLTATQNTKNGVDVLPKIIQTV GGGAVQERAPELDGGGPTEQD KSHSNSSTLSDRRLSNSLCSIE EEHRMVYEMVQRILLSTRGYV NFVNEVFHQAFLLPSCIAVTR KVVQVYRKWILQDKPVFMEEP DRKDVQAQEDAELGFSETDSK EASSESSGHKRSSSWGTHNSFT SAMSRGCVTEEG/TIQMLKAGV QALLQPVLCVFPLIPLPPLCNQA ARPAVVISPLGDLPLWLSVLGG PADQWHLSYLKPEGSSAYACIL EALASAGKGLWKVSAVGRKP WTRGRSDRKGTVGHQVQFLFF KDEGRVDSRILTLMVAVIRPN LCVYISRELWDDFLGVLISL TE WEELINEWANIMDSLTA VLAR TVYGVEMTNLPDLKLEQKEK KQRGKGCVLDPQKGTTVGRSF SLSWRSHPDVTEPMRFRSATT GAPGVEKARNIVRQKATAKRS QSISSNCVHLSALPATKSVPLLL HTLYKNKALKALGQPVGKAD QLVVAGSPSVCCVEDQWGRSN LEAMVLWLYCIPPDGDVLYL
4891	35259	C	4932	96	278	
4892	35260	A	4933	1	261	KLRLP PGHFGLLLLLSQQA KKG VTVLAGVIDPDYHNEISLLHN GGKKTRPAEMLAEGKG NTE WVGEEVSHQYQL*PHDQLQKR
4893	35261	C	4934	36	385	
4894	35262	A	4935	1	2349	
4895	35263	A	4936	207	561	QLAEPHPWIPGTRKDAQCLVGL FGFWRQH IPHLGLLWPIYRVT QKAASFEGWGP*EKALQIQPS VQAALPLGP*DLADPMVLEVS MADR CAGWSLWQAPIGELQQ KPLGFWSKALP

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4896	35264	A	4937	1	1375	MSTTQLDITMGAESLCNMETVQ VEDEGIQKLKEIRMVVEWITPFRP THPSCEGPEDIPLTNALQNTFVR AAPASLKSPPVALLSPVGYRT HAVVISPVPECRFGIDILSSWQN PHIGSLAGRAHQKQFVGSWQG QQYAFTVLPQGHINSLALCHNL IWRDLDFHLLSQGITLVHYTDD IMLIGSNLADPMVLEVSMADRC AGWSLWQAPIGELQKPLGFW SKALPSSADNYSFPERQFFACY WALVETECPLTGHQLTMQPEL PIMNWVLSDPSSHKVWHGQSG HGGRDGSGYSWTQQHGLPLTKG DLSMTTAEQIFQQRPILSPRY GTTPWGDQPATWRQKWQRFVL TGIDTYSRYEFAYPACHASTKT TIHGLMEFLIHGPHISIASDQ GTHLMAKEVRQWAHAHGIHW SYHVPHHPEVAGLIERWNEIGL LKSQQLQHQLVNRRLRRELQCWL
4897	35265	A	4938	1	324	INCLRNCKTYQA/RKPLWFYNT SLKFFLNKP/MLADVVEIQGTT VPAHRAILV/ARCEVMAAMFN AGIFQAMCLLCAE/MYQVSRL QHICELFII/TQLQSMPSRELAS NL

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4898	35266	A	4939	108	2304	VAAAYPPASPWPSPARSLAGA APAPLCVGPAAVEAREGDAAG DERIAGELAAARGPREAVSRCFS PSRRPALGFEIMSIHIVALGNEG DTFHQDNRPGLIRTYLGRSPL VSGDESSLLNAASTVARPVFT EYQASAFGNVKLVVHDCPVW DIFDSDWYTSRNLIGGADIIVIK YNVNDKFSFHEVKDNYIPVIKR ALNSVPVIAAVGTRQNEELPCT CPLCTSDRGSCVSTTEGIQLAKE LGATYLELHSLDDFYIGKYFGG VLEYFMIQALNQKTSEKMKKR KMSNSFHGIRPPQLEQPEKMPV LKAESHIYNSDLNLLFCCQC VDVVFYNPDLKKVVEAHKIVL CAVSHVFMLLFNVKSPDTIQDS SIIRTTQDLFAINRDTAFPGASH ESSGNPPLRVIVKDALFCSCLS ILRFIYSGAFQWEELEEDIRKKL KDSGDVSNVIEKVKCILKTPGKI NCLRNCKTYQARKPLWFFYN TSLKFFLNKPLADVVREIQGYG QCPAHRALIVAPCEVMAAMF NGNLHGKAKSVLIPVYGVSKE TFLSFLEYLYTDSCCPA/GIFQAM CLLICAEMYQVSRLQHICELFI TQLQSMPSRGTHGPWNLDIS/ DLL*KGPSFHHSWIAFSTWAYF HFHCYLYTLIFQFKRPGIFRDLF S/EGRNGSFLFGKRHRWGSPNM LLGRQLAGITGKYFTSPGNVG
4899	35267	B	4940	1	3117	MRVCARACVTRTRMVCVYAH TCVCVRTYAYVVRVVRVHVRA RVRVCA YARTRVRNLSILPFIQ LTLATPIHHIIHQEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLRMLEQTALAHN IPVQREVAPGVITETGYIQLFLP GWEIGFPLALLLAFLCSTSPGF GDPDGLGVIA YQDTVVRNAAT AISELNA LAVKGVILTGDNPRA AAAIAAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAGIAGMSGTDOAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL V'TLMTGLWLA VLADTGATV LVTANALRLRRR
4900	35268	A	4941	1	1162	

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4901	35269	A	4942	1889	3387	QWAIKQFKHAEKENPYLFGGG HLRAIFR*SGFQ*RQLHTMHWG AS/QQAEHP/LAQPSTRAQLRTP P/TADS/QRALVSGSGMKPRLNG ERVLICAAGKHPADAFTGLINE LESAGQTVVLVVRNDDVLGVI ALQDTRLADAATAISELNALGV KGVILTGDNPRAAAAIAAGELGL EFKAGLLPEDKVKAIVTELNQH APLAMVGDGINDAPAMKAAAI GIAMSGGTDVALETADAALTH NHLRGLVQMIELARATHANIRQ NITIALGLKGIFLVITLLGMTGL WLAVLADTGATVLFPPRLFEAR NSQVGNGETNQTRFLCAAPG GTFIADFTAGTGRRARPRNRNR RVVVSDFHQNMRRFLMEIVA ARFVVSXVAAHFRTFHYGGVIF ISRENVWIRGFESIFDHLERFR LLFTIDNPVGKVFVAALVGRV LGKHIQFDVVRVTTKLCESILQI VNFIFRQSQAQTQVSVQDRLTA LPQQINAGNRSRLMVGKQLLCI
4902	35270	B	4943	1	2104	
4903	35271	C	4944	1	1215	
4904	35272	A	4945	3	268	YEFNRPYPEIQRSGIS/KLLEPLL FAATSDSQLSKTEISSIKINSETV PVYQLRYNGNNALMFATYQD KMLVFSSTDMFLFKDDQDTEA
4905	35273	B	4946	1	1725	
4906	35274	A	4947	1	1437	
4907	35275	A	4948	2	736	QCPYPYIAATGRILVVTHLICLA PQIVENQVTVPLTTTMLSVPGA KTVRGFSQFGDSYVVYVIFEDGT DPYWARSRLVLEYNQVQGMPL AGVSAELGPDATGVGWIEYA LVDRSGKHDLADRLSLQDWIL KYELETIPCVSEVASVGGVVK YQVVIDPQRLAQYGISLAEVKS ALDASNQEAAGGS/SIELAEAEY MGGTCSAHGRALSRGVLWCRF SAIVRGPPRGMFCAGAAPNLI
4908	35276	A	4949	531	632	
4909	35277	A	4950	532	609	

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4910	35278	A	4951	1	525	LGVEATAMGDFGKAAEKLVPV VELAQACAHVMKSGIDLAVS YCMQVNHGFAQPLEFLLGGLD KVPVLLVFINGVATPLPGFQRT RMLGEAIGRFTSTPQYAGDTVN DEDISNTIRALFATGNFEDVRVL RDGELRKFPCTCESDDNFRPVT SVNYVIRHDWVGIRRVVPENE
4911	35279	A	4952	1	2769	
4912	35280	A	4953	1	681	
4913	35281	A	4954	1	1230	
4914	35282	A	4955	1	774	MLRTSDRPPYQPKRCIPLSVL EVLRCARRWSLRPYQLARAYI /ERYRHDRDIEREKRGRNLQEI RGLVEQTNASLLNENANKDSK AHERGDIHYHDLDYSPFFPMFN CMLIDLKGMLTQGFKMGNAEI EPPKSISTATAVTAQIGSVHIYG GTTINRIDEVLAFFVTASYNKH RKTAEAWNIPDAAGYANSRTIK ECYDAFQSLLEYEVNLTHTANV EGLTGDDGIAYEALKKNSQKPR MSASHNCELVSRLGRQYT
4915	35283	A	4956	1	1278	
4916	35284	A	4957	461	1002	SLSTKGYYAAKWCSTACAGS/T LLLVLLVWFIPKGFPGQDNGI IQGTILQAPQSISFANMAQLQRQ VADVILQDPAVQSLTSFVGVDG TNPSLNSARLQINLKPLDERDD RVQKVIA RLHTAVDKVPGVDL FLQPTQDLTIDTQGSRTQYQFT LHATSLDALNTWVPQLMEKI/Q QLPKLS
4917	35285	A	4958	1	291	MNPVDRPLLDIGLRLRLEFLRISG KGLA GLTIAPALLSLLGCKQED IDSGTVGLINTPKGVLVTQRRAR CTGCHRCIEISCTNFNDGSGVTF FSRIKPH
4918	35286	A	4959	1	306	MKNFEVLQPLQNSLSGLPLVW SERILQQINQLTHYEPVIGIMGK TGAGKSSLCNALFAGEVSPVSD VAGCTRDPLRFRLQIGEHFMTI VDLPGVGESGVRD
4919	35287	A	4960	2666	2775	
4920	35288	A	4961	9	308	GDLGDSRRHRAFLCHLPVELKTA LMFPVTLTRALMETAY/ATAVS A/NFRTESRGH/SRFDPP/RDD ENWL/CHSLYLPESESMTRRSV NMNPKLRPAFPKIRT
4921	35289	A	4962	1	1132	

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4922	35290	A	4963	1170	1352	RNLPDAAAGQSCAGEIRLYRQQT QRSRLQRWLHLACFRRCNLHR RELDATA*QHVRSRWR
4923	35291	A	4964	1	312	MRKLTALFVASTLALGAANLA HAADTTTAAAPADAKPMMHHK GKFGPHQDMMFKDLNLTDQA KQQIREIMKGQRDQMKRPPLE ERRAMHDIIASDTFDKVKA EA
4924	35292	A	4965	3	205	KDHIKGVLEAQNSLSTQVSLFF *SFFG*NSNMRLIQIYRSL/CTK AI*LMNFKRHK NQLVINYLRSR
4925	35293	A	4966	1	915	MTGVATARAGRLRRPLSVGQV PPFARLWKGVQTVERHMLANI GTGSQHPGCGFQLINQNSVIVF AAGEVNGFTSGDVQCLKMRSG DMNDIQRQRLLPDGNKFGEIQ TTIREYYKHYANKLEDLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIEAVVNSLPTKKSPGPE RLTAEFYQRYKEELVPFLKLF QTTEKEGLLPNSFYEASVLLIPK PGKDDTTKENFRPISLMNIDVKI LNKILANRIQQHIKKLIHNNQV GFIIIGVQGWFNICKSTNVIYHV NRTNDKNHIIISIDTEKAFD
4926	35294	A	4967	1	1338	

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4927	35295	A	4968	1	1928	PPLVIHRQTGSGEDLQQTPTDL QLRLVTIRRRKTNKQKGGPHQNP ISSRRHEITKIRAELEKETETQKTL QKKSMNPRSWFFERINKIDRL ARLIKKKREKNQIDAIAKNDKW DITHRIPTEJETIAREYKHLTY NKLLENLEEMDKFLDTYTLPR LNQEEVESLAHRLITGSEIEAITN SLTVIKKSPGPDGFVAEFYQRY KEELVPFLLKLFQSIEKEGILPNS FYEASIIISKPGRDTTKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHHQVGFPGMQGWFNIL KSNVVIHHNRTKDKNHMHISIEA EKAFDKIQQPFMLKTLNKL GID GTYLTYLKIIRAVYEKPTANIIL NGQKLEAFPLKTGTTRQGCPLSP LLFNVLVVLVGLVGAIRQEKEIG IQLGKEDVKLSLFADDMIVYLE NPVSAQNLLKLISNPFSEVSGYK INVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKT LNQKFSYWFRVNVKHYHRTFP LKETEFTIATLYNGASPRTAP KSTGTNGHQASGLPRF*RIAFCS ALVKSRRKLYQGYLPGQTD RR EEGVSWCPGGP
4928	35296	A	4969	2	237	QPVEDTWLSTPAAPMVDSL LIAR VRVMARGNAITLPVCGRDVK/F TLEVLRGDSVEKTSRVW/S GIET YQELVTEDALDDL
4929	35297	A	4970	1	1752	
4930	35298	A	4971	1	723	
4931	35299	A	4972	1	1701	
4932	35300	A	4973	1	1446	
4933	35301	A	4974	1	403	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEAKGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGLRLRAEDVFPVPV GVAAHKG/LALKGLRVLLVEV RHRV
4934	35302	A	4975	1	1374	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
4935	35303	A	4976	1	2259	MKLMETLNQCINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPVI GVA AHKGGVYKTSVSVHLAQ DLAL/KGLRVLLVEVHKRWS*N DEGYRHCTV***HPEARKITRR WRIGEADLVGVSSQAIRDAEK AGRLPHDPMEIRGRVEQRILVIQ LNKLII CVMCLVRDCDVLKTYF HR*SGLLPIKVAFTKP/HVSVHL AQDLAL KGLRVLLVEEPPSAPN LGIGTINVVCAADVLIVPTPAEL FDYTSALQFFDMLRDLLKNVD LKGFE PDVRILLTKYSNSNGSQ SPWMEEQIRDAWGSVMVKNV VRETDEVGKAAPMVDSL IARV GVMARGNAITLPVCGRDVKFT LEVLRGDSVEKTSRCDNLKTCH TSHGSVMAETA VINHKKRKNS PRIVQSN DLTEAAYSLSRDQKR MLYLFVDQIRKSDGTLQEHDI CEIHVAKYAEIFGLTSAEASKDI RQALKSFAGKEVVFYRPEEDA GDEKGYESFPWFIKRAHSPSRG LYSVHINPYLIPFFIGLQNRFTQF RLSETKEITNPYAMRLYESLCQ YHPLTIEKVMKPLITNTVTDEI ERANVFKMNGKWYLF TDSRGS KMTIDGINSNDIYMLGYVSNLS TGPYKPLNKTGLVLQMGLDPN
4936	35304	B	4977	1	1744	
4937	35305	A	4978	1	2367	
4938	35306	A	4979	1	1215	
4939	35307	A	4980	1	946	MKLMETLNQCINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPVI GVA AHKGGVYKTSVSVHLAQ DLAL KGLRVLLVEGNDPQGT A SMYHGWV PDLHIHAEDTL L PF YLGEKDDVTYAIKPTCWPGLDI IPSCALAHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVL I VPTPAELFDYTSALQFFDMLRD LLKNVDLKGQA PCMKVLTMS SSSAPSPWML
4940	35308	A	4981	1	1572	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4941	35309	A	4982	1	1617	
4942	35310	A	4983	1	550	
4943	35311	A	4984	1	3818	
4944	35312	A	4985	607	3777	
4945	35313	A	4986	671	3091	ARCQRPVGRPVDDLRLCLPRAT TPAPSPAPGLVVRRLAAPVPAA APVPAAPVPAAPVPAAPVPAAPV AAAPVPAAPVPAAPVPAAPVPA VPAAPVPAAPVPAAPVPAAPVPA AAPVPAAPVPAAPVPAAPVPAAP VPRFQSPNQASTSDSPHIGQLP HQTVPISDSFHTGQSPHRTDSTP DSPHTGQLPHRTVPTPD/ELPHR TVPTPDSFHTRQSPHQTASTPDS PHIGQLPHQTVPIQDSFHTRQSP HQTASTQDSPHHTGQSPHRTVPT PDSFHTRQSPYRTASTPDSPHIG QLAHRVTPDPSFHTGQSPHRT DSTPDSPHTRQLPHQTVPIQDSF HTGQSPYRTASTPDSPHTRQLP HQTASTPDSPHTRQSPHRTVPT PDSSPHQTVSTPDSPHTRQLPH QTVPTPDSFHTRQSPHQTVPPT DSPHTRQLPHQTASTPDSPTPD SPHTGQSPHQFPHQTVPTADSP HTRQLPHQTVPTADSPTPDSFH TRHSPHQTASTPDSPHIGQLPHR TVPTPDSFHTRQSPHQTASTPDT PHTRQLPQQTVPPTADSPTPDSF HTRQSPHQTVPPTDPSHTRQSP HRTVPTPDSFHTRQYYPQRTVPT QTASTPGSPHTKQSPHQTVPPT DCPHTGQSPYQTVSTPDSPHTR HSPHQTASTPDSPHIGQLPHQT ASTLDSPHIGRHPRQMAPTPESP HARQLPCQMAPTPDPTLDGPH
4946	35314	B	4987	1	891	
4947	35315	A	4988	157	1990	
4948	35316	B	4989	1	2157	
4949	35317	A	4990	1	378	MSIKGTLYLKVIAIYDKPTASSI LNGENLKAFLRLTGTRQGCLPY KINVYKSVALLYTTNDQGENQI NNSTPYTTAPRKIKYIGIYLTKE VKDLYKENYKTLLEKVIDDT/R WKHIPCWMGRINIV
4950	35318	A	4991	1	392	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
4951	35319	A	4992	3	1570	ETDFAFVGGAGVQWCDLSSPQ PLPPWVQAILLPQPPRGCCWSG IPKWSGISDEVQVWKNCKLDL AAATGKNCLGQGEALLTQMR TGNQREVSDDWEEFVYLRSRN PLMVNSNYMMDFLYVTPTPL QAAAGNAVHALLLYRHLNR QEIPVVRGPQWVRDGGVVLWP LGHVGPGRQLTAHGFIQTLLM GMRPLCSAQYEKIFNTTRIPGV QKDYIRHLHDSQHVAVFHRGR FFRMGTHSRNLLSPRALEQQF QRILDDPSPACPHHEHLAALTA APRGTWAVQVRLSLKTAQAEAL EAVEGAFFVSLDAPPAIGLTL EDPAASLDAYAHALLAGRGHD RWFVDKSFSLIVFSGKGLSV EHSWADCPISGHMWEFTLATE CFQLGYSTDGHCKGHPDPTLPQ PQRLQWALPDHHSISLALRG AKILSENVDCHVVPFSLFGKFI RRCHLSLDSFIQIALQLAHFRDR GQFCLTYESAMTRLFLEGRTE VRSCTREACNFVRAMEDKKKT
4952	35320	A	4993	1	1027	MPAKSPGDVLTGTDNIKIDVFK QTNQKSHTEKPYCEPCGKAF SEKSRRLRKHQRTHTEKPYKC DGCDKAFSAKSLRIHQRTHTG EKPFECEHCGKSFNYKSILIVHQ RTHTEKPFECNECGKSFHMS GLRNHRRTHTEKPYKCECG KAFKLKSGLRKHHRTHTEKPY YKCNQCGKAFGQKSLRGHH RIHSGEKPYKCNHCGEAFSQKS NLRVHHRTHTEKPYQCECG KTFRQKSNLRGHQRTHSGEKP YECNECGKAFSEKSVLRKHQR THTEKPYNCNQCCEAFSQKS NLRVHQRTHTEKPYKCDKCG RTFSQKSLREHQKAHPGD
4953	35321	A	4994	154	331	IPAAATCMGSLGGE*ETPGLWA RRSVKSRGLFPGLPSPRASVRS LLLLPAWAAFLGIVDTRPTAW RAFPWTLFLSVFCQFLDFPETS LSQKSLDTPSF

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4954	35322	A	4995	657	1455	PEPKAAVAPPPESPLPAGDSEC CLQPGHLLPASPRLPRPQAAS LAHRPEKSA PGADCPSGRR/GR PWTCGGLSGPAAAPRPCPLAPA FAPAFALGAQR/GPGPEQGGH ERQAERPGRRRRTRAYSARIY LPVAAEWPMGPGPEPGAGGRR RGEVPGGAQRSPARRRRGGPA AVSSGGRGVGGLRGAVLFQHP EQQRPVGLAGLGAQQAHPV WRYGPLST/PPALGPAAARGP\ GRRILFPFSFSPSAGAPGAASRP SPRRSP
4955	35323	A	4996	1	415	
4956	35324	B	4997	8	211	
4957	35325	A	4998	1	563	MDPNHEEIPDLPEKEFRRVKSK NHMTISIDA EKA FDN IQH R F M I K T L S K I G I Q G T H F N I K A I Y D K P T A S I I L N G E N L K A F P L R T G T S I V L E V L A R A I R R E K E I K G I Q I G K E E V K L L L F A D D M I V Y L E N P K D S Y R K L L E Q I K E F S K V S R Y K I N V Q K S I A L L Y A N S D Q A E N Q I N N P T S F T I A A K N K I K
4958	35326	A	4999	667	960	
4959	35327	A	5000	317	1157	EFRMDPAIALVLALSLTVPKLT VPDSPLRLYRSFCTSACTSNLV VHFA*KEK WPDV*LYTDSWAV ANGLAGWSGTWKKHDWKIDD NEIWGRGMWIDLSEWSKT VKIF VSHESAHHIT*KSSAEEDFNQ VDRMIHSVDTTRPLSPATPVITQ WAHEQSGHGD RDGGYAWAQQ HGLPLTKADLAMVTAECPIQQ QRPTLSP*YGTIPRGDQPA TW W QVDYIGPLSSWKGQRFLVTGID/ TSGYEFAYPARSSANSTIRGLM ECLIIHHHGIPHSIASNQLYS
4960	35328	A	5001	2	15246	

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4961	35329	A	5002	1	951	MALALNRYL/CLAVLPLITKCA PLFAG/TEHRAIMVDSMLHTVY R/LSRGRSLTKAQRDVIED/CLM SLCRLRLRLVFDVPIILNEFA/K MPLKLLTNHYERCWKY/YCLPT GWANFGVTSEEE/LHLTRKLFW GIFDSLAK/KKY/DPELYRMAM PCLCAIAG/ALPPDYVDASYSK AE/KKATVDAEGNFDPRPVET/L NV/IIPEKLSDFINKFAEY/HEK WAFDK/DKEIYRWPIKESLKAM /AWEWTIEKAREDLDPREGYN PQPPDLASV/ILSRELQAMAEQ LAENYHN/TWGRKKKQLEAK GGGTHPLLVP/YDTLTAKEKAR DREKAQSY
4962	35330	A	5003	273	478	
4963	35331	A	5004	2	622	GAPRSLSEKERQLMGMINQLSS FREQLLHAHYEQKKLAASQIEK QRQHMKLGKQ/QEQIARQQQ RLIQQHKINLLQQIQQLYAA QLAAMQVSPGGKLPQPGNL GAAVSPSTIHTDKSTNSPPPKSK TCCLLLWEDEHSASIPVTNQI HLHLASSITDHGGKVIWERCLE ESGKGVTFPDPWSPRWGRIPPE GSKEGFTKE
4964	35332	A	5005	3	512	
4965	35333	A	5006	1	642	MHAQTYAHTDTRAQCTSMK QVSLKPTTEAHKKERKPKPG KYICQYCSRPC/AKPSVLQKH SHTGYGCEMYPHGLEMERIPG EEFEPTGESTDSEETSATSG HPAELSPRPKQPLSSGLYSSGS HSSSHERCSLSQSTASQLEDPP PFVEPSSEHPLSHKPEDTHTIKQ KLALRLSERKKHQVIDRLSGSI LAGLSWQLLPQGEAL
4966	35334	A	5007	341	1020	TLNRRQGCCGSLWTRNSGILL FEISRPTYLPILLFLVKR/HKL KMSVLNMVVRHDGPGSTESAKA KEELIFRCRSHFRASPLFSQHA AADKHKFQRLTADMALAVTV YAPTTFPPSLLLFKQKSNGMH NLIATGHLLLVDPNRMVIRRV LSDPPFKICTKMAVVCYMFN EDVQWFKPVELRTKWSRRGHI QEPSGTHGRMKCSFDRKLKSQ NTELMNLYK

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4967	35335	A	5008	1	847	EKAQAELELAGFKDPAPGHTE ESMTHDKTKIPCKSPPELVDT ATSSKKWPRACGQKVEVKEEL LAVGKLTQTSGETTHTNKEPEG EGKGMKAFKQPAKQKLDPEN TGSRRLLPRVPKEKAQPLEDLAS FQELSQTGHTTELANGADSFT SAPKQAPDSGKPLKISRRVLQA PKVEPVGDLVGTGR/D/PVKSQSK SNTSLPPLPFKRGGCKDGSVTG TKRPHCMPAPEEIEELPASKKQ R/VVAPVRVGKSPPELVIMKRS LRTSAKRIEPAEDLNSNMKTNN
4968	35336	A	5009	9	1094	IRHEEESMTDDKTTIPCKSPPEL EDTATSSKRRPRTAQQKVEVKE ELLAVGKLTQTSGETTHTDKEP VGEKGVTGKAFKQPAKRKLDA EDVIGSRRQPRAPKEKAQPLED LASFQELSQTGHTTELANGAA DSFTSAPKQTPDSGKPLKISRRV LRAPKVEPVGDVVSTRDPVKS QSKSNTSLPPLPFKRGGCKDGS VTGTKRLRCMPAPEEIEELPTV SKKQRVAPRARGKSSEPVVIM KRSRLRTSAKRIEPAEELNSND MKTNKEEHKLQDSVPENKGI SLRSRRQNKTEAEQQITEVFVLA ERIEINRNEKKPMKTSPEMDIQNP DDGARKPIPRDKVTENKRCRLRS ARQNESSQP
4969	35337	A	5010	1	459	MAKPWRALCILLRSLDSFLQLS ASLTCFGFMHNTYKNRPWGV LRSSTERSPRKGTAGDMRAGGRF NAPLIGQDLLFKEHFASKALDT CTNIARSAKTQGGPVAAIILLL AFGPCIFNLRVVFVSSRIKAIKL QM/RLTIYRGPLDRPAGPSTGL
4970	35338	B	5011	1	687	
4971	35339	C	5012	194	418	
4972	35340	A	5013	17	396	
4973	35341	A	5014	1	70	

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4974	35342	A	5015	1	994	MGFVKVVKNKAYFKRYQVKF RRRREGKTDYYARKRLVIQDK NKYNTPKYRMIVRVTNRDJICQ IAYARIEGIMIVCAAYAPELPK YGVKIVGLTNYAAAYCTGLLA GPAGFFHRFGMDKFYEG/QVEV TGDEYNVESIDGGQGLHPAY WDA RPLRPTSPLAIKVFWLP*R GA\VDGGLVLFPPQYPNRPFWL WIPESQGNLNARRYHREGTIHG PRIVAGLHAPTLMEDEDA\YK KQFVRQYVKNSVTPD\MMEE MYKKAHAARIAENPVYEKKPK KEV\KRKRWNR\PKMSLAQKK DRVAQKKASPL\RAQERAAEKL NQTIIFYKDFSDIAN
4975	35343	C	5016	27	308	
4976	35344	C	5017	68	307	
4977	35345	A	5018	388	1485	
4978	35346	A	5019	3	1940	RDRMILLKMEQEIIDFIADNNN HYKKFPQMSSYQRMVLVHRVA AYFGLDHNVDQTKSVIINKTS STRIPEQRFCHEHLKDEKGEESQ KRFLKRDNSSIDKEDNQSVCS QESLFVENSRLLEDNSNICNETYK KRQLFRGNRDGSGRTSGSRQSS SENELKWSHDQRAWSSTDSDS SNRNLKAMTKTASFGGITVLT RGDSTSSTRSTGKLSKAGSESS SAGSSGSLSRTHPPLQSTPLVAG VAAGSPGCVPIYPENGIGGQVA PSSTSYILLPLEAATGIPPGSILL NPHTGQPFVNPDGTPAIYNPPTS QQPLRSAMVGQSQQQPPQQQP SPQPQQQVQPPQPMAGPLVT QSIPAKKELNAFRVRNQEQRDT GTLHEGSGKISRMVLGWEPLSP YAPDRDDVATQFGQMTLSRQS SGETPEPPSPGVYPSLMPQPAQ QPSYVIASITGQLPTGGFSGGP PISQVQLQPPSPQGFVQPPPA QMPVYYYPSGQYPTSTTQQYR PMAVPQYNAQRSSQMPQAAQ QAVLEVLSPVSTVMPKLAVAL VMAGFRLRLLESVLLQALW WSDHLSSFSELLCRLPDVLPES LLPLEYDHQKDAQGGQDYLTCM VLVTLLESPTGIQEDDSNEISVI

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4979	35347	A	5020	3	1353	GDAYALVLRVTLYCGKCHVNE VVLAIPFEILSTESIQDQI.PYSV MLMSMLAITEGRRSFVSVENA CSNYVTTVQVKEVNQMHSFN SCNAIHPRDHILEISGIPHTLTQ VEELEDASIQMSQTL.LLLIEHDP VSRSPAQLRLDAWLSPHTQNA GHPHALSTLDTKDNLEGLTRRC SLRLSNSISKSPSSPKPEPLLS RDISCWESLCCSSTYSKQNRSC DLIHGEVLGKGFFGAIKVTHK ATGKVLVMKELMRCDEENQK TFLTEVKVTLPSNLLPPGHDLL QTGAREQTGILKTGGLSVPGGA GHAAACRAGGVGPHCEHAVRP DPRLTPLALAQPPAGGCSTASIA PLFSIPAVSRVFRASRGLAACLE AEQAGRILTCEVCKLVVGLSL DSQQQLSSVLCGWLCCLSCPQL WSLNRHPQHHLVEMQNLKS HPRPGETESAL
4980	35348	A	5021	1	588	MEYPDGGSTLDLLEPGPLDETQ IITILREILKGLDYLHSEKKIHRG VKAANVLLSEHCEVKLVDFGM AGQLADTQTKRNTFVGTPFWI APENNPTLEENYSKPLKEFVE ACLNKELSFRTAKELLKHKFIL RDTKKTSYLTEIDRYKRWRA KQSQEDSSSEDSNSETDGGDSIG GSDSGDWIFTIQEKDPKNL
4981	35349	A	5022	1	1380	GPRASPPRARRGPAVPSQEVA VLSAMAHSPVQSLPGMQNLK ADPEELFTKLEKIGKSGFGEVF KGIDNRTQKVVAIKIIDLEAEAD EIEDIQEITVLSQCDSPYVTKY YGSYLKDKTLWIIMEYLGGS ALDLEPGPLDETQIATILREILK GLDYLHSEKKIHRDIKAANVLL SEHGEVKLADFGVAGQLTDTQI KRNTFVGTPFWWMVPEVIKQAG YDSKADIWSLGITAIELARGEPP HSELHPMKVLFIPKNNPPTLE GNYSKPLKEFVEACLNKPSFIP TAKELLKHKFILRNAKIKTSYLT ELIDRYKRWKAQESHDDSSSE DSDAEITDQASGGSDSGDWIF TIREKDPKNLENGALQPSDLDR NKMKDIPKRPSQWLSTIISPLF AELKEKSQACGGELGGPLKEL RGAIFYLAEACPGISDTMVAQL VQRLQRYSLSGGGTSSH

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4982	35350	A	5023	1	346	MAGEKVEKPDTKKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGGDKNGGTQVF QIITYSSYTQKVQLPKSTLKQRQ GPCPQ GAL
4983	35351	A	5024	67	599	SAKSEMAKEKVEKPDTKKK PEAKKVDAGGKVKKGNLKA KPKKGKPHCSRNPVLVRGIGRY SRSAMYSRKAMYKRKYSAAK SKVEKKKKEKVLRLNLLQNQVG GDKNGGTRVGLNFRKMPRIY PTEADVPRKLLSHGQKNPFSQH V/REKLASITPGTILILTGRHR GKR VVFLN
4984	35352	A	5025	101	202	PVPGTSSCTDRYHYKKH**KIN TKLVSKYILNM
4985	35353	A	5026	2	562	LRTVPDLPGRFRFRAMRTGQRR* PELPPDMNSLEQAEDLKAFERR LTEYIHCLQPATGRWRMLLIVV SVCTATGAWNWLIDPETQKVS FFTSLWNHPFFTISCITLIGLFFA GIHKRVVAPSIIAARCRTVLA EY NMSCDDTGKLLKPRPHVQ*QS SLIVMGLRIAFLRISDTAKSHKG FLRLDM

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4986	35354	A	5027	1	2090	MGAVFFMLFSWWITSGHIQLLC TRRRATVSTHQEFVVTVPFSL GLVVSGLDADTAMPGSAAEEQ FQWQSQDGGKDIEDELTTGLEL VDSICRSLQESGILDPQDYSTGE RVIHFGKTLGLSSEDYSIMEKG QMVKEVTVTQVSVLKANETM ASALCGEQEGHDDPLLLTVQMS TGNHYIKDNLFPVWVKWPSLLS QSALQLNSKPEGSFYYPASYHS NQTALGETTPSQLPARGTOAR ATGQSFSGQTTSRAGHLAGEPEP APPPPPPPREPFAPSLGSAPHLPD APPAALAAALYSSSTLPAPPP GGSPLAAPGGSPTKLQRGGSA PEGATYAAPRGSSPKQSPSRLA KSYSTSSPINIVVSSAGLSPIRV SPPTVQSTISSSPHQLSSTIGTY ATLSPTKRLVHASEQYSKHSQE LYATATLQRPGLAAGSRASYS SQHGLGPELRLQSPHHIDPI YEDRVYQKPPMRSLSQSQGDP LPPAHTGTYRTSTAPSSPGVDS VPLQRTGSGHGPQNAATAATFQ RASAAAGPASNYADPYRQLQY CPSVESPYKSGPALPPEGTLAR SPSIDSIQKDPKSPYILCDGGNPF CALVYRPPSSRERASSL/LKSMCY Q*NRLYPKFRRLVLSGFEGMQ RRFCASKGIKGRFCGSSLEQDC EHGGQHPCYPKLVPTLWNP HQ REGNQKNSE RV
4987	35355	A	5028	123	3825	
4988	35356	A	5029	1	593	MQVCSSGGRIILRVSGTERQLRR EGGRFCLGRGVRLREGGALR APFTAPSLTALPPDIVDIKPAN MEDLTVTTASESHPHHCNLFV YSSSKGFLRLCDMRAAALCDK HSKHPCDDIGPIQIIGHLRTSR GWMHLPALQSTFCRCRMDEQNL RAFLAPRLCDFSTSQPQGSPEQ PVMSGLISPWTKPSRSSVFSM
4989	35357	A	5030	1	894	

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4990	35358	A	5031	1	3115	RQICSMASELGARDDGGCTELA KPLYLQYLERALRLDHLRQTS AIFNRNISSDDSEGLDDSNPLL PQSGDPLIQVKEEPPNSLLGETS GAGSSGMLNTYSLNGVLQSES KCDKGNLYNFSKLLKSRKWLK SILLSDESSEADSQSEDDDEEEL NLSREELHNMLRLHKYKKLIQ NKYSKDKELQQYQYYSAGLLS TYDPFYEQQRHLLGPKKKFKF EEKKLKAKLKVKKKRRRDEE LSSEESPRHHHQTKV
4991	35359	A	5032	1	1522	MVAQASGQTIREAEVGGSLTA QEVEATSILLSDESSEADSQSED DDEEELNLSREELHNMLRLHK YKKLHQNKYSKDKWMSQLA ALNYLLAGGDEQKLLDLSYSP QNRQPAKAKAHNNNNNNNN NNNNHNKNPKRLDERELLY STATQSFDTNTRSFDEDAKES RAAALRAANKSGTGFESYSL ANPSIRAGEDIPOPTIFNGKLG YQLKGMNWLANLYEQRLERL RFLQLEQEHTCPQEGRAERLRG QPLKLWALLHFIMPTLFDShEE FNEWFSKDIESHAENKSAIDET KLKKVKKKRRRDEELSSEESPR RHHHQTKVFAKFSHDAPPGT KKKHLISIEQLNARRRKVWLSIV KKELPKKTLTYQDAPFHVVITS NQLVVQDVYFQVRKWQYMY LDEAQAALKSSSLTRSNARYPL VSSQRKIHDQVVTDDKSSKMDP KEEEYIPAKHEMENTKLQFYLS AIGEKQVRWKILLQFQCRNRL LLTGTPIONTMAE
4992	35360	A	5033	1	974	MGFHHIVARAGLELLTSGMCCY FAQDLRPEQSIKASLQRIILRKY EKCGHHNLQKKGKYKSVDEYK VHKGSYNGFNQCLTTTQSKIFQ CDKYVVKDFHKFSNSNRHMTKE NPFKCKECKSFCVLSHLTQHK RIHTTVNSYKLEECGKAFFNVSS TLSQHMRHTGQKHYYCQGEM GIAFNKSSHLNTHKIIHTGEKSY KREECGKAFFNISHLTTHKIIHT GENAYKCKECKGAFFNQSSLT RHKIIHAGEKPYICEHCGRFNL QSSNLTCHKRIHTGDKPYKCEE CGKAFFNVSSLTQHKRIQQQQQ QTIKQTKNLLNNNNKKLVV

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4993	35361	B	5034	22	684	
4994	35362	A	5035	1	1338	
4995	35363	A	5036	1	596	MGMTDMGSKSKKSQPPSPFP GGAPPPAIGAPAGRERPPGTGD PFNQRPDNLKTCHTSHGSM AETAVINHKRRKNSPRIVQSND LTEAAYSLSRDQKRMPLYLFD QIRKSDGTLQEHGICEIHVAK YAEIFGLTSAEASKDIRQALKSF AGKEVVFYRPGEDAGHEKGYE SFPW/FIKRSPE*RRGKFPPTQM GQD
4996	35364	A	5037	787	1692	
4997	35365	A	5038	289	1338	
4998	35366	A	5039	982	1347	
4999	35367	A	5040	1	780	
5000	35368	B	5041	148	334	
5001	35369	A	5042	2	545	
5002	35370	A	5043	1	732	
5003	35371	A	5044	1	1110	
5004	35372	A	5045	1	1170	
5005	35373	A	5046	1	870	
5006	35374	A	5047	1	1254	
5007	35375	A	5048	614	1236	TARVAAARRRCQWGSAGCS ALTLPRTSSLTLTETPIVQTRM VVRCPATSLPSQWRSCPSSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVTDRTVRTWIGEA VAAAAAD GVTFSPVPTPHTRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
5008	35376	B	5049	1	1281	
5009	35377	A	5050	2	893	
5010	35378	A	5051	1	1416	
5011	35379	B	5052	49	768	
5012	35380	A	5053	1	792	
5013	35381	C	5054	1	1461	
5014	35382	A	5055	887	1203	RPEKAR/IWGVTDRTVTRTWIGR AVAAAAADGVTFSPVPPTPHTR RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYVYTKVFALDVAAR RHRVQFAMPESDAVAMLKQLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5015	35383	A	5056	740	1431	CCQTLPVFHPHPHSHLGPRPCPP TH/HLPSEHRSFLFEAAACHSDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRHRLHR PQQSPPLGIPHPSLLLTAQVFIR DKLMERRNRRTRTEKARIWE VTDRTVRTWIGEA VAAAAADG VTFSPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
5016	35384	A	5057	1040	1477	
5017	35385	A	5058	1	1422	
5018	35386	B	5059	1	1404	
5019	35387	A	5060	353	870	AWSSPRSRCPLHRSRTPSLPRVEG QAHIGPGL/HRYQQGHQDLFIL RSDLPSQVFIRDKLMERRNRRTR GRTEKARIWEVTDRTVRTWIGE A VAAAAADGVTFSPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
5020	35388	B	5061	1	1612	
5021	35389	A	5062	2	429	WGHWASPRLWWAWGSPGPAG LKPPGTVAASTGFSQWLLYIETI SRTPELELKNSKVRKDVLS/R GPHSLYLVDQAQLEHAMEIAK VSVQALQAYRAPPRMEQANP KTPPDANLYKKGSPSPRRANT TRLGSRATKTIHPDS
5022	35390	A	5063	508	1007	PPLAQKQAVASQSHSPCGGFHR RWFMRMTGEIMKIITCFKLVP EEQDIVVTPEYTLNFDNADAKI SQFDLNAIEAASQLATDDDEIA ALTVGGSLQNSKVRKDVLSR GPHSLYLVDQAQLEHALPLDT AKALAAIEKIGFDLLIWTSSRI QAVALASPLSNT

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5023	35391	A	5064	1	1670	MNIEFFDPPIRVSGTLNRNIQH PFHLTGIRYCIDERQRTVNDVL QAHAGRVLQYQLPAPATATFR CQSRNRTENPQFLVCQWAGED QITQLLQEQWRVLIWMIFRTHN HMAGPRRWFRMLTGEIMKIIT CFKLVP EEQDIVVTPEYTLNFD NADAKISQFDLNAIEAASQLAT DDDEIAA/VLTVGSSLLQNSKVR KDVLSRGP HSLYLVQDAQLEH ALPLDTAKALAAALEKIGFDLL IFVKGTCLVLLVAFGLVTTTHFQ PCLFGVQNGEQETVQILLVGVV GGMERAERIIPFTLAINNQPTT RLTKTIAQGMPIIQRNIPNRIS LQPAPTPRHSANPATMQPHAQ ATPTPKPHTRITPTPRPPHQRSA TPGTQRTPTPGPQTARDRAKPK DHTRPQT AHTAHTSNDPQQR HRTQRHTNKQHPHPAPRLPT LPQNNKRQKPAESDTRKHHTP HMRQPTAHAETTARNTQAAQH CHTQNT PQANRHATGDRPEHH QARDRTRIDPKPNPDRTITTGHT KGTTYAHKHPTLATHHMTRPT TGHRRGTHH
5024	35392	A	5065	548	924	GLLRPRFSVNSPIIFNTWLLSAN SINWR*YGFMP SLLILL*LNPM GRYSGASLVSRMASTTLPGHS IAMRQPVCGIFALTRAISI/AM WDFHVEDFMPERMA LNLVLNS AI*LPKIFPARWMKFS
5025	35393	A	5066	33	424	CRFDEFWCDA/HAIFVAPTLY AYDFYADKTLVPLTDALANTW QKQFPLDYKGRLWGSVAFVI GSALTGKLVTFDYRVILALLT LGVASMLLGLIRPTIQPGASL QQUESTGWSAWLALVRQNWRF LA
5026	35394	B	5067	1	265	
5027	35395	A	5068	142	609	CLFRQVSAPHITRVCITRSAATI QTIDLNNLDTGD*LQAPFPVW LISPGPFHPTPSVTRVPLEKEIRT FAQLSVLHGINAEFFDKPLFS SLVLTLRDEGYISDSGDAEPAE TMKVYQLQTNIVIIHKCFKAGF TLAVGNQFLLINKQRASHQN

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5028	35396	A	5069	983	1387	LVWKVIPWRPAWKITLCLVNS CRRACLFAPAT*TANRLQAVC/ WLQSANPSINRGTLKESRTVA QRLSVLHGINAPEFFDKAVFSSL VLTLDREGYISDSGDAEPAETM KVYQLLAELITSDVRLTIESATQ GEG
5029	35397	A	5070	1	1815	
5030	35398	C	5071	1	354	
5031	35399	A	5072	1	678	MTDKQQGEKQKQKTEDKTKT KQKQRKNKTDKRRKTKTERNT QRTPERQTNTNQTRTKQ/RRPD TGVQTADTRQDTSARRLMRQP RSAAA WMAALRGARDPKLITM VPHSKISRSIVRKGLPMTETQRR TETSKNYRPREQQTRNRQQQD PRQQRITVQTHQQEERRETKDN NTHTKPHETLARRHRRHNIHAL AAADLVIEAASEVWKSCKRSL HSWRKFAPTNIDH
5032	35400	A	5073	93	729	SADPRNRDRTRAAKTRDAGK TDC*NL*THIETPDGDRYSRAG SCGPG/PLKRRNLNWKSKKRS HSWRKFARHKRY*PLTLRQSLY TAIAAEIKNPERVAGLHFFNPAP VMKLVEVVSGLATAAEVVEQL CELTLSWGKQPVRCHSTPGFIV NRVARPYSEAWRALEEQVAA PEVIDAALRDGAGFPMGPLELT GPDWAGPPFCCHLFGV
5033	35401	A	5074	145	1038	SILRLRQKRKQLTAYDFADNCD KALY*RNHRLREILALVCAHD RQKK/YLPSLAGFL*LKNEINRL SVRGW/SRRRSFSVR*/PFTNTD RARSHFYQFVIIDELQSLFQSHA DRRNQNNGFVSTGSTHVQGL TGQAVYSQVVRAAMNTDNLTF VNFCTVTEQLTAILQTEQRER DRFTLTVRDQYAVLTLTHTFRT YVVVVAEGGVQQTSTGSHGHE LRTEANQTTAWDHVVETYAAF TVWIHFVQVALTFAQLRHVRT LMLFFNVQSHVFIRLLFTTVDF EDNFRGTGYRFETFTTH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5034	35402	A	5075	39	4329	YAPATFSAATQPTPKKINNVPV RNSAMHWQTRIQQAQNGYWL EREQWLA VGEQWFWRMWWSG PHRAAAGRLCHHHGNDATWH RG*FHLCFRPCV**RIEQPQEGY AIIMETTPPGTG VNFVFSDDPAF DKGYAFDFFCLEPMSHAPDDH HRPEGGDLIALAPGESTTSEMS LRVPVANCAVTTASLDSYYGE AMAIGERAPVALLDFAASARL AVGEALTNIATQIGDIKRIKLS ANWMAAAGHPGEDAGLYEA
5035	35403	A	5076	1	625	MRASGTDEAVVLVPPIRMTLEQ ALEFIDDDDELVEGAAAFAFEAL MMGSGRDREIRYGE GSPWFDI VLP CGGGITLTLHKLRSAQPLL AVLNRLEQKKPVGLRYDPQAQ SLVCLPTQTRTGWNLNGFEASI THRALRTSRYGQYYCQGPR LTIRRTVIMTGSSDPHDTTDSNN DRVLGPSRYDGQYYCQGPRTL TIRRTVIMTGS
5036	35404	A	5077	3	516	ATLSCEVLENLAASPVVTTLE YTLFDGERV VHS SAIDHLAIEK LTSASLAFTVEQPQWSAESPY LYHLVMTLKDANGNVLEVVPQ RVGFRDIKVRDGLFWINRYV MLHGVNRHNDHRKRRGVGM DRVEKDLQMLMKQHNINSVRNA HYRKRNRKEVRTKKKIESIEEK
5037	35405	A	5078	3	678	ASYCYCTRNDELVA VCD SRLS QRQALAEYGNASVWDDPQA MLLAVKPDVVSVCSPNRFHYE HTLMALEAGCHVIAQAREM/CD TARKLGKVLAYDFHHRFALDT QQLREQVTNGVLGEIYVTAR ALRRCGVPGWVFTNKLQGG GPLIDIGHMLDAAVMYVLGFPR /SVEDSLCGTIELHSGCILWLETS FALNIREHAIMNIRFCGDKAGA SVFPAHIYTTATQR
5038	35406	A	5079	2	294	YSFMV/PIFGRRRWTVFSTAIL/I PCVWLGIAVQNPNT/PFGIFVIA LLCGFAGAN/FASSMGNISFFFP KAKQGA/PVFAF/LGVNVPQA DGSVMSLAMPH
5039	35407	A	5080	1	834	
5040	35408	A	5081	2	135	QYASALVSTAIALLVCLAFLY PAANSEIHLGLVSIFWGPDPG

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5041	35409	A	5082	1	324	MQGGYNIHPLDALDDAKLAPI AAKALSHTLLMFDNFYDVEEK AKRGNEYA/QVMQSWAD/AEW FLNRPALAEKLTVTVFVKTGET NTDDLSPAPDAWSRPDIPLHAL GC
5042	35410	A	5083	1	866	MGLAQAKLLIEAPVNGGRNYN GPKVAKFLVGGASLNDVYLHQ HDKYRYDRYHLIRNREKTHIM PEWVTQNMNGRGVNRLLDDVN RPKSPEIKNDIRLFRQELRDAAY HFQGDADNDQLSVTPLVGLGK SSLLIKITIFHRMRWAEQNLSICS SSFNRPAlFVRNIIQLREGKKV EITVGDKEHENDFYIPEDEPFKIIG ALPYLYEINLRRFLSRLQYYVN TDQLVVRVWKEDDNITYHLAK GWGWDKWMVITGINKLDPR AWRLDLENAILIHDPLQLELAPQ REKELE
5043	35411	A	5084	1	3483	VMFFFLPGLLMASWATRTPAIR DILSVSIAEMGGVLFLGSIGSMS GIL/SLGVVSETLWDT*/CHSW RCPAH*SG**Y*/VLALWLTSP LFAVGLGVFGASFGSAEVAINV EGAAGEREMNKTLGLPMMHGF YSLGTLAGAGVGMALTAFGVP ATVHILLAAALVAQIAAWYKAL QEIQIPDFIPRAPQRMADVAK TLAGEGRHLAIEAPTGVGKTL SYLIPGIAIAREEQKTLVVSTAN VALQDQIYSKDLPL
5044	35412	A	5085	1	848	MLVGKVVVSEGA SFRTHGAVD TSKAYVSLNSGWTHIADITTTN QNTLLNLNLANLMSDANVIMMD EPVTRSSVTASAENITLTTNTL SGNGNFYMRDTMANHQSDQL NVTGQATAGDSLTLVTTGGGD AAFTLGNAGRVFDIGTYEYTL DNGNHSWSLAENRAQITPSTTD VLNMAAAQPLVFDAELDTVRE RLGSGVKGVSYDTAMWSSAINT RNNVTTDAGLRAQAIKTVHHR QNRLIHFSLNGSTFNVYRHFRR TKTCPKDAETNGKEQGRCQPE CQT
5045	35413	B	5086	75	1777	

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5046	35414	A	5087	1	860	MKAPGLPADQQFFADLFSGLV LNPQLLGRVWFASQPASLPVGS LCIDFPRLDIVLRGEYGNLEAK QORLVEGEMLFIPARAANLPVN NKPVMLLSLVFAPTWLGLSFY DSRTTSLHPARQIQLPASLQRG EGEAMLSALTLSRSPLEQNIQ PLVLSLLHLCGSVVNMPGNSQ PRGDFLYHSICTWVQDNYAQP LTRESVAQFFNITPNHLSKLFAQ HGTMRFIEYVRWVRMAKARMI LQKYHLSIHEVAQRCGFPDSY FCRVFRRQFGLTPGEYSARFQG
5047	35415	C	5088	86	601	
5048	35416	A	5089	1	870	
5049	35417	A	5090	305	625	VAPGDRHAFPLAPSGLSPELTLP QTQCCAQATVQGLEGRSWSQ SGTSSLSPWSHTSLRRRRKEEG EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEE/EEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEAKTQ
5050	35418	B	5091	1	552	
5051	35419	A	5092	2810	3117	LTLNSHMAPALIPILAMSAPMT PMKN/LSQVHAQGLVIRDLPLIA SNFRNTEDLSSYLKRHNIVAIA DIDTRKHAACAVPNTLVARGL RKHLKRVAAPQHWIAG

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5052	35420	A	5093	2	1902	LKYPMKRVGKRGEGKFERISW DEALDTISDNLRLKDYGNEA VHVLVYGTGVDGGNITNSNVPY RLMNSCGGLSRYGSYSTAQIS AAMSYMFGANDGNSPDDIANT KLVMFMGNNPAETRMSSGGGVT YYVEQARERSNARMIVIDPRYN DTAAGREDEWLPIRPGTDGAL ACAIAWVLITENMVDPFLDK YCVGYDEKTLPANAPRNAHYK AYILGEGPDGIAKTPewaakIT SIPAEKIIQLAREIGSAKPAYICQ GWGPQRHSNGEQTsRAIAMLS VLTGNVINGINGNSGVREGATG SAVGEEVFNMTSGYQEILTD\
5053	35421	A	5094	8	456	LPIPSNRYSISYPILAMSAPMTP MKN/LSQVHAQGLVIRDPLIAS WFRNTEDLSSYLKRHNIVAI\
5054	35422	A	5095	377	1228	DIDTRKLTLLREKGAQNGCIIA GDNPDAAALALEKARAFPGNG MDLAKEVTTAEAYSWTQGSW TLTGGLPEAKKEDELPHVVAY DFGAKRNILRMLVDRGRLTIV PAQTSaedVLKMNPDGIFLSNG PGDPAPCDYAITAIQKfLETDVP VFGICLGHQLLALASDVEKNVV MITAQNHGFAVDEATLPANLR VTHKS/LFDRYVTGHSSHR*TG\
5055	35423	A	5096	1	519	FSFQRHPEASPGPHDA/APLFD KQARGRLCPAKPGWSCP RPW QPTFC/GQCCLKVRPGVIGDHF GALKFDCPTGFRITCLGRITPLFL PSSPIWNGCIFPIPVPGDCGEG VQIRSLSCMVHSGSISHAAGR EDALCGEMPFDQSIKQLCSVP CPGDCHLTewSEWSTCELTCID GRSFETVGRQSRRTFIQS FEN QDSCPQVLETRPCTGGCSPQA RPAAIRQCIPACRKPF SYCTQGG VCGCEKGYTEIMKSNGLDYC MKVPGSEDKKADVKNLSGKNR PVNSKIHDIFKGWSLQPLDP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5056	35424	A	5097	1	743	MCPAIDAVLVVYVNRKWTNLSDD PMPVGMGTVKYVLM SAPATT ASYIQLDFSPVVQQQKGTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVNI QDTMIGELPPQITKTLARFIPEV AVAYPKSKPLTTQIKIKKPPKV AMKTGKSLHLHSTLEMFAAR WRRKAPMSLFLEEHNKGG HSLHENQLQMATSLDRRG/N/YT GFITSYLEEAVIPVNDVLQVG LPLPDFLAMNY
5057	35425	A	5098	2327	3435	KTTTLEDNLGNTIQDIGPKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKRNVNKQDESLRS HYE*WGMLTDCVVMRDPNTK RSRGGCFVITYATVEEVDAAATN ARPHKVDGKVVEPKRTVSRRED SQRPGAHLTVKKIFVGKIKEDT EGFAVFTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQRGRSGRGGFGGNENFG CGGNFSGHGGFGSGHDGGGYG GSGDGYNGFGNDGGYPGGGPG YSGGSRGYSGGQCGNQDQSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSGYNDFGNYYNQY SNFGPMKGGN/FGRRSGP*GD GGQYFAKPPNHSYGGSSSSSS
5058	35426	A	5099	1	636	MRDPNTKRSRGGFVTCATVE EVDAAAMNARPCVVGRVTEPK RAVSREDSQRPEDETELHLRDY FEQYKGIEVIEIMTDQSGGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGSGNFGGGRGGGF GGNDNFGRGGNFGHGGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVYNNQSSHFGPM
5059	35427	A	5100	1	3622	MTGICYTEDERSYKKNQAFTA ASKKQKETQKFCLRVDDGQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPE PVALETSTVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAAQRAQSLEPYGTG LRLAMPGRPEPPVFRSQEVV ETMCPVPAATSNVHMKKISI TERSCDGAEMKWEDQNGID

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5060	35428	A	5101	1	782	MRRRLQLDSLHPPSCFSSTLK CGKAAAAACDSSDQIQLRLQT GHLPCSEASTICPPNHSSQSTLR PPLPPPHNHTLSHHSSANSLSN RNSLTNRRSQIHAPAPAPNDLA ITPESVQLQDSWVLNSNVPLET RFWCCQRFLVFPGLQLQLHTLS LPVWSHGALPVSLCIFTWLSH KDTSHFGLRVHLLSLPLEAKYS FYPGCPVLEAPAPNPLKGPWCLW GVGTFRRYCTTFLFNESEPKDL VGEKFKSDRLCREAHLQE
5061	35429	A	5102	3	1864	
5062	35430	B	5103	1	525	
5063	35431	A	5104	2	351	RPAVGAESKNPSKRHRDRUNA EULDHLASLLPFPDIISKLDKLS VLRLSVSYLRVKSFFQVVRQRR EIHGRNCQKRNQNLKDRGWQ WQMPKMWMITRANEGPCRS GPEHWTPRP
5064	35432	A	5105	1	375	RPLQKQRPVGAESKNPSKRHR DRLNAELDHLASLLPFPDIISK LDKLSVLRLSVSYLGKSFQFQ QGLAVADAEDVDHTGERRP MSFRPRALDTQALRRRTQFGLH LLMVNIAGLIATDRL
5065	35433	A	5106	407	910	NVTPAHYDEQQNFFAQIKGYIR CILFPDQFECLYPPVHHPCYR QSQV*LDNPDYERFPNFQNVVG YETVVGPGDVLYIPMYWVHHI ESLLNGGITITVNFYKGAFTP KRIEYPLKAHNKVAIMKNIEKM LGEALGNPQEVGPLLNTMIKGP IQLACQGSRRPAR
5066	35434	A	5107	237	908	HEKPGRQRETRSQNHSHHHHHH HHHHQEKIRIQTFTFP*EDTER SDCPQAKKRSRRNQPC*HLDF ELPAARAATQPVNSGARAGRA GATVPRHTATLLHHQRRDYA GGSLCDIDRAPDAKQGGKS*ES ETDSRFWKGTVC*DHTAGWVH GRPTTPHHSSPDSRNGGQFLHQ QIALAAGWREGASRPKQEP LQP GPEQQRGRREPVQGKAPSG HQS WP AE

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5067	35435	A	5108	57	873	SGLCTAAFFHHQMEVVHT*SVSSRS*R/PTTPVIAQWAHEQSGHGRHGGYAWTQQHGLPLTKADLAMATAECPICQQQKPTLSPRYGTIPQGDQPATWWQVDYIGPLASRKGGORYGFAYLARNVSAKTTHHGLMECLJHHHGIPHHASDQGTFFVAKEVRQWAHAHGHIFHHVAYHPEAGGLTEWWNGLKKSQQLRQLGDNTLQDWGKVPQKAMYALICQPIYGIVSPIARIHRSRNQGVKVEAPFTTIPSDPLAKCLLPVLVTLRSAGL
5068	35436	A	5109	1	311	QITMQPELPIMNWVLSVPSSHKMGHAQQHIQEV AQMPRVSTPATLPSLPQPALMAPWTVPYDQLMEEFKARARYAGTIQKWTAALQPLSRTSLKDSGEGTSKW
5069	35437	A	5110	3	591	DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYSFFKRQLLACYWVLVEIEHLMGHQVTMRPELPINC\VLSDPCHKVGHAQQHSIIKWRWYIHDWAEGETSKI.HEEVAQIPMVSTPSLPQPAPMASWEVPPYDQLTEEEKTRA WFTDGSARHAGATQKWTAVALQPLSGTSLQDSSEKSSQW
5070	35438	A	5111	1	582	
5071	35439	A	5112	1	635	

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5072	35440	A	5113	2	1538	FFPIGFWRQHPIRLSVLLQHIY* VT*KAASFEGWPKQEKAL*QV QAVVQVALPLGPYPADPMLL EVSVAADKDGCSLWQAPIGES QWRSLGFRSKALPSSADNYSSF ERQLLACYWALVETECLTLGH QVTI*PELPIMNWVLSDPSSHKV GHEQQHSIIKWRWYICDWAVV GRESTINGLAGWSETWKKHH WEMGEKQIWGRSMWMESEW SKTVKIFVSYVSAHQCVTSTEE DFNNQWDGMTCSVDTTPLSL TTSVIAKWAHEQSDHGGRYGG YAGAQQHGLPLTKADLAMTTA ECPICQQQRPSLSPQYGTISQGD QPATWWQVDYIGPLPSWKQR FVLTVIDTYSYGFGAYPEHNTS AKTTVNGPMECLIHRRHIGPHI ASDQGTFRFTAKEVWQWAHAH GIHWFYVYPHHPAAGLIGWW NGLLKSQQLQCQGLDNTLQGWG KVLQKAVCALNQHPYGTVSP VARIHGRNQGEVEVAFPIITS SDRLAKFLLPVSSTSCSAGL
5073	35441	A	5114	488	966	ILVSGKQGSVCPGPSSSGTRGSS SPGVAVSNKAAATVGPQ*VTQ QEGGPGSRQRTRAGSPVLPAG PSAVEGEEGSWTPGGPQVPRKR SAAPSRQR*HWLRCTPA*QRRG DWPRAAGRCHAAARPPAAGSRA PTKISARPTRISRLGPRAASKAQ RLQRL
5074	35442	A	5115	197	421	KLKATMNSFHKS*SCALVSTRP CSPRGDPRLATLTIPALVEPPCG TQDPKMAAEAPQRPGKRLGRN LLRRRPT
5075	35443	A	5116	3	5649	LLEKLRQRIHDKAVALERAIDE KFSALEEKEKELRQLRLAVRER DHDLERLRDLVSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ WLKEEMETKFSRWQKEQESIQQ QLQTSLHDRNKEVEDLSATLLC KLGPGQSEIAEELCQRLQRKER MLQDLLSDRNKQVLEHEMEIQ GLLQSVSTREQESQAAAEKLVQ ALMERNSELQALRQYLGGGRDS LMSQAPISNQAEVTPTRGLGK QTDQGSMPQRSDDST
5076	35444	A	5117	2	157	YLGRLHCLFSEHEHSSRKEMV LVEGLCSEQGRG*TLASSSER KPLENER

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5077	35445	A	5118	248	621	TDEPSLLSHTFCPKGALLSACSG ACPLSSGTQAGMPPSTEALQPC RGLTVPHQ/LG*RPQGMLWWK ALAADWSVEWQKGRRLGKA LSVTSRTGRLLCR*GSAEAAAS PLAASPRRSSRALGAGIP
5078	35446	A	5119	2	157	YLGRHLCFSEHEEHSRRKEMV LVEGLCSEQGRG*TLASSSER KPLENER
5079	35447	B	5120	125	994	
5080	35448	A	5121	1	550	RRYRPRRVQDPGGPAEAERGPP RRLLNARVHVCRAEASERAPGP CGRVSAHVERARDPRLE*QLED KAAPRQDFTQQLRGPEKH VWQEKEDMHKQLVEASETLKS QAKELKDAHQQQKLALQEFLE LNELMAELYSQKQKVWDKEEE MEVAMQKADMMWQE!*RSKK LRKRMLFSQMRWL
5081	35449	A	5122	135	638	GSFPGAPLQTLVTLGLAWQS SGWILRGWLVPVPRACKSPRGQ ALAICLSLRGLGARSTWAETRP QGPRGSLASLCPAHMDLSIWKT GDGGPRSAFVKVHQGSLNTFG VDTAARRLSQARTAPSPSV\SAP SSAAAPASAGPPAPGAPPTPA QALRPAPPSPRPAER
5082	35450	A	5123	193	610	VGELLPFRFKISLRPFLALCSSL GPCRQPHSGSVPA*NPLLGPR KSSPHSGCGLAPFAIPELLRLP LEGSAHCPAPEGAA SPPTS WDS ADPPCRETSIFAPPRVLTTPGPS APQASPSQPLFLTPRWDRLPES VL
5083	35451	A	5124	2446	2630	VGFFFFFWWGERGTGSYSVTQ ARVQ*YDLGSLQLLPPSFKGF CLSLPGSWYYRHGPPRLG
5084	35452	A	5125	3	710	EDGDWDQRRGGEAGDQDQRR GGEDEDQDQRRGGEDGNRDQ KRDGENDWDWKREDENDQDQ DEKREGEDGNQDQRRGGEDGD QDQRRGGEDGNQDQRRGGKD GDQDQGRGGEDGDQDQREG EDGDQEQRRRGEDGE*QDQRRG GEDGGQDQKRGGEDGNQDWS REGEDRD*HWRRGGEGVE*QD RRGGEDGE*GQRRGSEDGDWD RSRGGEDGDQDQRSVGHLC HSGPPASGCVS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5085	35453	A	5126	506	882	RCSGGGFDGNKGTALPTISA DTRCWRTRLRVQTMTCRFRRF KAFFGIMSCGRTGRILFPSPCS MSWIPCRANKS*GNVISQSPSK NR/WQIMMVIQLLNFYLPGLDFV SFRIMLKGNWEVTRTRG
5086	35454	A	5127	107	1327	ERRKRAVGGFDLVLGEQPSDKI FR*VIV*GLALWLPKSFVIPP AELAINPSAKCKTDMTVMEDA VEVR*VWLQD*GLDSLEVLLDS FGPVRDCSKDNGGCKNFRCS DRKLDSTGCVVGLPCKLVVDS SGCYDRHIGVDCSDGFNGGCE QLCLQMAFPDPDTLYNILMF CG*VELPARPLDGRSCQLITETC PEGSDCGESRELP MNQTLFGEM FFGYNNHSKEVAAGQVLKGT R*TSYT*N*YQQLPDGLVVATV PLENQCLEEISEPTDPDLTGE CAFSTLFGYPVLQHWKVR SVM YHIKLNQVAISQGEHCRLSCD GATSRADFVALLDQFGNHYIQE AIYGFEECSIWYPNKKVQRRRL WLEYEDISKGEWHACWQILSTF PWIVISLHNCLP
5087	35455	A	5128	3	23	FYSAFLVADKVIVTSKHNNDTQ HIWESDSNEFSVIADPRGNTLG RGTTIT*VSIPPSL

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5088	35456	A	5129	1	2462	MRALWVLGLCCVLLTFGSVRA DDEVDVDGTVVEEDLGKREGS RTDDEVVQREEEAQLDGLNAS QIRELREKSEKFAQAEVNR MKLIHSL* [*] NGIFLERLISNSS CVALDRLSLISLTDENALSVNE* LTVNKKCDKEKNLLHVQHTGV GMTREELVKNLGTIAQIWDQ ASFLNKMP* [*] SHRKMGPVNLPEL IGPVWVSGFLFPPLVADKIVIT SKHKQPIQHIWGVWTPNGIFL * [*] LLDPRGKHS* [*] DRGNRQFTLCP * [*] KEEASDLPWNLDTIKNLRQKN IHSFIKLFLLIYVWSSKTETV* [*] GA PWGEEAAKEEKEESDDEAAIV EEEEEEKKPKTKKVEKTVWDW ELMNDIKPIWQRPSEVEEVEY KAFYKFSKESDDPMAYIHFTA EGEVTFKSILFVPTAPRGLFDE YGSKKS [*] DIKLYVRRVFTDDF HDMMPKYLNFVKG [*] VDSDDL PLNVSR [*] ETLQHQHLLK [*] VIRKKL VRKTLDMIKKIADDKYNDTFW KEFGTNIKLGVIEDHSNRTRLA KLLRFQSSHHPTDITSLDQYVE RMKEKQDKIYFMAGSSRKEAE SSPFVERLLKKGYEVIYLTPEVD EYCIQALPEFDGKRQNVAKEG VKFDESEKTKESREAVEKEFEP LLNWMKDKALKDKIEKAVVSQ RLTESPCALVASQYQWSGNME RIMKAQAYQTGKDISTNYAS
5089	35457	A	5130	45	416	RWGLAMFPSLDNKSSETLSQKK KKKDLCPHISFEMDLTTADAR WVQDAATRLLATRCPPNSRG SR**ISWRAGCCPGGWAGPHW GHDGCL* [*] PSCVSSS
5090	35458	A	5131	3	477	GRLPRHRGGEPGAQAPAGRQP RGGAATAAGAPRAGGGAAA GNARRCREAAARDPHHGECSG PEPSQCEGAHQRAQRAQGD* GGSGATGEGRRGHDSHNPLG RVRGSTLPPS** [*] N* [*] VGL* [*] VPSWP QCGPAHPPGQHPALQEIHQRLP LESGGHRV

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5091	35459	A	5132	3	446	RTGSWGWASASQQRHKKDRGL DSAGSGWVSHILPVAPPADADA RPSASRWRQGSHPGRTECP SVQPLCLPPAGHHRNHSIASPS QTPPPRSLPGSQDKSLFLPRDRR TGEGEHGMN*APLSAPGTSCRS GGSTSWLPEILGPTQ
5092	35460	A	5133	352	588	DIFKVGCGFLFKRLRCQQRFFL LIFSSSTQSA*RVSNQPYH*EIK MAVYYGELRKNGLIQESCDNIQ PRQGSFNMDSMQ
5093	35461	C	5134	13	144	
5094	35462	A	5135	587	1078	LSQRFLSSRIKLQRLSLQNGIP QIKELDYLFRTNSNQINFNLISH RVRRARPAPPGRPNPSGPDPRP EPPARAGSSRRGPGEPPIRRQPQ RRFRRRGPDPRGRLSRGL*RRR ARPASQPQRQHHSRGPAGRPGV APRRPAGLAAAAERLTARGAA ASPAIPRA
5095	35463	A	5136	44	455	HLRNRTR/PSQITPHIYNHLIFDK /PLFNIWWENWLAICRKLKLD PFLTPTYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNR/LPT*WEKIF AIYP
5096	35464	A	5137	101	861	LIGYQPKMSRTRRIHSKRLPERIK YLGSQLIRDVKDLLKENYKPLL NEIKEDTNKWKNNIPCSWIGRISI VKMAIL/PQAICGKCLKDPFLTP YTKINSRWIKDLNVGPTTIKTLE ENLGNTIQAIGMGEDFMKTTPK AMATKAKIDKWDLIKLKSFCT AKETTIRVNRQPTWENIFTIYP SDKGLISRIYKELNQYKKK/TR NPIKK*VRDMNRHFSKEDIYAA HRHMKKCSSLLDIREMQIKTTM RYHLTP
5097	35465	A	5138	3	314	LKSFCMAKETTIRVNR*PTEWE NIFAIYPSEKGLIYRIYNEATNK DLVRRSGPLKTPKKKSQTLVLN LVTFRKTPALSEEKESAQVLWQ FKKPECVLTSKRVH

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5098	35466	A	5139	1	1278	MNIDAKILNKILANRIQQHIKKL IHHDQVGFPEMQGVWNICKSI NIIQHINRTKDKNHHISIDAEK AFDKIQQRFMLKTLNKLIGDGT YLKIIIRAIYDKPTANIILNGQKL EAFPLKTGTGQCPLSPLLFNIV LEVLRARAIMQEKEIKGIQLGKE EVKLSLFADDMIVYLENPVSA RNLLKLISNFSKVSQYKINVQK SQTLHTNNRQRESQIMSELPFT IASKRIKYLEIQLTRDVKDLFKE NYKPLLN
5099	35467	A	5140	1	430	GGVFFLRTPTDCCGMLQGAAG STGFYASEARPRGPACSLDRGS SSLLSWGLHQDPLFPAKQHRH EAGRADQNSPRRLSTG*QTPT L*RRPAAATGRRRAQPPRATSV SAPASPPCPRARPPHHARPPRVL ACQP*ATAPGP
5100	35468	A	5141	1	346	
5101	35469	A	5142	3	1336	
5102	35470	A	5143	5	283	
5103	35471	A	5144	1	1368	
5104	35472	B	5145	1	838	
5105	35473	A	5146	1	962	
5106	35474	A	5147	19	87	
5107	35475	A	5148	41	831	GLQNPKHQSSQLVDLKMKKSL LQCMFYQLIVLQ*YLK*YLGTO LTRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWIGRJNIVKMA ILPKDPTTAQLSPRGSTAQKGH WRPCPLPRGVPSPRGPTSH HHDPGPGGAPVRNTGSEWRQ KLRSGPKSDWAGRAQAPSLGE GGAKNGKSHPGSHRAFSLPRAP RRLLPGSQPGRFRGFLKQARGR AGEGHSAILLAPESPNAQVSNV TSATYRSNLSGLPRPCSVVLLG

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5108	35476	A	5149	1	2233	MKAIEIKTFETNENKDDTYTQNL WDAFKAVCRGKFTALNAHKR KQERSKIDLTLSQLELEKQEQ THSKASRRQEITKIRAELEIET QKALQKINESRSWCFEKIHKID RPLARLIKKEKNQIDAIKND KGDITIDPTEIQTITREYYKHLY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPTGSEIVAIINSL PTKNSPGPDGFTAIFYQRYKEE LRIKYLGILTRDVKDLFKENY KPLLNEIKEDTNKWKNI PCSW VGRINIVKMAILAQGNL*YIKFN AISIKLPFTFFIGL/EKNLTFKFIW NQKRS\RIAKSILSQKNKAGIGI TLPDFQITITYKATVTKTA\WYW YQNRDIDQWNRTEPSEITPHIYT ILNFDKPEKNKHGGKASLFIK W\WCWENWLACRKLKLDPELT PYTTINSRWIKDLNLRQIIKTL EENLDNTIQDIDIGKDFMTKTP KAMATKAKIDKWDLIKLSFC TAKETTIRVNRQPIEREKIFAIYP SDKGLISKIYKELKQIYKKKNK QPHQKVGEYEQILLKRRHLCS QQTHESMAHHHWPCREMQINT TMRVHLYTPVRMAIIKKSNNRC WRGCGEIGTLLHCWWDCKLV QPLWKS\VRFLRDLELEIPFDP AIPLGIYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTM IDWIKKMWHIYTMEYYAAIKID
5109	35477	A	5150	1390	3491	DLLTRTACAVPGWGCSRATC QARGWRLSSPPHPSPVQPLLC HLPYPPSPFSLLSNLTPFLRAFPR SLETS*KWART/WPGAVAHAC NPSSLGGRGRWIT*GREFETNL TNMEKPCLY
5110	35478	A	5151	310	445	YLTKIWPGAVAHTCNPSLTGGR GGWIT*GQEFETSLANMVKPHL Y
5111	35479	A	5152	44	1132	PQVIHPRAPKLLEIQEPWRWH DLNQDTPSALCQH*RTC*HRAE GVSWFKSWIHLGGSCNSSSLGA RGGWIT*GQEFETSLTNMAKPH
5112	35480	C	5153	183	323	
5113	35481	B	5154	504	2474	
5114	35482	C	5155	66	269	
5115	35483	B	5156	2414	3096	

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5116	35484	A	5157	9	239	HHHYCQHIIHHHHHHHHHHHHHH LPAPCRNLRV*PVCFRYKLFWH YGKQHLLFLDFLLSHSEWC VSHCGFDLHFSDD
5117	35485	A	5158	3	387	TDTKPLSCSSCPPRGKKPVSHR DQ*RRWGRRCRGEPGTEACWS AGALQF*KPRSRGGRTSKMTSG PSAEKGGG*AGRKPGRRHFGRR VLRHSCVLPVARELWGRHGPC GWRQKNVPWKWSELLPVVAP
5118	35486	A	5159	1	277	MPPPPPPSPGPGVGSRLPPG PAVTGNEKELRGN*VGLAPPR PRFRASRREGVTGKVHRPNRLQ LRAPPKG*SDQRGQNVPPSEAK SLC
5119	35487	A	5160	1	3285	
5120	35488	A	5161	3	194	IPLSLQSKVGGQLQDDLKVL NELYSVNQMGCLAL*QAEGSSI WQLAAIVHQQN*TPSWGQ
5121	35489	A	5162	520	844	VQAPGKCHAQMPAPAAPVPLG RSRNPGRLASAVPVSSLLRFLPF LQPIPPSDILPLSFEAVPSSPAE SGLHPCTRRRKARPPSC*VPLG LLSPQPHPPPHVWRKGIL
5122	35490	A	5163	1	794	FRGFLDRGDCAALPCTYPHSPC SH*GGNCLPSLLTRPCVKA*PQ MSGRKSSMRWRQRSLTAGT SS*TPTSSTMC*ALVGSSTWNC MLQAGSTAPGAGTPGSRPTWS SSSTCSWTAPSGRARCAASS SCAMSAARRGWTSACWRRTS RAWWTTSSPACASSATASVAA STASTWPAARTTGTAESSARP ARRASCTGSPARCWRRRPPT PSPGRPAPPSRRTRAQAGTSA LSPGACFGPRSCC*SSTCSSLSV APY
5123	35491	A	5164	3	57	RIGQGVPPVHS*VEGGPNVISIV LEYLRDTPPPVVCDSGRAS DILAFGHKYSEGG*VKVFLWC THKWKEDPM
5124	35492	A	5165	1	1326	
5125	35493	A	5166	2	337	YSVTMTPGKLRLTCEIDWPALE VGWSSEGLDRSLV*KVLCPEL VPSGGFLVSLTSRMKPTLTGS VKVLKDGMSGVCSFRCDVSR VSSFWWVRGLAGWSTTLRLKL
5126	35494	C	5167	339	548	

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5127	35495	A	5168	3	413	SQAFLPAASRRERPPPEVDPKA TDPKSGTRRLPPRLPCQWTTPE HSHTSQLNLSRAFPKEPNPAAT Q*NPSGASPRERPHARAQEDRN GEC*EGNGSRPDLEEEASTPRA SPTPSD*PLWLHPPLVLEITPL LQL
5128	35496	A	5169	3	479	FLHSTHIYWAHSMHELLKTAV VSISSGQCTSLNTESGIWGGVPE NAR/CPPAEGTVPASLQPRDPPR LPGSH/ASLPSAPPSRHVWTPP EP/EAAGPKPS*IRCRWPPAGAT TKANPKESGRVLESMLPLPKSR SAPVTFSAFACSGPLPERVHEVF RVGKLR
5129	35497	A	5170	81	329	QSVSSPSWFPQFPVQVQKVP QVYRGDLVV*KHIVAPPSPSS FSGHVRHDCFPFAFHDDRKFE ASPAMLPVSSLGPHYL
5130	35498	A	5171	335	467	MPSTPTARKPESPEALARVESIA CLPSPAP/PHCESPQASEETG
5131	35499	A	5172	1	2424	
5132	35500	A	5173	2	304	CLTKNTSATREKQVTELHRRSK LQFPAKTKALQTVIE*KDITLC *VKEHLYIVACWALRLHLVFLP TKAGISPALMKVSYPGKPLTLK QLGRLVILQE
5133	35501	A	5174	44	286	GVQNGVEELIVRRMQKSPGP GEMESGSLEKEPLGTQTGPVPS EGTE*TGPPPTPSLQTQGPQRT PSLQTQGPPTPSL*TTQGPLRTL SLQTQGPPTPSLQTQGPPTPS LQTQGPQRTPSLQTQGPPTPS
5134	35502	A	5175	206	384	KRVFAHQADGRARSGFISSAGP GSQAGPGQGTG*QREDVEAAG QPGSTAEGVRT*SDPG
5135	35503	A	5176	270	818	RNERKPSQRTAVGLGAGQLQP GQPGVQSEEPGLEAGCAAGV LPGPAEQDREGIYSK*KRVFAH QADGRARSGFISSAGPGSQAGP GQGTG*QREDVEAAGQPGSTA EGVRT*SDPGSSHPAAAFYEN IQDGEALGRCGAKRTATAAP*Q RG*EGF*AGPTAAEKNEEGPPP VFSLFNHSL
5136	35504	A	5177	122	436	LTSLSAISTKAKVSPLC SARAC SPSPAARAALGSPGFTC*GAGV APTPVVAAPAPATAPATAVAA AATTTVVSAAAMFTRRATRAAA ATGAWGFVAGAPWPLQT

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5137	35505	A	5178	20	1341	MRRCVAAPLAHRW*QKLGLP CTPTVCSFLSPQPPPRARSSSAT LSSGAPRAATPQPQTTPSSVQ PCAATPCARGGRPAPAGVTWP TTRPSMA*RTS*ASTTAPRMAP PRSHACARSHRPETARSARTAP RSAITRRAFTSTRPPPTTRTVAS SGTHTSGLSPTASRLARCRAPG RSSTIIT*TCRSPTRLCCPAQRPL PPASSPSSSRTSRSVWTRRCTRL RWTSSRPSPWMALRTVGTSTGP TA*RLRRCQASTWRSRSTSA PPSWCARWAAT*PLPSACQRK WSMLWRTGTARVSTSAACGAAP STSRSTSRPSTPMLRAPVPAGW QPPALHPQPPRPSHTRQPWPSA RRSCRWRTCTTRPASSTSSPRA T*TSHWPPTTRWRMSRCSTPTK TNCTCMRGLGTCQAGRLRGCP WPPGPSWAPWSRSPWCSLCSA
5138	35506	A	5179	47	598	ASGPASIVVLRRQQFIKFFLDEICS LEERVWCRRKCLLYLWKEPR AVQAKSRCSDIRRELYRPSVLA GLSGDFLRAGRYSAHTVNGAW SAWTSWSQWA**SRGI.LLALH NMLKIIIAFCSLQVATRIQSTFIS SWHLSPSLGSRSPSLYMSFGS VLCPLFISHDTSSYSTKSQFSFC LGWV
5139	35507	A	5180	236	690	LQNWSYLAEQCWNGGFIYLIM LRRFKHKAHSTYNGNSSNSEP GETPTL*LGDRATAKKGRTRKF GVISRPANKAPEESKGSAGE VSSDPSTELENGPDELGNHGV FQLENGPDSLKEVAGPHLERSE VDRGTEHRIPKTDAPLTTSN
5140	35508	A	5181	2	480	WPFWAMVQRPSSAILCGPATLP PNCRGACCACRATGALSAYP AIHRPATRPPAPPAGPLTSPPL SVQNSNPDPPLPSARPSGPAAPR HARHSPSELPAITLSARGSSAL CTKLKVEAAA*SCSASAWNWR LLPRNHVDSRCQPEPDGARARD GRGP
5141	35509	A	5182	3	153	
5142	35510	A	5183	3	239	
5143	35511	A	5184	1	394	
5144	35512	A	5185	1	435	
5145	35513	B	5186	84	2068	

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5146	35514	A	5187	149	832	DAGLSWREATRPGAPLHRPGC QDASTQMTFRPGDPGSSALFPLP SP*PEREELPMSSRRSPKPELP EACSRPPTRPRPRTATRGPLN GRLPRARLPVSAGAGALGGGR CRRRVAPRRVTPRLATRPSGVA PRGSG*AATTKLSLAFGVTPLA LTPWSRTPFRKREERPPF*YPRP ATPEASPAHVENFRSNQTRYTS AE*SGQQLERPSIAEISAQATVE PRSTI
5147	35515	A	5188	45	312	AEAQGGAAEAGHGCGGGPAPS QGCPARAAGARGWQPAPSPQK PTPSDTTPPPRTQPPVTQCHP VTQPPVTQPPVTQPRHPMKIPP G
5148	35516	A	5189	15	549	PRHKEPESQAPGRAPQAAAY QQAASPAR*QGGSCSRCPG*A VEAAPAP*GQALGCVSQGPA*V GPTRSPHPTAGLSRPHGPPSVRS TGWSPSSRLQAQEAPWPVAPT HIPPPLDPGQPHSCGLGAGCQP RAPAAPRAGHIP*EGAGPPPPWP SASAPPCASAPVWLWRFPPRET KT
5149	35517	A	5190	1	2445	
5150	35518	A	5191	1	708	FSEGRNRFNLVGPTFRFSTRQTL MWIPDSFFSLLSGRISTLRDET GAIFIDRDPAAFAPILNFLRTKE LDLRGVSINVLRHEAEFYGITPL EKIKMEYCFSCVMYS*QVCFE MFLVRRLLLCEELERSSCGSVL FHGYLPPPGIPSRKINNTVRSAD SRNGLNSTEGEARGNGTQPVLS GTGEETVRLANTIDSKYVAND DWLIFQYVDEEDLMNAIKDFSS VTKERTTFDTHL
5151	35519	A	5192	31	330	YGGTATVQRWAESRHVPFPSP QEQNANKICSCVEEKDSADSY GEIPWWQGPERCWPVRLMLAT LGDYKWWLTGIGTDS*LGFTIPT DHANAFSAKEIPQ

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5152	35520	A	5193	1	734	MISEVIVIQMLFLHAFSKVFSAL IKNNKKPLQDAQIKWKAISGLS GGMRRSECNRRERDQVTRTQCR DISQKIRGPGD*GMATSKNGAM A*QLGPGCQGDASTGNAEFGES AHAWSGGGRVPGVTGPDREEV GRSWQGTSCGGTSGCGRQL* DGVASRGRW/DPARPREQRAG VRQLAAPLGGP*SRRPWEPPGG SSCGRYLFAISSWSGVTVAQEG QRKRSGGK*RTERSGPGLRRL PPLLLTV
5153	35521	A	5194	3	449	EGQRSSSPATALLSSGPPSLKM ATSKNGAMA*QLGPGCQGDAS TGNAEFGESAHAWSGGGRVPG VTGPDREEVGRSWQGTSCGGG TSGCGRQL*DGVASRGRWDRR DRASSGRESGLHHSGARSLG APGSRPVEAPAGSEAKTPG
5154	35522	A	5195	606	841	CTVGFALPVFY*GFSH*CSSGIL V*NSRFLLCQALVSG*CWPH KMS*GGFPLLLTGIVSEGMPV ASLCISGRQL
5155	35523	A	5196	620	930	IPFISFSLIALARTSNTMLNRSG ERGHPCLPVVFKNASSFCPPS MILAVGLS*IALIILKYVPSIPNL LRVFSMKGK*ILSKAFSASIEIIM WFLSLALFI
5156	35524	C	5197	1	819	
5157	35525	A	5198	591	815	
5158	35526	A	5199	187	387	FFKTICFMVRVRKPPNRLCVS NMAVYFTWVQAGLHCSYPEH L*WSCRLPRRLGGVRL*PLEGE
5159	35527	A	5200	1	1197	
5160	35528	A	5201	119	375	ILDISPLSDE*IAKIFSHVSGCLFT LMVVSILA VQKLFSLIHSLSILA FVAIAFGVLDVK/CLVHA VVNLN GIA*VF*GFYGFRSNI
5161	35529	B	5202	1	1053	
5162	35530	A	5203	2	157	
5163	35531	A	5204	12	176	
5164	35532	A	5205	2	223	QTVLEDRSPRARWIF*G**GTIC SIPIPSFWWFSSNLSSHFCRSPP SSSPGGLPMCTCVSKFPWAVW PFSRY
5165	35533	A	5206	61	308	

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5166	35534	A	5207	487	898	DFAEVAYQLGISSGVCRTTDFH EPRMLLSDRSSGSFVTHSVFLS FSSLKCL*SPLVHDALHQAHPH GKSRLRFLGSMACCMKFTCPP TLSTVPSSTPFSFCSLIKTRSAT LLKLWSISLRFLHWSWSSAFRV
5167	35535	A	5208	9	191	IPQHYYPPKTKPGRI*ISE*INNRL* NCGNDQ*LINQKESRTRWIH SRILPKTNREP NHE
5168	35536	A	5209	1	1989	
5169	35537	B	5210	1	1488	
5170	35538	A	5211	929	1209	IPFISFSCPIALARTSNTMLNRC ERGHPCLPVPVFGNASSFCPFS MILAVGLS*IALIILRYVPSILNL FRVFSMKGC*TLKAFSVSIEII
5171	35539	A	5212	242	642	FSLKRSFTSLVSWIPRYFILFEAI VNGSSMLIWLVSCLLLMYRNA CDFFPILY PETLKLKLLISSSLY LW*NSAVNLSGPGLFVGRLLII ASISEPAIGLFRDSPSSWFSLGR VYYSRNLSSSRFSSFLV
5172	35540	A	5213	747	885	
5173	35541	B	5214	115	1267	
5174	35542	A	5215	209	322	
5175	35543	B	5216	1	3321	
5176	35544	A	5217	390	655	CLFPVHYRLHAMMHQMKNP VLVLGIGGFILGILVIGGPVSLF KGS*KLLGIETGKISLDHPVPG GTPTKMALYEHFMNTKEFGIE
5177	35545	A	5218	3	221	
5178	35546	A	5219	798	914	FVFLWDRW*YPLYHFLCLFDS SLFFSLVLVAVYQFC
5179	35547	A	5220	12	460	YLCMLHEVLVLCFSVPSGHFSF SLN*LF*LA VPTVYQGLSFLA QA*ASQVDFRQLCWQQEFQAS GS*LAGLHGSGIH*ARPLGSWL QLPFQESEWFCLSGVPGATVVS /CTF**SPF*LV*DGISLWF*FAFL *WPVMMSIFMCLLAA
5180	35548	A	5221	3	508	AERNRSRQGVGAGAGDHEVLQ LLPDKWKQKILCPVQLLRGAW SNYYSPDANRQP**VQGNALHF AECWPHGEDSQPTVPTSQGRM LAGPARHLPHPHVPSPSGSLRG SDSEDTHT*GTVAGSGCLHCLAP GHLHPGWPPSRVLPIDRSVHQ GPGRKAPPTPRVTLFT

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5181	35549	A	5222	584	1052	LRKAAASGSFVFVAPDPNTDTG SSQCESESGSRGCSMGHQRS QHYYHHHHHHHHHHHHHHHH HLDTGWRGE*SRHSAGLCPPSQ RRLHSCQTSPSCSPSGHRCI*LT GIEAA*CHSL*PYQKDACHHFE EHSPPP*RPFLPRHHLHPQSS
5182	35550	A	5223	1614	2308	LRKAAASGSFVFVAPDPNTDTG SSQCESESGSRGCSMGHQRS QHYYHHHHHHHHHHHHHHHH HLDTGWRGE*SRHSAGLCPPSQ RRLHSCQTSPSCSPSGHRCI*LT GIEAA*/WS*PLTLSKRCVSP RAQSSSVTSTSAQASSAPPEKK *L*PERPYSSHPASVADLQMC LPLNRITGQTNRLHRAILLRW MRSCNLLTCTVLSNVFSFSELS YSRNTMCRG
5183	35551	A	5224	3	407	SVGLILPSSLQHYYHHHHHHHH QHYYHHHHHHHHHHHHHHHH ADLPTCAPHQGIRPFGGFPQTS GSPGLPVYAEQGTTERLSLQGT CGCGQAGLLCWGPPVASTSVG FSLESSVSPQVPLSPGAGTDA
5184	35552	A	5225	1	1287	
5185	35553	A	5226	3	1315	STMALLHSGRVLPGIAAFAHPG LAAAASARASSWTHVEMGPP DPILGVTEAFKRDNTSKKMNLG VGAYRDDNGKPYVLPSVRKAE AQIAAKNLDKEYLPIGGLAEFC KASAEALGENSEVLKSGRFVT VQTISGTGALRIGASFLQRFKF SRDVLFPKPTWGNHTPIFRDAG MQLQGYRYDPKTCGFDFDTGA VEDISKIPEQSVLLHACAHNPT GVDPRPEQWKEIATVVKKRNL FAFFDMAYQGFASGDGDKDA WAVRHFIQGINVCLCQSYAK NMGLYGERVGAFTMVCKDAD EAKRVESQLKILIRPMYSNPLN GARIAAAILNTPDLRKQWLQEV KGMADRINIGHAGLQLVSNLQG REGISTH\N\WATHSPTKLG MFC FHRG*KLEQVERLIKEFSIYMTK DGRISVAGVTSSNVGYLAHAH
5186	35554	B	5227	57	386	
5187	35555	A	5228	1485	1883	
5188	35556	B	5229	117	641	
5189	35557	C	5230	1	552	
5190	35558	B	5231	250	378	

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5191	35559	A	5232	3	1117	TPDPGQGCSEGGIVHETRPSPQP LCQGSCAVGCSPGLLLR* ALGKIPGHRGPAFLPAVESAH VVPGLPGLTRETLPAPLGPHRPP QPPQGPLSTAPPAPLVSLGPHV PGLPGPPPGCPSPLPLRPCPPPS WLRPHRPVQPWGWT*GSGWRP RCRPGAAGRNPGLPRACCRGL CRGPH* RPGGPRPGHSGPRTSS WGRMTGNRPSPASAG**PRHR R* TSAERPSPQQSASRTGGRS PLSHPGSWWGVMGPPGLWAG APSMWG* GPGSRVAGSGRRP TSRPPHYPPHPPGTWPSGAQS GRR*QAQTPGAATEG*GGWGL PPKPWCPQDQFLGVQDWVLP NGARVGGTAWKRESVLVPG
5192	35560	C	5233	229	522	
5193	35561	A	5234	1	972	MTAEYYKLKQVVTPIAAAVPD VVSLLLEQINISLCTWYAVIDL NACFYIPVHKAHQKQFAISRHG QQYTFTVLLQRRDLDFLSLQ DITLVHYVDGIMLIGSSEQEVA STL.DLLVRHLHARGWEINLTKI QGLATSVKFLGVQWYGACRDI PSKVCDKLLHLAPPTTKKEAQH LAASFEWGPEQKGLQVQVAV QAALPLGLYDPAADPMVLEVS VADRDVWVSLWQAPIGESQWRP LGFNKALPSADNYSPPERQLL ACYWALVETEATPVITQRAHE QSGHGGRRDGGYAWAQQHGLP LNKADLAVATAKCPISQQQRPI
5194	35562	A	5235	3	246	
5195	35563	A	5236	3	841	
5196	35564	A	5237	1	746	RDLDFLSLPQDITLVHYVDGIM LIGSSEQEVA STL.DLLVRHLHARGWEINLTKI QGLATSVKFLGVQWYGACRDI PSKVCDKLLHLAPPTTKKEAQH LAASFEWGPEQKGLQVQVAV QAALPLGLYDPAADPMVLEVS VADRDVWVSLWQAPIGESQWRP LGFNKALPSADNYSPPERQLL ACYWALVETEATPVITQRAHE QSGHGGRRDGGYAWAQQHGLP LNKADLAVATAKCPISQQQRPI
5197	35565	A	5238	1	483	
5198	35566	A	5239	1	1908	
5199	35567	B	5240	1	2718	

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5200	35568	A	5241	522	693	LDFFLVFLQQFLPRPSSSEI*MLP GFPAAYAGPVAAAAVAAARGSGRKYVGTGDSQA
5201	35569	A	5242	1	225	MGRNQSRKAENSKHESTYSPP KDHSSSQAMEQSWTENGFEKL GFRKKEALYYLDLTASCQSQEL FQKWVSLCCPD*SYSPPKDH SSSQAMEQSWTENGFEKLGFR RKEALYYLDLTASCQSQELFQK WVSLCCPD
5202	35570	A	5243	1	1129	PWISAPVPVDVVEGAMDSVT LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRN YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNRHTVS SSGGNRLPNPGDRSCDNLKTC HTSHGVSMAETAVINHKKRKN SPRIVQSNLDTEAAAYSLSRDQK RMLYLFVDQIRKSDGTLQEH D GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAKGEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYKSL CQYRAFVNGGEEKARGKPIL CRYGVGM

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5203	35571	A	5244	1	1753	MVDSLIARVGVGMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLTGGQTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELHDEQMAALYRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISHLIIHAEDTFLPFY LGKKDDVITYAIKPTCWPLDII PSCLALHGIEIELMGKFDEGKLP TDPHMLGLAIETVAHDYDVIV IDSAPNLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDIKGFEPDVRILLTKYSNS NGSQSPWMEEQIRDAWGSMLV KNVRETDEVGKAVINHKKGK NSPRMVQSNDLTAAAYLSRD QKRMLYLFDVQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSLAGKEVVFYRPE EDAGDEKGYESFPWFQKQSEE/P QSGNFYTDTLGMAEFRGGGLR ATAGPRLSRTDCQGTKEKVVH KTVFDKTP/VWPKRLKSPSCK NRWP*KMQKLSVCTASSPGQ LSTVRVTQREICFPVVRREVL IGTLTQTRKGQISVRA
5204	35572	A	5245	337	1977	

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5205	35573	A	5246	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDQMAALSRLG NDYRPTSA YERGQRYASRLQN EFAGNISALADAECNLTCTHT SHGSMVMAETAVINHHKRRKNP RIVQSNLDTEAAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPPDFRRRLQGFCFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPLDIIIPSCALHRIETEL MGKFDEGKLPTDPLMLRLAIE TVAHYDVVIDISAPNLGIGTIN VVCAADVLIIVPTPAELFDYTS LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGNSVLRK
5206	35574	A	5247	1	1383	
5207	35575	A	5248	1	1731	
5208	35576	B	5249	1	1290	
5209	35577	B	5250	1	3345	
5210	35578	A	5251	1	1959	
5211	35579	A	5252	3	2356	
5212	35580	B	5253	334	1710	

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5213	35581	A	5254	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGRRLRRAEDVFPV NVSKSDDTLKINGVEDHKITFD GDGKTYQNVQQFIDEGNVTS DNHTLRDPHYVEDKGHKYLVF EANTGTENGYYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGHIENNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRM LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPPLYESLCQYS
5214	35582	B	5255	1	1452	
5215	35583	A	5256	1	1323	
5216	35584	A	5257	1	1557	
5217	35585	A	5258	1	2259	
5218	35586	A	5259	1	2418	
5219	35587	A	5260	1	1218	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGRRLRRAEDVFPV GVAAHKERNQNSIRYISNRLAR RECHDSPEEGTGNTSRKERLQG RLPSRGLTESQEHLLDTRKQFW FEDFKDGLGPIKCDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLSAS NYQRMDFRRRLQVVCVMEIN KQTSMLRSYI
5220	35588	A	5261	1	2028	
5221	35589	B	5262	1	1653	
5222	35590	A	5263	1	1446	
5223	35591	A	5264	1	1788	
5224	35592	A	5265	22	1893	

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5225	35593	A	5266	1	2144	MEKKITGYTTVDISQWHRKEHF EAFQSAVQCTYNQTVQLDITAF LKTVKKNKHKFPAPAFIHILARL MNAHPEFRMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYTTQGDVLMPL LAIQFFDMLRDLLKNVDLKGFE PDVIRILLTKYSNSNGSQSPWME EQIRDAWGSMLKNVVRTEDE VGKDTGVRKISGVKIMPMGV AVVNCCTYGSDYRVWLASWM MSQWLHYPEWYRKENKHKFY PAFIHILARLMNAHPEFRMAMK DGELVIWDSVHPCYT VFHEQTE TFSSLWSEYHDDFRQLHIYSQ DVACYGENLAYFPKGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYTTQGDVLMPL LAIQFFDMLRDLLKNVDLKGFE PDVIRILLTKYSNSNGSQSPWME EQIRDAWGSMLKNVVRTEDE VGKQIRMGTELEFFRLSETKEI TNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRM PDFRRRLQCDNLKTCHTSHGS VMAETAVINHMKRKNSPRIVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHGDGICEIHV AKYAEIFGLTSAEASMDIQHAL KSFSGKEVVYRPEEDAGDEK/ GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFLSE
5226	35594	A	5267	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYV VFALAGSPEDADDTIYMFYQK CDNLKTCHTSHGSMVMAETA V1NHKKRKNSPRIVQSNLDEAAY SLSRDQKRMLYL FVDQIRKSDG TLQEHGDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRKPDGSGIVSLK/ID WIIKRSQLPQSAFYQFMGLRR ESFYFRWERTLGPLKSFVSKR GTEAGKFRLLAALLVRL
5227	35595	A	5268	1	1395	

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5228	35596	A	5269	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAAGTVAEYNGYHV VFALAGSPKADDDTSIYMFYQ KIRRKNGPVSAFTSDGKIRLFY TDYSGKHYGKQSLTTAQCDNL KTCHTSHGVSMAETAVINHKK RKNSPRIVQSNDLTEAAYSLR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDPGSGIVSL/KIDW/II/ RYQLPKVPSPEARKITRRWRJ/V KQRI*LGFLRLSEMPRKQGDY RTRIWKFEGLSNVLVIQLNKLII ICVMCLVRDCDVLKTYFHR
5229	35597	B	5270	1	1668	
5230	35598	A	5271	1458	2675	CDNLKTCHTSHGVSMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRSQND*RR GI
5231	35599	B	5272	1	1317	
5232	35600	A	5273	1	987	
5233	35601	A	5274	1	571	
5234	35602	A	5275	1	4161	
5235	35603	A	5276	1	1228	
5236	35604	A	5277	387	3466	
5237	35605	A	5278	1	6721	
5238	35606	A	5279	1	1651	
5239	35607	A	5280	5082	5879	
5240	35608	A	5281	1	231	NHLAVRRLTELSGGQRQRAFL AMVLAQNTPVLLDEPTTYLDI NHQVDLMRLMGLRTOGKT VD*VRDLNQVSRYC
5241	35609	A	5282	1	303	CLRILCPYPYIPLTEKTLA*PAL YTELTAADMAETCKQFLPEFSL TFSFQGWKEKETEYAEVLERNF ERDRQLTYTAHGPBKADLRIQE SGVPYNEILVTL

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5242	35610	A	5283	1	273	TNSSVGPGRLL*QTAAPHRGK LKVFFGACAGVGKTWAMLAE AQRLRAQGLDIVGVGVETHGR KDTAAMLEGLAVLPLKRQAYR GRHISEF
5243	35611	A	5284	66	1200	HILPAGHPTLRHSLFPHQQGRSS VQSALGAASGNGLKLVGRFEW GPSRRARSQYPDATGYDQPKPI SAAVKEFFGSSQLSQFMDQNNP LSEITHKRRISALGPGLTRERA GFEVRDVHPHYGRVCPITPE GPNIGLINSLSVYAQTNEYGFLE TPYRKVTDGVVTDIHYLSAIE EGNYVIAQANSNLDEEGHFVE DLVTCRSKGESSLFSRDQVDY MDYSTQQVVSVGASLIPFLEHD DANRALMGANMQRQAVPTLR ADKPLVGTGMERAVAVDSGVS GGVVQYVDASRIGIKVTKTRCI RVKQVSTSTLPLFLESNPLF WMAVLVSAGILQWPIGRLAD KFGRLLVLRVQVFVVLGSIAM
5244	35612	B	5285	1	862	
5245	35613	A	5286	1	579	DPRD*RLKVAK*MVTLFGPQFV RELQQRGFDFLDLKFHDIPNTA AHAVAAAADLGVWMVNVHAS GGARMMTAAREALVPRPDAP LLIAVPV*RSIKASDLVDLGMTL SPADYAERLAALTQKCGLDGV VCSAQEA VRFKQVFGQEFKLV TPGIRPQGSAGDQRRIMTPEQ ALSAGVEYMENGRPGTQSVK
5246	35614	A	5287	484	978	GIVRIPIRLADIKCWRAVLVNY THYSYQANLCCANLE*ADLSGS VLDCANLQGVKMLCSNAEGAS LKLCNFEDPSGLKANLEGANLK GVDMEGSQMTGINLRVATLKN AKLKNCNLRGATLAGTDLENC DLSGCDLQEANLRGSNVKGAIF EEMLTPLHMSQSVR
5247	35615	A	5288	3	504	YRLSQSSSKSLVSRSLNMRFIS SVMFMFEPTSSSENRFSPSCSE MSSSEATLRSFFLGTTSPCRSM VGLQLVKSSQSSSVSSSHVRL SQSSSKSKVSRLAGT*EGSEKRS FREEKVPCLRLGLPESTLYAHC SV*SRTHVFSGTSHHSSKVAVG MSIVQMRKL

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5248	35616	A	5289	2	442	HVIWHMPRKTSKCRQLLCSGA SRNADTAARQSTCSSHRPPGKIP SLGPRRVPGCSSVPSSRGEQSTG SPAAPRCQDVTHTTEASQEEQP* LRGTHGPASTPEQGTAKAKVR DRRAVVHPGKTGIPSAAG*KGR GRPEPPGAAVQVE
5249	35617	A	5290	151	1185	YVDQVTHITESPLPSVSYSAFAG SLISAVDPVATIAIFNALHVEED TEKGHVRLTPASPSTFFFFSTE EKYAPGSCCRKA AVL*LLHISH QLSLDSPSLTVVIYVLKHIDLRK TPSCRHCEI*VGDHTAVLSVLFS PSLGIMAILFSGIVMSHYTPREA SP*SCCLFTVSSHVTVCCHPGLRG AIPYALSLHLDLEPMKQRQLGT TTIVIVLFTILLGGSTMLIRLM GLPGGAPRWQQLVAVGPPFLP AQGNTVESEHSELTEEEYEAH YIRRQDQLSLFN*N*SCLWPSPC LPPPP*TPHTKHPVASPPFHGPA PDALTAWLCLSTQDLHHGRQ MKTLT
5250	35618	A	5291	5	198	VCGRQQSLEAGL*GAATPFVAF PRPWSAVRVKEYGYTRLHLIN GTHIHQQVSDDQAFACHP
5251	35619	A	5292	137	308	HLERTGPNLPPGARLATRPTTR LPAASPRGRDTPLPIPIFYSETE AKGEAPYIEPE
5252	35620	A	5293	612	1078	RPPEKKERGRVRGRRRGGGGK RRRRKRRKRRKSGKREDAAAA AAAAQSPRTAPAPD*ERRPQP APSARAPPRLLPAPRRSRPAQV PPDSASPWAAAAGLALPPQCP GGGARPLRLLPQPPAPGGTAR WEPRRPRPAAAAGLLQSPGFLP RQS
5253	35621	A	5294	515	817	LALPHLPSNLLKGLKWLKA*S RPSRTPSFG*LSQWKHALKRLK PVITCLLQHGLKPINSPYNSLIL PVLKPKPKYKLVQDLRLINQIV LPIHPMVSQA
5254	35622	A	5295	1	951	
5255	35623	A	5296	1	1077	
5256	35624	B	5297	87	1423	
5257	35625	A	5298	29	234	
5258	35626	B	5299	77	327	
5259	35627	B	5300	1	235	
5260	35628	A	5301	2	2144	
5261	35629	A	5302	1	855	
5262	35630	A	5303	845	1057	

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5263	35631	A	5304	1	933	
5264	35632	A	5305	1	954	
5265	35633	A	5306	1	1603	MEAEKFHQMPVSRRTRKASG VIQSKSENLRTRGANSALKRL KPVITRLLQHGLLKPINSPYNSPI LPVLKPKPKPYKRFLAFYGWSPR SLIVDSCSKLEQHSTLSRVILVIY KGFCFRNHHQTGFSPAGANQ RGPLAATLSGPGGEGQSAVACL TGEKKNHGAQYANRLSPRVG RFINAAGTTGFTGTGKRAVSATQ LMDFAFGTITITQDFRLLGQTS VDRLQLSQGQAVKGNQLLPV SLVKRKTTLPANTQTASPRALA DSLMLQARQVSRLESGQSSQLS SLRLTLPDLRSLPDHGHRRAS GNSHSGSPKPPCLPLISPHLNP QVWDISTPSLATDHMPITILKS NVTLPNLKCCQYPIQHALKRL KPVITRVLQHGVLKPTNSPYNS PILPVLKPKPKPYKLVDRLINIH IVLLPIHPMVPNPYTLSSIPPSTI HYSVLDLKHAFITPIPHSSQPL LAFTWTDPDHQAQQITWAVL PQRFPRTGPHYFNQAQISSSV TYLGIIILIKTYVLSLPIVSD
5266	35634	B	5307	1	874	
5267	35635	A	5308	144	539	
5268	35636	A	5309	1165	1639	PHPAVASRRGRAGPGGLSAPER TPSSELSPLSKGDLRKTHRTFSP Q*GDLRKTHRTFSTR*GDLRK HRTFCTR*GDLRKTHRTFSTR* GDLRKTHRTFSTR*GDLRKTHR TFSTR*GDLRKTHRTFSTR*GDL RKTHRTFCTR*GDLQKTHRTFS TR*GDLRKTHRTFSTR*GDLRK THRTFSTR*GDLRKTHRTFCTR* GDLRKTHRTFSTR*GDLRKTHR TFCTR*GDLRKTHRTFSTR*GD LRKTHRTFSTR*GDLRKTHRTF CTR*GDLQKTHRTFSTR
5269	35637	A	5310	235	453	SHWPWLCSSSTCSSQRSIVSSG MARGPFLRKRDLLFPFPPPGSH GLELLEIIFHQGISQVHLLHLQ VWL*NLNVDPSSSLPAENATGP GFVPPPLAPVRGPLFPVDAARGP FLRKRDLLFPFPPPGAMFGASR DYFPFGDFPGPPAPFASMAFL N

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5270	35638	A	5311	2	2333	TGRGYCGDHESFSGAMEEPGA TPQPYLGLLLEELRRVVAALPE GMRPDSNLVGFPPWELVICA VGFFAVLFFLWRSFRSVRSRLY VGREKKLALMLSGLIEEKSLL EKFSLVQKEYEGYEVESLKD SFEKEATEAQSLAETCEKLNRS NSELEDEILCLEKELKEEKSKHS EQDELMA DISKRIQSLEDESKSL KSQVAEAKMTFQIFQMNFERL KIAIKDALNENSQLQESQKQLL QEA EVWKEQVSELNKQKVTFE DSKVHAEQVLNDKESHIKTLTE RLKMKDWAAMLGEDITDDD NLELEMNSESENGAYLDNPPK GALKKLIHAAKLNASKTLEGE RNQIYIQLSEVDKTKEELTEHIK NLQTQQASLQSENFHFNENQ KLQKQLKVMTELYQENEMKL HRKLTVEENYRLEKEEKLKSV DEKISHATELETYRKRAKDLE EELERTIHSYQGQIISHEKKAHD NWLAA RNAERNLDRKENA HNRQKLTETELKFELKDPYA LDVPNTAFGRGSRGPGNPLDH QITNERGESSCDRLTDPHRAPS DTGSLSPWDQDRRMFPPPG QSYPDALPPQRQDRFCNSGR LSGPAELRSFNMPSLDKMDGS MPSEMESSRNDTKDDLGNLNV PDSSFPVAKKEATGPGFVPPLA PVRGLFPVDARGPFLRRGPPFP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met lud	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5271	35639	A	5312	141	2788	GLRVLPSPSSPRSLRSGPLRLP GADSGSGPKAVCSPPFIVAPTG RGYCGDHESFGAMEEPGATP QPYLGLLLEELRRVVAALPEG MRPDSNLYGFPWELVICAADV GFFAVLFFLWRSFRSVRSRLVY GREKKLALMLSGLIEEKSLLLE KFSLVQKEYEGYEVESLKDAS FEKEATEAQSLEATCEKLNRSN SELEDEILCLELKEEKSKHSE QDELMADISKRIQSLEDESKSL KSQVAEAKMTFQIFPMNEERLK IAIKDALNENSQLESQKQLLQ EAEVWKEQVSELNKQKVTTFED SKVHAEQVLNDKESHIKTLTER LLKMKDWAAMLGEDITDDDN LELMNSESENGAYLDNPPKG ALKKLIHAAKLNASKLTLEGER NQIYIQLSEVDKTEELTEHIKN LQTEQASLQSENTHFENENQKL QQKLKVMTELYQENEMKLHR KLTVENYRLEKEEKLKSVDEK ISHATELETYRKRAKDLEEL ERTIHSYQGQIISHEKKAHDNW LAARNAERNLNDLRKENAHRN QKLTETELKFELLEKDPYALDV PNTAFGREHSPYGPSPLGWSS ETRAFLSPPTLLEGPLTLSPLLP GGGGRGSRGPGNPLDHQITNER GESSCDRLTDPHRA LSDTGFLS PPWDQDRRMMFPFGQSYDPS ALPQRQDRFCNSGRLSGPAE
5272	35640	A	5313	217	447	FORMSGL*GYSPPLGGQPAL*E CQGAADSAGGIRGLDSERSLGR PAASGPNTALGWQAQPS*Q AGPELPRAEFLQA
5273	35641	A	5314	3	287	TLRNRHRELRTCLSGPGLGLPT QVSVVAGGCCVCPSSSQSPVPR PPALSAAPWHSRAGCPPSGGL *PQRPLILWNQPLSNTLLEKELA PPPAH
5274	35642	A	5315	3	468	ALARSPAG*PQSPDGLCFRHR KGERRPAAPAGQCPAGRQRHY PAAGRDKPGRAPGADR*AGPI LHLHYLPAPCGGGTPGDSNPRR APAQRSE*CTPPPPQ*RNNRKPS TRAGLLPS*HVQLSGGLTLC GDRVS*WPGVLAAPGPGPCT HL
5275	35643	B	5316	64	288	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5276	35644	A	5317	73	265	NGRTSRCSFSPGKH*EYCSGTFH PLQVVVGKIYSNLDKIL*ASRAR WGLCSRKPGYWSCTQPTSS
5277	35645	A	5318	125	461	
5278	35646	A	5319	298	593	LGVEVEPVTGGDAVIGASHDAF LQVNIESIVPEHSTRCKLLGKFI RIWIKYFRHLVHGGGSAPVSLV TGPVHGDSLLGFPVAPEPPRVVE PARQVRAHAVVVAGPLRRGRG LGRHRLRARG*GMPQSVRGA CGAQGHGPAGEDQRLPRERG PAGQVQPGVVPGLQDPEGCL RVQDQ*PGLREQSPHRADA*S ILSKFE*IFPTTCSGWNVPEQYS QCLPGEKHRDWPR*LHHLI*PA QI.PPPVTTSTGHPSAIEGLETP RSPLTPGPPGKSIIPHPQSPDCD GTDCAAFPENIIRLSRKICKRG
5279	35647	A	5320	1124	1835	HSLHFPKFPFLTLITLGLLM AVPPGLITTHQQRQAML*YKPL ARLLEPLISFSPWSILKEITSQC SICYSTTPQRLFRPPFPETHQTR GFAPPR/HWQIDITHMPQVRKL KYLVLVDVTGSKKATVVISLL SDIIPRFGLPTSIQSDNGPAFISQI TQAISLALGIQRTHGLLKTHLT NLSHQLKKDWITLLPSLLRIQ ACPRNATGLHSDG/VGPKLLPG SPFQLHHTWDSP
5280	35648	A	5321	1	1758	
5281	35649	A	5322	1	1967	
5282	35650	A	5323	76	1908	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
5283	35651	A	5324	524	2144	QSDLSASQHGFLPLATEVRSRG AASCPDSDSICPAPIAPGRATP PQANCWASEGTLRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLFSNLQGP RSRPVAFLSKQLDLTVLGWPC LRAAAAAAALIVLEALKITNYAQ LTLYSSHNFNQLFSSSHLTHILF CSPGFSFCTHSLLSLPQLPIVPGP DFSPASHIILDTPDPHDCISLIH LTFTFPFHISFFPAHPDHA*FIN GSSTRPNRHTPAKAGYAIVQVT SPPLKTSHFSLSIVEIYPQGNFS VFHLLFFYSSGIIQAPLLSLHIKL RDLPPRPTGKSALLNMPVRKRL KYLVLVDTGSKKATVVISSLL SDIIPRFLPTSQSDNGPAFISQI TQAISLALGIQRTGILLKTHLT NLSHQLKKDWTILLPLSLRIQ ACPRNATGLHSDGEARSSFAQH HFNFIHTGTVPDVFVPIQLLNE DFEDPCLGYLPSPEISICLEPTSW SKDRSCSSGEGSAGQTVTGD HKAQTPELDQPASLNCPLD
5284	35652	A	5325	1	420	RTRGGEKE*EEKQRSRR*RIK*E EEEE*RRSRGAGDKG*NERRRR NRGEPVEKEEDRRRRKQWRR GEEKRRRRGRNCGGGGEEKE DGRRRRLPCFLLPSLLVSLW LVSFPCVFGFGAPAVVFARF RGLRAFCRF
5285	35653	A	5326	2	467	
5286	35654	A	5327	269	777	
5287	35655	A	5328	2443	2627	VGFFFFFWGGERGTGSYSVTQ ARVQ*YDLGSLQLPPSFKGFS CLSLPGSWYYRHGPPRLG
5288	35656	A	5329	57	394	
5289	35657	A	5330	33	311	HNTLPKTKPWQEPGDEEPQOE EPPTESRDPAPRLPRSP* WRSQRPQGLTRPPPEPLRPHGS PPAHLSLFCQRSCPGPQERPHPS TM
5290	35658	A	5331	226	406	
5291	35659	B	5332	51	90	
5292	35660	A	5333	1	348	PPSQRV*GWHEMRQGGRRQHAQ PVLSSQGLTAGCHHHQCRRP LACDVRPVVYVEKVSRDHGLVS GQHN/PAPESQGGSTSPRHTGR KQARAGGEKKVTS DPANTAQH NPNTGSRGRP
5293	35661	A	5334	109	380	

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5294	35662	A	5335	448	724	WPSRSALAAAGGRTAPTSPRSRAG PPAR*RGAGRESARGTS*GIRPRS QPARRPCPPAPVGRGLPPGPAP PPPRAAPREPPRCRAAAHTSRP AGS
5295	35663	B	5336	1	1554	
5296	35664	B	5337	99	366	
5297	35665	A	5338	1	714	
5298	35666	C	5339	391	689	
5299	35667	A	5340	2	614	
5300	35668	A	5341	2	461	
5301	35669	B	5342	45	1148	
5302	35670	A	5343	215	849	IKRLPLMKRMWL*LQPESLEIA GILVQ*MIE*QPKKGTNSIPVSK PSP/VVQKPNGQWRQVQDLRLI SDAVIPLYPVSNPYTLLSQILE EAEWFTVLDLKDFAFCPLRSD SQFLLAFEDPTDHTSQLTWTVF TQGFMDTPHLFGQSLAQDLGH FSSPGTLVLQYVDDLLAKQQA TLDLLNFLANQGYKLSKLKAQ LCELLVFSSCARMHS
5303	35671	A	5344	1	1035	MGQVWALVRSTLELFTDDEE EGEYDEVTEEVTEQVYLPAKA KVAQEEVHPYPSAPPHYFYEE KEWPDPPDLSFLEDTRKVVAP VTEQHLERLLSVLFRQEFSLRD ERDDAVEQLRGVCIRAWKIT GGEQYPSFSAVKQGPKEYADF IAWNLLRQESLKKVISDSAAQD IVLQLLAFGNVNLDCQAALRPI RGKAHLVDYIKACDGIGAKQD SERFAFTIPVNNLQPAKHFIY FTDGSSNGKASYSKGQGNQ PIWILSRHLKPYHEPDAKEEIPG G/CPRTPLWQPCRD*C*GGP*/P VTSNTR*TPPTWGQIKLSQM VEENLRKAGQLVTMTVYWN
5304	35672	A	5345	1566	1767	KGGSWSQRHSQACGYTCRKS GHWAKECPQPGIPKPRPCVGP H*KSDCSTHLAANPRAPGTLAG SGL
5305	35673	B	5346	1	3429	
5306	35674	A	5347	1	1776	
5307	35675	A	5348	1	933	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5308	35676	A	5349	1	1743	MGKVVAVVRSTLELFHTDDEE EGEYNEVTEITEQVYLPAKAK AVKEREQRGNITATFEPPFKLL KEFKQAINQYGPESHFVGMGLL KNVAVSSQMIPTDWDALTOAC LTPAQFLQFKTWWAHEASIQ ACNAQAQPNITITGQLLGVG WAGLDAQVVMQDDAIEQLRG VCIRAWEKIPLCGEQYASFAIK QGPKEPYVDIAWLQESLKKVI ADSAAQDIVQLSAFDNANPDC QAAL*PIRGNAHLVDYIKACDG IRGNMHKATLLVQAMAGLRVD KGNPLLPAGCFNCGKHGHTKQ ERRKKSVSQAARWGKRKTADP EICPKCKKGKYWANQCHSKFD KDGTLSIGNAMRAEQDCEWFT FTIPAVNNLQPAKHFRFTDVS SNGKASYSGSKGGQARVQLFE NASVRATNSDLPQSSLWCRRT SVSAVLVSATIPISRVQGPSQV LGQGEKQTNQNVVPNPYTL QIPEEAKWFTALDKDAFFCIPL HSDSQFLFAFEDLTDHTSQT LW TILPQGFDRDSPHLFGQALADL GHFSSPGTLVLQYVDDLLATS SEASCQATLDLFLSFLAN
5309	35677	A	5350	1	1085	
5310	35678	A	5351	1	3105	
5311	35679	A	5352	1	5172	
5312	35680	A	5353	41	324	
5313	35681	A	5354	18	270	KLSQVCIDLL*IREGERDMYPG WAKFSPSPYSLKGT*PIAQVLW SFGDFFYC/IPSTLPTPKS WRLFESPFESLTPVSLVWWPC
5314	35682	A	5355	80	384	SNRRTGAWGKCQLMSS/PLTE PQVTLTIDSQEIFLLDTGA AFS VLISCPQLSSRSVTI*GILGQPV TRYFSHLLSCNWTLLFSHAF L VMPESTPLLGR
5315	35683	C	5356	99	317	
5316	35684	A	5357	388	476	KVCPRPCRTSM/LPIRII*KLPQV CLDLL*IEGEGDMYPG*AKFPS PYCLKGT*PGTIAGSWARGVSA AASPSYSSPSY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US/N 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5317	35685	A	5358	254	849	LQPESLEIAGILVQ*MIE*QPKKGTNSIPVSKPS/GVQKPNGQWRQVQDLRLISDAVIPLYPVSNPYTLLSQILEEAEWFTVLDLKDAFFCIPLRSDSQFLAFEDPTDHTSQLTWTWFTQGFMDTPHLFGQSLAQDLGHFSSPGTLVLQYVDDLLAKQQAATLDLLNFLANQGYKLSKLKAQLCELLVFSSCARMH
5318	35686	A	5359	1	909	
5319	35687	A	5360	153	436	CFCCCVEGKNPRNLQRTTKTPRLSVMSPSSCRGRGIWPNPGTC/RPSPSLI*SRSRQTWRITTPCQQGNKTGQRMNLN*QEQAEGG*QTPLS
5320	35688	A	5361	1	1632	
5321	35689	C	5362	1	675	
5322	35690	A	5363	604	1047	SNNRTDNPTSVAYLSKETDVVAKGWPHCLWVVVAAILVLEAIKIIQKGDFTVWTSHDVNGILGAKGNSWLSDKRLRYQAALLLEGPVLQIHCTCVALNPAIFLPEDGEPIKHDYQQIVAAQTYYVT*EDLLEVPLANPDNLNLTNGSSFV
5323	35691	A	5364	749	1002	QLKKGTSNLLVSKPSVWIPGTGLTQIMGTGVANIC*PVF*KD*GELGKMNYAMMSTITQKKEENPAFLKWLWEALRKYTPLSP
5324	35692	B	5365	114	2309	
5325	35693	A	5366	413	1157	
5326	35694	A	5367	105	478	YGHCCYDHRICFFPATEQKVCPCAAQ*PL*LRGDDPEMSVYI*QLPLYSSDLLSAANEVQILAFQGDVSPFPVATTDTLSTVTNFPFNQGVNDFFDFKQFLHSSRDFCFGRVFSNFE
5327	35695	A	5368	531	1087	RLQPPGAPVEDITRPVSAKPRDADRNSTGCYLV*LQHQRQTESGRQLSGL*GPGCNGVH/ASLYRTSAMFAERFGSYRRSTTAGIPSLRLKSTIRSDRSRRKAQRKRCGQVMPQHRRSIRPLLPITPPLNRNLHRSRPHRSRNRWSRLNRRLKHHLLRRSQNRSSRWKKKLHRRVKPMCLNWR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5328	35696	A	5369	544	1381	VNPALQVLVVAITPPSPSPSCI RVLTRVSNIAIAKPLCLAVCAV VEGGRIRALVAVAAWGAAGVTG GPAGLIACGPVSPSVIRGQFRHA GISFFLYAIGGEMVPAVRRQNH TPA*HKRFKAFQLAHNAVN AEHFAGGDRHLFSLNQCQCVV KHHVRRDITFIGYRFTQFA
5329	35697	A	5370	81	863	AYGNPVEIAGGARQAGVNFITG VFRPRFSRRWRRISGETCKLWW RRWRSAAWASINQTFASWSTLIF RAISNPIIRKPDAPGVMACPRKR CCFTIRLIWRGCAVWKRSE GQLQDIERHKLNAMGAFAEAQ TCRRLVLLNYF/GRRASGAVRE LRYLPRSAETVRRFNRCSDCPF HHWSCSAVWDGLCGGSDSCC GVSRARLFASPVNLPITGEIPER GFHPFCGRRTTENGKNHPRNLFI WRSNCSVLPVKVMSCSSTPCP
5330	35698	B	5371	12	273	
5331	35699	A	5373	145	336	SEEEEEEEEEEEEEEEEEEEEE E*EEGESAIICAKVCISVFPRRK NELNMAITPNTIPKLNHW
5332	35700	A	5374	294	657	VAPGDRHAFHGGGSGLSPELTL PQTQCCAQATVQGLEGRSWS QSGTSSLSPSWHTSLACPQKEE GEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEAKTQ*KSG QK1*TDSPQKK
5333	35701	A	5375	2	588	SRPGITGSTISYGDPGHGAGPPG ADLGPASRLKPERAAGAQLAA GEARQSGDPGLPGPGHSLGTA PC*VDKGWGHVPSTVHHQRQP QPGGLRAPGTALLAGTQPSHPA AGWPWPQQRGVRVLGGRRDS *VGGG*GQHNKALWGPR*PHT EQKPRKLSRIPLRAAGGEKRG CGCDRAGCLVLGPPQLPAQGL
5334	35702	A	5376	1	445	SLSHRAGGGGVGGGAVCLFS PPRTKRESAPESPSRLVGHSPVP S*GAPSTRGSVSRILTSGGTHER SNGLTCHRNQAGTGPSALRSGR P*CLSRANPPGSKRSAGPVHEE RT*PCRLSGSAGITQ*DGN*KAG PRVPEAPERGCATC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5335	35703	A	5377	3	313	QNDEVAFRKLLKHIEDVQGKSY LTFNHGMNLTNDKMCMSVKK WQTVIEAHVDVKTNGYLLCL FCVGFTKKCNQIWKTSLF*QQ SNMEDFFVLTTGIIHSHLEPFLV VTDDQ
5336	35704	A	5378	45	764	TSFLTGGGKGS/KKKVVDPFS KKD/WL*YVKHRAMFNIRNIGK DVGSPRTQGTKIAS/DGLKG/RV FEVSLADLQNDEVAFRKFKLIIT VEDVQGK\NCLTNFHGMMDLTP* QKCCSMVKKM/WQTMl*SSPL MVKT\TDGLLASVSCVGFTKK VRNNQIRKTSYAQQVQRQIRK KMMEIMTREVQTNDLKEVYNK LIPDSIGKDIEKACQSIYPLHDVF VRKVMLKKPKFELGKLMELH GEGS
5337	35705	A	5379	3	501	SSARFVSSSSGGYGGGYGGVL TASDGLLAGNEKLTMQNLNDR LASYLKVRALAAKILSDMRS QYEVMAEQNRKDAEAWFTSRT EELNREVAGHTEQLQMSRSEV TDLRRTLQGLEIELQSLSMKA ALEDTLAET/EGDVRADSERQN QEYORLMDIKSRLEQE
5338	35706	A	5380	1	716	AQLKVKFWYWPEAGAGGLRR FKHY\YTPFKDCRDKILGATIKN SRIVLQIDNAGLAADDFTKFE TEQALRMSV*ADITGLRRVLDE LTLARTDLEMQIEGLKEELAYL KKNHEEEISTLRQVGGQVSVE VDSAPGTDLAKILSDMRSQYEV MAEQNRKDAEAWFTSRTTELT REVAGHTEQLQMSRSEVTDLR RTLQGLEIELQSLSRLWGFCC PLEGVFWVEGWEGRDPYPRLF
5339	35707	A	5381	3	832	
5340	35708	B	5382	141	1067	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \-possible nucleotide insertion)
5341	35709	A	5383	3	1316	GVAPSVLRAMTSYSYRQSSAT SSFGLGGGSRVFGPGVAFRAP SIHGGSGGRGVSVSSARFVSSSS SGAYGGGGYGGVLTASDGLI.AG NEKLTMQNLNDRLASVLDKVR ALEAANGELEVKIRDWYQKQG PGPSRDYSHYYTTIQELRDKIL GATIENSRIVLQIDNARLAADDF RTKFETEALRMSVEADINGFR RVLE*S*TLAQEPNLEDARIEG LKEELAYLKKNHHEEISTLKG KCEAQVSVVEVD/SA/PGTRSSPK ILSDMRVQYEVMAEQ/NRKDVA EA/WFTSR/TERIETREVA WPHR SSFQMSQAPRLLDLAAATPQGS *DLSCQSQLEPLKAALGKTPLA ENRKA/RFGNPQLAPYPQALDS AVI*KPQLG/DIVAKLDSSTGRI QEYQ/RLMDIKFARLEQEIHP NRSLA/LEGQEDHYNNLFAASK
5342	35710	A	5384	23	279	GCLRGSLERCGLTKLNLHEISG PESRVQQLSSREEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEERKK ECSKAQCKHFPLSEVL
5343	35711	A	5385	1	507	MEKNEKEEEEEKKEKSKKK EEEEEEEGGEEEEEGEGGEE EEEEEEEEEEEEEEEEEEEE EEEE/EEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKKKKKK KKKKKKKKKKKKKKKKKKKK RKKKKKEEEEKVVEEDEFIWF LGNSLYFPFSHFAWSQIPSRD EGERRLRVNSMIMDFTSNTNH
5344	35712	A	5386	3	259	
5345	35713	A	5387	53	387	LEEEKEEEKEEEKEEEEEE KE/DEEGEEGGEGEGEGEGE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEMIVLKIIVAKQLF
5346	35714	B	5388	1	1446	
5347	35715	A	5389	3	122	
5348	35716	A	5390	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEKI FLGHRVGI
5349	35717	B	5391	1	1269	
5350	35718	B	5392	44	244	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5351	35719	A	5393	1	626	EEGEVEEEEEEEEEEGEGEE EEEEEGEGEGEGEGEGEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEQEEEEEEEEEE EEFFAAAAAASRDSHTSL TYWPPCPALROTLVSNCS CTSGDSFW*ETTIPAMSSCS QHSLHQLGIIPQILMRMAS LRRICEDHPATAEQ**HV*GPPD
5352	35720	A	5394	2	506	
5353	35721	A	5395	1	480	
5354	35722	A	5396	1	492	
5355	35723	A	5397	1	870	
5356	35724	A	5398	111	407	
5357	35725	A	5399	1	651	
5358	35726	B	5400	1	2427	
5359	35727	A	5401	571	966	SPFTNSRLTIFISFECGQIAEIY LSQPFMVRIMATEPPINLQPGN FTL DIVSRDHTAL*PGRQEQNS VSKKKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKKKK
5360	35728	A	5402	1	1674	
5361	35729	A	5403	1	306	
5362	35730	A	5404	2	431	
5363	35731	A	5405	1	585	
5364	35732	A	5406	1	708	
5365	35733	A	5407	3	595	
5366	35734	A	5408	287	659	
5367	35735	A	5409	1	633	
5368	35736	A	5411	3	634	
5369	35737	A	5412	344	481	
5370	35738	A	5413	1	525	
5371	35739	A	5414	1	501	
5372	35740	A	5415	1	461	
5373	35741	A	5416	302	567	MLCCLEISSTRYPKSLSSSKFH KSLGQGQNAASLFAKT**RESPL LQFPASSSSPSETTSAWTLFISL SAFLTAKAFNKSLGGSKLSH
5374	35742	A	5417	251	844	NLGRGQSITLDFCAPGLIPCG SCQGLGLPHSEATARAVYWPL SAMAGVAGTQGTSLDSSLFA KT*QESPLLRFPTSSSPSETTSA FILLFISLSEFLSKPFNKSLGGSK LSHIFVSSSEPSKLSQPLHMPQ ARISSFTSGHTDDSTVLFSVLLK LPLPVPSQAFSLKPGSIVMLLS WSDNFNIPSISDSDA
5375	35743	A	5418	1	1113	
5376	35744	A	5421	1	337	

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5377	35745	A	5422	2	680	
5378	35746	A	5423	144	373	
5379	35747	A	5424	1	597	
5380	35748	A	5425	3	3319	
5381	35749	A	5426	1	612	
5382	35750	C	5427	46	168	
5383	35751	A	5428	1	663	
5384	35752	A	5429	10	417	IAIMNDTVAIRTRKFMNRLLE RKQMVIDVLHPGKATVPKTEIL EKLAQMYKTTPDVFVFGFRTH CGGGKTTGFGMIYDSLDAEK NEPKHRLARHGLYEKKKTS*K QRQERTNRMKKVRGTAKANV VAG*KPNE
5385	35753	A	5430	67	263	GKTTGFGMIYDCLDYAKKNE PKHRRARHGLYEKKKTSRKQR KERKNRMKKVRGTAKANVGA GKK
5386	35754	A	5431	2	537	TPGSTTTTKFPTASTSEDRSPIM NDVTVTIPH*EKFMQTPTYFRGN QMVIDVLSPPGKGDCPKHRK FGKKLAQNVPRPTPD/VIFVFWI QNFI FG GGTGFGMIYGFPGI YAKEKMNPDRHLCMDGLVL RKEKGPSRKANGKGTARNRIG RKVPGGTGKGNVGCWAKRR NEVSSS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5387	35755	A	5432	1	2195	ARGLSMGH*FP/PHFQCALA*M PAPGRGPPPLP/CPDAPPACA ATMERPEAGLRVAPRSPVQPGC TSVLPAKRFNARILWLKRPQR QLWSLWRAQATVSLGGFHV LSLQVHRINARVKEAWQLPPRF QMMYQKAWVLRQKPAAAVEP SQRNSPRAMLGNGVLEPPPRV STRALPSGAVGRGLPPSRPKND TATGSLHPELGKAAADIQFHPVR AATGASPCCKSIGTELPKALGAH VLLQCALDVGHGVEGELWSFK TRQPSDFSIFSPFPFYSTKPPLS SWPIPNEPLGTPPRRGRGGAEG LLTSQCSHILNGLCTGGINSNE CENVSRKKKMSEEFANTMDS LVDMPFATVDIQDDCGIFDVW KLVRVNCQEILANRHPGRAMRK VVLTKTSWEGESLAVGKLPLK RLVSLDCQLRCLQCECGILIRQ HVVWLERTTGHWHPRSSQSCR LNTTSTALEHCNAFIYNTVCSH KLKDHSHDNGKSSGLNPVAA PHSCIVMGHILTLITTSYTPLT KPDTPDLTKKEGLISQDSSSLEV LLHTDPLGKRGTPDPRVDDDSL GKFPVTNSQARKRILEPDDFLD DLDEYCEDAPKHRGKCGSA HKELDASNLEDQDKPYACDIC GKRYKNRPGLSVHYAHSHLAE EGEDKEDSQPTPVSQRSEEQK SKKGDPGFALPNNYCNFCLGNS
5388	35756	A	5433	1	580	FSPLIHILSGHSTCFRHRVGG KVTDQQDPKAEFFLVQNKMK SLPCLLLSTQTRQPSDFSIFSPF PPFYSTKPPLSSWPVLNELLGTP PRRGGGRAEG/PHFPVGPGR GAPSPRRGGWPGGLTPQPPS RTGRLARGADPPTSLPDGAA GRAGG*PHHLPPGRGGWPGRG APHFPVGAGQRRLLFC
5389	35757	A	5434	405	685	KVSHVYFYPHRPRNHPSQFFPH PSRLSIPQNRHCHHGGS/RNEPL GTPPR/PGSWPGRGAPHFPETFN HGRRWKGSRHVFTWPEQERE WGSATHF
5390	35758	A	5435	1	654	
5391	35759	A	5436	1	426	
5392	35760	A	5437	1	548	
5393	35761	A	5438	1	459	
5394	35762	A	5439	1	346	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,440,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5395	35763	A	5440	1	1248	
5396	35764	A	5441	1	1257	
5397	35765	A	5442	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRSLH AKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKIKNLQNRSTTWKLN NLLNDYWIHDEMKAIEKMF ETNENKDTTYQNLWDAFKATA SKTNKEKEKNQIDTKNDKGD TTDPTEIQTIREYKHLANK LENLEEMDKFLDTYTLPRLNQ EVESLNRPTGAEIVAIHNSLPTK KSPGPDGFTAEFYQRYKEELHI NRAKDKNHMISIDAFAKAFDKI QQPFMLKTLNKLGDGTGFKIIR AIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLFNIVLEVLR AIRQEKEIKGQLGKEEVKLSIF ADDMTVYLENPIVSAQNLLKI SNFSKVSGYKINVKQSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKINPCSWVGRIN IMKMAILPKVIYRFNAIPKLP TFFTELEKTTLKFIWNQK/RARI AKAILSQKNEAGGITLP
5398	35766	A	5443	1007	1719	TEPKTKT*LSQ*MQKKPLTKF NNPSC*KLSIN/IVLEVLRARIR EKEIKGQLGKEEVKLSLFA MIVYLENPIVSAQNLLKLSNFS KVSQYKINVKQSQAFLYTNNR QTESQIMSELPFTIASKRIKYLG QLTRDVKHLFKENYKPLLKEIK EDTNKWKINPCSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELEKTTLKFIWNQKACIAXSI LSQKNKAGGITLP
5399	35767	B	5444	1	1020	

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5400	35768	A	5445	1	1576	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSQYRIN VQES/QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKF1WNQKRARIASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNYLIFDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPLTPYTRINSRWIKDLHV RRKTIKLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYA AKKHKMKCSSLA IREMQIKTTMRYHLTPVRMAII KKSNNR/CAPGTPERQNHSL WKG*SQEPGLAQWIPLPWSP AS*DPLA*NSCCQHSLKSTWD AQACARKLRTLIGYRNCQLE
5401	35769	A	5446	1	984	
5402	35770	A	5447	1	1563	
5403	35771	A	5448	1	1449	
5404	35772	B	5449	1	1605	
5405	35773	B	5450	1	1569	
5406	35774	A	5451	1	690	MSELPTIASKRIKYLGIQLTRD VKDLFKENYNPLLNEIKEDTNE WKNIPCSWVGRINIVKMAILPK ATVTKIAWYWYQNRDIDQWN RTERSEIMPHIYNYLIFKKPEKN KQWGKDSLFDKWCSENWLAIC RKLKLDPLTPYTKINSRWIKD LNVRPKTIKLEENLGITQDIGI GKDFMSKTPKAMATKAKIDK WDLIKLK/FCTAKETTIRVNRQS TKWEISSL
5407	35775	A	5452	1	1919	

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5408	35776	A	5453	1	1416	MIILIDA EKAFDKIQQPFMLKTL SKLGT DGT YLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTTRQGCPL SPLL FNIGLEDLARAIRQEK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQI MSELPTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQWNRTEPSEIMPHTYNYLI FDKPEKNQWQKDSLFFHKWC WENWLA VCRKLKLDPLTPYT KINSRWKDLNIRPKTIKLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRPQTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL
5409	35777	B	5454	1	810	
5410	35778	B	5455	1	1277	
5411	35779	B	5456	130	1701	
5412	35780	A	5457	1	1395	
5413	35781	A	5458	3	1646	
5414	35782	A	5459	1	759	
5415	35783	A	5460	2821	5781	
5416	35784	B	5461	1	2025	
5417	35785	A	5462	1	3663	
5418	35786	B	5463	1	2265	
5419	35787	A	5464	1	2241	
5420	35788	A	5465	1	2478	
5421	35789	A	5466	1	2067	
5422	35790	A	5467	1	2988	
5423	35791	B	5468	1	2061	
5424	35792	A	5469	1	2141	
5425	35793	A	5470	1	400	
5426	35794	A	5471	2	2507	
5427	35795	A	5472	1	768	
5428	35796	A	5473	1	1527	
5429	35797	A	5474	1	1293	
5430	35798	A	5475	1	1038	
5431	35799	A	5476	1	1572	
5432	35800	A	5477	1	1290	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5433	35801	A	5478	1	524	MSELPFRIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNK WKNISCSWVGRINIVKMAILPK/ VKHR/FSACIQLGRSGTTGLE ALAM*PIWPQVEV*VKFPALPS GASSTKGGCVP*QIQVEERLLS WKL*QA*TSWYQQRQSSSL RERK*PKSIQRNVRLSYYP
5434	35802	A	5479	2	1547	
5435	35803	A	5480	1	2376	
5436	35804	A	5481	1	1824	
5437	35805	A	5482	1	1071	
5438	35806	B	5483	1	1839	
5439	35807	B	5484	1	1368	
5440	35808	A	5485	1	1884	
5441	35809	A	5486	1	1053	
5442	35810	B	5487	1	2532	
5443	35811	A	5488	1	2373	
5444	35812	A	5489	1	2361	
5445	35813	A	5490	1	2274	
5446	35814	A	5491	1	1686	MASPGAPTASPPIHSELLTATR EAQRHHPVPRGQDLVTSEFSL SFCFSAAFIFELLGNSSEGVTDL RLWLCQPAPRCGEWTYNPLEQ CCDDGVILDNLQTRLGSSSTCF WPCFQHCCLSLGSONQTVVRF KVPGMKPDCKSSPITRICAQAG VQISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASQ RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA LIAKSILSQKNKAGGITLPDFKL YYKATVTKTAWYQNRDID QWNRTEPSEITPHIYNLIFDKP EKNKQWKGDSLGNKWCWENW LAICRKLKLDPFLTPYTKINSRW IKDLNVRPKTIKLEENLGITIQ DIGMSKDFMSKTPKAMATKDK IDKWDLIKLSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSLSLAIREMQIKTTNQNHM RYHLTPGHG
5447	35815	A	5492	1	1872	

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5448	35816	A	5493	195	1494	PPGQHLQRRCLLRVSGFSENAK KGMLEVLARA\NRQEKKIKGIQS GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKALGYKISV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYGF NAIPKLPMTFFTELEKTTLKFI WNQKRARIAKSILSQDKAGGI TLPDFKLYYKATVTKTACNSN GSQSPWMEEQIRDAWGSMLVK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTD\TSLTSPAAPMVD SLIARVGVMMARGNAITLPVCGR DVKFTLEVLRGDSVEKTSRVW SGNERDQELLTEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLGGE DDEQMAALSRLGNDY
5449	35817	A	5494	1	1845	
5450	35818	A	5495	1	2109	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, ~-possible nucleotide insertion)
5451	35819	A	5496	1	2535	MKSGHPEKEQDNDVQETREIT IRGLLCTALMRHSTGAIAIYLG VLSGSASLLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETHIVLPSNVIN FSQAEKPEPTNQGDLSKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIVYVLGLDICRPFVSRVSEE GRMGQRGEEDANSDFPPASLL CLICQEQGVNGESCSPVGMYYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAFAFDKIQQHF MLKTLTKSLGIDGTYLKIIATYD KPTANILNGQKLEAFPLKTGTR QGCPSPPLFNIVLEVLAIRAIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSDQNLKLSNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPICSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELEKTTLKFIWYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNLYFFDNPDKNKK WGKDSLFFNKWCWENWLAICR KLKLDPLTPYTKINSRWIKDL NIRPKTIKLEENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLSFCTGKETTRVNRQPT
5452	35820	A	5497	3	2284	
5453	35821	A	5498	1	1245	
5454	35822	A	5499	1	1140	
5455	35823	A	5500	383	1185	
5456	35824	A	5501	1	3159	MLEVLAWAVRQEKIKGIQLG KEEVKLSLFADNMTVYLENPIV SAQNLKLSNFSKVSGYKVS GQKSQALLYTNNRQTESQIMSEL PFTIASKRIKYLGIHLTRDVKDL FKENYKPLLKEIKKDTNWKWNI PCSWVGRINIVKMAILPKDIIQE NFPNLARQANIQIEIRKTPORY SSRRATPRHIVRFTKVEMKEK MLRAAREKASHHTYSKIDPILG SKPLLKSKCRTEIITNYLSHSAI KLEFRIKNL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
5457	35825	A	5502	583	2515	MQKKPLTKFNPPSC*KLSIN*LI SNFSEVSGYKISVQKSQAFLYT NNR/QESQIMSELPFTIASKRIKY LGQLTRDVKDLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKAIYRFNAIPIKLPM FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNLYIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFPTYTKINSRWIK DLNVGPNTIKTLEENLGITQDI GTGKDFMSKTPKAMATKAKID KRDLIKLSNFKTAKETTIRVNR QPTKWEKIFTTYSDDKGLISRIY NELKQIYKKKTNNPIKKWAKD MNRHFSKEHIYAAKHKMKCS PSLAIREMQIKTMTMYHLTPVR MAIHKSENNSLLAAGGGNRRRT ANVVAHGAFANLLTLDKKTLEI LVHYDPSEIRILMKKARVLLKQ KAKTAEATPPRKDALLPFPKE ETPKLFKTLGGTGKASLARLL KLKREQAQKKESEGGESE KENEDKQKENEDKQKENEDKG KENEDKDKGREPEEKPLDRPEC TASPIAVEEPHSVRRTVLPRT SRQSLISMASAEAGGEEVLTIE
5458	35826	A	5503	1	2463	
5459	35827	B	5504	1	1221	
5460	35828	A	5505	1	4494	
5461	35829	A	5506	1	2825	MARTSYGQHFFPTLISMNIDSG RQNGIPKLSYSYSLKPMNTLC YLVRKRDLEGVLKRLITWESSL DYPGGPSVITKVLIRQKEGQSQ RTRYDNGSRGWSDAIAVKRPQ AKECGWPLEAGKGKEWILRKE CIPANTLMLAQCPPTLRVGGVS CSAWRMIONSDGERKKRNRIQL QAVRLSKVHIDTFRNFRFVHS RELSKGAEKSSSLKKGLEQVII WTKRCQCGESRCTKKVEERKV LHNTFISTSTTITLTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, √=possible nucleotide insertion)
5462	35830	A	5508	1184	4791	TSMQKSSIKYVQTESSTSKSLSTMIKWASSLGCKAGSVYANQ*M*SSI*TEPKTKTI*LSQ*MQKPL/YKIQQPFMLKTLNKLQNL LKLISNFSKVSGYKINVQKSQA FLYTNNRQTESQIMSELPFTIAS KRKYLGIQLTRDVKDLFKENY KPLLKEIKEDTNKWKNIPCSWV GRINIVKMAILPQVIYRFNAIPIK LPMTFFTELEKTTFKFIWNQKR ARIAKSILSQKNKAGGITLPDFK LYYKATVT
5463	35831	A	5509	516	2233	
5464	35832	B	5510	286	4131	
5465	35833	B	5511	1	4911	
5466	35834	A	5512	1080	3119	SSGLHPWDARLVQYTQINKCN PAYKQSQRQKPHDYLNCRKK AFDKIQQPFMLQTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSLLFNIVL EVLARAIHQEKEIKGQLGKEEV KLSLFADDMIVYLENPIISAQNL LKLISNFSKVSGYKINVQKSQTF LYNNNRQTESQIMSELPFTIALK RIKYLGQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIVNQKRA RIAKSILSQKNKAGGITLPDFKL YYKATVTKTAWYVYQNRDID QWNRTEPSEIMPHIYNYLIFDKP EKNKQWGKDSL FNKWCWENW LAICRKLKLDPFTRYTKINSR WIKDLNVRPKTIKTEENLGITI QDIGVGKDFMSKTPKAMAACA KIDKWDLIKLSFCTAKETTIRV NRQPTTWKIFATYSSDKGLISR IYNELQQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKHKMKK\ CSSSLAIRVEMQIKTMMRYHLTP VRMAIHKSGNNRIRRHQPRS AMFFCCCPGEGSGLQWELL LAAWTVLPYPCPAA TVGRFLKQ AQTADHSFLGHVVRVPSSRSW TDKEILSLVNNRQNEVVQLIG LCGTHTISPTQHPATG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \-possible nucleotide insertion)
5467	35835	A	5513	2494	4549	LQTLQGYSNSKQHGTTGKTFA WYWYQNRDIDQWNRTEPSEIT PHIYNLYIFDKPDKNKKWGKDS LFNKWCWENWLVICIKLLDP FLTPVYTKINSRWIKDLNVRPKTI KTIEENLGNTIQDIGMGKDFMS ETLKARATKAKIDKWDLIKLS ECTAKETTIRVNRQPTKWEKIF AIYSSDKGLIPRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEDI YAAKKHMKCCSSLAIREMQI KTAMRYHLTPVRMAI
5468	35836	A	5514	1	5582	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQAADLIDYQTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTQIITNYLSDHS AIKLELRKLNLTQNHSTTWKLN NLLLN DYWVYNEMKAEIKMFF ETNENEDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQKLEKEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFERINKIDRLARLIKKKRE KNQIDTIKNDK
5469	35837	A	5515	3371	5375	TDTSQKKTTFMQPKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRSWYFEKINKIDRL LARLIKKKREKNQIDAINKDKG DITTDPTIEIQTTR EYKHL YA NKLENLEEMDKFLDTYNLPRL KQEEVESLNRPGRSEIVAIINSL PTKKSPGPDGFTA EFYHRYKEE LVPLLLKLFQSIEKEVILPNSFYE ASIIIPKPRDRTAKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5470	35838	A	5516	314	2695	GSACRDPDPDPLRLVGGGAAA PPCSSVSPSAWRQSRPREYYEG GRGLHAPDRETALGLGIATSER MLGICRGRRKFLAASLSLLCIPA ITWIYLFSGSFEDGKPVSLSPLE SQAHSPTYASSQRERESLEVR MREVEEENRALRRQLSLAQGR APSHRRGNHSKTYSMEETGD SENLRAGIVAGNSSECGQPVV EKCRRNPLHFHLIADSLAEQILA TLFQTWMVPAVRVDFYNADEL KSEVSWIPNKHYSIGYGLMKLV LTKTLPANLERVIVLDTDTFAT DIAELWAVFHKFKGQVVLGLV ENQSDWYLGNLWKNHRPWPA LGRGYNTGVILLLLDKLRKMK WEQMWRLLTAERELMGMMLSTS LADQDIFNAVIKQNPFLVYQLP CFWNVQLSDHTRSEQCYRDVS DLKVIHWNSPKKL RVKNKHVE FFRNLYLTFLEYDGNLLRREL GCPSEADVNSENLQKQLSELDE DDLCEYFRFRERFTVHRTHLYFL HYEYEPADSTDVTLVAQLSM DRLQMLEAICKHWEGPISLALY LSDAEAQQFLRYAQGSEVLMS RHNVGYYHIVYKEGQFPVNNLL RNVAMKHISTPYMFLSDIDFLP MYGLYEYLRKSVIQLDLANTK KAMIVPAFETLRYRLSFPKSKA ELLSMLDMGTLFTFRYHVWTK GHAPTNFAKWRTATTPYRVEW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5471	35839	A	5517	3	2079	GKPVSLSPLESQAHSPTYASS QRERESLEVRMREVEEENRALR RQLSLAQGRAPSHRRGNHST YSMEEGTGDSNLRAGIVAGNS SECGQQPVVVEKCRRNPLHFHLI ADSIAEQILATLFTWMVPAVR VDFYNADELKSEVSWIPNKHYS GIYGLMKLVLTPLPANLERVI VLDTDITFATDIAELWAVFHKF KGQQVLGLVENQSDWYLGNL WKNHRPWPALGRGYNTGVILL LLDKLRKMKWEQMWRLTAER ELMGMLSTSLADQDIFNAVIKQ NPFLVYQLPCFWNVQLSDHTRS EQCYRDVSDLKVIHWNSPKKL RVKNKHVEFFRNLYLTFLFYD GNLLRRELFGCPSEADVNSNL QKQSELDEDDLCEFRERERT VHRTHLYFLHYEYEPADSTD VTLVAQLSMDRLQMLEAICKH WEGPISLALYLSDAEAQQLRY AQGSEVLMRHNVGYHIVYKE GQFYPPVNLRLNVAMKHISTPY MFLSDIDFLPMYGLYELRKSV IQLDLANTKKAMIVPAFETLRY RLSFPKSKAELLSMLDMGTLFT FRYHVWTKGHAPTNFAKWRT ATTPYRVEWEADFEPPYVVR DCPEYDRRFVGFVGNKVAHIM ELDVQYEFIVLPNAYMIHMPH APSFIDITKFRSNKQYRICLTKL EEFQQDMSRRYGAALKYLTA
5472	35840	A	5518	403	2757	
5473	35841	B	5519	128	353	
5474	35842	A	5520	2	333	
5475	35843	B	5521	25	1359	
5476	35844	B	5522	1	1113	
5477	35845	A	5523	1	2526	
5478	35846	A	5524	3	555	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5479	35847	A	5525	1	1710	MSQGTTPWGPTPAGTTPSEVH RPFPPVPVPVPEPVSERSFPVRG VCGQAKSGLRRGAARLAPAAAY LFTTRQQTRELIHSACVSISVNTM HGLSVAINSRRCTYYRKYYVIDF SKSEIIGIPISKNIDLTVGTTVTQ LQNLNTVGIHGRGGRGQVAAL NCDRQGHLLWLFTRTVHWRM GNDRTFWGLLDTVSELMFIPGN PKHHCGPPVKVGAYGVTFGLV HWCAGACQDTPCKMKDKLLHL APPTTKKKAQYVVGLLGFWRPI YRVTQKAASFEGPEQDKALP QVQAAVQPALLFGPYDSADPM VLEASVADRDAVWSLWQAP/IS HKMGHAQQHSIIKW*YICDW ARAGPKGTTAPMASWGVLVD QLTEEEKTRAFTDGSARYAG TTQKWTAALQPLSRTSLKGS GEGKSSQWAEQLQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDKWKGDKKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
5480	35848	A	5526	1	438	
5481	35849	A	5527	1	612	
5482	35850	A	5528	2	736	EKCAMTALSSKLISQQKAFFAK MVVDVAVMMLDDLQKLMIGI KKVQGGALEDSQLVAGVAFKK TFSYAGFEMQPKKYHNPKIALL NVELELKAEDNAEIRVHTVED YQAIVDAEWNILYDQKLEKIH SGAKVVLKSLPIGDVATQYFA DRDMFCAGRVPEEDLKRTMM ACGGSIQTSVNALSDVLRGRCQ VFEETQIGGERYNFTGCPKAK TCTFILRGGAEQFMEETERSLH DAIMIVRRA
5483	35851	A	5529	3	474	
5484	35852	A	5530	374	968	
5485	35853	A	5531	1	568	
5486	35854	A	5532	1	2136	
5487	35855	A	5533	1	240	
5488	35856	A	5534	248	1034	
5489	35857	A	5535	1	1602	
5490	35858	A	5536	120	340	

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5491	35859	A	5537	2	408	DEDDDDDEEDDEDDDDDDF DDEEAEEKAPVKKSIRDTPAK NAQKSNQNGRDSKPSSTPRSK GQESFKKQEKTPKTPKGPSSVE DIKAKMQASIEKGGSLPKVEAK FINYVKDCFRMTDQEAHQDLW QWRKSL
5492	35860	A	5538	194	1027	WSFISIHLLSYLSACHLMEDS/ MDMGMRLRPQNYLFSCELKA NKDYHFKVDNNEHQPLPLTTI NLGAGAMDELDIVEAEAMNYE GSPKIVILATLKMSVQPTVSLG GAFETPPVVLRLKCGSGPVHIS GQHLVAVEEDAEEDEEEDV KLLSISGKRSAPGGGSKVPQKK VKLADEDDDDDEEDDDDED DDDDDFDDEEAEEKAPVKKSIR DTPAKNAQKSNQNGKDSKPSS TPRSKGQESFKKQKTPKTPKG PSSVEDIKAKMQASIEKAH
5493	35861	C	5539	212	367	
5494	35862	A	5540	14	1515	
5495	35863	A	5541	1	540	
5496	35864	A	5542	1	1881	MDAALDDLIDTLGGPEETEEEN TTYTGPEVSDPMSSTYIEELGK REVITPPKYRELLAKPIGDDAI DALSSDFTCGSP*LYPSQVFHLL DLLPFPSPGYQRLQLQHILA/AVP FKVAGSGGADCILHMEVRDTA SDTGAGAAALDSSVFSVGLDGF SLHSDRSKSSSSSSMSDSLRLG LFSSGSGNSGFPSSLVAGFNLYS DGI VSSSPHFSFSSLAFASSSTS LIERSSSGSACRPVSEADRASS
5497	35865	A	5543	1	930	
5498	35866	A	5544	1	183	
5499	35867	A	5545	1	555	
5500	35868	A	5546	162	499	FPGSGNMAKDAGLIEANGELK VFIDQNLSPGKGVVSLVAVHPS TVNPLGKQLLPKTFGQSNVNIA QQVVIGTPQRPAASNTLVWVG SPHTPSTHFASQINQPSDSSPW/S AGKR
5501	35869	A	5547	2	451	LVAEFAADNHILPNESA YDQK NIRRRVYDALNVLMAMNIISKE KKEIKWIGI.PTNSAQECQNLEV ERQRRLEIRIKQKQSLQELILQ QIAFKNLVQRNRHAEQQASRP PPPNVSIHLFPFIIVNTSKKTVIDC SISNDKFEYLFNFNDNT
5502	35870	A	5548	37	162	

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5503	35871	A	5549	205	616	RKLHGSQSSITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRGNNQHISSTYDINR ADAQVRRRAVNNYDIHMSNSF NGQSEHQVWIGGQFTFIKFPIN SVSIRCARQEGIMSSPGQVQG
5504	35872	B	5550	1	1407	
5505	35873	A	5551	3	416	MLPARMC GGIVSG*OFITGNSY DHDYEFELGTRSA*KLKLFST LPD*QLPAGSGEGPYHLEGQLS YCHRGGEKALALLSSPTSKTR SPSEPDEQDEQKLRFCKRHLY GQQPRSPVEIRLQHVIAIAYQTH HAYD
5506	35874	A	5552	1988	2137	LVITTLPLACGTAK*E*VNVTS FGSRPICSTSPVLFSL*GPVKF IDT
5507	35875	B	5553	1	561	
5508	35876	A	5554	1	492	
5509	35877	A	5555	3	1055	
5510	35878	A	5556	1	634	
5511	35879	A	5557	1	723	
5512	35880	A	5558	1	384	
5513	35881	A	5559	1	792	
5514	35882	A	5560	3	1607	HCTRM SVK WTSVILLIQLSFCFS SGNCGKVLVWAAEYSHWMNI KTILDELIQRGHEVTVLASSASI LFDPNSSALKIEIYPTSLTKTEL ENFIMQOIKRWSDLPKDTFWLY FSQVQEIMSFIDITRKFCCKDVV SNKKFMKKVQESRFDVIFADAI FPCSELLAEI.FNIPFVYLSFSPG YTFEKHSGGFIFPPSYVPVMSE LTDQMTFMERVKNNMIYVLYFD FWFEIFDMKKWDQFYSEVLGR PTTLSETMGKADVWLIRNSWN FQFPHPLLPNVDVFGGLHCKPA KLPKEMEDFVQSSGENGVVV FSLGSMVSNMTEERANVIASAL AQIPQKVLWRFDGD/KPDTLGL NTRLYKWIQNDLLGHPKTRA FITTHGGANGIYEAHYHGPVGI PLFADQPDNIAHMKARGA AVR VDFTMSSTDLLNALKRVINDP SYKENVMKLSRIQHDQPVKPI. DRAVFWIEFVMRHKGAKHLRV AAHDLTFWQYHSLDVIGFLLV CVATVIFIVTKCLFCFWKFAR KAKKGKND
5515	35883	A	5561	2	1600	

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5516	35884	A	5562	2	1624	AATGKQALHCIRMSMKWTSAL LLIQLSCYFSSGSCGKVLVWPT EFSHWMNKLTILDELVRQGHEV TVLASSASISFDPNPSTLKFEV YPVSLTKTEFEDIKQLVKRWA ELPKDIFWSYFSQVEIMWTFN DILRKCKCDIVSNKKLMKKLQE SRFDVVLADAVFPFGELLAELL KIPFVYRPRFSPGYAIEKHSGLL LFPPSYVPVMSSELSDQMTFIE RVKNMIYVLYFEFWFQIFDMK KWDQFYSEVLGRPTTLSETMA KADIWLIRNYWDFQFPHLLPN VEFVGGGLHCKPAKPLPKEME/E FVQSSGNGVVFVSLGSMVSN SEERANVIASALAKIPQKVLWR FDGNKPDTLGLNTRYLYKWIPQ NDLLGHPKTRAFITHGGANGIY EAIYHGIPMVGVPLLADQPDNI AHMKAKGAAVSLDFHTMSSTD LLNALKTVINDPLYKENAMKLS RIHHDQPVKPLDRAVFWIEFVM RHKGAKHLRVAADHDLTWFOY HSLDVTGFLACVATVIFITKC LFCVWKVVRTGKKGKRD
5517	35885	A	5563	1	225	
5518	35886	A	5564	1	3210	
5519	35887	A	5565	1	835	
5520	35888	A	5566	222	477	HPRCLSPKGILKYLTKKYLKKN NLRDWLRVVANSKESYELRYF QINQDEEEDEED*ISFIWKILYE FLNKTDWDPKKKKTKKKKK
5521	35889	A	5567	1	778	MAAAAAAGDSDSWDADAFS VEDPVYKVGGGTAGGDRWG GEDEDEDVDNWDDEDEKK EEAEVKPEVKISEKKIAEKIE KERQKKRQEEIKKRLEPEEP KVLTPEEQLADKILRLKKLQEE DLELAKETFGVNNNAVYIGDAM NPSSRDDFEFGKLLKDINTQYE ESLYYARFLEVLVRDVCISLEID DLKKITNSLTVLCEKQKQEKQ SKAKKKKGGVVPGGGLKATM KDDLADYGGYDGGYVQDYED
5522	35890	A	5568	1	897	
5523	35891	A	5569	1	2658	
5524	35892	A	5570	1	441	
5525	35893	A	5571	3	427	

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5526	35894	A	5572	1	952	PRLVLLKMAPI.DLDKYVEIARL CKYLPENDLKR.LCDYVCDLLL EESNVQPVSTPVTVC.GDIHQGF YDLCELFRITGGQVPDTNYIFMG DFVDRGYYSLETFTYLLALKAK WPDRIITLLRGNHESRQITQVYG FYDDCLTKYGNANAWRYCTK VFDMLTVAALIDEQILCVHGG SPDIKTLADQIRTIERNQEPHKG AFCDLVWSIDPEDVDTWAIN PRGAGWLFGAKVTNEFGS*ST NLKLCIRAHQLVHEGYKFMFD EKLVTVWSAPNYCYRCGNIA MVFKDVNTREPKLFRAVPDSE RVIPRRTTTPYFL
5527	35895	A	5573	54	588	
5528	35896	A	5574	1	4287	
5529	35897	A	5575	1	507	
5530	35898	A	5576	1	1416	
5531	35899	A	5577	1	841	ILLWDVDGGTLQIDKYLYSSED YIKSGALLACGIVNSGVRNECD PALALLSDYVLHNSNTMR.LGSI FGLGLAYAGSNREDVLTLLL MGDSKSSMEVAGVTALACGMI AVGSCNGDVTSTILQTIMEKSE TELKDTYARWLPLGLGLNHLG KGEAIEAILAALEVSEPFRSFA NTLVDDVCA.YAGSGNV.LKVQQL LHICSEHFD/SKEEEDKDKKEK KDKDKKEAPADMGAHQGVAV LGIALIAMGEEIGAEMALRTFG HLLRYGEPTLRRVPLALAL
5532	35900	A	5578	2	391	AFGVTEPGCYGV.DVDTGKSTL FVPRLPASHATWMGKL/HSVLT SQKPSVLLTLRGVN.TDSGSVCR EASF.DGISKFEVNTILHPEIVE CRVFKTDM.EVLRYTNKISSE AHREVMKAVKVG.MKEYELER

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5533	35901	A	5579	18	1541	RRCRANMAAATGPSFWLGNET LKVPLALFALNRQRLCERLRKN PAVQAGSIVVLQGGREETQRYCT DTGVLFRRQSEFFHWAFGVTEPG CYGVVDVDTGKSTLFVPRLPAS IIATWMGKIHSKEHFKEKYAVD DVQYVDEIASVLTSQKPSVLLT LRGVNTDSGSVCREASFDGISK FEVNNITLHPEIVECRVFKTMDM ELAEVLRYSNKISSIEAHREV/MK AVKSGEWKEYGVGKASFEHY\ CYSRG/GMRHITSYTCILRAVG *GTS AVLTFTHAGAPNDRTIQ NGDMCLFDMGGEYYSVADIT CSFPRNGKFTADQKAVYEAVL LSSRAVMGAMKPGDW WPDMA HRLAYRIHLEELAHMGILSGSV DAMVQAHLGAVFMPHGLGHF LGIDVHDVGGYPEGVERIDEPG LRSLRTARHLQPGMVLTVEPGI YFIDHLLDEALADPARASFLNR EVLQRFRFGGVRIEDVVVID SGIELLTCVPRTVEEIEACMAGC DKAFTPFSGPK
5534	35902	A	5580	1	98	
5535	35903	A	5581	1	810	

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5536	35904	A	5582	1	861	MLKEIIDDTNKWKHIPCSWMGRISIVKMTILPKAIYKFNAVLIKIPPSFFTELEKTILKFLCNEKRAKAKARLNKKNKSGGITLLDFKRYYSIAIVTKTVWYWKYKRNRIHQRRNRIENPEINPNTYSQLIFNKANKNIKWGNDFLFSKWCWDNWLATCRRMKLDPHLSPHTKINSRWIKDLILRPETTKILEDNIGKTLDDVGLGKDFMTKNPKANARKAKINIWDLIKLKSFFTAGKGTVSRVNRQPTWEKIFIHTSDEGLLISRIYNELKQISKKKITNNPIKKWAKDMNRQFSKEDVQMANKYMKKCTSTLIANLICREMQIKTTMQYHLTPARMAIIKSKISRCWHGCGDQGTLLHCWWECKLVQPLWKTVWRFLKELKVELPFDPAIPLGTHPEEKSLCKDCTCMLLAAQFTIAKSWNQPCKPSVNEWIKKLCPRWLLSKWASA*NKWKHIPCSWMGRISIVKMTILPKAIYKFNAVLIKIPPSFFTELEKTILKFLCNEKRASRAKARNKKNKSGGITLLDFKRYYSIAIVTKTVWYWKYKRNRIHQRRNRIENPEINPNTYSQLIFNKANKNIKWGNDFLFSKWCWDNWLATCRRMKLDPHLSPHTKINSRWIKDLILRPETTKILEDNIGKTLDDVGLGKDFMTKNPKANARKAKINIWDLIKLKSFFTAGKGTVSRVNRQPTWEKIFIH
5537	35905	B	5583	473	1694	
5538	35906	A	5584	1	429	
5539	35907	A	5585	572	1149	PPVSHSMTLGNLSYLFAPNWTITPAW/CNTLDPSEGFQWQASLSLPSHQQFEHTCPEWLPTYSWPCKVGPDYLSICQPECKQHFQESLLESSKQNIYETCAIYVSSPGERILNQRFGPHGAFILVREYDDIRFHSQPPSTCPNFGPSYYTARESAYALKLRALIIQISQSTKMQRNLGNPILPAIHQQPPQ
5540	35908	A	5586	1	804	
5541	35909	B	5587	1	1995	

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5542	35910	A	5588	74	1128	LLLDL*VD*SPSRPLEMRFRV*P MKRCTLKKNYLSFLVYISRL *NRVKAIM/VGKAIEWKTIELPL PRKTVNQKQYRIPGGIAEIST11 KELNNAGMVIPTTSPFNSPIWP VQKIDGSRWMTVDYCKLNQV VTPIAATVPYVVSSELEQIN/TSPG T/WNRKRFNCNRSRLHLKLLCHL GHMTQQI*CFLRQCWHIGMLF GPEICGCTLSGQKL/WKIFVSH AASFWSPEQEKALQQVQAVV QAALPLGPYDPADPVLLEMSV ADRDVWILWQAPISEQWRPP GFWSKALPSSADNYSFPERQLL ACYWTLVETERLTMGHQVTIPP ELPIMNWVFSDLSSPKMCHPQQ
5543	35911	A	5589	1	1337	MIISIDA EKAFDKIQPFMLKTL SKLEETASPSPVVATYTPQPM PSAFPPLSEEINPVL PETTVMAS PEAVTRQDNVDSPOKPPPTPMF ASRPITRLKPRRAPSEEGIQLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGAKWKPLEQPP PRKIVIQKQYHIPGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSRWMTVNYHKLNQVET PIAAVDPDVSLLEQINTSPGT WYAAIDLNVVFSIPVYKAHQK QFAFSWQQQYTFFTFLPQGYIN SPDITL VHYIDIMLIGSSEQEV ANTDLLPARVASWGVYPDQL T/GGRED*GLLHRWSCRICRHH
5544	35912	A	5590	2	693	KIVN/QKQYHRIHGGIAEISATIKD SKDTGVVIPTTSPFNSPIWVPVW KTDGSRWMTVDYHKLQDVVTPI AAAVPDVVSLEQINTSPGTWY AAINLENAFFSIPVHKANQ/KQF AFSWQQQYTIAPVQ/VKFLG IHWFVACQDIPSKIKDKLLHLA PPTNKKEAQCLVGLFGFWRQH PHLRVLLQPIYQVTLKAAIFEW GPEQEKALQQVQAAVQAAALPL GPYDPTDPMVLE

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5545	35913	A	5591	1	1011	MVSTPATLPSLPKALMASWG VPYDQLTKEEKTRVWFTDGS RYAGTTQKWTAVLQPLSR TKDSSEKSSQWAEQAVYLV VHFAWKEKWPDPVGLYTD SWAVANGLAGWSETWEKQD WKIGDKEIWGRGMWMDLSE SKAVKIFVSHVSAHQRVTS AEFEFNNQVDRPL/PVFTQ WAHEQSGHSGRDGGYSWA QQTGLPFTKADLAMATAE CPICQQRPTLSPLYS TIPQGDQPA TWQIDYIGL PLPSWKGQKFVLTVIDTYS RYFAYPAHNASAKTTIHGL IECLHCYGIPIHSIADQSIH /TTKEVQ*WAH AHGIHWS YHVSHHPEAAAGL
5546	35914	A	5592	7	278	SASCTAAFHQMEVVYTRSG SRS*R/PTIPVIAQWDYDHN GHGGRDGGYPWAQQHELPL TKADLATATAECPICQQRPS LSPRCGTIPR
5547	35915	A	5593	1	237	
5548	35916	C	5594	63	116	
5549	35917	A	5595	2	739	HKMGHAQQHSIIKW*YICD WARAGPKGTTAPMASWGVL YDQLTEEEKTRAWFTDGS ARYAGTTQKWTAAALQPL SRITSLKSGEGKSSQWAE LQAVHLVVHFSWKDKWPD VRLYIDSWAVANGLAGWS GTWKKHDKWIGDKEIWGR GMWMDLSEWPKPVKIFG SHVSAHQWVISAEDFNNQ VDKMTCSVDITQPLSPAT PVITQW AHKQSGHGGRD GGYTWAQQHGLPLTKTGL AMATAECP
5550	35918	A	5596	1	354	
5551	35919	A	5597	3	592	
5552	35920	A	5598	126	365	QLAEPHPWLDP*KAGAFW GPEQKKALQ*VQAAVQAAL PLGPYDPADPMVLVSVAD KDAVWI FHLSGSDRWRR TYRCL
5553	35921	A	5599	1	483	
5554	35922	A	5600	1	1908	
5555	35923	B	5601	141	1569	
5556	35924	B	5602	46	1533	
5557	35925	A	5603	61	448	WRFLGPWRIVSCWFCGWE ERR EGSFAFFVGIPARMSA ARESHPHGVKRSASPD DDLGSNNWEAAAYLGNE ERKQKFLRLMGA/GKGEE DQKINEELESQYQHSMD SKLSGRYRRHCGLGFEV EDHDGEGD

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5558	35926	A	5604	1	404	PWRIVSCWFCGWEEERREGSAFF VGIPARMSAARESHPHGVKRSA SPDDDLGSSNWEAADLGNEER KQKFLRLMGAGKKKEHTGRLVI GDHKSTSHFRTGVEDHDGEGDV AGDDDDDDDDSPDP*SPDDSES DSESE
5559	35927	A	5605	2	434	LGPWRIVSCWFCGWEEERREGS AFFVGIPARMSAARESHPHGVK RSASPDDDFFLFAIMNGK*KIV NSHRCSVKAKSRQQLGSSNWE AADLGNEERKQKFLRLMGAGK KEHTGRLVIGDHKSTSHFRTGE ED*KINEELESQYQH
5560	35928	C	5606	909	1096	
5561	35929	A	5607	1	309	PQPAAMAAYIWLIRHGESAW NLETFSFGWYDATLSLAGHKE AKRGGQALRGLFQVPLAPEAV GTVWCWSWRTPCALKQL*PRPL KRRLRILADRHATQPRPQQ
5562	35930	A	5608	93	914	SQSVPHQPAPAMAAYKLVLG/ RHGESAWNLENRFSGWDDADL SPAGQRGGERFAAQLQDAGY EFDICFTSVQKRAIRTLWTVL/ DAFDQMWLASGEGWGFNER HYWGS*PGLN*KQKLAAKIG*G PRLKIWRRSYD/VPPPPMEPDH PFYSNISKDRRYADLTEDQLPS C/ESLKDITARALPFWNIEIVPQI KEGKRVLIAAHGNSLRGIVKHL EGLSEEAIMELNLPTGIPIVYEL DKNLKPDKPMQFLGDEETVRKA MEAVAAQGKAKK
5563	35931	A	5609	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFYSPLDLLKLHDERVLVAF GQRDGIIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANY VSIRFGRPRLTSNEKLMASMF HSIKFVVLADP/RQAGIDSLRK IYEIYSDFALKNPFSLEMP
5564	35932	A	5610	1	663	
5565	35933	A	5611	1	2034	

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5566	35934	A	5612	374	1106	IPVSRQGSQDWRFFSVYVVNKA GGLIYQLDSYAPTGLRLEKTF YPLDLAGSS*HDERVLVAFGQR GRHPEWGHAVLAINGMDVNG RYTADGKVEVLEYLG*PLLNY VSIRFGRPRL/TSNEKLMGLP CFHSLFAIGSQACLPGTREASR HLKILGRQDTFKLHICYQTLTG IKFVVLADPRQAGIDSLRKI YEIYISDFALKNPFIYSLEMP IR CELFDQNLKLALEVAEKAGTF
5567	35935	A	5613	1	336	
5568	35936	B	5614	60	2175	
5569	35937	A	5615	2	198	
5570	35938	A	5616	1	449	
5571	35939	A	5617	1	771	
5572	35940	A	5618	18	736	EAMSSKVSRDTLYEAVREVLH GNQRKRRKFLETVELQISLKNY DPQKDKRFSGT/VQVGTVLIPPS PQCPRACPSAGSR*AGGGHVG TDVLG*FRPPAPGRRGWTDPHP GS*NMRRGGVGRPPSPASLRS QAGCW*M*TLRVRLGWLLRSQ TLHRLGTPGLGVTWCWCCPPK RRLKSTPRPKFSVCVLGDQQHC DEAKAVDIPHMDIEALKKLNK NKKLVKKLAKKYDAFLASESLI
5573	35941	A	5619	24	698	EAMSSKVSRDTLYDAVREVLH GNQRKRRKFLETVELQISLKNY DPQKDKRFSGTVRLKSTPRPKF SVCVLGDQQHCDEAKAVDIPH MDIEALKKLNKKNKTGSRSWP KKYDAFLA/SQSPLIQADSPKSL GPISLNGKRSKSSPLLTHNKNM VAKVDEVKSTIKFPNWRRCCL CL AVAVGVHVKMTDDELVYNIHLA VNFLVSLKKNNWQNVRLYIK SPMGKPQRLY
5574	35942	A	5620	1	843	

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5575	35943	A	5621	3	1215	LLIMADPRDKALQDYRKLLLE HKEIDGRLLKELREQLKELTKQY EKSENDLKAQSVGGQIVGEVL KQLTEEKFIVKATNGPRVYVVG CRRQL*QKVSLKPGTRIVALAD MTTLTIMEDILPRIEVDPLVYN MSIHEDPGNVSYSEIGGLSEIQI RGI*GEVIGLPLYKPQSYFQRVG IIPPKIGCLLYGPPGTGKNT/LLA RAVASQLDCNFLKVVSSIVDK YIGESARLIREFNYARDHQPCI IFMDEIDAIGGRRFSEGTSADRE IQRTLMELLNQMDGFDTLHRV KMTMATNRPDTLDPALLRPGR LDRKIHIDLPNEQARLDILKIHA GPITKHGEIDYEAIVKLSDG/FN GADLRNVCTEAGMFAIRADHD FVSTGKTSLKAVRKVADSKKL ESKLDYKPV
5576	35944	A	5622	104	173	
5577	35945	A	5623	1	1140	
5578	35946	A	5624	1	528	
5579	35947	A	5625	1	1083	
5580	35948	A	5626	1	471	
5581	35949	A	5627	1	2322	
5582	35950	A	5628	1	678	
5583	35951	B	5629	213	1477	
5584	35952	A	5630	2	339	FGLHKWGLGLEASSPCGPLTPS YLGFPRPHPGTLGLGRFWPFLA LQSLSETPSHARMPRVTVARTS PETLEISPLRAAT*NHRSSGHTC FRERMLRVSCRLSLDLSSSWVR
5585	35953	A	5631	1	783	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5586	35954	A	5632	92	2746	ASRMTVLQEPVQAAIWQALNH YAYRDAVFLAERLYAEVHSEE ALFLLATCYRSGKAYKAYRL LKGHSCTTPQCKYLLAKCCVD LSKLAEGEQLSGGVFNKQKSH DDIVTEFGDSACFTLSLLGHGII VQTERAAKGTAFSKRLCLHTF PWTPLPLEVEIGERPLPHQTFN FTS*RNFANCLHTSGTKQVTN HVFHRQPETVLTETPQDTIEL NRLNLESSNSKYSLNTDSSVSYI DSAVISPDVTPLGTGTSILSKP VQNKPKTGRSLGGPAALSPL TPKFWGFLPIRKPPSPGDSY LQNYTNTPPVIDVPSTGAPSKK TFRVLQSVARIGQTGTSVFSQ SGNSREVTPIAQTSSSGPQTST TPQVLSPTITSPNALPRSSRLF TSDSSTTKENSKKLKMKFPPKIP NRKTKSKTNKGGITQPNINDSL EITKLDSSIIEGKISTITPQIQAF NLQKAAAEGLMSLLREMKGK YLALCSYNCKEAINILSHLPSHH YNTGWVLCQIGRAYFELSEYM QAERJFSEVRRIENYRVEGMEIY STTLWHLQKDVALSVLKDLT DMDKNPESGTQRGRESPRMC GADSQIEKSQSSYFIQDLRSFDY VKFAVVTKIRAWCAAGNCFSL QREHDAIKFFQRAIQVDPNYA YAYTLGHEFVLTEELDKALAC FRNAIRVNPRIYNAWYGLGMI
5587	35955	A	5633	260	678	GEFSIFFWVWN*LLLWHQETFS I*NLFSSH*TSITYQATEEGDFDII QMKLIHFGDSIFIYLLKLLINRK P**EAAISI*V*TWRSRFSHFQLR *HQTQVTNHSWFTEAR*LTDLV KSKSPTIPCSRFKANTLF**SDP
5588	35956	A	5634	1	1452	
5589	35957	A	5635	2	1563	
5590	35958	A	5636	1	444	
5591	35959	A	5637	2	345	

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5592	35960	A	5638	2	1721	RSREAAA VAAAAATTAFCGR1 WNPCAALTMKQSSNVPAFLSK LWTLVEETHTNEFTWWSQNGQS FLVLDEQRFakeILPKYFKHNN MASFVRQLNMYGFRKVVHIDS GIVKQERDGPVEFQHPYFKQGG DDLLENIKRKVSSSKPEENKIRQ EDLTKIISAAQKVQIKQETIESRL SELKSENFSLWKEVSELRAKHA QQQQVIRKIVQFIVTLVQNNQL VSLKRRRPLLLNTNGAQKKNL FQHIVKEPTDNHHHKVPHSRTE GLKPRERISDIIIVDVTDDNAD EENIPVIPETNEDVISDPNSCSQY PDIVIVEDDNEDEYAPVIQSGEQ NEPARESLSSGSDGSSPLMSSA VQLNGSSSLTS:EDPVMTMDGFP FGMDNIQSFWGRVELLDYLDLS IDCSLEDFQAMLSGRQFSDPDL LVDLFTSSVQMNPTDYINNTKS ENKGLETTKINN VQPVSEEGK ENLKS(KPDK)QLIQYTAFFLLAF LDG\NPASSV*TGRTTASFRKF CPL*DKPIEVDELDDSLDPEPT QSKLVRLPLEL TEAEASEATLFLY LCELAPALDSDMPLDLS
5593	35961	A	5639	2	251	QLRSPLKWKKAQRQPLAIAHV LLLRPRKKRONGFTVRYARLL STLPRSWRRKQWY*AQNHVRS PEWKWHYQSL
5594	35962	A	5640	70	297	
5595	35963	A	5641	3	985	
5596	35964	A	5642	1	3501	
5597	35965	A	5643	1	1752	
5598	35966	C	5644	1	879	
5599	35967	A	5645	21	519	LHHPVRTLSRCRFVGVCRWSTPG PVCGLISSGGCRTVDIAALQLW LRGLALPEQLLRVDPHPQACRR LPREPPGPGQTFTGREPPQAVS TKEASSNNLHAPERTVAGLTFT TEQVRALEGVFRHHQYLGPLE RNWLAREMQLSRSR*KPGFKI AG*NTNGKCRTPS
5600	35968	A	5646	90	2401	
5601	35969	A	5647	776	1018	
5602	35970	B	5648	1	1296	
5603	35971	A	5649	1	1257	
5604	35972	A	5650	731	4841	
5605	35973	A	5651	325	9497	
5606	35974	A	5652	1	322	
5607	35975	A	5653	1	819	

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5608	35976	A	5654	56	251	
5609	35977	A	5655	149	701	
5610	35978	A	5656	3	415	
5611	35979	A	5657	3	467	AIASPRAGIRHELTSTMAAGK NKRLTKGGKKGAKKKAV/DNII NIGKTLVTRTQRTKIASDGLKG RVFEESLADLQNDVTDGYLLRVI *VAFTTERTNQ/REVFNKLIPDS IGKDIEKACQSIYPLHDDFARK VKMLKKPKFELRKLMEHGG
5612	35980	A	5658	2	418	PRVRADGKNFRLTKGGELGAR NKVVDPFSKKDWYDVKAPAM FNIRNIGKTLVSRQTGKTIASDG LKGRVFEARLADLQNDVAFIK CKLITDDVHGKNCLTIFHGMDL TRDKM/CSLGKKWQTMIEAHV DVKTTDGYLL
5613	35981	A	5659	3	121	
5614	35982	A	5660	1	237	
5615	35983	A	5661	25	967	FSPAAGIRHEGLTSTMAVGKN KRLTKG/GKKGS/KKKVVDPPF R/KDWY*RRKHPLMFHYKNIG KTLVLTQDPKGPKIA/SDGLQGF VCLKVSLADLQNDVSRKF RLITEVCFRGKNLP*LTSHGAW DLYPVTMKCSHGQKNWQTM DSSR*MFKTNPMPGYLALRLFLC /VGFT*KNRNQFRLRKAPPYAS ATQQVPPKSRKKM/MEIMTPR GARQNDLEKKWVNKLIPRQAL GKDIRKGPQSYFIPLHDVLR EKLKLEGS/KF*IGESSLGASM GGRAVVPGKSHLGTGTGAKVG TSLMGYEPPVPRILV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US/N 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5616	35984	A	5662	1	2142	MIILIDAEKAFDKIQPFMLKTL NKLIGDGTLYKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSISVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLAIRAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSL FNKW CWENWLAICRKLKLDPLTPYT KIHRSWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELQIYRKK/TNN PIKKWAKNMNRHFSKEDIYAA NRQMCKCSSLVIREMQIKTTM

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5617	35985	A	5663	1391	2742	KKRESSLTHVMRPA SF*YQSQAE ETQKKRILDQY P**TL MQKSSI K/YLAKRIQGHKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHHIISIDAEKAFDKIQPPF MLKTLNLKLELETTV KFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSL FNKWC WENWLAICRKLKLD PFLTPYTK INSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIFTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSSEDIYA AKKH MKKCSSLAIREMQIKTTMRVH LTPVRMAIIKSGNNRHAPFSIH THIMFGSLYLIQKDL SILGFW YPRGILEPIY
5618	35986	A	5664	1	1910	MTIIHIIIIIIITIIHVIITINIVIT TTILTTVIISSTIIHITFVFETGAI KLEIRIKLTLQNRSATWKLNNL LLNDYVWHNEMKAEIKMFET NENKDTTCQNLWDTFKAINKID RPLARLIKKKREKNQIDA IKND KGDITTDITGIQTITIREYYKHLY ANKLENREEMDKFFDTYTL PRL NQEEVESLNRPI TGSKIEEINSL SIKSPGPDGFTA EIFYQRYKEE LVPFLLKLFQSIEKEGILNSCCE ASHILIPKGRD TT KENFRPISL MNIDAKILNKT LANRIQQHITK LIHHIVQVGFI PGMGWFNIRKS INNWKKTTLKLIWNQKRACITK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEASEIIPHTYNYLSFDKPDKN KKWGNNSLFNKWCWENWLAIC CRKLKLD PFLTYTKINSRWIK DLNFGTETIKTLEENLGNIHDI GMGKDFMSKTPKAKATKAKID KWDLIKLSFCTAKETTIRVNR QPTWEKIFAIYPSDKGLISRIY KELKQVYKKKTNNPIKKWAKD TNRHFSNEDIYA ANRHMKKCS SSLAIREMQIKTTMRVHLPVR MTIIKSGSNRQ/W*ASGHVRC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
5619	35987	A	5665	1	2460	MPHAGHARSPGHTLIKLAEWWM MSRWMEWNPFGPLSIDAKCHK DLPRDIQDFSEKGVDFVLNYSK ALNQEEVESLNRPIITGSEIAIIN SLPTQKSSGPDGFTAIFYQRYK EELVPFLLKLFQSEKEGILPNSF YEASILIPKPGRYTHKKNFRPI SLMNIDAKILNKILANRIQQHIK KLIHQDQVGIIPIGMQSWFNHKK SINVIQHINRTKDKNHMIISIDAE KAFDKIQPFMLKTLNKLGIK YLRIQLTRDVKDLFENYKSL NEIKEDTNKWNIPCSWIGRMN IHKMAI/LPKVIYRFNVIPIKLPM FFSELEKSTLKIWNQKRARIK TILSQKNKAGGIMLPDFKLYYK ATVTKTAWYQYQNRDIDQWN RTEPSEMTPHYNHLIFDKPDKN KQWGKDSL FNKWCWENWLAI GRQLKLDPLTPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI SMGKDFMSKTPKAMATKAKM DKWDLIKLSFCTAKETTIRVN RQPTWEKNFAIYSSDKGLISRI YKQLKQIYKKKTNNPIKKWAK DMNRHFSKEDVYAANRHMKK CSSSLAIREMQIKTIMIYHLTPV TMAIIKSGNNRCWRGCGEMG TLLYCWWDCKLVQPLWKTW QFLRDLGLGIPDPAIPLGIYPK DYKSCCYKDTCTPKLARDQI HILKQHRKLETRQKQYRAW
5620	35988	A	5666	689	1909	LIA YQPKKSRTRWIHNQILPERI KYLGIQLTRDVKDLKEKYKPL LNEIKEDINKWNIPCSWIGRIN LVKMAIL/PQAICRKLKLDPLT TYTKINSRWIKDLHVRPKTTKT LEENLGNTIQDIGMGKDFMSKT PKAMATEAKIDKWDLIKRRKSFC AAKETTRVNRQPTDWEKMFA IYSSDKGLISRIYEELKQIYKKK TNNPINKWAKDMNRHFSKEDI YAANRHMKKCSSSLAIREMQIK TTVSPFAAQWVSQRYGK WQEA HPSNNNDGKGYRGKPRFQSLSD VHGPQDQKKIIESALPPTPTFI NILMNAKTIENGQFPYLLNALK QQQPHDAENLFTWGKENAIV SPCIEVSAALSQWK VPAWPQRS GIPNRILRSPIGLGSWVAFDL VWVRGDPTALK

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5621	35989	B	5667	1	1962	
5622	35990	B	5668	1	1851	
5623	35991	A	5669	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNCKSN VIQHINRAKDKNHMIIISIDAEKA FDKIQQLFMLKTLNKLGDGTY FKIIIRAIYDKPTANILNGKKLEA FPLKTGTRQGCPSPLLFNIVLE VLARAIQKEIKEIGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLEKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTPQSEITPHIYNLIFD KPDKNKQWKGKSLFNKWCWE NWLAICRKLKLDPLTPYTKIN SRWIKDLNVRPKTTKLTLEENLG ITIQDIGMGDMFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFTTYSDDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSPLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGC GEIGTLLHCWWINWMKKTWH IYTMEEYASIKKNEFMSFAGA* MKLETII
5624	35992	A	5670	2	1967	

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5625	35993	A	5671	1039	2272	KKRESSLTHVMRPASF*YQSQA ETQKKRILDQYP**TLMQKSSI K/YLAKRIQGHKKLIHHDQVGF IPGMQGWFNIRKSSINVIQHINRA KDKNHMIIISIDA EKAFDKIQPP MLKTLNKELEETT VKFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDLSLFNKWC WENWLAICRKLKLPFLTPYTK INSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIIFTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYAAKHH MKKCSSLAIREMQIKTTMRVH LTPVRMAIHKSGNN
5626	35994	A	5672	1	3477	
5627	35995	A	5673	1	2814	
5628	35996	A	5674	1	2093	
5629	35997	A	5675	1	2724	
5630	35998	A	5676	1	4680	MDKFLDITYLPRLNQEEVESLN RPITGSEIVAIINSLPTKDDPGPD GFTAIFYQRIKYLGIQTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWYGRINIMKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARITKSILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNR AEPSEIML PIYNYLIFDKPDKNKQWGKDSL FNKWCWENWLAICRKLKLPFL LTPYTKINSRWIK
5631	35999	B	5677	1	1989	
5632	36000	A	5678	1	2784	
5633	36001	B	5679	1	3573	
5634	36002	B	5680	1	2630	
5635	36003	A	5681	5339	10577	
5636	36004	A	5682	1	873	
5637	36005	A	5683	1	672	
5638	36006	A	5684	1	435	

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5639	36007	A	5685	I	1011	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGGGLQPGQR VLYKQSIAGRARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMLATIIANC IVLALQHLDPGDKTPMSERLD DTEPYFIGIFCFEAGIKIALGFV FHKGSYLRNGWNVMDFFVVVL TGRKAGLGCCSGVSEGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSSELKE/DVRIHRK EAKNLEKRLDKM/VNRSNVEK TLNDPMELKTMARELCDACTS FSS*FNQVEEKVSVIEDQMDEM K*EEKFREKRVKRNEQSLQEIW DYVKRPNRLRL
5640	36008	A	5686	I	1539	
5641	36009	A	5687	I	756	MDDPRLNVKPLTESLETYSKGS KGLEGDVITDSKLNDCRCPST KLPEEGLGSNCCSAIFAVLQPL LVIPRQTGSGVDHQQTPDRLM TVRRKMNMKGIASTSTKRTK KDIHTKTPSVCHQHQRPKDCSP SPATEQSWMENDLEELTEIGFR RSVITNFSSELKEDVRIHHKKAK NLGKRLDEWLTRINSVEKTLND LMELKTMARELHDSCTSFNSRS NQAEKVSVIDQFNEIKREEK FREKRVKRKN
5642	36010	A	5688	I	1008	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGGGLQPGQR VLYKQSIAGRARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMLATIIANC IVLALQHLDPGDKTPMSERLD DTEPYFIGIFCFEAGIKIALGFV FHKGSYLRNGWNVMDFFVVVL TGRKAGLGCCSGVSEGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSSELKEDVRIHRK EAKNLEKRLDEWLTRMNSVEK TLNDLMELKTMARELDACT FSSQFDQVQEMVSVIQDQISEM KREEKFREKRVKRNE/QLQ*I WDYVERPNRLRL
5643	36011	A	5689	I	672	
5644	36012	A	5690	I	807	
5645	36013	A	5691	I	1617	

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5646	36014	A	5692	1064	1893	LLEGSININKKDIYTKTQSVGRQ HQRPKVDKTTKMRNQNRKA ENSKNQSASSPPKDCSSSPAME QSWMENNFDELTEIGFRRSVIT NFSCLKEDVQTHCKEAKNLKK RLDECLTRINSVEKKTLNDLME LKTMAQELHDTCTSFNTQFDQ VEERSVIEDQINEIK*EEKFRE KRVKINE*SCQEIWD*VKRPNI HLITVPESDGEKGTLENTLQDI IQENFHNIAEQANIQIEIQRTA QRYSSRTATPRHIVRFKAVEM KEKVLRAARKKG
5647	36015	A	5693	3	620	EAGWLLSSVDEVMKENDEL DSISLQKQILSLKSAKIALTESL ISFRERAIEVEKQTQALIM*VAD LQGGNDQTFQGLDGTSELTLI PGDPKHHCPPGPKVRAYGDO VINGVLAQVQLIVGPVGPWTHP VVISPVPECVIGAILNSWQNP HIGSLTGRVRAIMVGISWQGGQY TFTVLPRQYINFPALCHKTAKR HTARR
5648	36016	A	5694	1	1098	
5649	36017	A	5695	2	563	IIRRAVFRWFVG*RSWGLNMIR PQNTKDSNSNCKLEKTDSPWC ELFKELYKINAFDTPDLSLLMRG NEFSDPIHHTFDHMRWRTKEHNE AGWLLSSVDKVMKENDELGDS ISLQKQILSLKSAKIALSESUS CRERAIEVEK*T*ALIMLVADL Q*KVHAQPHHAQPRQVSTVKV RALIVLQEVTD
5650	36018	A	5696	1	499	FVLVDVNNMWHRYASMLYER RLLIICSKLSTLTACIHGAAML YPMYWQHVVYTPVLPPHLLDYC CAPMPYLIGIHLSLMEKVRNMA LDDVVILNVDNTNLTETPFDDQ SLPNDVISSLKNRLKKVSTTTG DGVARAFKKAQAFFGSYRNA LKIEPEEPTFCEEA
5651	36019	A	5697	1	795	
5652	36020	A	5698	103	3531	
5653	36021	A	5699	1	2073	
5654	36022	A	5700	1	901	
5655	36023	A	5701	148	639	
5656	36024	A	5702	1	318	REYGTPEQELNALLTLNFLSL PKGQMLSAAEQHLQKPAKTE A/GRMIWQRDPITKIWEIGKIT WGRGYACVSPGQNHQSVWIPS RHLKSCGHGDAKEEIPGGS

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5657	36025	A	5703	1	612	PTRPIKHITDIPYNSEGOAIVER MNLSLKQQLQKHKKGGK/SKD YGTPHMQLNLALLTLNLSLPLK GQILSVAEQHLQKPAKTEAEQ LVWWRDPITKS*EIGKIITWGK GYACVSPGLTQQPIWIPSRHLK PYHEPDAEEEEIPGSGRGPPPPV/ DSHVETDAEEPHCHEQHLNNT ATHLGTDDQEA VTAGGRKPEES KTTSHNK
5658	36026	A	5704	2	791	
5659	36027	A	5705	2301	2620	DGQQLIALHRLALRELQQAGH AGLPQQA KILFDGGSEIGKIRGL QRPRAKNRLSGRGPLREPSPK*F FGVQGRKTLNRTLKGAPH*NL AAKAGKPLSPCTSGRIRM
5660	36028	A	5706	1	1010	MDDIPQEA GRYRHNQAYAYS QGDGAEDDDERIVRFHTRVT DSDTLASDAARLTCRHGLGNQ GSDLVLYGTSTPKNLIWVRVH VVGHRPDRRFFAFDVWSPRLI VDSCSKLEQHSTLSRAILLIYKG FCRFRNHQTFSPAGANQRGP LAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGFPTGKRAVSATQLMD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQANVQQFIDEGNYTS GDNHTLRDPHYVEDKGHKYLV FEANTGTENGYQGEESLFNKA YYGGGTNFRKESQKLQQSAK KRDAELANGALGHIELNNDYTL KKVMKPLITSNTVTDEIERANV FKMNGKWYLFDTDSRGSKMTID GINSNDIYMLGYVSNLSLTGPYK PLNKTGLVLQMGDPNDVTF YSHFAPVPAKGNVVTSYMT RGSSR*RQRP*IPCIRSQHGNRK RIPR/SKNLYLTKRTTAAARTSS VKKARSFSLRALKNAMLS*RTAP
5661	36029	B	5707	1	1149	
5662	36030	B	5708	55	3947	
5663	36031	B	5709	4	885	

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5664	36032	A	5710	461	1560	SLQTRDLPISEPPSNRIFACWGK PAWTACCNLSLRARR*RAISCCP SH*KRIPRRRIFI*PKRTTAAART SSVKKARSFSRALKNAML*RT APSV*S*IMITH*KK*SR*SLQ TRDLPISEPPSNRIFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGIPDWKAGSERNAI NGAIALIEGFRPLTLEPSSLIVNS CSKLEQHSTLSRAILLIYKGFCR FRNHQTGFSPAGPNQRGPLAA TLGPGGEGQSAVARLTGEKK NHIPGAQYANRLSPRVGRFINAA GTTGFTGKRAVSATQLM
5665	36033	B	5711	1	1458	
5666	36034	B	5712	1	3573	
5667	36035	A	5713	606	1005	GGMLCGTLSPDGEQGSAAVAR LTGEKKHPRGDQ*QKAPLLAR W/RNPLMQLAQ/PDFTGKRRAI DTHRSVSHAHIIITHSSTLSSDIS HTDAPNTSSNNYVIAITSPSDTA PSTRPLHRIHHHTPIPIATLARP
5668	36036	B	5714	1	1566	
5669	36037	C	5715	29	2314	
5670	36038	A	5716	597	1384	ISYTVPEALSARSNPAACQHAS CRPAACPVASVGSRPQAPGGA GGHRHWPRRRWRLRQRPSPA PGRPRRRPRPRRHRRRRPRPH HHAPPPRPSCAETRSRRGGGRR PLPRPLPPGAAGAGHREVGDK AGAAGCGRRVVALAA/PVSPPS SPSSPSPLLAAVGVAGCFSAE LSDSRLLAPGGEGPLARSPAR CDPAAGSACPAWSSRQRRC ELMCAAGISCWHTGHCTWCSL SFMPVLVLMILAASFRPVAVSSH
5671	36039	B	5717	1	3873	
5672	36040	C	5718	356	784	
5673	36041	A	5719	1303	1664	KRRDEIIPCVLKQLLVTFITCR ASCINESANARGEAVCVLGAR VV/SSFHQ*DGQQLIALHRLALR ELQQAVHAGLPQQA KILFDGGS EIGKIPYKSKE*PENRLSVVPVW EQUESTLASV

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5674	36042	A	5720	453	915	TVSRWAMLEHILLFSREPSNKE PET*AHSM*ADDKRFAAYKKK TKGGTERWDKYGRPPANGIRT GENNAKTEHLRDRDQKR/PRER ERAR*TTTEITEQEGSG*GEPVEQ MRKKRAQAWSRRKSTGSGQTET RSVRVTRVGLKTASESRRTM EQN
5675	36043	B	5721	319	1469	
5676	36044	B	5722	164	3112	
5677	36045	A	5723	1	1102	MRWTPGHEITKALQTFQRYTGI QHVHRIGMAERMWCDNRNR HTVSSSGGNRLPNPEHFEAFQS VAQCTYNQTVQLDITAFLLKT KKNKHKFYPAFIHILARLMNAH PEFRMAMKDQVDSCKLEQHS LSRAILLIYKGFCFRFNHHQTGF SPAGANQRGPLAATLSGPGGEG QSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAAGTTGFPYTK RAVSATQLIYRELFPQPLVQLD PCSVPQMPPSPKSRRAWVSDI ALLEFQKKKEMEKKKEKERKK ELQGGRRRRGGGWGKGRER GGRGKKRRGGGEAIRDAEKAG RLPHPDMEIRGRVEQRVGYTIE QINHMARDVFGTRLRLRAEDVFP VIGVAHKGGVYKTSVSVHLA QDLALKGLRVLLVEGNDPQGT ASMYHGWVPLHIHAEDTLLP FYLGEKDDVTYAIKPTCWPLG DIIPSCALHRIETELMGKFDG KLPTDPLMLRLAIETVAHDYD VIVIDSAPNLGIGTINVHPAWS AISLLEYSPLAGFVASIPAPL QLVPRWDTKPVLEDASASSRFS IPQRNPTHILHTTSFPCNDPTV DAWMRFLITWCLYTSPTYSLM GELFPFYQGMLESTKQGSQVR KVFVWTLVPNNNTQPSRAI LLIYKGFCFRFNHHQTGFSPAG ANQRGPLAATLSGPGGEGQSA
5678	36046	B	5724	90	6258	
5679	36047	A	5725	837	1485	
5680	36048	A	5726	1	2993	
5681	36049	A	5727	1	123	
5682	36050	A	5728	1	960	
5683	36051	A	5729	507	755	NKRGYKQMEEHSLMGRKNQ YRKNGHTAQNL*IQCHPHQA TNDFLHRIKGNDFQVHMEPKK SPHRQVNPKEQSWRHAT

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5684	36052	A	5730	274	882	PDQVDRGGAHWQTDADDPWL ADHLQHCQRCGEILRHYSGGIR GNVSAYKCAEHVPAFARLRN PQCGDFQLRDYRLFDSPGVKRR EL*TA YRFCHVAP*LMDLRSG WAAGAVYRYQSH*FTADRLRSV VDMDEAGNHHSQQT\SQDQKI KQRTFSLISGS*TTTRTHGHREGN ITHRGLSRPNTARILCASKAHLG LPLRSSLP
5685	36053	A	5731	114	329	
5686	36054	C	5732	1	1983	
5687	36055	C	5733	1	588	
5688	36056	A	5734	1	597	
5689	36057	A	5735	1	721	MTSYNEQNKKPVTDPNEMAIH EDSNQEFKIAVVNETQSRSSP TEHLMTPPLPTREQPPLT VIF HYLPKSYKTAPPLSPFDSLFGL SQPAPRDMDEAGNHHSQQT K QEOKTKHCMFSLTSGS*TMRT H GHREGTVIHRGLLGQFSQQLN KSEFNTVCREKSGRVLQVNM ESPL*MIQDALQDQTPPKGPITV FL*LFYLDHLLRSSHKVASYLST ESRSRGSITVLFIRCSEP
5690	36058	A	5736	417	696	DRNRKANTACFQHSQVGEQ* EHMDTGKV*SI*YGNYEHTSTC ERMEIQKATTEHLNL*S*SGSFL RFTWKMLQFSKISR SFYQVLKH QQKIM
5691	36059	A	5737	325	1489	RSPTLLMHVHYIKVISWRELLLI WLRANASINPGVEQSPSGDPK TVTGPFPLRLEAADWVEEASVP KGVHIALSSQEQRAGDPRDLEA PSNLVISERTHRFRVSWTPPSD SVDRYKVEYYPVSGGKRQEVV RTPGPVPLRLPAIIPQAAWLI.A HLPAPSA PPTLEPTKHTEAQSQ RCWSLLCSVTEVAAPSQVVK EAPPSFHTGTENGYQGEESLFN KAYYGGGTNFFRKESQKLQQS AKKRDAELANGALGHELNNDY TLKKVMKPLITSNTVTD EIERA NVFKMNGKWYLF TDSRGSKM TIDENKIPRNPTYKGREGPLQGE LQTTAQGNKRGYKQMEEHSM LMDRKNQYRENGLT AQAPQPP PSGI*GYTAPCFPWENLI
5692	36060	B	5738	1	873	

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5693	36061	A	5739	274	716	QACYIYTTEYYAAIKNDEF/TVL CRDMDEAGNHHSQQTVTRTKN QTPHVLTHRWELNNENTWTQE GEHHTPGPVMLDSAPPTLGHQT PGSSAFGLWDLHQRLRLPRPQT KGSTVGFPGSEAFKLGLGHYW LSFFPSLQTAYRGTLPFNH
5694	36062	B	5740	134	2283	
5695	36063	A	5741	3	872	
5696	36064	A	5742	1	480	SKLNSGDGCWSGARRGSAHSR SPLPSPLRPRAKMA TEGLHENE TLASLKSEAESLKKGLEERAK LHDVELHQVAERV/VGPGAVC HEDQKDPQRPREQSPVHGLVQ R*EEDRELVTGWEGDRVGFLLH HKQGARGHHALHVGDMCLC PIGMCHCLWWFG
5697	36065	A	5743	3	387	AKMATEGLHENETLASLKSEA ESLKKGLEERAKLHDVELHQ VAERV/VGPGAVCHEDQKDPQ RPREQSPVHGLVQR*EEDREL VTGWEGDRVGFLLHKKQDPDSER RWHMCPVGRGERAAAAELPRT
5698	36066	A	5744	1	1575	
5699	36067	A	5745	20	510	
5700	36068	A	5746	1	1392	
5701	36069	A	5747	1	1560	
5702	36070	A	5748	3	325	
5703	36071	C	5749	206	409	
5704	36072	A	5750	1	855	
5705	36073	C	5751	233	571	
5706	36074	A	5752	1	3600	
5707	36075	A	5753	1	4137	
5708	36076	A	5754	3	1357	
5709	36077	A	5755	3	194	
5710	36078	A	5756	3	269	
5711	36079	A	5757	1	1770	
5712	36080	A	5758	164	411	RKNRKPNTAFLTHKWELNNEN TWTQGGNITHQG/CWGVQG*R RDSIRRN1*CKCRVPGCSKPPW HVVYTYTNLHILHMPRT

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5713	36081	A	5759	1	3095	MKMADAKQKRNEQLKRWIGS ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLLKLLHR GADINYNVDGLTALHQACID DNVDMVKFLVENGANINQPDN EGWIPLHAAAACGYLDIAEFLIG QGAHVGA VNSEGDTPLDIAEEE AMEELLQNEVNRQGV DIEAAR KEEERIMLRDARQWLN SGHIN DVRHAKSGGTALHVA AKGY TEVLLKLLIQAGYDVNIKDYDG WTP L HAAA HWGKEEACRILVD
5714	36082	A	5760	1	591	FTVTRCYAVAQEGTYFDGSGY AALVKEGYKVQSDVNITLEVS NIPRRNGVFLGISTAIVHAI GLEL VDGKVL FHVNNGAGRITAA YE PKTATVLC DGK WHTLQANKSK HRITLIVDGN AVGAESPTQSTS VDTNNPIYVGGYPAGVKQKCL RSQTSFRGCLRK LALIKSPQVQS FDFSRAFELHGVFLHSCPGTES
5715	36083	A	5761	340	739	
5716	36084	A	5762	1234	1897	
5717	36085	A	5763	1	4070	VTPRAAWLGLGFRGSAVLGLC WQPRSPPSRAAGMMNRTPDQ ELVPASEPVWERPWSVEEIRRS SQSWSLAADAGLLQLQEFSSQQ TISRTHEIKKQVDGLIRETKATD CRLHN VFNDFLMLSN TQFIENR VYDEEVEEPVLKAEAEKTEQE KTREQKEVDLIPKVQEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVEILILEPKDLYIDRPLP YLIGSKLFMEQEDVGLGELSSE EGSVGSDRGSIVDTE
5718	36086	A	5764	1	972	

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5719	36087	A	5765	1	2193	MVPYSLLVTWLQKALGVRQY HVASVLCQRAK VAMRPFEPKY IHYDLLEKNINIVCK*LNRLTL SEKIVYRHPDDPTSQEIERGGTY LQQWPDSVTMQD/ATAQMAM LQFISSRL/SKVTMPSTIHC DHLI EAQLGSEKDLHQAKDINHEVY NFLATGSVKYGLSFWKPGSGII HQIILENYEYPGVLLIGTDSHTP NGGSLGGICIGVGA/DAVDVM TGIPWELKCKPVIGVKLMGSL GWTSPKDVILK VAGILTMKGG TGAIVEYHGPVVD SICTGMVT VCNMGLEIGTTTSVFHYNLRM KKYMSKTCQADIANLADEFKD HLVPDPGCHYDQLIEVNPSELK LHJNGPFTPDLAHPVAEVGKVA EKEEWPLDI*VGLWGCTNSSY EDMGCSAGVAKQALAHGLKC KSQFTITPCSEQIRASIEQDGYA QTLRDVGGIVLANACGPCIGQL HRKDINKQEKNIIVTSYNRNF GHNDTNPETHAFITSPETVTA AIVGTLKFPNETNYLTGKDGGK FKLEAPDADELQAEPGPGQDT YQHP*PWGTTD HISAAGP*LKFR GHLDTISNNLLSGAINIENGKAN SVHDAVTHEFGPPDTARYKK YGISWVWIGD*NYGKGSSWEH AALEPHRLGGRAITKSFARIHE TNLRRQGLLPLTFADPADNKIH LVDKLTIQSLKDLT/PGKPLKYI
5720	36088	B	5766	3	1205	
5721	36089	A	5767	435	1428	
5722	36090	A	5768	1	615	
5723	36091	A	5769	79	381	DKPOPHLQHTRTSKRLNRSSQA FLQNLPLQELATSAGNLAIRP NACSLGFLVSRVPSLAATPRAP WNSGPRLSD*LLPRSSRLSS*RL TLPDRLGSPVDH
5724	36092	A	5770	38	452	
5725	36093	A	5771	435	524	
5726	36094	A	5772	284	411	
5727	36095	A	5773	1	354	
5728	36096	B	5774	1	942	
5729	36097	A	5775	1	417	
5730	36098	A	5776	88	279	EDLGRSQSESLGPEFG*VVAIE TIWPTPEKIFTICLSGSHSQSPW NSGPRLSD*LLPRSSQLSS*RLT LPNRLRSLQDHHRCR

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5731	36099	A	5777	206	816	FIDSMSPSRVQ*LSSQNWKKL L*ISYGTKNPEA*PKQS*AQRTK LEASH*LTSNCTTSLH*SKQHGT GTKTEKT*AIPFT*AWAKTS* LKHHQKWQQKPK*TKKIKYLG IQLTTDVKDLFKENYKPLLNEI KEDTNKWNIPCSWIGGINIMK MAILPKVIYRFNALPIKIPMTFF TELEKTTLNFIWNQKRARIAT LSTKNKAGGITLADFKLYYKPT LVKTAWYWYQNREENLGNTIQ DIGMGKNFMTKTPKAMATKA KIDKRDLIKPKSFCIAKETTRM NRQPTWEWELFAIYPSDKALIS GIYKDLKQIYKKNNPIKKWA KEMNRHFSKEDIYAANRHVK AHHHWSSEKCKSKPQ
5732	36100	A	5778	502	600	
5733	36101	A	5779	51	452	ADKQLQQLRQNGCTKITSILI HQQTNRPNHE*TPHNCFKE NKIPRNPTYKGCEGLQGELET TAQGNKKGYQMEEHSMMLG RKNQYRENGHTAQELEKTKVH MEPKSPHRQVNPKEQSWR HHIT
5734	36102	A	5780	381	528	LPPPLPAGLC**DQQQNSNAPLI H*EKERPDDSYRIFLPRYHFHD DRI
5735	36103	A	5781	1	477	
5736	36104	A	5782	180	496	TPHNKYKENKIPGNPTYKGCE GPLQGEQTAAQ*NRGQKQM EEHSMMLMDRKNKYHEN/EPYSP R*FIDSMSPSNYQ*LSSQNWK KLL*GPYGTCKEPT*PRQS
5737	36105	A	5783	1	533	MGPEICTDKLSDADVTVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIEHSIKWKNIPSSWVG RISIMKTAIILPKVYIRIKDDEWN IYRRYTEFRSLHHKLQNKYPQV RAYNFPPKKAIGNKEAVLCHG R*HDCISRKPHRLSPKSP*ADKQ LQQLRQNGQCAKITSILYQ*QT NREPHE*TPHNCFKENKIPRN PTYKGCEGLQGELETQAQGN KRGTFHQMEHSILMGRKNQY HENGHTAQGLHPDKRR

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5738	36106	A	5784	599	870	TPANQQHYRRMTLQLKENQTN RKRRQKQHQKRPKNPIQRS ATSKIKGDGSIQ*MLPWGQSP QKALTLATAPEQRKDTTPVVRGL SLQD
5739	36107	C	5785	1	1170	
5740	36108	A	5786	317	960	KWPYCPQRQFIDSMSPSSYQRL SSQNWKLL*SSYGTKKEPTSP SQS*AKRTKLEASRYLTSNYTT RLQ*PKQHGTTKTEI*INGTQQ SPQK*/OPHVYNYLIFNKPEKKK QWKGDSLNFKNWDMDEVGNHH SQQTITRTGNQTPHVFTHRWEL NNEITWTQGAGHHTPGPVVGL GAGRGIALREIPNANDELMVQQ TNMAHIYLCIKPARCADVP
5741	36109	A	5787	903	1050	LPPLPAGLC**DQQQNSNAPLI H*EKERPDDSYRIFLPRYHFHD DRI
5742	36110	A	5788	281	491	SFGYIPNSNGMAGSNGISSRSLR NRHTDFHNG*TSLSHQQCKSV PISPHPLQHLLFPDFLMAIALTGV R
5743	36111	A	5789	1	381	
5744	36112	A	5790	1	3231	
5745	36113	A	5791	1312	1463	KGSATCSPQANATTTTALQML GGIPWGNACGIFTRPPPTYLN THLSTR*RPLLLLLKCVR*KGSA TCSPPQANATTTTALQMLGGIP WGNACGIFTRPPPTYLNTHTLS TR
5746	36114	A	5792	811	1065	IS*VSFMSITH**WKKKEQQLLG CWL*A*M*SMLICV*RER*THKL E*LILCI*RMKKILEIQKGMFKL LPY*TKRIMLK/TLNRQLNSTVS SLHSRVDSLEKSNTKLIIEELAIA KNNIQLQEENHQLRSENKLLIL MKTQQHLEVTKVDVETELQTY KHSRQGLDEMYNEARRQLRDE SQLRQDVENELAVQVSMKHEI ELAMKLEKDIHEKQDTLIGLR QQLEEVKAINIEMYQKLQGSSE GLKEKKEIIVRLYWSALCG
5747	36115	A	5793	1	1353	
5748	36116	A	5794	78	503	TKELLHSKRNYHQSEQATYRM GENFCNLLI*QRANIQNLQ*TQT NLQEKKNQPHQVGEQYQQT LKRRHLCSQKTHEKMLITGHQ GNTNQNHNEIPSHTS*NGDH*K VRKKQGHG*SWKPSFSANYRK DKKPNSTCSHSQ

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5749	36117	A	5795	2	200	YGLMIRTIPVDPTRITTSVSLTV RLATMNP RSRPAPVDLTAPGPP HLHKNQKSSQHSQYLDLTSYC
5750	36118	A	5796	76	195	
5751	36119	A	5797	1	2445	
5752	36120	A	5798	207	475	TNLQEKKNQPHQKVGKGYEQT LLKRKHSCSQQTYEKMILITGH QRNANQNHNDIPS HSS* NNDH* KDRKQQMLERM*RNRNAFTLL VGV
5753	36121	B	5799	1	681	
5754	36122	A	5800	1	798	
5755	36123	C	5801	78	245	
5756	36124	A	5802	16	491	EPYPDRPREPKRDPESWSGLW DKGGLVLSLGRTRTEAHTALS RLRASMWIDRSTRASVHFTLY NPPTQLFTSVSLRVEILPTGSLV PSSLVESFSIFRSDALQYHMLML PQLVFLALSLIHLVCVQLYRMMD KGVLSYWRKPRNWLEVASLVS FSFEK
5757	36125	A	5803	3	2791	
5758	36126	A	5804	219	392	
5759	36127	A	5805	1	1044	
5760	36128	A	5806	1	360	
5761	36129	A	5807	1	528	
5762	36130	A	5808	127	360	
5763	36131	A	5809	1	421	GRRSRLAMRPLSMSYFDLSDV TTPESTKNLVESSMVNGGLTSQ TKENGLSTSQQVPAQRKKLLR APTLAELDSSESEETLHKSTSS SSVSPSPFPEEPVLAEAVFTRKKP PKFLPISSTPQPERRQPPQRRHSI EKETP
5764	36132	A	5810	328	1086	
5765	36133	A	5811	1	2076	
5766	36134	A	5812	1	450	
5767	36135	A	5813	901	1506	
5768	36136	C	5814	17	106	
5769	36137	A	5815	24	330	ARDQPI/PKKGTVGEFEPADNK CLLRATDGGKKKISTVSSKEVN KFQAMAYSNLLRANMDGLKKR DKKNKTKTKTSSSSSSSSPA AATAATTAATTAATAAQ
5770	36138	A	5816	1	2247	
5771	36139	A	5817	1	339	
5772	36140	A	5818	3	463	
5773	36141	A	5819	3	83	
5774	36142	A	5820	1	642	
5775	36143	A	5821	2	583	
5776	36144	A	5822	193	409	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5777	36145	A	5823	3	425	
5778	36146	A	5824	1	450	
5779	36147	B	5825	82	2096	
5780	36148	B	5826	1	1554	
5781	36149	A	5827	129	522	LCTDNIEITSKVHLHCSHHGAG LGTCSPCLCLSLPPPWAPVQPEP PR*APPPAPQRPVPSTIQGRKRL QLHS*SQ*DH/DAHAKVCSFTPE PARPRTHQKEETPNTSEHQKKQ TPDTPPLRTVTLTARLHGF
5782	36150	A	5828	1	541	
5783	36151	A	5829	1	714	
5784	36152	A	5830	188	287	KELPSGGHYNCRAPSSPHAGS S*SGHQPNSSQ
5785	36153	A	5831	71	689	SPVLDCCPGPLPSEESW/EQPV TRQYPLRPEVHKGLQNVKHLK APGLVRKCSHCNTPIIGVQKP NGQWRLVQDLRLINEAVVPLY PVVNPNTLLSQTPEEAEWFMV LDLKDFAFFCIPLHSDSQFLFAFE DPTDHTSQITWMVLPQGFDRSP YLFQALAQDLGHFSSRGTLVL QYADLLFATSEASCQATLID LLNFLANQ
5786	36154	B	5832	45	1148	
5787	36155	C	5833	233	319	
5788	36156	C	5834	11	133	
5789	36157	A	5835	215	849	IKRLPLMKRMWL*LQPESEIA GILVQ*MIE*QPKKGTNSIPVSK PSPVVKQKPNQWQVQVQDLRLI SDAVIPLYPAVSNPYTLLSQILE EAEWFTVLDLKDAFFCIPLRSD SQFLAFEDPTDHTSQLTWTVF TQGFMDTPHLFGQSLAQDLGH FSSPGTLVLQYVDDLLAKQQA TLDLLNFLANQGYKLSKLKAQ LCELLVFSSCARMHS
5790	36158	A	5836	1	449	MNKELGISSYKFCGMGRKTSVS AAKSVSATIPISRVQGLLQVLG QEVFLLLCQDQEEQAKREKRD QRKATALAMALRQITNLGGSER IENGAGQSPSRACYQCGLQGHF KKDYPTREPAAPCPLC*GNHW KMHCPGRQSCDSHLAITHL
5791	36159	A	5837	1	723	
5792	36160	A	5838	186	602	
5793	36161	A	5839	1	843	
5794	36162	B	5840	1	1779	
5795	36163	A	5841	1	1182	

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5796	36164	A	5842	23	302	LSQWKNRWTRTFLASLSVIANI LEPLLNILHVAVWLM.PN* [*] S* [*] V KKQVIM/FWNWWVLGLTDFKN EATDPRVCSWPCWLRSEADL CGECYSS
5797	36165	B	5843	1	2622	
5798	36166	A	5844	279	1024	
5799	36167	A	5845	3	3619	
5800	36168	B	5846	1	1898	
5801	36169	A	5847	1	420	
5802	36170	A	5848	1	1632	
5803	36171	A	5849	1	597	KYLTKKTQAASVEAVKMLDEI LLQLSASVPVDMVMPGEFDPNTY TLPQQPLHPCMFPLATAYSTLQ LVNTNPYQATIDGVRFLGTSGQN VSDIFRYSSMEDHLEILE*LRVR HISPTAPDTLGCYPFYFCGNTPS FGSKIIRGPEDQTVLLVTVPDFS ATQTACL VNLRS/LACQPSISFG FGAEDDDLGGGLGWAPDSKKW
5804	36172	A	5850	1	1490	RDAARRALNLLGLEAVWTKQ VRSVAMFSEQAAQRAHTLLSPP SANNATFARVPVATYTNSQPF RLGERSFSRQYAHYATRLIQM RPFLENRAQQHWGSGVGVKKL CELQPEEKCCVVGTLFKAMPL QPSILREVSEHNLLPQPPRSKY IHPDDEL VLEDELQRIKLKGTID VSKLVTGTVLAVFGSVRDDGK FLVEDYCFADLAPQKPAPPLDT DRFVLLVSGGLGGGGGESLLG TQLLVDTVGTQLGDEGEQCSA AHVSRVILAGNLLSHSTQSRDSI NKAKYLTKKTQAASVEAVKM LDEILLQLSASVPVDMVMPGEFD PTNYTLPQQPLHP/CMFPLATA YSTLQLVTNPYQATIDGVRFLG TSGQNVSDIFRYSSMEDHLEILE WTLRVRHISPTAPDTLGCYPFY KTDPFIFPECPHVYFCGNTPSFG SKIIRGPEDQTVLLVTVPDFSAT QTACL VNLRLSLACQPSISFGF AEDDDLGGGLGLGP
5805	36173	B	5851	13	441	
5806	36174	A	5852	3	279	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5807	36175	A	5853	23	841	EKAKEFRRAEEKKKEVPAPVET LKKK*RNFAELKIKRLRKKFA QKMLQRARRKFIHEKAKH\YH KEYRQMYRTEILMA\RMARKA GNFYVPAEPKLA\FVIRIRGINV SPKVRK\VLQLLRLRQIFNGNLL *SSTKASINMLRDCRSHILAWG VPQILKSVNELIYK\IRGYGKINK KRIA\LTDN\ALIASLGGKYGIL LAWEDLIHEIYTV\GK\RFKEAN NFPVGP\SNLSSPPRWK*KKKTT HFCKKVEDAGNREGRTSRNP YLEGMDLRCLP
5808	36176	C	5854	57	287	
5809	36177	A	5855	1	450	
5810	36178	A	5856	1	549	
5811	36179	A	5857	3	581	EQRKIPLVPENLLKKRKAYQAL KATQAKQALLAKKEQKKGG LRFKRLESFLHDSWRQKRDKV RLRRLEVKPHALELPDKHSLAF VVRIERIDGVSLLVQRTIARLRL KKJIFSGVFVKVTPQNLKMLRIV EPYVTWGF\PNLKS\VELILKRG QA\KVKNKTIPLTDNTVIEEHLG ECYSLGVSWGRKPGSLKL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *~Stop codon, /~possible nucleotide deletion, \~possible nucleotide insertion)
5812	36180	A	5858	1	2652	MFGRSRSWVGGGHGKTSRNIH SLDHLKYLHVLTKNNTTVTEQ NRNLLVETIRSITELIWDQND SSVDFDFLEKNMFVFFLNILRQK SGRYVCVQLQLTLNLFENISHE TSLYYLLSNVYVNSIIVHKFDFS DEEIMAYYISFLKTLCLKNNH TVHFFYNEHTNDFALYTEAIKF FNHPESMVIARVTRITLVYK DNQAMLHYIRDKTAVPYFSNL VWFIGSHVIELDCVQTDDEHR NRGKLSDLVAEHLHLHLYND ILIINCEFLNDVLTJILLNRLFLP LYVYSLENQDKVFLIIHAPLV NSLAEVILNGDLEMYAKTEQD IQRSSVLPPTSSLWQGSLSLNQ LQSGHLKCSHLCGAQAADS VTGEIPAIRSLWELISAGSKART FFFLKMLIGFWEKVDCEYQRR QVLSTRLEALPSNRLTDVAAV HSSCMLGFGSTAPRGSWIGDPA AVHLPLPGELAEHLGSKGTTTV TKHQPAKPSIRCFIKPTETLER SLEMNKHGKRRVQKRPYK NVGEEDEEKPTEDAQEDAE KAKGTEGGSGIKTSGESEIE MVIMERSKLSELAASTSVQEQN TTDEEKSAATCSESTQWSRPF LDMVYHALDSPDDYHALFVL CLLYAMSHNKENLLKKRKAYQ ALKATQAKQELLAKKEQKKGK GLRFLKLESFLHDYWQQKPKD
5813	36181	A	5859	1	405	LEISIMAAISIGYTFSAVCFHSA NSNADHEGFLJGEVQRQETFSIS DSQISNTEFLQVIKVIWYRFR RNTQQQMSYREQVLHKQLTRI LGPVPLVFLFSFISTANNSTHA LEYVFLFRPNRRYNQRISLAIPN
5814	36182	B	5860	1	843	

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5815	36183	A	5861	3	1260	EISIMAAISISGYTFSAVCFHSAN SNADHEGFLLGVEVRQEETFSISD SQISNTEFLQVIQIYNHQPCKSL FSFYDYASKVNEESLDRILKDR RKKVIGWYRFRNTQQQMSYR EQVLHKQLTRILGVPLVFLLF SFISTANNSTHALEYVLFPRNRR YNQRISLAIPNLGNTSQQEYKV SSVPNTSQSYAKVIKEHGTDF DKDGVMMKDIRAIYQVYNALQE KVQAVCADVEKSERVVECSQA EVNKLRRQITQRKNEKEQERRL QQAVLSRQMPSCSLDPAFSPRM PSSGFAAEGRSTLGDAEASDPP PPYSDFHPPNQESTLSHSRMER SVFMPRPQAVGSSNYASTSAGL KYPGSGADLPPQRAAGDSGE DSDDSDYENLIDPTEPSNSEYSH SKDSRPMAPHPDEDPRNTQTSQI
5816	36184	A	5862	1	742	
5817	36185	A	5863	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFVQNCLS LARSDSREQGLVLMVESNRNE VVPVGVSYSKDGAKSLKGDVP ASEVTSKDSFQSFPSSAEEC GDDEKIKVDDPLTRTCNQASG SAPQQDYDKLKAFGGENSST GLSPSGNMEKNVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSAI MALSAKKAASDSCKEPV
5818	36186	A	5864	2	626	LCQHNRKIKHGIRKVVYACSHCP DSRRTFTKRLMLEKHVQLMHS LKDPDLKE/TDRCHQ*GGNRNK RRH/LSSPVPVSGSWKNQFSR/CA MCGFTTENLLQFHEHIPQHKSD SSSYQCQECGLWYTSHSVLSRH LFIVHKLKEPQPVSKQNGAGED NQQENKPSHEDESPNGTVSDRK CKVCVKTFETEAAALNTHMRIH GMAFIKSKRMSSAKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5819	36187	A	5865	1	765	MQRDVYISHVRKEHGKQMKK QPCCCQRDKPFSSSHSLCWHNR1 KHKVIRKVYTCSHCSDSRGTFT KQLMLEKHVQLTHGIKDPDLK E/TDRRHQ*GGNRNRKRPQGPQ SQVEVERTGSGVQASQ\GAITQ PLKCLKINVKVHKCARA\GFT TENLLQFHEHIPQHKSDGSSYQ CREHLFVVHKLKEPQPVSKQN GAGEDNQENKPSHEDESPNG AMSDRCKCKCAKTFETEAALN THMQTHGMAFIKSKRMSSDEK
5820	36188	A	5866	878	1095	AFFLDTLYTQFSRC*SRAVFVFA HPTAMACSSRR/LIRVQEQDAA QVTHQSFKDDL CVVLGDTLHH RFLLIFRH
5821	36189	A	5867	1	1137	
5822	36190	A	5868	1	1380	
5823	36191	A	5869	55	558	
5824	36192	A	5870	1	897	
5825	36193	A	5871	1	565	
5826	36194	B	5872	22	1696	
5827	36195	A	5873	295	522	
5828	36196	A	5874	3	3678	IPAPVSGRPPGLLAEGKLSGPR PMCRTRLGSHTAASAPARMWL FHTLLCIASLALLA AFNV DVAR PWLTPKGGAPFVLSLLHQDPS TNQTWLLVTSPTKRTPGPLHR CSLVQDEILCHPVEHVPIPKGRH RGVTVVRSHHGVLICIQVLVRR PHLSSELGTGCSLLGPDLRPQA QANFFDLENLLDPDARVDTGD CYSNKEGGEDDVNTARQRA LEKEEEEEDKEEEEDEEEAEAGT EIAHLDGSGSID
5829	36197	A	5875	1	3189	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5830	36198	A	5876	1119	2463	LRAGGPGQGGKGAHPGRRVD ELL.LGHPTAVGCAGTDCPTPT PGGLWV*GVQEESDLPTAVDS SRPDIRDQAWASVHWELVYVHG SSFINT*GERGAGY/AVITW/STV VEARSMPPQGTSAQKAEI/AFIR ALELSEALAKTVRQRCVSCRQ HHARQGPVAVPPGIQAYGAAPFE DLQVDFTEMPKCGDIRKIVTGD VNTPAILGVVSSPPSHIGNNITE DPELQPILAGLSMYLVTVLR NLLIILAVSSDPHLHTPMCFFLS NLCWADIGFTLATVPKMIVDM QSHTRVISYEGCLTRISFLVLF CIEDMLLTVMAYDCFVAICRPL HYPVIVNPHLCVFFLLVYFFLSL LDSQLHSWTVLQFTIKNVEISN FVCDPSQLLKLACDSVINSIFM YFHSTMFGLPISGILLSYKIVP SILRISSSDGKYKAFSTCGSHLA
5831	36199	B	5877	1	1830	
5832	36200	C	5878	109	245	
5833	36201	B	5879	1	801	
5834	36202	B	5880	171	288	
5835	36203	B	5881	49	502	
5836	36204	B	5882	1	639	
5837	36205	A	5883	1	821	MSGQFDFLLWTPEDNSDESD AEGEHGDGAEAEAPPVPRPGP KPAGLGRRPCPYEQAQGGDGP EEQWMSFCWDIPRKSAGPRERI TLRRHLEDGCGKVSKKKAQICR QQKDPQEESPAQFYERLCEAYG MYTPFDPDSPENQRMIMHALV RQSAEDMRRLQKQAGLAGM NPSQLLERASQVFVNRDAV/TP** GKQOREWRERG*YDSQYRRGG TQPCDIVPNIRRRER*YHSQYRR RARPPGP*SERGALRPGSLPRQ AA*RVPSGPADGQ
5838	36206	A	5884	1	1860	

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5839	36207	A	5885	2745	3732	IRIGKNYFKVHMEPKKSPHRQV NPKPKEQSWRHHTT*LQTLQG YSNQNSMPGTPQ*PSTPAPGG NLNRNPOSSDLLQVTKQQGQAL AIQREAPLHRIPAPEAIPWYFQP QPA*TLQGSPPVDPSSAMM/SR RAHRSRGPDRQGYPLQGD*PGE PRPQEH*RGHSQERLPSSEKQTP ICPPAQATQHPEEPDAHQPYKH LFQVCAHQGHVPAQRRN*PGY WERYHSAEDPELQPILAGLSLS MYLVTVLRLNLLIS
5840	36208	B	5886	1	2379	
5841	36209	B	5887	1	6741	
5842	36210	B	5888	165	928	
5843	36211	A	5889	56	2028	
5844	36212	B	5890	1335	3804	
5845	36213	A	5891	365	1573	
5846	36214	A	5892	1	1491	
5847	36215	A	5893	25	458	
5848	36216	A	5894	1	1194	MGGNAADKFRAGVELALQSG NKVCVCSPRTTISGDAVAPRSV LPGCRHPIGEISQSHCWAGRS LSSRKRGSLFRMGFIKVVKNK AYFKRYQVKFRRRIRKGTQDY YARKRLVIQDKNKYNTPKYR MIVRVNTNRDNIICQLYA/RRIE GDMIVCAAAYCTPNLPKIWV*RV GLTNVAAAAYCTGLLLVARRLL NRFGMDKIYEGQVELTGDEYN VESIDGQPGAFCTCYLDAGLAR\ TTTGKNVFGAPEGLWMGGLS IPHSTKVRFGVYDSEISKEFNAIE VTSGKHIMGPCKCLQNYMRYL MEVEDIEDAYKKQFSQYIKINS VTPDMMNEEMYKKAHAHAIRE ESSSMEKKAQGGKFKKKRWNR PKMSLAQKKDRVAQKKASFL QSSRSGLLESLETPAIFP
5849	36217	A	5895	1	1191	
5850	36218	A	5896	21	159	PRSSVRPAGGFSSTCPPSWAAS RSCCTSHGCGHQ*CAAGTGQTR L
5851	36219	A	5897	1	1062	
5852	36220	A	5898	1	246	
5853	36221	A	5899	1	642	
5854	36222	A	5900	2	648	
5855	36223	A	5901	1	555	
5856	36224	B	5902	151	513	

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5857	36225	A	5903	1	2915	VSLAFCQPLSLSLSPLLPLASSL APERTHLPGGSLLLSPSPFAR PREPRGCVTAAPPDKMDTAE DICRVCRSEGTPEKPLYHPCVC TGSIKFIHQECLVQWLKHSRKE YCELCCKHRFAFTPIYSPDMP SRL PIQDIFAGLVTSIGTAIRYWFHY TLVAFARWEVLLPACRIYKCL FLGSVSSLLTLPLDMLSRKNLL ADCLQGC/VVVTCTLCAFISLV WLREQIVHGGAPIWLEHAAPPF NAAGHHQNEA
5858	36226	A	5904	3	907	
5859	36227	B	5905	102	406	
5860	36228	B	5906	1	5241	
5861	36229	A	5907	1	519	
5862	36230	A	5908	1	3067	TRDAAMAEAALEAVRSELREF PAAARELCVPLAVPYLDKPPPT LHFYRDWVCPNRPCHRNALQH WPALQKWSLPYFRATVGS TEV SVAVTPDGYADAVRGDRFMM PAERRLPLSFVLDVLEGRAQHP GVLYVQKQCSNLPSELQLLPD LESHVPWASEALGKMPDAVNF WLGEAAAVTSLHKDHYENLYC VVSGEKHFHPPSDRPFIPYEL YTPATYQLTEEGTFKVVDEEA MEKAEVSRCTLLTVRVLQA
5863	36231	A	5909	1	429	
5864	36232	A	5910	1	690	
5865	36233	A	5911	1	376	
5866	36234	A	5912	1	471	
5867	36235	A	5913	1	606	
5868	36236	A	5914	3	2756	SPGGRTPAARDSIVREVIQNSKE VLSLLQEKNPAPFKPLAIQAG DDNLMQEQINQNLAEEAGLNITH ICLPDSSEAEIIDEILKINEDTRV HGLALQISENLFNKNVNAKLP EKDVGVDINLGLKLVGRDAH ECFVSPVAKAVIELLEKSGVNL DGKKILVVGAGHSLEAALQCLF QRKGSMTMSIQWKTRQLQSKL HEADIVVLGSPKPEEIPLTWQIP GTTVLNCSHDFLSGKVGCGSPR IHFGGLIEED
5869	36237	A	5915	3	404	RLKEKKLVKEVIAVSCGPAQCQ ETIRTALAMGADRGHVEVPPA EAERLGPLQVARV/AVVTADLR LNEPCYATLPNIMKAKKKIEV IKPGDLGVDLTSKLSVISVEDPP QRTAGVKVETTEDLVAKLKEIG

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5870	36238	A	5916	1	334	
5871	36239	A	5917	88	870	MADVRLVAVKRVIDYAVKIR VKPDRTGVVTDGVKHSMPFC EIAVEEAVRLKEKKLVKEIAV SCGPAQCQETIRTAI\MGAD RGIHVE\VPPAEAEERF/GVPLQV ARVLGQAWQRRRLDLVLLGK QAM\ACTDCNQ\TGQMTAGFLD WPQGTFA\SQVTLEGDKLKVER EIDGGLET\RLKLP\AVVTADLR LNEPRYA\TLP\NIMKAKKKKIE VIKPGDLGVDLTSKLSVISVEDP PQRTAGVKVETEDLVAKLKEI
5872	36240	A	5918	1	774	
5873	36241	A	5919	1	1557	
5874	36242	A	5920	1	759	
5875	36243	A	5921	305	638	
5876	36244	A	5922	364	540	
5877	36245	A	5923	9	111	
5878	36246	A	5924	1	594	
5879	36247	A	5925	169	594	
5880	36248	A	5926	37	936	
5881	36249	B	5927	91	2043	

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5882	36250	A	5928	1	2298	MSRKGPRAEVCADCSAPDPGW ASISRGVLVCDECCSVHRLGR HISIVKHLRHSAWPTLLQMVH TLASNGANSIWEHSLDDPAQVQ SGRRKANPQDKVHPIKSEFIRA KYQMLAFVHKLSCRD/DDGVT AKDL\$KAN*HSSVRITGKPKW TCLRLLSVLGA/QANFFHPEKGT TPLHVA AKAGQTLQAEELVVY GADPGSPDVNGRTPIDYARQA GHHELAERLVEQ/QYELTERLA FYLCGRKPDHKNHGYIIPQMAD SLD\$SELAKAAKKKLQALSRL FEELAMDVYDEVDRRENDAY WLATQNHSTLVTERSAPFLPV NPEYSATRNQGRQKLARFNAR EFATLIIDILSEAKRRQGGKSLSS PTDNLELSLR\$QSDLDDQHDYD SVASDEDTDQEPLRSTGATRSN RARSMDSSDLDGAVTLQEYL ELKKALATSEAKVQQLMKVNS SL\$DELRLRLQREIHKLQAEENLQ LRQPPGPVPTPLPSERA EHTPM APGGSTHRRDRQAFSMYEPGS ALKPFGGPPGDELTTTLQPFFHS TELEDDAIYSVHVVPAGLYRIRK GVSASAVPFTPSSPLLSCSQEGS RHTSKLSRHGSGADSDYENTQS GDPLLGLEGKRFELGKEEDFH PELESLDGDLDPGLPSTEDVILK TEQVTKNIQEL\$RAAQEFKHDS FVPCSEKIHLAVTEMASLFPKRP
5883	36251	A	5929	1	924	
5884	36252	A	5930	214	387	RRAFHPTPVTSARSTLH\$FGQL RLPHSM*SGGTLISM MQANQS LSLEFSK WTSFPLD
5885	36253	A	5931	1	1639	
5886	36254	A	5932	1	1098	
5887	36255	A	5933	1	546	NSSQVLQF*YLVVNEAPFRLLT MPQYPYQINITADQLWGSVAVL V*MH\$NGLPGLCI*AWKTTSG GEQYPSSAIKQGPKEPYADFIA RLQESLKKVIADLAAQDIVLWL LAFDNANPECQAALRPGRKAH LVYDYTKVCDGIRDKLHKATLL AQAMAGLRMGKGNTPFPGACF NCGKHGH

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5888	36256	A	5934	1	648	MGQVWGLVHFTLEV FHTGD EEE EEQYSEVTFDVTEHVYLP KVAKEEEAGIQQARQEGDLEA WQFPVRIHPPDQENITATFEPF PFKLLKELKQAINQYGPSPFV MGLLKNVTVSSQMIPDGDPLT RACLTQAQFLQFKTWWADEAS IQAARNAWAQFQINITADQLLG VGGWAGLDAQFVMQDDAIEQ LRGVCIAREKVI*CGEQYPSF
5889	36257	A	5935	120	254	
5890	36258	C	5936	366	479	
5891	36259	A	5937	1	933	
5892	36260	A	5938	1	840	MGKVWGLVIHSTLEL FHTDVEE EGEYNEVTEEVTKHVYLP KAAKEGEVHPYHSAPPHYFFE ENDPPDLSFLEDGTGRLAAAA TTKANA/KQPLLLSPSMHR/PLP TRPLLAGIATALPQGV*PLIAP PTRPHLEHCSTQ*RPQAPTLGE ITPVTVPQAPLHPRAVQPW/HST PTRSWLQAVMPGIAPSRSPPW AVQLRLTYLGCLSTTPAAVQS LSQPPASVRQARVPQAPASSLC QEKPPSPPPVAPHGAAAAARPP SYHSSCASVAVVAANVLIG
5893	36261	A	5939	1	134	MGQVW*KSQSPKA*EPGVSCP RAGRREASVPRWYSS
5894	36262	A	5940	1	1158	
5895	36263	A	5941	1	673	MGIALGSPPTTGPKAMKQNL SIG PAGILLPQPVMTPGCPAAAPPV APRCGYVLS EDAWGNLQGLCT GLSCGQPVAPWATDSGGAQDP VALLPPFSPRGLLGPSCMQRSQ VVKGGRQSEISSQNKKVIADLA AQDIVLQLLAFDNPANPDCQAA LRPIRGKAHLVDFIKACDVIGGI PNLLHPRGLRAITIAVFGKQIR TSGSNPLRSTFLSRSRISKNCSEA EV
5896	36264	A	5942	1	1182	

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5897	36265	A	5943	1056	2128	TQPPTWGQIKKLSQMVEENLR KAGQLVTMNNLMVAMIVVITT TEEQEYSEVTEEVTEQVYLP AKVAKEGEVHPYPSAPPHYF EKEWPDPDLSEFLEDRQKVVA PVTVRAAPRATVLSIQAGIQQ AR*EGDLEAWQFVRHPPDQ GNIIVTEFPFPLFKEFKQAVN QYGPSPFVVMGLLNVAVSSW MIPTDWDALTRACLTQAFLQF KTCAMKQGPPEPYVDFIARLQ SLKKMIADSAAEIVLQLLAFD NAHPDCQAALRPIRGKAHLVD YVKACDGIGEYTPSTYEKKVN CKTASCRSFRYPPEGIVITGDD SSMRVVVPEDLPVGGQDVEVED RDIDDPDPV
5898	36266	A	5944	1	300	
5899	36267	A	5945	1	373	
5900	36268	A	5946	1	2976	
5901	36269	A	5947	287	544	
5902	36270	A	5948	831	4555	
5903	36271	C	5949	108	434	
5904	36272	C	5950	145	402	
5905	36273	A	5951	3	1104	GSRPGGHTLQSHRGRHAQGLR SPLLAAPVCLGCTWQRRFLW SLKI*RLLCWF/CRRLQINCKN KPAIPRGPT/GPSEKSGLLQDQ GDTTNTTEENSKLENIFGRVIKE NFQSLVRDLDIQYKKHKEHPG NSSQKDHHLGTLSSGYPKLRQR KES*ELSDRSTRKISQS/YNLYTP NTGAPRFIKQLLTDLRNEIDSNT IIVGYSTPLTALDRSSRQKVND ETVDLNYTLEQMDLTIYRTFH PTTTEYTFYSTVHGTFKIDHMI CHKMSLNEFKKTEIISSTLSDHS GKLEINSKMNQLQHANTWKL NNLLLNEHWVWNEIKMEIEKFF KLNDSDNTTYQNLWDMAKAV LRGKFIALNTYIKKMM
5906	36274	B	5952	1	2367	
5907	36275	A	5953	21	132	WREGARQCQEDPAEFLSD*DW ADPGPPHNAPGQNVH
5908	36276	A	5954	1	1461	

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5909	36277	A	5955	31	802	SAWWNSRELLDPQSRSGGCF *EYPPTSGTEQESVSGNRALCSS LRMNGDQNSDVYAQEKQDFV QHFSQIVRVLTEDEMGHPEIGD AIARLKEVLEYNAIGGKYNRGL TVVVAFRELVEPRKQDADSLQ RAWTVGWCVLQLQAFLVAD DIMDSSLTRRGQICWYQKPGV GLDAINDANLLEACTYRLKLKY CREQPYLNLIELFLQSSYQIEI GADPGPPHSPPRAMWILSDSLK RGTNLLSSTRQLSTPSTFL
5910	36278	A	5956	1	532	RLNEAEQKYKDIQDKLQIIEET NARAPECMALKADVAKKRA YNEAEVLYNRSLEYKALKKD DEQLCKRIEELKKR/VL.TN/RLE PERLERQKKISWLKERVAFQ QENSVNQIEIQFQQALEKDKKE HGKIKREKLDVKHALSYNQL LKLKDSKTDRLKRFPGNPVPA LEAIDD
5911	36279	A	5957	121	475	
5912	36280	A	5958	131	2891	
5913	36281	A	5959	131	3101	
5914	36282	A	5960	44	292	CQDYRWLLASSVLCWLY*KTQ QSDTEDLLCSAPTGPPEEDD GKS*PEKCRQMT*KKWSINCKC FFASSHTTSLIGLFLR
5915	36283	B	5961	26	239	
5916	36284	A	5962	131	3121	LVSFLLFDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPSSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPPIVASE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTSTIIT TTVITTEQAP
5917	36285	A	5963	1	1185	
5918	36286	A	5964	495	636	PSVVLDDINVSFNHWSAIFLTME/ PFCHRVRSHAMESR*GSVLP*N KPQ
5919	36287	A	5965	2	376	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5920	36288	A	5966	3	688	GTSAGDGC PHPTVLWPPDIMP PKKDVVKKPAGPSISKPAKP AAAGAPPAKTKAEPVQPAPQ KTQEPVDLSKVVFIEFNKDQLE EFKEAFELFDRVGDGKILYSQC GDVMRALGQNPTNAEVLKVLG NPKSDEMNVKVLDFEHLPLML QTVAKNKDQGTGYEDYVEGLRV FDKEGNGTVMGAEIRHVLVTL GEKMTTEEVEMLVAGHEDSNG CINYEELVRMVLNG
5921	36289	A	5967	54	540	AVYMCDLTENQTADLIPSTVEF KEAFQLFDRTGDGKILYSQCQ DVMRALGQNPTNAEVLKVLGN PKSDEMNVKVLDFEHLPLMLQ TVAKNKDQGTGYEDYVEGLRVF DKEGNGTVMGAEIRHVLVTLG EKMTEEDVHMLVAGHEDSNG CINYEAFVRHILSG
5922	36290	A	5968	1	405	
5923	36291	A	5969	93	506	
5924	36292	B	5970	43	615	
5925	36293	A	5971	2	598	TRTSLHAALFSWDVPGTSLTEFI SHLEVKKGMLVGIVGKVCGCK SLLAAIAGELHRWEQVQCGL HTLH*APEQMLRGHVAVRGLS KGFLATQEPWQFATIRDNLIF GKTFDAQLYKEVLEACALNDD LSILPAGDQTEVGEKGVTLSSG QRARIALARAVYQEKELYLLD DPLAAVDADVNPACTGCNP
5926	36294	B	5972	137	371	
5927	36295	A	5973	1	1398	
5928	36296	A	5974	1	915	
5929	36297	A	5975	40	564	
5930	36298	A	5976	62	280	
5931	36299	A	5977	17	744	
5932	36300	A	5978	1	537	
5933	36301	A	5979	242	576	AANSLYKGSNSAALIILVGP*IS CLTHPVYMK*AP* TICLLYSM VILKALFFPQNINIFLPVKSRRHS
5934	36302	A	5980	924	3473	
5935	36303	A	5981	1	604	
5936	36304	A	5982	288	732	RNCIANYDFLILPTSF*WCSEFFV LLFLFLSLSSSLKLHSDLDKGE GTAKYTLSGDGAGPVFTIDETT GDVHAIRSLDREKPFYTLRA QAVDIETRKPLEPESEFIIKVQ DIANDNEPKFWG WDLMAVATGP QK WSPVG*VGQIKIL
5937	36305	A	5983	1	1510	

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5938	36306	A	5984	1	603	
5939	36307	A	5985	250	505	GFSPTWQ*MNTHPSLMCFSPSR TTGSAAN*RGQKSGVPFWS* SHVKGKDQIPVPCPCTTAPVT MESTCIC*PTHVCKTLMV
5940	36308	A	5986	3	131	RVLVDPDIRGAI*AVPKSPSIKSY PALRALFLLPPYPDDLGI
5941	36309	A	5987	1	913	
5942	36310	A	5988	5	177	
5943	36311	A	5989	3	383	
5944	36312	A	5990	1	1323	
5945	36313	A	5991	342	594	
5946	36314	A	5992	1	321	
5947	36315	A	5993	3	601	
5948	36316	A	5994	1	1023	
5949	36317	A	5995	1	606	
5950	36318	A	5996	1	1536	
5951	36319	A	5997	2	1394	
5952	36320	A	5998	371	1045	
5953	36321	A	5999	3	360	
5954	36322	A	6000	1	636	
5955	36323	C	6001	1	861	
5956	36324	A	6002	1	711	

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5957	36325	A	6003	18	2446	AGSPPRADAAAGLWERGHLLS AAVAAMGKRDRADRDKKKSR KRHYEDEDDEEDAPGNDPQE AVPSAAGKQVDESGTKVDEYG AKDYRLQMPLKDDHTSRPLWV APDGHIFLEAFSPVYKYAQDFL VAIAEPVCRPTHVHEYKLTAYS LYAAVSVGLQTSIDITEYLRKLS KTGVPDGMQFIKLCTVSYGKV KLVLKHNRVYVESCHPDVIQHL LQDPVIRECLRNSEGEATELIT ETFTSKSAISKTAESSGGPSTSR VTDPPQKSDIPMDLDFEYEQM DKDEEEEEETQTVSFEVKQEMI EELQKRCIHLEYPLLAEDFRN DSVNPMDINIDLKPTAVLRPYQE KSLRKMFNGRARGSVIVLPC GAGKSLVGVTAACTVRKRCLV LGNSAVSVQWKAQFKMWSTI DDSQICRFTSDAKDKPIGCSVAI STYSMLGHTTKRSWEAERVME WLKTQEWGLMILDEVHTIPAK MFRRLVTIVQAHCKLGLTATLV REDDKIVDLNFLIGPKLYEANW MELQNGYIAKVQCAEVWCP MSPEFYREYVAIKTKRILLYT MNPKNFRACQFLIKFHERRNDK IIVFADNVFALKEYAIRLNKPYI YGPTSQGERMQILQNFKNPKI NTIFISKVGDTSFDLPEANVLIQI SSHGGRRRQEAQRLGRVLRAK KGMVAEEYNAFFYSLVSQDQTQ
5958	36326	A	6004	1	933	
5959	36327	A	6005	1	879	
5960	36328	A	6006	1	727	
5961	36329	A	6007	1	1509	
5962	36330	A	6008	1	1698	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
5963	36331	A	6009	2465	2751	VPTSSAPMPWPSRQWERSRT MTVISSSQLMALGP*RTAQVLA AAPA*LGASSAARGIDPQAGKT QKVIETDIATMQLCANKLDKKDF FGKSDPFLVFYRSNEDGTFITICH KTEVVKNLTNPVWQFSPVRA LCNGDYDRTVKIDVYDWD RD GSHDFIGFITSYRELSKAQNNQ FTVYEVLPNPRKKCKKKYVNS GTVTLSSFSVDSEFTFVDYIKGG TQLNFTVAIDFTASNGETRMSE KVGGNPLQPTSLHYMSPYQLS AYAMALKAVGEIIQDYDSDDL FPAYGFGAKLPPEGRIHQFPLN NNDEDPNCAIEGVLESYFQSL RTVQLYGPITYFAPVINQVASLP
5964	36332	A	6010	1	1059	
5965	36333	A	6011	255	405	
5966	36334	A	6012	251	1199	
5967	36335	A	6013	1	1791	
5968	36336	A	6014	335	984	
5969	36337	A	6015	1	127	LPLRLSYEIVLYFTF*KPEHNKS HFLESHLRNTRSA LNTRK
5970	36338	A	6016	1	774	

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5971	36339	A	6017	186	2699	PRGAKPAVPAGPERPGPGPGPC SPRPMVLPTCPMAEFALPRHSA VMERLRRRIELCRRHHSTCEAR YEA VSPERLELERQHTFALHQR CIQAKAKRAGKHRQPPAATAP APAAPAPRLDAADGPEHGRPA THLHDTVKRNLDSATSPQNGD QQNGYGDLFPGHKKTRREAPL GVAISSNGLPPASPLGQSDKPSG ADALQSSGKHSLGLDSLNNKKR LADSSLHLNGGSSNPSEFPLSLN KELKQEPVEDLPCMITGTVGSIS QSNLMPDLNLNEQEWKELIEEL NRSVPDEDMKDLFNEDFEEKK DPSSSGSATQTPLAQDINIKTEF SPAAFEQEQLGSPQVRAGSAGQ TFLGPSSAPVSTDSPSLGGSQTL FHTSGQPRADNPSPLMPASAQ AQNAQRALAGVVLPSQGGPGA SELSSAHQLQQAIAKQKREQML QNPQQATPAPAPGQMSTWQQT GPSHSSLDVPPYMEKPAASPSY KQDFTNSKL/PHDA*CE*EFP SARRPLPPAQCEPAESPATE*LES ELRE/YTRGLCWIRQYKTPFSL QSGLWARQPGVWPEQASPDGL SSPAAVPYKSRAELPVSD EAKA RKYAFPTGSTWPGAEPFQCPC ASPGYQCWDPAACRVRGQLPQ QLPLSQQPATGRCAEASVAFG PTETKGA AAKAFTATAVPSEAT APSRGTGEATVSPSPDPTTPVP
5972	36340	A	6018	1	1062	
5973	36341	A	6019	3	566	ASRPVPTLRLVVPASQCGSLIG KGGCKIKIESTGAQVQVAGD MLPNSTERAITIA GIPQSIIECVK QICVVMLESPPKGVITPYRKP SSPVIFAGGQAYTIQQQYAIQ PQDLTKLHQLVAMQQC/HFPMTHG /NTGFQWALESS/FPFV/KGYW AGLDASAQTTSHELTIPNDLIGC IIGRQGA KIN
5974	36342	A	6020	2	531	TLRSSWQVVRTGTAQAATVRG FPPHPPRPASSTLTLEGPPLEAY TIQQQYAIQPD LTKLHQLVAM QQSHFPMH/GDGIHSDYSAG/LD ASA/QTTSHELTISKRLIGLA*S GRSRAPKINGGSRQMSGAQIKI ANPVVEGSTD*GRFTITGSAASIS LAQYLINVRLSSETGGMGSS

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5975	36343	A	6021	181	1369	PLKVVQLPRTLDMDTGVIEGGL NVTLTIRLLMHGKEVGSIIIGKK GESVKKMREESGARINISEGNC PERIITLAGTH*LPSFKAFAMII DKLGRRDISSMVTNSTAAQLGP PVTLLKGLAPAS/QCQSLIGKGG CKIKEIRESTGAQVQVAGDMLP NSTEAGHHYLLGIPQSIIECVK QILRGSCWETLFPSSPPKGVTPA YRPK/PSSSPVIFVAGPGQVPA QAATVRAFTTPRPGCSTLTWE GPPLEAYTIQQQYAIQPDALT L/HQLAMQQSHFPMTHGNTGF SGIESSFPEVKGYWAGLDAS AQTTSHELTPNGFDWAGIIGA FKGAKINIEIRQMSGAQIKIANP VEGSTDRQVTITGSAASISLAQ YLINVRLSSETGGMGN
5976	36344	A	6022	1	690	
5977	36345	A	6023	1	399	
5978	36346	A	6024	3	397	
5979	36347	A	6025	3	249	
5980	36348	A	6026	177	477	
5981	36349	A	6027	49	451	
5982	36350	A	6028	1	1305	
5983	36351	A	6029	1	568	
5984	36352	A	6030	207	1053	PLTFGPARWRETPPSLYKEFSG LFGSFFLSSAWGAHNLRALFLL LPSSRIQPTPWVFGDLKSPAGL QVLNDYLADKSYIEGYVPSQA\ DVAVFEAVSSPPADLCHALR WYNHIKSYEKIEKASLPGVKKA LGKYGPADEVDTTSGGATDSK DDDDIDLFGSDDEEIESEKPKRL REERLAQYESKKAKKPG/LVA KSSILLVKP/WDIDETDMAKLE ECVRSIQADGLVWGSSKLVPV GYGIKKLQIQCVVEDDKVGTD MLEEQITAFEDYVQSMDDVAFF
5985	36353	A	6031	1	211	
5986	36354	A	6032	27	241	EVFGSWWQVPHEWLGSVLVV MSEFLFH*LM*ELVLKR*CLS HLSLAPFLAM*YACSSSPSTMI VSFFFF
5987	36355	A	6033	1	588	

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5988	36356	A	6034	279	1333	LIFCGCWLFASLTVMEAAHFFE GTEKLLLEVWFSRQQPDANQGS GDLRTIPRSEWDILLKDVQCSII SVTKTDKQEAAYLSESMFVSK RRFILKTCGTLLLLKALVPLKL ARDYSGFDSIQSFYSRKNFMK PSHQGYPHRNQEEIEFLNAIFP NGAGYCMGRMNSDCWYLYTL DFPEERVISQPDQTEILMSELD PAVMDQF*HEDGVTAKDVTRE SGIRDLPGSVIDATMFNPGYS \MNGMKS\DGTYWT\IHITPEPEF SYVSFETNLSQTSYDDLIRKVV EVFKPGKFVTTLFVNQSSKCR RLGLPQK\IEGFKRLDCQEGWF KDSNFFVTSFAKKQQQQQS
5989	36357	A	6035	1	687	
5990	36358	A	6036	1	894	
5991	36359	B	6037	1	1458	
5992	36360	A	6038	1	1062	
5993	36361	A	6039	1	1218	
5994	36362	A	6040	277	3508	RSGRIAWAQEMDAAGRCHLL PLPAARGPARAPAAAAAAS PPGPCSGAACAPSAAGAGAM NPSSSAGEEKATGGSSSSGSG AGSCCLGAEAGDPRGAGSAA AAGAAALDEPAAGQKEKDEA LEEKLRNLTFRKQVSYRKAISR AGLQHLAPAHPLSLPVANGPA KEPRATLDWSENAVNGEHLWL ETNVSGDLCYLGEENCQVRFA KSALRRKCAVCKIVV/HTTACIE ELEKINFRCKPTTFREG\GS
5995	36363	A	6041	45	155	
5996	36364	A	6042	1	979	
5997	36365	A	6043	3	1042	
5998	36366	A	6044	2	401	
5999	36367	A	6045	1	5772	
6000	36368	A	6046	16	5678	VTSGRLLFYFRSMGPGCDLLLR TAATITAAAIMSDTDSDEDSAG GGPFSLAGFLFGNINGAGQLEG ESVLDDCKKHLAAGLGLGLG SLITELTANEELTGTGDGALVND EGWVRSTEDAVDYSINEVAE DESRRYQQTMGSLQPLCHSDY DEDDYDADCEDIDCKLMPPPPP PPGPMKKDKDQDSITGEKVDFS SSSDSESEMPQEAQTAESEDG KLTLPLAGIMQHDA TKLLPSVT ELFPFRPGKVLRLR
6001	36369	A	6047	1	354	

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6002	36370	A	6048	1	666	
6003	36371	A	6049	129	456	TYPVAVGESSRRPERSRGVPGPD AAAESHFRPGRI SNPLHRAEQ GHARAEGSGVFRPHRGRGLRL LRVQAPDQVDAPVHG*VAPPAP GARDAQTCRSHECPRTPLDEV
6004	36372	A	6050	1	1095	
6005	36373	A	6051	171	619	
6006	36374	A	6052	1	621	
6007	36375	B	6053	1	181	
6008	36376	A	6054	1	905	
6009	36377	A	6055	1	855	
6010	36378	A	6056	2	244	
6011	36379	A	6057	3	829	LTDCLKDVLIPPFNRMILLEVT FGKLYAWTVQNILNVLMDASA KFKELGIQPVPLQTITSENPLGP SLGSIPQARFLLMMLSLTLQH SANNLDLLNSGTLALTQTALR LIVLPDVELLI*DHLL*MQTSIV* LPVLALLAQHRSFGPSCDNVE EDMNAsAQGASATVLEATRKE TAPVHLPVSGPELAATMKIGTR VMRGVDWKWDG/QEAEQTER NIHPPTMMFTSTINLLQTLCLPA RVHAEIMQSEATKTLGGLLQIL VESGITDKTRME
6012	36380	A	6058	133	5421	IFVFGCPGSPRLQMVENRYTES FFTGQNCNRNEKVTLVRIADLE NHNNDDGFWTVIDGKVYDIKD FQTQSLTENSILAQFAGEDPVV ALEAALQFEDTRESMHAFQVCG QYLEPDQEGVTIPDLGSLSSPLI DTERNLGLLLGLHASYLAMSTP LSPVEIECAKWWQSSIFSGGLQT SQIHRYNEEKDEDDHCSPPGGT PASKSRLCSHRRALGDHSQAFL QAIADNNIQDHNVKDFLQCQIER YCRQCHLTPIMF

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6013	36381	A	6059	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAQSGCSR ARHQKARSMPLQDQHLALAIL LELAQVRGTLSQMLSAIILLLQ LWDSRAQETDNERSAQGTSTL LLSLQTTFQSIICSKDTPPSEGN MHLISGPLSPSEFLRESFFTVQ NCRNNEEVTICKADLENHNK DGGFWIVIDEKVYDIKDFQTS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFVGVQYLEVR LYALSDAEDGRGVTL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTAPASKSR/CSHRWALG DHSQAFLLQAIADNNIQDHNVK HQQGRSYKEVCTPVIERLRF SNELRPVGNLDSISEFKLLSSL PRWRIAQKIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRP/IAIKSPKTITSEN LGPSLGSIPQARFLLMMLSMILT LQHSANNLDDLNSGTALTLTQT ALRLIGPSCDNVEEDMNASAQ GVSAATVLEATRKETAPVHLPVS GPELAATMKIGTRVMRGVDW KWGDQDGPPGLGRVIGELGE DGWIRVQWGTGSTNSYRMGK EGKYDLKLAELPAAQPSAEDS DTEDDASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFAASL QRQRWVAVSLPHALVKSQTVP
6014	36382	A	6060	1	7297	
6015	36383	A	6061	32	259	SLRVTPGGNRVSEKKDRKKTG R/PPELERKSHTERLYLEEGSAE PA*VGRRAPESVNDRGGAIQRA QRGQAPPLPR
6016	36384	A	6062	3	437	
6017	36385	A	6063	1	425	MTELTPLWKPLKNSPMFRVIAR AFCVTFILVSTHQEMLTITSEN LGPSLGSIPQARFLLMMLSMILT LQHSANNLDDLNSGTALTLTQT ALRLIGGTPVELPAELAAPAFR AAAA/VDKNPRRRGQKVA VAK SGDGRGKKS

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6018	36386	A	6064	2	14566	RRGGRALRVRPETWEEAGEKM PSEFCLAAQARLDSKWLKTDI QLAFTRDGLCLGNEMVKDG EIVYTGTESTQNGELPPRKDD VEPSGTTKEDLNDKEKKDEET PAPIYRAKSILDSWVWGKQPDV NELKECLSVLWKEQALAVQS ATTLTALRLKQRLVILERYFIA LNRTVFQENVKVKKSSGISLP PVDKSSRPAGKGVGLARVG SRAALSFAFAFLRRWRSGEDA DLCSELLQESLDALRAL
6019	36387	B	6065	75	581	
6020	36388	A	6066	517	5495	ESFFTQGNCRNNEKVTVFRIAD LENHNNDGGFWTVIDGKYVDI KDFQTSQSLTENSILAQFAGEDP VVALEAALQFEDTRESMHAF VGQYLEPDQEGVTIPDLGSLSP LIDTERNLGLLGLHASYLAM TPLSPVEIECAKWLQSSIFSGGL QTSQIHYSYEEKDEDHCSSPG GTPASKSRCLSHRRALGDHSQA FLQAIADNNIQDHNKDFLCQI ERYCQCHLTTPIMFPPEHPVEE VGRLLCLCLKH
6021	36389	A	6067	1	1851	
6022	36390	A	6068	53	423	YHLTLIHGTVSATRPGHCSP GKLPWSVPSLQCTPSSPECRSV *RQL*HGHMHELLYIITKADSVI TASCLISRSEWWDGGTVSLV QRFVDYGSQCQRPHRTGCASS SAPQRASSVAPG
6023	36391	A	6069	1	49	EWSGTRTWWRPWCRT*CRT
6024	36392	A	6070	1	726	
6025	36393	A	6071	368	485	
6026	36394	A	6073	1	414	
6027	36395	A	6074	3	535	RRREFFPAKERESASMSSPEE*P/ DMAKGA PPSQPPNSVPAD/CS RSVRLSSSNFEESLRTEDDEGQ EGQDSMSRAKANWLRANFKV RMQLQEARGEEMSKSLWFKG GPGGGLIIDSMPDIRKRKPIPLV SDLAMSLVQSRKAAITSALASS TLNNEELKNHYKKTLQALIYP ISC
6028	36396	A	6075	1	222	
6029	36397	A	6076	2	284	NGIPDFSNTLLRGLQMPGARG PCCGSQRHINLLMGTGVFLVK MKA/NEFFLDSETRLCIAPEG WREQPQKTSMTNTFTLFLRIKFF VSHYGLL

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6030	36398	A	6077	91	749	
6031	36399	C	6078	1	380	
6032	36400	A	6079	1	877	MPPRDLAPALLVAVLVLLYLL VSAAAAPSSDSTPENVCVET TTNFIWELSSPHNTSAVLLVVF HKGPSPKFEVKLKKNANGLGFS FVQMEKFCSCSLKSDLVRIKRL FPGHPAEENGAIAGDIILAVN GSPRKASSRCRGSWAMQLSV QAGPSFASYYPAAVEVLHLLRG APQEVTL LCRPPP GALPELEQE WQQQKYKCAWAIVNEAEVEE VVEVAGTVEFFGDQGA*CHHP ACSGKPLGW HGGLSRKCPRLFF RGATRV TGAQGLKEVKQQSFR SNMMWLGLRL
6033	36401	A	6080	1	1683	
6034	36402	B	6081	66	1214	
6035	36403	A	6082	1	5694	
6036	36404	A	6083	3	483	SSLTSSMEDPAAPGTGGPPANG NGNIGGGKKGQAAPKGREAFR SQRRESEGSVDCPTLEFEYGDA DGHAAELSELYSYTENLEFTNN RRCFEEDFKTQVQKKEWLELE EDAQKAYIMGLLDRLLEVVSRE RRLKAARAVLYLAQGTGCECD SEVDVLHWSRY
6037	36405	A	6084	1	2646	
6038	36406	A	6085	115	1289	FSPLEPRLCSLGGWGALQAGEP CQPSRAGCGREGATMGCTLSA EERAALERSKAIEKNLKEDGIS AAKDVKLLLLGAGESGKSTIVK QMKIIHEDGFGSEDVQKYKPV VYVNTIQSLAAIVRAMDTLGIE YGDKERKADAKMVCDDVSRM EDTEPFAELLSAMMRLWGDS GIQECFNRSREYQLNDSAKYYL DSLDRIGAADYQPTQDILRTR VKTTIGIVETHFTFKNLHFLRLD VGGQSRERKKWIHCFEDVTAIL FCVALSGYDQVLHEDETTNRM HESLMLFDSICNNKFFIDTSIILF LNKKDLFGEEKIKKSPLTICPEY TGPNTYEDAAAIIQAQFESKNR SPNKEIYCHMTCATDTNNIQVV FDAVTDIIIANNLRCGGLY
6039	36407	A	6086	1	1053	

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6040	36408	A	6087	2	377	IYDGFDFGFAKGQIKGWTVDVG GWTGQGGSIKTRVLPKGY MEEIATQMRTHSINALLIIGGFE AYLGLLELSVFVTLKLFYQHFM HVLTLIPNRRVPICTSPSACC LWSVSHAFRCAYEQN
6041	36409	A	6088	1	591	
6042	36410	A	6089	1	2391	PGRAAPLGLLAMDADDSRAPK GSLRKFLLEHLSGAGKAIGVLT GGDAQGMNAAVRAVVRMGY VGAKVYFYIEGYQGMVDGGSN IAEADWESVSSILQVGGTHGSA RCQAFRTREGRLKAACNLLQR GITNLCVIGDGSALTGANLFRK EWSGLLEELARNQIDKEAVQ KYAYLNVVGMVGSIDNDFCGT DMTIGTDSALHRIEVDAIMTT AQSHQRTFVLEVMGRHCGYLA LVSALACGADWVFLPESPPEEG WEEQMCVKLSNRARKRLNII IVAEGAIDTQNKPTSEKIKELV VTQLGYDTRVTLGHVQRRGTP SAFDRILASRMGVEAVIALLEA TPDTPACVSLNGNHAVRLPL MECVQMTQDVQKAMDERRFQ DAVRLRGRSFAGNLNTYKRLAI KLPPDDIPKNTCNVAVINVGAP AAGMNAAVRSVAVRVGIADGH RMLAIYDGFDFGFAKGQIKGWT TDVGGWTGQGGSIKTRVLP GKYLEEATQMRTHSINALLIIG GFEAYLGLLELSAAREKHEEFC VPMVMVPATVSNNVPGSDFSIG ADTALNTITDTCRJKQSASGT KRRVFIIETMGGYCGYLANMG GLAAGADAAYIFEFPDIRDLO SNVEHLETKMKTTIQRGLVLRN ESCSENYTTDFIYQLYSEEGKG VFDCRKNVLGHMQQGAPSPF
6043	36411	A	6090	1	459	

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6044	36412	A	6091	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLSNPIKRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNLYSDHSAIKL ELRIKNLTQSR
6045	36413	A	6092	1	3654	
6046	36414	A	6093	1	5127	
6047	36415	A	6094	1	3663	
6048	36416	A	6095	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRLDQLDLSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRIKNLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKA VCRGK FIALNAHKRKQERSKIDTLTSQ LELEKQEQTHSKASRRQEITKIR AELKEIETQ
6049	36417	A	6096	1	5073	
6050	36418	A	6097	1	3489	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTTEITNLYSDH SAIKLELRIKNPTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIPLNAHKRKQERSKIDTL TSQLELEKQEQTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKTDRPLARLIKKR EKNQIDTIKNDK
6051	36419	A	6098	1	3235	

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6052	36420	A	6099	1	3070	MATLIPLLFHKHPHLTQRYQFN VRGGCPTSTAIAITLDPRTAVFP LMSVFQTSAPWPFWGFTHTQTP VPQPLKVKIHSSADTAADIQAN RVWSGPPANSKRPAEEGKLT NRKDIHTKNPSVRHHHQRPKV DKTTKTGKKQRRKTGNSKKQS ACPPPKERSSTATEQSWTEND FDKLREGFRSSNYSKLQDEIQT KGKEVENLEKSLDECITRITNTE KGLKLENYVKNEETSGANAI NWKKGINKIDRLARL
6053	36421	A	6100	1	3297	MKAIEKMFETNENKDTTNQN LWDAFKAEEVESLNRPTGAEL GAIINSLPTKSPGPDGFTAEFY QRYKEELVPFLLLKFSIEKEEL LPNSFYEASILIPKPGRDTTKEE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDA EKAFDKIQQPFMLKTL NKLGDIGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNILLEVLARAIQKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPTYKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYA AKKHKMKCSSLAIREMQI KTTMRYHLTPVRMAIHKSGNN
6054	36422	A	6101	1	2563	
6055	36423	A	6102	1	3417	

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6056	36424	A	6103	1	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSASEPPSAIPKAQV SSTEKLRNCIDDLKPFPAALASEL SRRAKALQIAGFPPMKVPRDTI SKVCCLKTVGKLCHSGEESRK CTLICNNKHYPIDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAKYSSLEAKLCQIESKYL ILLQEMKTPVCSEDDQGPTRV AQLLEDALQVESQEQPEQAFV KPHLVSEYDIYGFRTVPEDDEE EKLVAKVRALDLK
6057	36425	A	6104	1	4371	
6058	36426	A	6105	1	1825	MVKGSIQEEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTROKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEITNYLSDHSAIK LELWIKNLTONHSTTWELNNLL LNDYVWHNEMKAEIKMFFETN ENKDDTTYHNLWDTFKAVCRGK FIPLNAHKRQKERSKIDTLTSQ KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKREKNQI DAIKNDKGDITTDPEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPIGTAE IVAIINSLPTKKSPPGPDGFTAKF YQRYKEELVPFLKLFQSIIEKE GILPNSFYEAHILIPKPRDRTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIGM QGWFNIRKSINVIQHINRAKDK NHMISIDAFAFDKIQPFMLK TLNKLGIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNP CSWVGRINIVKMAILPKNILITL QLLLVLPSTLPLWLPALAGQ
6059	36427	A	6106	1	4449	

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6060	36428	A	6107	824	3693	AWKGTDDRSTRQKVNKDTQELNSALHQAADLIDYRTLHPKSTETYTFSSAPHHITYSKIDHIVGSKALLSKCKRTEITNYLSDHSAIKLELRKINFTQSRSTTWKLNLLNNDYVWVHNEMNAEIKMFFETNE NKDDTTYQNLWDFAKAVCRGKFIALNAHKRKKQERSKIDTLTSQLKELEKQEQTTHSKASRRQEITKIRAELEKETQKTLQKINESRSWFFERITKSDRPLARIKKKREKNQIDTIKNDKGDIT
6061	36429	A	6108	1	3297	
6062	36430	B	6109	112	3300	
6063	36431	A	6110	3	3316	
6064	36432	A	6111	1	3457	
6065	36433	A	6112	1	3170	MVKGSIQEEELTILNIYAPNTGAPRFIKQVLSDLQRLDSHTLIMGDFNTPLSTLDRSTRQKVNKDTQELNSALHQAADLIDYRTLHPKSTETYTFSSAPHHITYSKIDHILGSKALLSKCKRIEITNYLSDHSAIKLELRKINLTQSRSTTWKLNLLNNDYVWVHNEMKTEIKMFFETNENKDDTTYQNLWDFAKAVCRGKFIALNAYKRKEERSKIDTLTSQLKELEKQEQRHSKPSRRQETKMRAELEKETQ
6066	36434	B	6113	1	4753	
6067	36435	B	6114	1	3384	
6068	36436	A	6115	1	3345	
6069	36437	A	6116	1	3780	
6070	36438	A	6117	1	3720	
6071	36439	A	6118	1	3894	
6072	36440	A	6119	1	3335	MVKGSIQEEELTILNIYAPNTGAPRFIKQVLSDLQRLDSHTLIMGDFNTPLSTLDRSTRQKVNKDTQELNSALHQAADLIDYRTLHPKSTETYTFSSAPHHITYSKIDHIVGSKALLSKCKRTEITNYLSDHSAIKLELRKINLTQSRSTTWKLNLLNNDYVWVHNEMKAEIKMFFETNENKDDTTYQNLWDFAKAVCRGKFIALNVYKRKKQERSKIDTLTSQLKELEKQEQTTHSKASRRQETKIRAELEKETQ
6073	36441	A	6120	1	3780	
6074	36442	A	6121	1	3852	
6075	36443	A	6122	1	3345	
6076	36444	B	6123	1	6136	
6077	36445	B	6124	1	3924	

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6078	36446	B	6125	295	4185	
6079	36447	A	6126	1	405	
6080	36448	A	6127	1	1059	
6081	36449	A	6128	2	518	EKATCDENDSVSNIA TEIKGQ QSVVHVSPQKQSAWKVIFKKKV SLLNIA TRIIGGGKSGTVSSQKQ PPSKATSDKTDALNIA TEIKDG LQCGTVSSQKQPALKATTDEED SVSNIA TEIKDGEKSGTVSSQKQ PALKATTDEKDSVSNIA TEIKD GEKSVTVSSQKQPASK
6082	36450	A	6129	1	843	
6083	36451	A	6130	1	432	
6084	36452	A	6131	2	835	CGSAQAAAAAAEEATEKIPAL RP/ASAVGAAGALAVLRDPRA WREAGSKS/PETPFS* CQGA/HG GGQFCPSGTAFPGKMKVMMR KRKKKGQCLPGICRSLKRRKSP RSPGM/IGYSTLSIPPEMLASYQ SYSSTFHSLEEQQVCMA/G*HR QMPGADKPVRAQQRVLAGVW AGFTMRHQSRLY*ECSCIGVIFR HRCVAHLLGRAIGALFVITPA GERGMCCAKILGNARVFPVT TL*NDGQCQACMHAG/TTLED P GKNYISSPSSSSSSPSSPRVPS
6085	36453	C	6133	278	446	
6086	36454	A	6134	1	1152	
6087	36455	A	6135	1	639	
6088	36456	A	6136	12	1436	
6089	36457	A	6137	367	1056	
6090	36458	A	6139	1	4263	
6091	36459	A	6140	1	1311	
6092	36460	A	6141	1093	1358	MQKKPLTKFNNPSC*KLSIN*V LMGRISK*VTTTATTTTITTTT TTTTTTTTTATTTTTTTTTTTT TTTTTTMGPTLPLPIGLGS
6093	36461	A	6142	1	699	
6094	36462	A	6143	1	489	

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6095	36463	A	6144	5	916	ALGGTPMLGKLAMLLWVQQA LLALLPTLLAQGEARRSRNTT RPALLRLSDYLLTNYRKGVPRV RDWRKPTTVSIDVIVYAILNVD EKNQVLTTYIWYRQYWTDEFL QWNPEDFDNTKLSIPTDSIWVP DILINEFVDVGKSPNIPYVYIRH QGEVQNYKPLQVVTACSLDIY NFPFDVQNCSTFTSWLHT/SPG HQHLFVALARKGEIRQECLHEP GRVGVAAGGAALLSGVQHGKQ* LLCRNEVLCGHPPAAPLLCGQP ATAQHLPHGHHGRGLLPAPQQ WREGLFQNYTPPGLLGLPDHFR
6096	36464	A	6145	5	756	
6097	36465	A	6146	1	471	
6098	36466	A	6147	184	1097	ALGGTPMLGKLAMLLWVQQA LLALLPTLLAQGEARRSRNTT RPALLRLSDYLLTNYRKGVPRV RDWRKPTTVSIDVIVYAILNVD EKNQVLTTYIWYRQYWTDEFL QWNPEDFDNTKLSIPTDSIWVP DILINEFVDVGKSPNIPYVYIRH QGEVQNYKPLQVVTACSLDIY NFPFDVQNCSTFTSWLHT/SPG HQHLFVALARKGEIRQECLHEP GRVGVAAGGAALLSGVQHGKQ* LLCRNEVLCGHPPAAPLLCGQP ATAQHLPHGHHGRGLLPAPQQ WREGLFQDYTPPGLLGLPDHFR
6099	36467	A	6148	3	672	
6100	36468	A	6149	3	398	LRKIKIDLGKFSNDPBGYIDVLQ GLRQSFDTWRDIMLLDQSLT PNEKSAAKTAAREFGDLWV/S FQN*SCKTNRSSNGAPDAVHD *D/PTADPWTGPLAHALMLMTL KAPLTRKSQLHDPYYPAPIQQA V
6101	36469	A	6150	1	420	

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6102	36470	A	6151	1	878	TLLPPRPGVGS DYPNIPGCPMW GNKDPGEGTLER GKVEDASQR TSRTLKETS GKA EHRKKQDGK CSPQGKNAL KMYSGEFDPVRV CVPFSLDLKQLKIDLGRFSDNP DGYIDV/LQGLGQSFDTLWRDI MLLLDQTLTPNERNATITAAARE FGDLWCLSQVNDRMTTEERER FPTGQQA VPSADPH* DTESEHG DWCCRHL L TCVLEGLRKRKK AVNFSVMSTVTQGKEENPTAFL ERLREALRKHTSLSPDSIEGQLI LKIKFITRSAADIRKQTSKVHLR PGAKLKTPY
6103	36471	A	6152	1	417	
6104	36472	A	6153	1	415	
6105	36473	A	6154	1	234	
6106	36474	A	6155	1	335	TCPIVPG/QEMIIEISKGRSGLGL SIV*GKDTPLNAIVIHEVYEEGA AAVDGRLWAGDQILEVNGVDL RNS SHEEAIT ALMQTPQKVRLV VYRDEA HYRDEENLEIFPVDLQ
6107	36475	A	6156	109	4687	
6108	36476	A	6157	109	4991	
6109	36477	A	6158	3	862	
6110	36478	A	6159	1	1857	
6111	36479	A	6160	3	100	
6112	36480	A	6161	1	537	
6113	36481	A	6162	125	1184	
6114	36482	A	6163	875	1506	LSIYLV TQKAA/SSEWGP EQEK ALQEVQAAVQAA LILEPYDPA GPVVLVSLADRD A VWSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQHSI I KWKYIHD RARAGPEGTNSSARYAATM*K WTASALQPLSRKSLKDSSEK SSQWAE LRAVHLAVHVAWKE KWPDPVRLDTDSWAV/ANGLAR WGTWKEHDRKIGDKEVWGR GTRI
6115	36483	A	6164	1	1566	
6116	36484	A	6165	1	1098	
6117	36485	A	6166	1	538	
6118	36486	A	6167	410	625	LTLVPFSFVVL TPLPKGNTRY *TGIL*GWNLSWKGT L GFSVTA QPSSGTPRTALGSR TT KPLLVSL LQV

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6119	36487	A	6168	821	1428	QVTDVQDFLCKCIQWRRTVR GDLQ/PFTRVTVHWGKGNQDT FQGLDITGSELTLPDGPKRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQ/NSHIGSLTGRVRA TMVGKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT GVIPTSPFNSPI*PMQKTDGSW RMTVDYL
6120	36488	A	6169	203	850	DVEHVKGKMRRRWRRRVVAD GNVVKPMSCAGDLQ/PFTRVT HWGKGNQDTFQDILLDTGSELT LIPGDPKRHC GPPVKIGAYGGQI INGVLAQVQLTVDAVGPWTHP VV/I/SPVPECIIGIDILSSWQ/NSH IGSLTVHLSSDPKGCHEWGP QEALQEVQAAVQAALILEPY DPAGPVVLEVSLADRDVWVSL WQAPIGESQQRPLGFWSKALPS
6121	36489	A	6170	1	864	
6122	36490	A	6171	1	205	VPDFPAKPIQGFHNSRYL/REA VHGAEVHAFIAGQPLT**ELM SIFPQFQFFLYRRLDSHSGSQW I
6123	36491	A	6172	1	3039	
6124	36492	A	6173	1	1364	MIISDAEKAFDKIQPFMLKTL SKLEETASPSVVA TYTPQPM PSAFPLSEINPVL PETTVMAS PEAVTRQDNVDS PQKPPPTPMF ASRPITRLKPRRAPSEEGIQLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTFSQLQN LNTMGIFGSCDRSQVAALNHQ RQVPELIIGIDILSSWQNP HIGSL NGRGYINSLALCHNLIRDLDR FLLPDQITLVHYIDHIMRLDSVK DKWLHLAPPTKKEAQLVGL/ FGFWRQHS/LWROPLACYWAL VETEHLTMGHQV/TMQPELPIM NWLISDPSSYKPAPMASWGV YGQLTEEEKTRAWFTDGSARY TETTRKWTAVAIQPLSRTSLKD SNEGKSSHQA KNGITVLACVI DPDYQDEISL/LTPQWRCHPGSS VWRASSLGISHPP
6125	36493	A	6174	114	1996	

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6126	36494	A	6175	1	475	MGRNQNRKAENSKNWNASSPP KEHNSSPAREQNWREDEFNLT EVGFRRSVITNFSDLKEHVLTH CKEAKILEKRLDKWLTKITSVE KS/CK*PDG/D*KPQYENFMKHT QASIALDLIKRKKRYQ*LKIKLM K*SKKTR*EKKKYKLPSENTTN TSMQIY
6127	36495	A	6176	179	393	NKRGYKQMEEHSLMDKKNQ YYENGHTAQGN*AGEGNKGYS IRKGTGSQIVPLCR*HDCISRKPD CLSPKSP
6128	36496	A	6177	1	710	MARELRDECTSFSSQFHQLEER VSVIEDQNMENKQEEKFREKGI KRSEQSLQEIWDYMERPNLCLI GVPESDGENGIKLEDTLQDIIQK DFPNLGRQANIQIEIQRMPQR YSSRRATPRHIVRFTKEIQTIR EYYKHLANKLENLEEMDKFL DTYTLPRNLQEEVESLNRPTGS EIEAIINSLPTTKSPRPGFTA YQRYKEELVPFLKLFQSI GILPNSFYEAHILPKLGRD KENFRPISLMNIDAKILNKILAN QMQQNIKNLIRHDQAGFIPGMQ CWFNIRKSINVIQHINRTKDKN HMIISIDAFAFYKIQQPFILKTL NKLLENKIPRNPITYKGCEGPLFK ENYKLMLEKEIKEDTSKWKNIP WSWGRNIVKMAILPKVIYRLS AIPKLPIMIFFTELEKTLTKFIWN QKRACIAKSILSQKNKAGGIML PDFKLYYKATVTKAAWYWYQ NRDIDQWNRTEPSETIPHIYSHL IFDKPDKNKKWGDFLFNKWC WENWLAICRKLKLDPLTPYTK INSRWIKDLNVRPKTIKLEENL GNTIQDIGMGKDFMCKTPKAM VTAKIDKWDLIKLSFCTAKE TTVRVNRQPTWEKIFAIYSSD KRLISRIYKELKL*PCSI*SQVA *CLQLCSFGLGLTWQCRLFFGSI
6129	36497	A	6178	464	724	IGEVLLDNILQRFVQLGSILPTF RYTNQT*IWSWTLFWLVS
6130	36498	A	6179	1	2022	
6131	36499	A	6180	1	882	
6132	36500	C	6181	1	1935	
6133	36501	A	6182	1	672	
6134	36502	B	6183	140	2195	
6135	36503	A	6184	26	354	

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6136	36504	A	6185	86	747	SLEDAMSLKDDDSGDHDQNEE NSTQKDGEKEKTERDKNQSSS KRKAVVPGPAEHLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFASIVEQFWRFYSHMVRPGDL TGHSDHFLKEGKIPMWEDDA NKNKG/KWIRL/RKGFGRGW ENLILAMLGEQFMVGEIECGG CGVCPAFQEDIH/IWNTASDQ ATTARIRDTL\RRVL\NLPANTI MEYKN
6137	36505	A	6186	23	127	
6138	36506	A	6187	2	419	
6139	36507	A	6188	1	714	
6140	36508	A	6189	19	373	AVFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFLL FFFFKLKELRLV*PLNPEN*ESC PLFSPVNLDMPTFKDKRWKV NWARSTSRQQLLESARTKSWA EREGGTRWRAW
6141	36509	A	6190	227	420	KNFLPNCASAKELFFFFFFFFFLL LLLLLLYFKF/M*WFKHLAF PLLAFILSPITAL*RGVFHH
6142	36510	A	6191	400	582	
6143	36511	A	6192	1202	1678	
6144	36512	A	6193	2	109	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL
6145	36513	A	6194	110	377	QWISRQKPYKPEKRGDQYSTFL *EC*ILVPLFWLVGFLRPDLL V*WAYGCP*HFLHFNLGESNN YVSWGCS
6146	36514	A	6195	1	381	
6147	36515	A	6196	1	759	
6148	36516	A	6197	1	609	
6149	36517	A	6198	2	1178	
6150	36518	B	6199	159	290	
6151	36519	A	6200	716	1001	SMPASTHLIVGSCSWKMVIVL PLVTHLFTALTVPWNLPWVEL YWNM*TM*LRSMKESLMATIF TLPELKA/VLHEKLQ*LQSTEDL *HGLLGG
6152	36520	A	6201	5772	5971	TANIIMTGSNSHITILTNVNRL NARIKRHRENCIKSQDPSVCCI *ETHLMCRDITYRLKIKGWSN
6153	36521	A	6202	1	974	
6154	36522	A	6203	1	600	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
6155	36523	A	6204	51	424	MAPKQDPKPKFQEGERVLCFH GPLLYEAKRVKVAIKD/ITREIH SYITVVGIKIGMNGFRRAKYSN TWTPICRNSENFKKPSKFVL* T EY*GEMPVDF*FWTWNQWRSC WLPCLYNDTSDLSAGV
6156	36524	A	6205	1	3827	MQKAIRLNDGHVAPLGLLARK DGTRKGYLSKRSSDNTK WQTK WFALLQNLFFYFESSRPSG LYLLEGVCVCDRAPSPKPA SAK EPLEKQHYFTVNF SHENQKALE LRTEADAKDCDEWVAIAHASY RTLATEHEALMQKYLHLQIVE TEKTVAKQLRQQIEDGEIEIERL KAEITSLLDNERIQSTQT VAPN DESDIKKIKKVQSFLRGWLCR RKWKTIQDIYIRSPHADSMRKR NQVVFMSLEAEAY
6157	36525	A	6206	1	900	
6158	36526	C	6207	172	501	
6159	36527	A	6208	499	848	KIRVPAA VAGLSPPLGPWSLRS PSQPERCCPWRNSSWWTAPRTS IITAAGKVSAPRLSSISCTTRGS WVKTPPTRARMVIASSNLERP SALSRM*PTSQSMTRKRWWRL WPSTTL
6160	36528	A	6209	3	495	SCAQTFPKLDTFLEHIKSHQEEL SYRCHLCGKDFPSLYDLGVHQ YSHSLLPQHSPKKDNA/CLQVF PCERYLRRHLPTHSGGRFKCQ VCKKFFRREHYLKLHAIHSGE KPYKCSVCESAFNRKDKLKRH MLIQYDEVQRQGLGMVPGTQKV LNKCFCHNVKKKK
6161	36529	A	6210	667	2142	
6162	36530	A	6211	1	396	
6163	36531	A	6212	213	446	
6164	36532	A	6213	101	580	VAGVGS LPRSMEDDAPVIYGLE FQARA/LTPQTAETDAIRFLVG TQSLKYDNQIHIDFDDENNIIN KNVLLHQS/AGEIWHISASPADR GVLTTCCYNRTSDSKVLTCAA V WRMPKELES GSHESPDDSSSTA QTL/ELLCHLDNTAHGNMACV VWEPMGDG
6165	36533	A	6214	1	933	

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6166	36534	A	6215	3	404	RLKEKKLVKEIVASCGPAQCQ ETIR TALAMGADRGHVEVPPA EAERLGPLQVARV/AVVTADLR LNEPCYATLPNIMKAKKKKIEV IKPGDLGVDLTSKLSVISVEDPP QRTAGVKVETEDLVAKLKEIG
6167	36535	A	6216	1	408	
6168	36536	A	6217	88	871	MADVRLVAVKRVIDYAVKIR VKPDRTGVTVDGVKHSMPFC EIAVEEA VRLKEKKLVKEIVAS SCGPAQCQETIR TALAMGA/D RGIHVEVPPAEAEFR/GVPLQV ARVLGQLAKKEKVDLVLLGK QAMACTDCNQ/TGQMTAGFLD WPQGTFA SQVTLEGDKLVER EIDGGLETIRLKLPAVVTADLR LNEPRYATLPNIMKAKKKKIEV VIKPGDLGVDLTSKLSVISVEDP PORTAGVKVETEDLVAKLKEI
6169	36537	A	6218	1	1023	
6170	36538	A	6219	110	842	
6171	36539	A	6220	1	122	
6172	36540	A	6222	1	1257	MNDATAVQEGSQMYSWQKLT PTGPFIMQPEGMGRLFAINKMA EGFPPEHYEPIETPLGTNPLHPN VVSNPVVRVLYEQDALRMGKKE QFPYVGTTRYRLTEHFHTWTKH ALLNAIAQPEQFVEISETLAAAK GINNGDRVTSSKRGFIRAVAV VTRRLKPLNVNGQQVETVGIPI HWGFEGVARKGYIANTLPNV GDANSQTPYKAF/LGQHREGV RN*LHHA AFSGA*LQCFQYAH NSRKNN
6173	36541	A	6223	737	941	WLRMMEHRLFPLWKRESKKA HYVQSSVLLCLGMLR*KYKGG KGKKERKKDEKRKGNGKKRI KIHSI
6174	36542	A	6224	1	1072	
6175	36543	A	6225	1	585	
6176	36544	A	6226	1	930	
6177	36545	A	6227	28	392	AGEVPLQLPPAAVCSACLQRP LWNSSFFL*SCLHALFH*VDL QSLIAFLLD*SS*YLCMLHEV LVLCFSAPSGLHLCSSLS*LF*LAI HLTFFQGS*LPCIGLEHASLAQR SLLLPF
6178	36546	A	6228	1	271	SAIVTFVCFMKFSCCVFQLHQV FHVLFKLVILVSSCNLFSRFLA SLHWVTTCFSFSEEFVITHLLKP APVNSSNSFSVQFCSLAGKEL

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6179	36547	A	6229	1	1089	MGWRPRWLPYLYWGFQSDLC PHCKRKAQEEDSLAAQAASHP RLSANSKNNSWKGQYSYALFK AMRHMLCIGYGRQAPAAVSDV WLTMLSMIVGATCYAMFIGH/ ATALIQVLDCSRRQYQEKVVL REHPNIGSSQEGGTWHQTVGL QQTSKDFDANDPILKQDTQEW SGSATFTSDGKIRLFYTDYSGK HYGKQSLTTSANTGTENGYYQ GEESLFNKAYYGGGTNFFRKES QKLQQSATTRDAELANGALGII ELDNDSPKKRGATQRSSENI TLKAYKRDVRSLLMLTRNEDV ADSLNSSKKRQNYQLPSIRSVT RCKKIGVCAKIGCGQGTHYLS VSILNTADRRRLGFRTRSMY
6180	36548	B	6230	1	1140	
6181	36549	A	6231	3	204	GSDYELGLW*PWLTSATDLH GECYSS*SGASGVVRSWLARG LAGFRSEADLRGRESVAVTN
6182	36550	A	6232	1	1296	
6183	36551	B	6233	1	1686	
6184	36552	A	6234	1	627	
6185	36553	A	6235	570	736	SATFGRSSRSGCSGFPAASRRG RLPLSPPPWPAVRVYPCGMLD NKASAAHPKKK
6186	36554	A	6236	1	103	
6187	36555	A	6237	699	887	GLQPPAPRETRPLY*TLAWNLI FLFVSPLDSCDLVRSVLTCLSP GNSPSFDMHRYQLPCVH
6188	36556	A	6238	2	803	
6189	36557	A	6239	2	1277	YKETYLIHLHFTTGLSIAYFNF GNQLYHSLLCIVQLILRLMG RTITAVLTTCFQMA YLLAGYY YTATGNYDIKWTMPHCVI.TLK LIGLAVDYFDGGKDQNSLSEQ QKYAIRGVPSLLEVAGFSYFYG AFLVGPQFSMNHYMKLVQGEL IDIPGKIPNSIIPALKRLSLGLFYL VGYTLLSPHITEDYLLTEDYDN HPFWFRCMYMLIWGFVLYKY VTCWLVTGVCIL.TGLGFNGFE EK GKAKWDACANMKVWLFET NPRFTGTIASFNINTNAWVARYI FKRLKFLGNKELSQGLS\MLFLF LWHGLHSGYLVCFQMEFLIVIV ERQAARLIQESPTLSKLAITVL QPFFYLVQQTHTWLFMGYSMT AFCLFTWDKWLKVYKSIYFLG HIFFLSLLFILPYIHK\AMVPRKE

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6190	36558	A	6240	56	324	
6191	36559	A	6241	68	487	
6192	36560	A	6242	52	457	
6193	36561	A	6243	263	787	SLEV*KWPGVACRLQL*P/MVP APKS*ESKSAGSLNTPSAICRDA SGRGLARPWLKSKCLACHLV DTRSKTAGGLAPVPSAHLISVR EREPLCAVLVSQLEFRVGVGL VGPTLGARREPCWPQAMGDLA PEPVAALRLISRRLPAFPWGR ARDLQAMPEPPTHSMGSCAPE PPR
6194	36562	A	6244	3	236	
6195	36563	C	6245	1	1608	
6196	36564	B	6246	1	1083	
6197	36565	A	6247	823	1055	KQKDGTPAPWSRGRSSGRLG THRSRRGWAEQAWRAAGPET CPAGRQLRPGEKSSAPG*RSR RKDAYEMDTAKKK
6198	36566	B	6248	1	390	
6199	36567	A	6249	27	363	
6200	36568	B	6250	1132	1268	
6201	36569	A	6251	11	489	
6202	36570	A	6252	356	638	
6203	36571	A	6253	1	507	
6204	36572	A	6254	80	336	
6205	36573	B	6255	100	912	
6206	36574	B	6256	821	2992	
6207	36575	A	6257	2	602	
6208	36576	A	6258	1	519	
6209	36577	A	6259	3	228	STGVVPSQRTCLLEKASVLFNT GALYTQIGTRCDRQTQAGLESA IDAFQRAADMSPGLTRRLGP TRWHQGTPH
6210	36578	A	6260	1	963	
6211	36579	A	6261	1	925	
6212	36580	A	6262	1	397	
6213	36581	A	6263	1	2625	
6214	36582	A	6264	11	241	SLQHLNPATFLPVSKSPVKHNC VEVLDSVYSSGPNHRDHP*TSV DWELYMDGSSFTNPCKVTLKK TTSPAPVTPGS
6215	36583	A	6265	1	1662	
6216	36584	B	6266	1	897	
6217	36585	A	6267	3	258	
6218	36586	A	6268	1	279	
6219	36587	A	6269	1	258	
6220	36588	A	6270	1	639	
6221	36589	B	6271	1	1935	
6222	36590	A	6272	698	1643	

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6223	36591	A	6273	91	386	IFDFLLYYVSGCNSIAEPQHFT TTVTRCSPVAFVEFPSSPQLKN DVSEEDQK\KPIENEMSGKGG SWVLFTKGEVQEWRESGLNPT KFNMGPLIYS
6224	36592	A	6274	1	2538	
6225	36593	A	6275	1	471	
6226	36594	A	6276	152	520	CPLTLLPSRGAGLGTCSPPCLS LPPTPWAPVRPEPPRRAPPAPR RPVPSGTKEQTTQGLRNASARR GTGRQLHLSPGVGSTG*SQGL
6227	36595	A	6277	831	1449	HPQWQLRRVCWVSSGAGLAL CSISCPALAAFPVRVGLGTCSPPC LSLPPTPWAPVRPEPPRRAPPAPR PPSPIDHPRAEEYE/PHGAGL AGSSTCSPSAESTG*SQLGS*VV RVRGFILVSETKNPPIDTFGL PPGSSAASLTVQVTRL*ISAIL PHLLSRPCSNARGPVPAVPG AAVRAPAAGRWCGGARGRG RRGGGH
6228	36596	C	6278	1	426	
6229	36597	A	6279	1	535	MKHSGAQLASPSGS\PLGPQVE LPASPVCACTSQPLGGRWDW APWSRGWCSSGRLGPHRSPWS GWE\LRHGGQLVPSAPREGS* GPARNP/GTAPGRPAAPS\GGPP SPRPRTPAGPQALRAAPVP\LA PLPPLPAS*GSLQPWPA*KE APTVCQCAEGLLKCRQSGSPGR GGAESE
6230	36598	B	6280	1	1743	
6231	36599	A	6281	1	428	GTR EEHLKRSRGRIALPIEACV MLLLETGMKEEGLFRIGAGASK LKKLKAALDCS\LTWDEFYSD PHAVAGALKSYLRELPEPLMT FNLYEEWAQVASVQDQGQKT FKDLWRTCQKLPQNFVNFY LIKFLAKLAQTSDV
6232	36600	A	6282	135	512	LPFRGAGLETCSPPCLSLPPPPW APVRPKPPR*APPPAPRRVPST TQSLGPHCFYEL*HSP*RSAAS LLKPARP*AHREERTTP/GRSAL/ TSCNTHREGLO/PSLRKKETPNT SEHQKEQTPDAPP

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6233	36601	A	6283	698	2233	IQAAMQAAAPQFGPSTED*CCPIT SEAPWAIMDAKLRLKPPSHPL VSPHLNPQVWDTSSPSLA TEHA SLTISLKPNIHPYPAQSQYSIPQH ALKGSKPVITRI LEHGLLKPIN PYNPILPVQKLDKSYRLVQHL CLIQVLPIHPMPNPYTLSSSI PFTTHYSVLDLKHAFFTIPLYP SQPLFAFTWTDPDTHQAQQTIL AVLPQCFIDSPHYFSQAQISSSS VTYLGILMKTHIGLGAVEQGV VLVGEARAAQEPMEWVGSG MVGCRSRALPRGKA AKARREI ERSAVTIVPVLDFNPAFHIDPTT PDHHDICSLIHLTFTFPFHSFFP VPHLEHTWFDGSSTRPNCHSP AKAGYAIVSSTSHIETALPRST TSQQAKLIAYTDSKCAFHILHH HAVIWEERNFLTMQGASIIINAF LIKTLKDLLPKEAGVIHCKGQ QKASDPITQDNAYADKVAKKQ LAFQLLSLTA VFLLLIRPLSPTSP LKLPLNLFPHKANDS
6234	36602	A	6284	1	1239	
6235	36603	A	6285	1	477	QRPPHG VFLVGVAGR VHGP ASHKAGPQLGDVGVCAQGG QVGPLVLQPVVEHIQQLPG/AG HCAHQ*QGSPS*SSLPRPERSLQ CRRPQGATA TIRSTWWGPRGP VCTAALVPLCWPGWPVQKDEL QAVRSHSALASAMQTCSLAGP GLGSSHARLTA
6236	36604	A	6286	1	1134	
6237	36605	A	6287	673	836	
6238	36606	A	6288	1	225	
6239	36607	A	6289	1	468	
6240	36608	A	6290	495	1637	ESQVLSNVSPHVKKV*NMASWE GKDLTVPPQPDTRKGSVLRISK RGRNASCS*DKRKASVCLSLG NGMSRYKTRLYAPSTEIGKNRL RAGGGTCGQYCFVKH
6241	36609	A	6291	1	507	
6242	36610	A	6292	215	389	
6243	36611	A	6293	1	255	
6244	36612	B	6294	69	1055	

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6245	36613	A	6295	23	1596	IKPQRWGGETRAEMLKILKTREP FLLQRIASPRQQWKNAGQRRS WFFERL/NKIDRLARLIKKKRE KNQIDAINDKGDITDPTIEIQT TIREYYKHLKYANKLENLEEMD KFLDTYTLPRLNQEELESNNRPI TGSEIEAIHSSLRTKKSPGPDGFT AEFYQRYKEELVLFLLKLFQSIE KEGILPNSFYEASIIIPKPGRDT TKKENFRLISLMNIDVKILNKIL ANRIQQHKKLVHHDQVGFIPG MPDWFNICKSINIIHHINRTNGK NHMIISIDAEKAFEKIQCFMLK TLNKLIGDGMYLKIIIRAIFDKPT ANVILNGQKLEAFPLKTGTTQG CPLSPLLFKIVLEVLAIRAIRQEK EIKRIQLGKEEAKLSLFADDMIV YLENPVSAQNLLQLRSNFSKV LGYNKINMQKSQAFLYTKNKQT ESQIMSELPFTIATKRIKYLGIQL TRDVKSLFKENYKPLLSKIKED TNKWKNIPSSWIGRISIAKMAIL PKVIYTFNAIPIKLPMTFTFTELEK
6246	36614	A	6296	1	1488	
6247	36615	A	6297	1	1401	
6248	36616	A	6298	2	1256	
6249	36617	B	6299	84	955	

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6250	36618	A	6300	735	2718	RSFPRSRPSPFLLLSRYLRIHMV FSVLPGFLQNPKYLLSGSLQEK FRTPGINSKTLDPNRYVHKVRR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITTDATIEQTTIREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPIITGSEIEAIINSL PTKRSPGPDGTAEFYQTYKEE LVFPPLKLFQSTEKEGILPNSFY EASIIIPKPGRDTTKKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHYDQVGFIGMQGWFNKRK SINVQIHINRTNDKNHMIISDAE KAFDKIQQPFMLKTLNKLGDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCLSPLLFNI VLEVLARAVRQEKEIEGQLGK EEVKLSLFADDMIVYLENPIVS AQNLKLLISNFSKVSQYKINIQK SQAFLYTNNRQTESQIMSELPFT TASKKKIYLGILTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPI SWVGRINIMKMAILPKVICRFN AIPKLPMPFFTELETTTLKFIWN QKRARKSILSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTPESEIMPHIYNYLIF DKPEKNKQWGKDSL FNK* CWE NWLAIWRKLLK
6251	36619	B	6301	1	2907	
6252	36620	A	6302	1	2358	
6253	36621	A	6303	1	1866	
6254	36622	A	6304	1	885	
6255	36623	A	6305	1	1059	MKNNSSEFPELLIPRQRSGV DLQQTPTDLQLRVLTVRRTN KQDIHTKTPTVRRHHQRPKNP WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLEKEVQEQT QSKASRRQEITKIRGELKEIETQ KTLQKINESRSWFEKINKIDRL LARLIKKKREKNQIDTIKNDKE DITTDSTEIQTIREYYKHLYAN KLENLEEMDKFLNIYTLPLNLQ EEVESLNRPIITGSEIEAIINSLPT KKSPGPDGTAEFYQSYQEELV PFLKLFQSEIEGILSNSFYKA NIILIPKPGRDTTKKENFRPISLM NIDAKILNKILANRIQQHIKKLI HHDQVGFIGMQGWFNI
6256	36624	A	6306	1	1692	

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6257	36625	B	6307	1	2871	
6258	36626	A	6308	2	2315	
6259	36627	A	6309	1	1210	MMSFHLSVHTAIDGSHSSCS AWCSPIRDYFEQENNSSSSCC CCCYHCHRRKHCCKGLSFPGE MPLSPGHFNKMMYSVSELMQG SGSGTFIPLPAELSLWLLVTNTK GQRMKNDAEIQTITREYYKHL YANKLENLEEMDKFLDTYTLPL RLNQEEVESLNRPTSSEIVAIIN SLPTKKSPGPHGFTAEFYQRYK EELVPFLKLFLQSIEKEGILPNSF YEASILIPKPGRDTTKKENFRPI SLMNSDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIIIDAE KAFDKIQPPFMLKTLNKL/GIK YLGQLTWDVKDLFKENYKPL LKEIKEDTNKWNIPCSWVGKI NIMKMAIPPKATSPLESYKREK
6260	36628	A	6310	1	2745	MEGEMNEMKREGKFRKRIKR NEQSLQEIWDVYVKRPNI.RLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIEIQRTPQRY SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHLKST YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNLLLN DYVWHNMKAIEKMFETNEN KDTTYQNLWDTF

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6261	36629	A	6311	1	2052	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRKIKNTQNRSTTWKLN NLLLN DYWVHNEMKAEIKMFF ETNENKDKTYQNLWDAFNAV CRGKFVALNAHKRQEGSKID TLTSQLEKEKQEQTHSKASRR QEITKVRALKEIETQKTLQKIN ESRSVARLIKKKREKNQI/DAIKN DKRDITDPTEIQTITREYYKHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIITGSEIVAIIN SLPTKKSPGPEGFTAIFYQRYK EELVPFLKLFQSTEKEGILPNS FYEASIIIPKPGRDTTKKENFRP ISLMNIDAKILNKILAKRIQQHI QKLIHHDQVGFIPGMQGWFNIC KSINVIQHINRTKDKNHMISID AEKVFDKIQQRFMLKTLNKL LEVLA RAVRQEKIKIGIQLGKE ELKLSLFAADDIMIVYLENPVSA QNLLKLISNFSKVSEYKIN VQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDVNWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTSFTLEKTTTFKIWNH KGARIAKSILSQKNKAGGITLPD FKLYYKATVTKTAWY

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6262	36630	A	6312	2	2143	SSDGSWWTGFQWREWRQAGR SVNSWDNPKQEVRASSKDKSR GSIQEAMRMQSSAKLLCSAWT LAYSIARTLSSDSEGQPPVIH RQTGSGEDLQQTPTDLQLRVLT IRRKTNKQKGHPHQNPISRRQ EITKIRAEKKIETQKPFKKINES RSWFFKINKIDRLRLARLIKKKI EKNQIDAINKDKGNITTNPTIEQ TTIREYYKHLANKLEHLEEM DKFLDIYTLPRLNQEEVESVNR PITGSEIEAIIINSLPTKKSPGPRF TAELYQRYKEELVPFLKLQFSI EKEGILPNSFYEAIIILISKPRGR TTKKENFRPISLMNIDAKILNKI LANQIQHHIKKLIHHQVGFIPG MQGWFNILKSINVIHINRTKD KNHMIISIEAEKAFDKIQPFML KTLNKLIGIDGTYLTYLKIIRAIY DKPTANIILNGQLEAFPFTGT RQGCPLSPLLFNIVLEALARAIR QEKEIKGQLGKEDVKLSLFAD DMIVYLENPVSAQNLLKLISNF SEVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLENIK EDTNKWNIPCSWIGRINIVKM AILPKTLNQKFSYWFRVKNKHYI HQRTFPLKETEFNTIATLYNGA SP/CTAPKSTGTNGHQASGLPRF *RIAFCSALVKSRRKLYQGYLP GQTDREEGVSWCPGGP
6263	36631	A	6313	1	3018	
6264	36632	A	6314	1	2016	
6265	36633	B	6315	1	1215	

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6266	36634	A	6316	1	2268	MAGYPSETKPPEERSDSNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDLQLRVLTVKRKTNKQKG HPHQNPRTSPSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFIKEVLRLDQ RDLDSHTIMGEFNTRLSTLDRS MRQKVNKDIQELNSALHQADL IDISRNHLPKSTEYTFFSAPHRT YSKIDHIVGSKALLSKCKRTEII TKCLSDHSAIKLELRKLNLTQNC SITWKLNNLLNDYVWHNEM KAEIKMFFETSENKDDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKTDLTSLKELEKQEQT HSKASRRQEITKIRAEIQEIETQ RTLQKISESRWFFEKINKIDRS LARLIKKKREKNQIEAIKNDKG DITTNPTETQTTIKEYYKHLYK NKLLENLEMDKFLNTYTLPRLN QEEVESLNRPIITGSEIVAIINSLP TKKSPGPDGFTAIFYQRCKEEL VTFLKLFQSIKEGILPNSFYE ASINLIPKPGRDITTKENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSQIVPVC*H DCVSRKPHHLS PQSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE*TPIHNCFKENKIPRNPT YKGCCEPLQGELOTTAQ*NKR GHKQMEEHSMMLMDRKNQHRE NRHTAQGNL*IQCHSHQATNDF
6267	36635	A	6317	1	1797	
6268	36636	A	6318	2	2063	
6269	36637	A	6319	1	1212	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
6270	36638	A	6320	1	2718	MALFRVGM TTRRLGHANKFTR DLLVKRLLEYFVVEIIPGLRTK TTLVGPLETGYTSSDVNSPHF MLDIALSHNVKSTQLLRPWR NIDCSRNIHNAKKEEQMGDDE INRQQECSSSPAMEQSWTENDF DELREFVFRSSNYSELQEFIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQETKIRAELEKEIE TQKTLQKINESRSWFFKINKID RPLARLIK KREKNQTDTIKND KGDITDPTIEQTIREYYKHLV TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPIGTGEIEAHNSL PTKKSPGPDGFTAIFYQRYKEE LVPFLLLKLSQIEKERILPNSSYE ASIIILPKPGRDTTKENFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KLISKFSKVSQGHKINVQKSQAF LYTDNRQTESQIMSELPFTIASK RKLYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNI PCSWVG RINIVKMALLP RFSAPIKLPMPT FFTELEKTTLKIWNQKEP/CIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNLYLFDKPKD KKEWGGKDSL FNKWCWENWLA ICRKLKLPFLTPYTKMNSRWI
6271	36639	A	6321	1	2307	
6272	36640	A	6322	1	1989	
6273	36641	A	6323	1	3285	
6274	36642	A	6324	3	4732	
6275	36643	B	6325	1	2693	

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6276	36644	A	6326	603	2976	DNTARGTIRQQHLLFTNIRCSA ASAAADTQANRVWSGPPANSNR PAAARVLTVRRKTNKQKGHPH QNPICTSFSSSKTKETQITIREYY KHLVYANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRITSDIE AIINSLPTKKSFGPDGFTAIFYQ RYKEELVPFLLKLFQSIKEGIL PNSFYEAIIILPKLGRDITKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHQDQVGFIPMGQ WFNICKSINVIHHMKRTDKDKNH MIISIDAFAKAFDKIQPFMLKTL NKLIGDGTLYKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLNFIVLEVLARAIRQEKEIK GFQLGKEEVKLSLVDEMILSL ENPMVSAKNLLKLISNFSKVS YKINVQKSQAFLYTSNRQTESQ IMSELPFTIASKRIKYLGIQLTGD VKDFFKENYKPLLNEIKEDTDK WKNIPCSRVRGINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIKSLSQKNK AGGITLPDFKLYYKATVTKTAC HRVGRAQQHSISKWKWYIHDW SQVGPEGTNDSARYPDITQKW TAAALQPLSRITSLKDSHEGKSS QWAE LRAVHLVLRFAWKEKW PDVQLYTDSWAVASGLAGWS GTWKKHDKWIGDKIEWGRATP VIAQWAHEQRGHGGRDGDYA
6277	36645	A	6327	3193	6107	SMKTGLEKKMKRNEQSLQEIW DYVKRPNLPLIGVPESDGDNAT KLENTLQDIIQENCNPLARQANI QIQEIQTTPQYSSRRATPRHIIV RFTKVEMKEKMLRAAREKGRV THKGKPIRLTAALSAETLQARR DRRPIFNILKEKNFQPRISYPAK LSFVSEGEIEYFTDKQMLRDFL MTRPALKELLKEALNMETTGA PRFIKQVRLRELQRDLDTHTITG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADL
6278	36646	A	6328	1	1808	
6279	36647	A	6329	1	4695	

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6280	36648	A	6330	1	2915	MIMGDFNTPLSTLDRSTRQKVN KDTWELNSALHQADLIDYRTP HPKSTEYTFFLAPHHTYSKIDHI AGNKALLSKCERTEIHTNCLSDH SAIKLQLRIKKLTQNHSTTWKL NNLLNDYWVHNEMKAEIKIF FETNKNKDTTYQNLWDTFKAV CRGKFIALNAHKRKQERSKTD RTSQLKHLENQEQTTHSKARRS WFFEKINKIHRPLARLIKKKREK NQIDAINKDKGDIITNPTEIQT REYYKHLTYN
6281	36649	B	6331	1	6730	
6282	36650	A	6332	1	378	
6283	36651	A	6333	3	1700	
6284	36652	A	6334	1	1759	
6285	36653	A	6335	2	409	
6286	36654	A	6336	1	2051	MFGRSRSWVGGGHGKTSRNIH SLDHLKYLYHVLTKNTTVTEQ NRNLLVETIRSITELIWGDQND SSVFDFLEKNMFVFFLNLRQK SGRVVCVQLLQTLNLFENISHE TSLYLLSNVYNSIIVHKFDFS DEEIMAYYISFLKTLCLKNNH TVHFFYNEHTNDFALYTEAIKF FNPESMVRIAVRTITLVYKVV DNQAMLHYIRDKTAVPYFSNL VWFIGSHVIELDDCVQTDDEHR NRGKLSDLVAEHLDDLHYLND LIINCEFLNDVLTDDLNRFLFLP LYVYSLLENQDKVFLIIHHAFLV NSLAEVILNGDSEMYAKTEQD IQRSSVLPTLSSLWQGSLSLNLQ LQSGLHKCSSHLGCAQAAADS VTGEIPAIRSEWLISAGSKART FFFLKMLIGFWEKVDCEYQRR QVLSTRLQALPSNRLTDVAAY HSSCMLGFGSTAPRGSWIGDPA AVHLPLPGELAEHLGSKGTTTV TKHQPPQAKPSIRCFIKPTETLER SLEMNKHGKRRVQKRPNYK NVGEEDEEKGPTEDAQEDAE KAKGTEGGSKGIKTSGESEIE MVIMERSKLSLAASTSVQEON TTDEEKSAATCSESTQWSRPF LDMVYHALDSPDDDYHALFVL CLLYAMSHNK/GKSPEKEEGLS GTQSHPGKAGTFGKEGAERK
6287	36655	A	6337	2	2753	
6288	36656	A	6338	1	577	
6289	36657	A	6339	1	849	

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6290	36658	A	6340	1	1293	
6291	36659	A	6341	1	861	
6292	36660	A	6342	154	6208	RRAPGKIPGQASAFGLGRTWSRP CLRTQLCVIVSCLAKAGVQGYL VGSPGGAKRFLFSERTGFSFKL AAMSSWLGLGSLGQSLGQV GGLASLTGQISNFTKMDLMEG TEEVEAEIPDSRTKEIEAIHAIL RSENERLKKLCTDLEEKHEASE IQIKQQSTSYRNQLQQKEVEISH LKARQIALQDQFLKLQSAAQSV PSGAGVPATTAASSFAYGISHP SAFHDDDDMDFGDISSQEQEINRL SNEVSRLESE
6293	36661	A	6343	3810	5310	SQGTCPVDRPCNVSG*RI/SIEEI EAGRIPNPHLGPVEERLALHVL QQQGLVPEHVESRPLYSPLQPD IEQAFPSFGRKSRWIRVIPPRFF LRCIWNTNRDVLDDLSLTGEK MSDIYVKGWIMIGFEEHKQKT VHYRSLGGEGNFNRWIFPFDFY LPAEQVCTIAKKDAFWRLDKT ESKIPARVVFIQWINDKFSFDD FLDPYAIVSFLHQSQKTVVKN TLNPTWDQTLIFYEIEIFGEPAT VAEQPPSIVVELYDHDITYGADE FMGRICQPSLERMPRLA WFL TRGSQPSGELLASFEIQLREKPA IHHIPGFESEDTLPPPPQREA NIYMPQNIKPAQRATIEILA WGLRNMKSYQLANISSPSLVVE CGGQTVQSCVIRNLRKNPNFDI CTLFMEVMLPREELYCPPI TVK VIDNRQFGRRPVVQGCTIRLSLES FLCDPYSAESPPQGGPDDVSL LSPGEDVLIDDDKEPLIPQNYA
6294	36662	A	6344	1	527	
6295	36663	A	6345	5251	5711	PPQRGPSSSCYSRSQRSVSRCP SRHRPSAASPRGRPSGRSGLLA GLRLWAGAGCFQCPCLQRL FSPEALRPQAPAHKGLFSGSLW PQQRSHQGLRAAATS*DRRAAG ALCKWCPRPSGTPRGEHLS*EN ESLPP**RWAHQTAQESQTS
6296	36664	A	6346	1	924	
6297	36665	A	6347	1	894	
6298	36666	A	6348	1	525	
6299	36667	A	6349	6	343	
6300	36668	A	6350	1	2693	
6301	36669	A	6351	26	353	
6302	36670	A	6352	1	9182	

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6303	36671	A	6353	1	8655	EA AKDLADIAAFFRSGFRKNDE MKAMDVLPILKEKVAYLSGGR DKRGGPILTFPARSNHDIRIQE DLRLRLISYLACIPSEEVCKRGFT VIVDMRGSKWDSIKPLLKILQE SFPCCIHVALIIPDNFWQKQRT NFGSSKFEFETNMVSLGLETKV VDPSQLTPEFDGCL EYNHEEWI EIRVAFEDYISNATHMLSRLEEL QDILAKKELPDLEGARNMIEE HSQLKKKVIKAPIEDLDLEGQK LLQRIQSSESF
6304	36672	A	6354	1	1338	
6305	36673	C	6355	152	404	
6306	36674	A	6356	137	1278	MDSQPNSTRGQSGRR/MEIKGI QLGKEEVKLSLFADDMIVYLEN A/TSQPKISLS**ATSAKSQDTKS MCKNKHHSYTPITDKQRAKS* VNHSQLLQRE*NT*ESNL*GT* RTSSRKTTHNCMSMK*KRIQTNG RTFHAHG*EESIS*KWPYCPR*F IDSMPPSSSYQ*LSSQNWKRL SSSYGTTKEPASPSSQS*AKRTKL EAS/LLPDFKLYYKATVTKTAW DMDEAGNHHSQQTITRTKNQT PHVLTHRWELNNENTWTQEGE HHTPGLVVRSPDPEQNFKAVR CLDLPD/PSSSFLAVLTFHFKA FLQSLR*DKPRS/SPALGTWHP *KITPKKQ/HQAITKPNTYEYRTA VKPSVVGALPDINSFLKLGGLH RITNGCLLD

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6307	36675	A	6357	1	2569	MRTKTQHTRISWDAFKAVCRG KFIALNAHKRQERSKIDTLTS QLKELEKQEOTHSKASRRQEIT KIRAELEIETQKSLQKINESRS WFFERINNDRPLARLIKKKREK NQIDTIKNDKGDITDPTIEIQT REYYKHLVANKLKNLEEMDKF LDITYTLPRLNQEEVESLNRPTG SEIVTIINSLPTKKSPPDGFTAE FYQRYKEELVPFLKLQFSIEKE GILPNSFYEAIIIPKPGRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIIHDDQVGFIPGMQ GWFNIRKSINVIQHVNRADKDN HMIISIDAEKDFDKIQPFMLKT LNKLGIDGTYLKIIIRAIYDKPTA NIILNGQKLEAFPLKTGTGRQGC LSPLLFNIVVEVLASAIRQEKEI KAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFIIASKRIKYLGIQLTRDVKDLF KENYKPLIKEIKEDTNKRKNIPC SRVGRINIVKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKRAHIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYSYQNR DIDQWNRTEPSEITPHIYNLYIF DKPEKNKQWKGDSLNFNKGW ENWLAIWRLKLDPPFTPTTKI NSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTP/TSNG NKRQN*QMGSNETKELLHSKR
6308	36676	A	6358	1702	2252	FLSLFFISLASSLSILIIHIMNSW IPHSPIFDLNVESRLCPLGDIM M*IPLTWYLVTCITLSREITTV PRGLARLWSFTRICPRTHCKPIP A/VLLRAGCPPSCWWDQDTHS QLPSKRSSYLFFCTVTEYPFLO *WP*NHGTPC*TAPLWSMF/PCS CWYPVTGPGVSCSPSCVQVFS FISHL*VRTCGVWFFVLAIVC*E *WFPASSMSQAVLVTVL*YSL KSGSVMPA/FSFGLGTWRCL LFFGSIRTLK*IFPIL*RKSLVA* WGWH*YKLRWAVWPFSSRY*F FLPMSM/VMFFHLFVSSFISLSS GL*FSLKRSFMSLVSWIPKYFIL FEAIVNGSSLMIVLWVCLLLLH KNACDFCTLILYPETFLKLLISL RRFVAETMGFSRYTIMSSANR DNLTSFFPN

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6309	36677	A	6359	207	1209	IPRHHPPKTKPGRS*/TP*IDQ*Q ALKLRQ/CINSLPTKKSPGPDGF TAKFYQSPSLTGKNDKEPEILPY FHADFLVVPGTHQASVLMVL GHKSPFHRNSPPSVCMANFFQT KPPSQSIHNAVNTHTDPLFLVL LKDRGLLVWCHESQGDLEIWH LVLLDSKCCFGSMTHRMEWSG PSAAGLLEFAGGPLQTLFAVVS AVEAAEQRIILLNSKCCCLIPLE ALSQRGIW/PWQGSVPVRPWTTT TLWPVRNQTQQTSLMPCQL EGKEPLALPTKEAEIEGRRTGEI KKVERDSNTNKEELLLDLAFK VSSFLDKLEEVVELLVIGELQL YPSK
6310	36678	A	6360	544	678	AFHHVSFGCINVFF*EVSVHML CPLFDGVVFFLVNLEFFVDSG
6311	36679	A	6361	7	94	VRTSGVWFFVLAIVC*E*WFP SSMSLIY
6312	36680	A	6362	381	431	ATKQDSVSKKKEEEEEEEEEEE EEEEEEEEEEEEEEEEKEK/GNK ERKK/DKGKARQVQARQIYLLS LHLGRIRKVPNNKA*SSCP
6313	36681	B	6363	1	603	
6314	36682	A	6364	1	987	
6315	36683	B	6365	1	444	
6316	36684	A	6366	977	1177	RTSISSPVSTCSPLVMTLLPQP TVPWWRMWRPCTQ*RNAITFSP AVAMGLPVEAVICLSV*DSPA
6317	36685	A	6367	1148	1395	
6318	36686	A	6368	33	663	VHVLGDDTDETNHHSQQTIA RTKNQTPHVLTHRERLSLRGL HSCAYSLHRWLGAHQKGS NTKGGCGGQGPRTSERGPASGEF SENCTSLGQRGVFSPPRRALL HSPSDGSPVPLGAVDSSP/PASTR RDWSHWAVGKPSPEREPAGKV T*TTTQLQPASP*REHPLLSQH GHCLKISLPLPTVLSPPPLSLC SNVTFTSTRPLT
6319	36687	A	6369	1	1314	
6320	36688	A	6370	120	410	
6321	36689	A	6371	1	492	

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6322	36690	A	6372	3	945	EEVPRSMKSKKKRKRKRKRKR EEEEEEEEEEEEEEEEEEEE EERRVEGEVEGEVEGEVEGE PSHLEKMYVRNKNMTMYEVCLM PIGIKQVNVGAMQCILVAPYIS PIVGVINFNDQVNSQGGGSKME DGIHFRGKVMHLHVGRKRQRVK KGLGYAFISSMKTNEYTKLVVP EWGLAEKIPKNVEATLELGNRR SKKTGGILPLLWNFELERDEL GYLVEEISKQPSIQMTWVLLK AFRFQIEAEKPSSENLPDNDVIE KKNPFSSEKGFMLAAEICISNEE WNGVNPQDYGGKWLQGMA EVFTATPSITGLEA
6323	36691	B	6373	1	792	
6324	36692	C	6374	348	884	
6325	36693	A	6375	1	588	
6326	36694	B	6376	1	5339	
6327	36695	B	6377	520	3146	
6328	36696	A	6378	1	2044	
6329	36697	A	6379	1	585	
6330	36698	A	6380	1	2433	
6331	36699	B	6381	53	441	
6332	36700	A	6382	2	425	
6333	36701	A	6383	1386	2569	FLRKHRESGKDEEMTALCSFPG VAGEDELQVIQPEKSVSVAAGE SATLRCAMTSLIPVGPIMWFRG AGAGRELIYNQKEGHFPRVTTV SELTKRNNLDFSISISNITPADAG TYYCVKFRKGSPDDVEFKSGA GTELSVRAKPSAPVVSQPAVRA TPEHTVSFTCESHGFSRDIITLK WFKNGNELSDFQTNVDPAGDS VSYSIHSTARVVLTGRDVIHSQV ICEIAHITLQGDPLRGTAANLSEAI RVPPTELVTSQPIRAENQANVT WQVSNFYPRGLQTLWLENGNV SRTETASTLIENKDGTYNWMSS WLLVNTCAHRDDVVLTQCVHEH DQQQAVSKSYALEISAHQKEH GSDITHEPALAPTAPLLVALLLG PKLLLVVGVSAIYICWKQKA

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6334	36702	A	6384	1	2453	MEPAGPAPGRLGPVLCLLLAAS CAWSASRQLPAVQVLRGDVTC GSDHVFLLAYIKHLAVAGRRRA LKATVHVHQRTLLRPGGCGSV PGKRAVTLISKSDGQPAPPGA PAGNTNTFLVCSCGFPDLQSSR GPERALCAFIQCLMVRPEQRE KNWPGPRGRSMARPGWNAKPP VVQAKAFKNWAVLELSTVSAR NLTGSRJPRENTKVILIGTIWVL CFLGSA LGVCDPGGTHSHLAM HVVFPGVGSNNPSIVIIIRPIL QIKSQRSRVGETTFPGVSWVAEL ESKSKHTFSQCQALLQPWGRK LSSCSQRTYNLLVCIQSMNVI DKHLRKHGRSVAGEEELQVI QPDKSVLVAAGETATLRCTATS LIPVGPIQWFRGAGPGRELIYNQ KEGHFPRVTVSDLTRNNMD FSIRIGNITPADAGTYCVKFRK GSPDDVEFKSGAGTELSVRAKP SAPVVS GPAARATPOHTVSFTC ESHGFSPRDTILKWFKNGNELS DFQTNVDPVGESVSYSHSTA KVVLTATREDVNSQSFW*GPTVT LQGDPLRGATANLSETIRVPPTLE VIQQPVRAENQVNVTCQVRKF YPQRLQLTWLENGNVSRTETA STVTENKDGTYNWMWLLVN VSAHRDDVKLTCQVEHDGQPA VSKSHDLKVSAPKPEQGSNTA AENTGSNERNIYIVVGVVCTLL
6335	36703	A	6385	1	405	
6336	36704	A	6386	91	2926	PACPSPLPFTNTDTHIDTSSPA SRSTRCLCISTHGVLAQSGGSSG GPAVPTVQRGIKMLVSGCAIIV RGQPRGGPPPERQNLNIRAGN LARRAAATQPDADKTPDEPWA FPAREFLRKKLIGKEVCFTIENK TPQGREYGMIIYLGKDTNGENIA ESLVAEGLATRREGMRANNPE QNRLSECEEQAKAAKGMWSE NGSHTIRDLYTIENPRHFVD SHHQKPVNAIIEHVRDGSVVRA LLLDPYYLVTV
6337	36705	A	6387	2	448	
6338	36706	A	6388	1	645	
6339	36707	A	6389	1	294	

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6340	36708	A	6390	23	321	RGREHTQGIPGAGKRWH*FKV LLTQ/CW*SEFSVIRQFKAGPGG LDQFRDRSK/RWLRDLRGRLLG SLNASLVLRALFSGNWGLTAN QL*LAVGAKGDPEA
6341	36709	A	6391	1	1599	
6342	36710	A	6392	1	561	
6343	36711	A	6393	1	1833	STLASSEGQGGFWRGPRLAILL LLFLGPCHARSHDGKYSREKN QPKPSPKRESGEEFRMEKLNQL WEKAQRQERYPCRRRRRVKQV AAGTPRVFLKTPMEGVFELCRP SGPHYLISNAGVRLDLLNSPVL SIPESLRGKVNDLQNKKELLER KGRGETGLARPMHDLTAAQGG YGCALVHGAQVEGAGAGQGWA GTVHATCRGETGTACQEAALVT ATACSSCQRGQTRAPQGOHTL ESMGLNCLPQGAASGSDHHCG PRISDLPGSAARTSRWPASSELH LPPVRLAELHADLKIQUERDELA WKKLKL DGLDEDEGEKEARLIR NLNGHWRAEDAHQDGGVYNK WDIPTVVGVGVAIALVAVKL FFLPINIRCVLSSEPATLHSLQV ASVLWSLEFLPYGSRSPVVIQET VILAKYGLDGKKDARQVTSNS LSGTQEDGLDDPRLEKLWHKA KTSKGFSGEELDKLWREFLHH KEKVHEYNVLLLETLSRTEVHPG PQDGVASTGREHSPMETLQFEE LKHFEAKIEKHNNHYQK/QLEIA HEKLRHAESVGDRRSV*SASPR ESTPCLEGRTKGAGLPR*KKHL QDLSGRISRARHKRTLKALGS
6344	36712	A	6394	1	185	DFFDNSAQVTIAGIPCDIRHVSP RKIECTTRAPGKIV*GSPPLSQA EGFFLKLEMLLRDWN
6345	36713	A	6395	1	1512	
6346	36714	A	6396	117	268	QSLLELYLHLYLHLCYLHLANK QELTLTWYKE*CTFFLPSPV*NP HQNLA
6347	36715	A	6397	1	500	

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6348	36716	A	6398	1301	2565	TLLTILPFYLFKNRSTL.TGYLR WILSTKLFLCSTLWLAPTFLFLIP/ LPDPHDCISLIHLAFTFPFHTSFF PIPHPDHTWFDGSSTWPNRHSP AKVGYAIVVSSTSIIEATLPPS TTSQQAELIALTRALALAKGLH VNIYTDSKYAFHILHNAVIWA ERGLSTQRSSIIASI.KTLLKA ALLPKEAGVIHCKGHQKASDPI AQGNAYADTKFLDLAFPLR LSFTCQITQAVSQALGIQWNLH TPYRQSSGKDWTVFLPLALHR IRARPREATGYSPELLYGRFTL LSPNLVPDTSPLGDYLPVLWQA RQEIHQAAANLLSTPDSQLYED TLAGRSVLIKNLTPQTLQPRWT GPYLVIYSTPTAVRLQDPHVV HRSRIKLCPSDNQPNLSSSWKS QVLPSTSLKVTLISEEQ
6349	36717	A	6399	581	2517	LFLGYSHTSLLPFPVQSLHL PLYLHTLTHKYGIPLPPWRPIM HPLPSH*NLITLTLNANIPSCST L*KD*SLLSLTCYSMAF*/QPIN PYNSPILSVQKPKPYSSFRVY SLFVESPTITIVPGPDFNLASHIIP DITPDYDCISLIHLTFPFPHVS FFPVPHPFHTWFDGSSTRPNCH TPAKAGYAIVSSTSIIEVTTLPHS TTSQQAELIALTRTLAKGLC VNIYTDPISTCTMLFYGLKCFLT MQGSSIIASLIKTLKAAALLPK EAGVIHCKGPKQKASDPIAQDNT YADKVAKKAASVPTSIHSSFS PSHLVTPTYSPETSTYQSLPTQ GKWFLDQGYLLPASQAHSILS SFCNLFHVGKPLARLSELLISF PSWKSILKEITSQCSICYSATPQ GLFRPPFPKHQAWGFVPTQD WQIDFTHPQVQKLLYLLVW VDITFGWVEAFPTGSEKATVVI SSLLSDVIPRFLCPTSQSNNGLA MISQITQAVSQALGIQWKLCTP YHPOSSGKVKWANGLLKTHLT KLSLQKKDWTVLLPLALLRIR ACLRNATGYSPELLYRCSFLL GPSLIPDTRPTWTAPPKTWHPY YLLSSHTPIHRSQLLIHALLLFTL PVYTVSPSHHS

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6350	36718	A	6400	281	1095	DCSKNRHSQVIAEGNICKIQE VRRKEDTQGEKDPESLLPL LAPGPTE/YSTYYNISVAKAELL NKLKDQPEMAEIGLGEEDVDH ELAQQKIQLIESIRKLSVLREA QRGLLEDINANSALGEEVEANL KAVCKSNEFEKYHLFVGDLDK VVNLLLSLGRLARVENALNSI DSEANQEKLVLEKKQQLTGQL ADAKELKEHVDREKLVFGMV SRVLPDQQLQDYQHFKVMSA LIJQRELEEKILGEEQLKCLR ESLLGPSNF
6351	36719	A	6401	1	972	
6352	36720	A	6402	514	736	
6353	36721	B	6403	446	991	
6354	36722	A	6404	521	903	NIKPASQISPG*/*VHSSPTQRLS APPSAA/GRLLSLSLPAGLVGGD TARCIPAGRLRLPCSWLDPGKL LHLSLKSXGSGRSGAGTLQEG NQSVCIQAEKPLKPAIQTSQ MNVLCRAYSWVIDWD
6355	36723	A	6405	11	545	
6356	36724	A	6406	3	2920	
6357	36725	A	6407	1	2388	
6358	36726	A	6408	275	479	
6359	36727	A	6409	1	3810	
6360	36728	A	6410	7	1047	
6361	36729	A	6411	1	705	
6362	36730	C	6412	304	638	
6363	36731	A	6413	99	759	WAYLDFWM*HIPHLGVLL/SAH LLSDLNSCF*MGSRTEGSATG PGSCSAALPLGPYDPAADPMVLE VSMADRDASPHDPLAKFLFPVP MTLHLSALLEVLVPEGGTLPPGD TTTIPLNW/IVKIAT*TLWVPPTF KFTGCRNLNTMWKLPRLGASTL *SNSLRCTLTFSHDWSGWDAG HQVIRPHGFAGYNTCGCFHRL MLSACGFSRQMVQAVNGSTTL GSGG
6364	36732	A	6414	1	685	
6365	36733	A	6415	1	1359	
6366	36734	A	6416	3	7714	
6367	36735	A	6417	1	723	
6368	36736	A	6418	1	528	

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6369	36737	A	6419	38	530	HSPRRSAASLLSQRDHEPHQKE ETPNTSEHQKEKTPDTPPLRTV TLTVRVHGFLEIVSETKNPPIPD TKLRG/ERLQGFGLAGERSE/GC RPSP*VLQLIKAVVTQRLGGR WDWAPWSRRWCSSGRLRPHR NQWSGWEAQAWGLQVPEPCP AGRQLRPGEKSSTAP
6370	36738	A	6420	1	649	
6371	36739	A	6421	1	987	
6372	36740	A	6422	1	924	
6373	36741	A	6423	1	435	
6374	36742	A	6424	1	147	
6375	36743	A	6425	1	1107	
6376	36744	A	6426	3	913	
6377	36745	A	6427	1	159	
6378	36746	A	6428	313	1083	
6379	36747	A	6429	1	1245	MAQELRDTCTSFSSRFQDQVEER VMVIEDQINEMKQEEKFREKR VKRNKQSLQEIWDYVKRPNLR LIGVPEKNLEETDKFLDITYTLPR LNQEEVESLNRPTDSEIEAIINS LPTKKSSGPDGFTAIFYQRYKE ELP/RQRHNKKREF*TNIPDEHR CKSPQ*NTGKPNPAHQKAYPP *SSGLHPWDARLVQHTQINKRN PAYKQNGQKPHDYLSRCRKG L*QNSAALHAKNSQ*IRY*WDI SQNNKSYL*QTHSQYHTEWAK AGSIFPENWHKRGMPSLTTPIQ HSVGGSGQNGQAGERNKGYSI RKRGSQIVPVYR*HNCISRKPH HLSPKSP*AGKQ/SSAKSQD/DKI NVQKSQAFLHTNNRQTESQIMS E/APIHNCYKENKISRNPYKGC EGPLQGEQTTAQRSKKGHKQI
6380	36748	A	6430	39	314	KSECLITYTKGSQRLASNGTKLD GE*L**VDRIRLQKIGNDKLLPA KGGCSNPQRS*KPRKKIRQMA N*NKQHRGDLK*PDGAENHGT RTT
6381	36749	A	6431	213	843	VDRSRLQKVSNNKLL*AKGEC NPLQGS*KP*KKIRRMAN*NKH CREDLK*PDGVENNGTRTS*FM HKLQ*PI*SSGRKGISD*R*N**N KIHQG*NEGKSVKGSQRESSY PQRKAHQTNSSGLSRNPTSQKK VGANIQHS*RKEFSTQNFISSQT KLHK*RRNKIFYRQADAERFCH HQACVTRAPEGSTKHGKQPV PAPAKTGQIV

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6382	36750	A	6432	1	2112	MRAFVVLMDVSKLPSEGGPG LRSNQQHMRMFLTSVDRGSVS LLADAVAAATPQGKTSQPRGPS NLAAADLRVAEESGMENFLK MSFDSIRPAQDGGCTPEISMVTP SPGWSVHTGDLGDHPLPRMVS AHRRSRWSPPPQDGGCTPEISM VIPSPGCSVHTGDLGDHPLPRM LSAHRRSRWSPPPQDAQCTPEIS MVTSPGWSVHTGDLGDHPLP RMVSAHRRSRWSPPPQDAQCT PEISMVTPSPGCSVHTG
6383	36751	A	6433	1	648	
6384	36752	A	6434	1	1539	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE/ SAN*NQCCREDLK*PEAEIHGT RTS*HMHKLQ*PI*SSGRKGVSD *GSNQ*NK*WGEWNQVGKHS A GYYPGELPQPSKAGQHSNSGNT ENTTKILLEKSNPKTHNCQIHQ G*NEGKSVKGSQRERTREARA NKFKS*QKARYN*QCRTERD RNTENPSKN**IQEPVF*KDQQN **NASKTNKEEKREESNRNRKK **KNRTVKPHVSFTLLPALSHVS EKNEAESMNSLIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKMSMA RELHDTCTSFNSRFDQVEERS V AIEDQTNEINNGENGTLENTL QDIQENFPNLARQANIQEIERR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKGLERQEQTN SKASRRQDITKISAELEIETQK TLQKINEFRSRFFKKINKIDKTL ARLIKKKREKNQTDIAKNDKR DITTDPTIEIQTITREYKHL YAN KLENLEEMDKFLDTYTL PRLNQ EEAESLNRITITGSEIAINSLPT
6385	36753	B	6435	137	586	
6386	36754	A	6436	129	506	
6387	36755	A	6437	1	237	
6388	36756	A	6438	182	1034	

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6389	36757	A	6439	203	650	SAIVCGSPRLRLMQAVSSRINSA HSRGAIYSQASSAAACPSVSI AF LRR*IEANVS/WIRTLSTLCTPK CGPGFKHRIVLCKSSDLSKTFPA AQCPPEESKPPVRIRCSLGRCP PP RWVTGDWGO/CDSRDFRPGRR RRDFCRNCRAGAGAH
6390	36758	A	6440	207	426	AECTRAIPK/HSCYPVLLIVVS P*KKQNCSLGELSCWRRRES CRS SWSNKALPSLTRCLRGFV CGLS CYKGSS
6391	36759	A	6441	524	783	TAVLAARISNQWILSCWS/AVG CTPKCGPGFKHRIVLCKSSDLS KTFPAAQCPPEESKPPVRIRCS LG RCPPPRWVTGDWQGLSPTREK
6392	36760	A	6442	1	1524	
6393	36761	A	6443	1	8738	
6394	36762	A	6444	1	642	
6395	36763	A	6445	1	549	
6396	36764	A	6446	8	434	
6397	36765	A	6447	1	2922	
6398	36766	A	6448	18	1158	FLDFDCPYGSAHITGLRFWLPW YRKQRQRYWGSNGCMPPPSLR VPERCPSHTEPRNL TGA*ELLLL GLSEDELPQLAGLSLSMYLVT VLRNLLISLAVSSDSHLHTPMC FFLSNLCWADIGFTSAMVPKMI VDMQSHSRVISYAGCLTQMSLF AIFGGMEENMLLSVMAYDWF VAICHPLHYPVIMNPHLGVFLD LGAFLLSLLDSQLHSWIVLQFTF FKNVEISNFV*DPSQLNLACSD SVINSIFIYLDSIMFGFLPISGILW SYANNVPSILRISSSDRKSKAFS TCRSHLAVVCLFYGTGIGVYLT SAVAPPLRNGVVASVTYAVVT PMLNPFIFYQRNRDIQSALRRLR SRTVESHDLLHPFCVGGKKGA
6399	36767	A	6449	2	1535	
6400	36768	A	6450	1	635	
6401	36769	A	6451	222	1040	
6402	36770	A	6452	2	1135	
6403	36771	A	6453	1	576	

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6404	36772	A	6454	2	694	QCGGIQRSHGWSWSEASDSVW QLQSMWMLDKLTGVFAPRPST GPHKLR/ECLSRIFLRNRLKYA LTGDEVKKNCMQRFIKINDGKV RTVDITYPVGFMDVVISIDKTGR EFPVLIYDTKG/RAFAVHRITPE EAQVPSCAKVRRDLCSGAQKGIP HLVTHDARTIPLRSPSSKVNDA TIQNDLEDWARFT*FSSKFDNW *TCCMGDWEGA*P*GRNVVLI HQQRRRAPWDLF
6405	36773	A	6455	1	243	
6406	36774	A	6456	3	766	
6407	36775	A	6457	1	741	
6408	36776	B	6458	500	8643	
6409	36777	A	6459	1	7863	MKPRTLTVRVLTALKVARLESV PSDVQMCSEFLPSDSAQALASP SGSRRTGAAGGAAYQSCAVLPH SSALWVVDGTRCRGAGGSAHQ GGSATQEPTEVERVEGSGMAGCR SRVLPHWKAANVLGMSVESAP AVEEEKGEELEQKEKEEEDTS GNTTHSLGAEDTASSQLGFGVL ELSQSQDVEENTVPYEVDKQL QSVTTNSGYTRLSDVDANTAIA HEEQSNEDIPIAEQSSKDIPVTA QPSKDVHVVKQNPPTA
6410	36778	A	6460	2	669	ERRRRRLTIPCPPPHAPPTGGQ ACRENAEGIL*AANTSEPGKDA EK*KIKV*LAP/CSHSGSSLQSDP HFGCSLGPS/DPALGLSGCILPPC SGSYLAAPNRSRIPKPKPW/H /ESYLPASVVRPHGTQAPGLWPE RGL*PAGFLRPEPVRAASER/Q EAVSPER*VPRPPKAQQLHGQS PDPSSLCTALRQDHTHWLDARS VYPDWRGQWPPLHQDCGHG GWR
6411	36779	B	6461	241	369	
6412	36780	A	6462	1	510	
6413	36781	B	6463	1	630	
6414	36782	A	6464	229	561	SCRGYSRILLFHKSSWCSQVIS IFRYNIICSRLPKSWKWRLPVY MNWL*YHWFQYHSSINFISFR SMWFIHNFKRSPAFILSGSWSIS IARWQIFVFFTFGSRTKV

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6415	36783	A	6465	1271	1710	TEGLGHRSSSETPGGAALDALTG ERPRVACFPAARGRLRPRRL MIGPFETGGGQRLTLRPRRRR QRRRP/WQGLERPHVRNWGIEL ETLRDAFRPQPSVWRTARGE GKRKGRLVECLGSQRKVLGV LLYAVTRGSPFNLFTRD
6416	36784	B	6466	1	772	
6417	36785	A	6467	1	1272	
6418	36786	A	6468	3	236	
6419	36787	C	6469	1	457	
6420	36788	B	6470	148	324	
6421	36789	A	6471	1	1407	
6422	36790	A	6472	1	651	
6423	36791	A	6473	619	835	
6424	36792	A	6474	52	535	
6425	36793	A	6475	319	647	LCRIYMYFCVMKNWMSLW KLCTNKR*RIDKPTLHQVVVRK *LTPGLMKNQVDSLELLETRSL KKDPVELGSKSLRCCQTEPV NLLPHVSIKTKI*SRILRLQRP
6426	36794	A	6476	39	515	
6427	36795	B	6477	1	807	
6428	36796	A	6478	3	247	GANICCW*GLQE/VFHSW*KTQ EPSWLHLVDPTTGLQVELPASP APFARIPQPLGGRWDWAPWSR GWCSSGRLGQHRSPWSG
6429	36797	A	6479	27	363	
6430	36798	B	6480	1132	1268	
6431	36799	A	6481	1628	2008	
6432	36800	A	6482	953	1087	
6433	36801	A	6483	2	443	QLAGRCGGRGMSGNRGC/WGA CGPAGVPGG/CWAWCALHSEE PASPALRSISRRLAAFPGRAR DLQPAMPEPTPSVGSAAQAS PTSAAPCSMAPSIDHPRAEECV ARRGTGRHDELIVALPFMMIPW HSSIQPFTHPFNWNFG
6434	36802	C	6484	175	423	
6435	36803	B	6485	122	608	
6436	36804	A	6486	644	1149	KTMHWKAPLMSWHMRASSQ KQTRTGTQT/MEAQLQLQRY QEALLQVLRKGEKAFNMGN SEVLQRADESCSQFYERLYEAF QLCSPFDPEATENQCMVNAV VGQTQGDIRRLKLECFGTGM NVTQVLEVATKVYTNCEETQ GKGQFAGGSTYKGGCECPKTK
6437	36805	A	6487	1	2847	
6438	36806	B	6488	329	742	
6439	36807	A	6489	1	1035	

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6440	36808	A	6490	13	630	INPPPPFRPEPPSSNSPKMTDH KGERGEATRYMFSRPFARKHG VVPLGPHICRIYRKGDIVDMKG MGYCSKKGIATKCYHGNLE GVLPMLPQHACWPFVYNQFVL GQSFFPRELMCRJEHI*ALLRAR DKLPETVLKENDSEKERSPNEK GTWGSNLKRHPGSTPEEAHFV RTQWGRSLELAGTLFPMNFMG IIGVKEIK
6441	36809	A	6491	1	1020	
6442	36810	A	6492	1	330	
6443	36811	C	6493	250	372	
6444	36812	A	6494	1	345	
6445	36813	A	6495	2	335	TVRAYNVQHAVGIVVNRQVK GKIPAKRINVGIKHKHST*EN FLKRMKENDQKKKEAKEKVT WIQLKHQSAPPRE/AQCERTNG KEPELLEPLPYEFMHNTHYIHIYV CVH
6446	36814	A	6496	2	490	
6447	36815	A	6497	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQ/RKAPGKNLVYISLVLRA L*G*DLTHHIIILFPFFLL**PAPP REAHFVRTNGKEPELL
6448	36816	A	6498	54	553	
6449	36817	A	6499	131	803	TMFCQTGSSVRRVGGPWAEN RTAMLRPCGGTFARKTRLSRLG NSPKMNEQQRGKRRGTPIIMFS KGLLRKHGVVPLAHIFMRVYK KGDIVRHPRGMGYLVPKREL PQSCYPWPKPGRSLTNVTPAML VGHLL*NKQV*GQRFPLKRN MWRI*APFRHFLRSPRLASLKT CGRENGSRKKERPKPGGKVTW GFQLKRRHLGFPQEEATFLK EPIGREGP
6450	36818	A	6500	1	489	

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6451	36819	A	6501	29	2028	ENEEEGEKMASTDYSTYSQAA AQQQYSAIYTAQPTQGYAQTT QQAYGQQSYGTYGQPTDVSYT QAQTTATYQGTAYATSYGQPP TGYTTPTAPQAYSQPVQGYGT GAYDTTATVTITTQASYAAQS AYGTQPAYPAYQQPAATCPT RTED* ¹ ANKPTETSQSQSSTGGYN QPSLGYGQSNYSYPQVPGSYP MQPVTAPPSYPPTSYSSTQPTS DQSSYSQQNTY GQPSY GQSS YGQSSY GQPPPTSYPPTGGSY SQAPSQYSQQSSSY GQSSFRQ DHPSSMGVYQGESGGFSGPGE NRSMSGPDNRGRGRGGFDRGG MSRGGGRGGRGGMGSAGERG GFNKP GGPMDGEPDLDLGPPV DPDEDSDNSAIYVQGLNDSVTL DDLADFFKQCGVVKMNKRTG QPMIHIYLDKETGKPKGDATVS YEDPPTAKAAVEWFDGKDFQG SKLKVSLARKKPPMNSMRGGL PPREGRMPPPLRGPGGPGGP GGPMGRMGGRGGDRGGFPFRG PRGSRGNPSGGGNVQHRAQDW QCPNPGCGNQNFARTECNQC KAPKPEGFLPPFPFPPGGDRGRG GPGGMRGGRGGLMDRGGPGG MFRGGRGDRGGFRGGGRGMD RGGFGGRRGGPGGPPGLME QMGGRRGGRGPGKMDKGEH
6452	36820	A	6502	1	693	
6453	36821	A	6503	3	657	
6454	36822	A	6504	1	434	
6455	36823	A	6505	208	443	

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6456	36824	A	6506	3	2650	LLPAFLLLCSDSHLQFCSQFAP RKTQGSQSVNNIQANIHKKN NHLMKKNDQKFKDLPMAGH PIHHQAQGGGAKNPQEQRRP MGQTTLPAEQEESRVKCKNCG AFGHSARNKTCPIKRWGALPL QVLGSHKEKENLKPAKALPFT TPGPFTTNDREKERSPSSTMNPS EMQRKASPRRWKHHNQTPSIH KVNKMVMSEEQMKLPSTKKA EPPTWAQLKKLTQLPKKSLEN TKVTQTPENTLLAALMIVST/A GAAAAANYTYWAYVPFPLIRA VTWMDNPIEVVYVNSAWVPGP TDDRCPDKEEGMMINISTGY RYPPICLGRAPACLMPIQNL VEVPTVGTTSRFTYHTGLLTFR DVAIEFSQEEWKCLDPAEDSY TRRKANSCKGPKYKNECGKAF TQNSNLTSHRHSGEKPYKCS ECGKTFTVRSNLTIHQVIHTGE KPYKCHCEGKVFHNSYLAH RRIHTGEKPYKNECGKAFRGH SNLTTHQLIHTGEKPFKNECG KLFTQNSHLISHWRIHTGEKPY KNECGKAFSVRSSLAHQTIHT GEKPYKNECGKVFRVGRGVS GTTCLLSVFQVITVSSRSRAS ENRATQSILILAPPTSRGSGPG ASVLRRLAQTRKMAWTESCT AACAFPSCLVLLYRGRGVPTDL QVPAFLFTSQSKLRPGSRTKSS
6457	36825	A	6507	54	360	CSTMNPSEMQRAPPRRQRHRS RAPSAHKMNRMMSEEQMKL PSTKKAEPPTWAQLKKLTQLA KKKLENTKVTQTPENMLLAL KTVSTVSAGVPSSEESD
6458	36826	A	6508	525	3656	SSTMNPSEMQRKAPPRRRHR NRAPLTHKMNMVTSSEQMK LPSTKKAEPPTWAQLKKLTQLA TKYLENTKVTQTPENTLLAAL MIVSMVVSLLPMPAGAAAAANY TYWAYVPFPLIRAVTWMDNPIE VYVYVNSAWVPGPTDDHCPAK PEEEGMMINISTGYRYPPICLGR APACLMPIQNLVEVPTVGT TSRFTYHTIDLMTEKVVVLA EVLLRFLKPGEDPTARYVSNK KCQPSVDWPTTISQRRGY
6459	36827	A	6509	1	246	
6460	36828	A	6510	1	246	

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6461	36829	A	6511	1	279	
6462	36830	A	6512	1	363	
6463	36831	C	6513	109	245	
6464	36832	A	6514	2	429	LMTFCWDTPRQSGVPRRMPH TGTWRTVGIRCPKKKLRANS SMMRGKVQFPRP/DIAYGAAPF EDLQVDFREMPKCGGNKYVLV LGRTYSGWVEAYPTRTEKTR E VTPVLLRDLIRRFRLP L WIGSDN GPAFLAALVQKTAK
6465	36833	C	6515	31	895	
6466	36834	A	6516	2	4735	
6467	36835	A	6517	263	418	
6468	36836	A	6518	120	295	YDPLPTWILGKISQRGAEEPAQ HPGCQL*LPPP/SPRTSSSPSCA GLTSVSPRPRFPR
6469	36837	A	6519	1	1758	MKIRRRFPSSLQLSADLQVPVR KAPRQGVSQEKRTKPSLELMIS GTISQEDIRNNVTRGCTPPAIQR VISSPLLAIRNNVTEGVYTPCD TGGRVHLPPVILLISRDGGHDIS FNIAVDVHSPCDTDPNIQGV EYDMTPNIAMNVQPPGISQKRCT LPAILGLISYASSVNIRSNITGWL YIDRYVGSVILYPLGIRMGVT GEMKGERRRGLHAATKWLEE HAPADYQNPQEYGRGTQLPGTQ PQLDPHEREDMQLNRDREAL LEGFKRGAQKATNVNKVSEVI QGKEESPAQFHQRLCEACAKQ VLVNGDAVSREEKRKENERQA RRNADLLVSCNSQSGPPKEARE ELWTKDYRPGQDLRLLSQATL TFHPTVPSPTLLGLLPAEDSWF TCLDLKDAFFPIRSAPESQKLFA FQWEDPESALAKTVRQRCVSC RQHHA/GKVQFPRP/DIAYGA AAFEDLQVDFTEMPECCGNKY LPVLGRTYSGWVETYPTRA EKAREVTRVLLRDLIPRLPFRIG SDNGPAFVADLLQKTATVLGIT RKLHAASRPQSSGKGIQNNRTG GVVYTPCDIESHVILFRSGY
6470	36838	A	6520	1111	1342	MFVPHIGFQNTAALCLRLGLGVL FP*PVGFPAGSCLL*WNRHWH VPDFSCVTTPOEWCGGVSDVC CGHPHAEPHLQ

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6471	36839	A	6521	1	1144	MIRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVD LRLHQAQLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRALAAATALLVQEANKLTG QKLNKASRAVVTLMNTKGHH WLTNATLTDYQTLLENPRITIE VCNTLHPATLLPVSKSPVKPGC VEVLDSDSSRPDLWDQPWASV DWELYLDGSSFFNPQGEVEG/S RGDTSELPPCWVCGIPALTQRL EKQHLPPSGHQGSLKHLIWDLL LLTKKRTFSSMI
6472	36840	A	6522	1	554	
6473	36841	B	6523	63	620	
6474	36842	A	6524	1	796	SRTKNYQPVDLRLHQAQLT FHPTVPNPSTLLGFPPAEDSWFT CLDLKDAFFPIRLAPERQKLFAF QWEDPESGWPPCWRALAAATL LVQEANKLTGQKLNKASRA VVTLMNTKGHHWLTNATLTD YQTLLENPRITIEVCNTLHPAT LLPVSKSPVKPGCV EVDSDSS RPDLWDQPWASVDWELYLDG SSFFNPQGEVEGSRGDTSELPP CWVCGIPALTQRLKQHLPPSG HQGSLKHLIWDLLLLTKKRTFS
6475	36843	A	6525	3	2640	
6476	36844	A	6526	2745	3732	IRIGKNYFKVHMEPKKSPHRQV NPKPKEQSWRHHTT*LQTLQG YSNQNSMPGPTQPSTPAPGG NLRNPQSSDLLQVTKQQGQAL AIQREAPLHRIPAEIPWYFQP QPATQLGSPVPDPSSAMM/SR RAHRSRGPDROGYPLQGD*PGE PRPQEH*RGHSQERLPSSEKQTP ICPPAQATQHPEEDAHQPYKH LFQVCAHQGHVPAQRRN*PGY WERYHSAEDPELQPILAGLSLS MYLVTVLRLNLLIS
6477	36845	A	6527	1	1860	
6478	36846	A	6528	1	1458	
6479	36847	B	6529	1	1503	

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6480	36848	A	6530	3	515	TISQKRCTLPAILGLISYASSVNI RSNITGWLYIDRYVGGSHVILYP LGIRMGVGTGEMKGERRRGLHA ATKWLEEHAPADYQNPQEYGR TQLPGTQPQLDHEREDMQRL NRDREALLEGFKRGAQKATNV NKVSEVIQGKEESPAQFHQRCLC EAYRMYTPLDHDSPENQRMHI MALVRQSAEDMRRLKQKAG LAGMNPSSLLEIASQVFVNRDA VSPKENSKEGGQARRHDDLF SPVEPDCVEVLDSIHSSRPDLRD QPWPSGDW/RTICGWEQLLQPP RRERCRCVSDNPGH/WLLKPHR CPRPLQARKLNSLLSLGP*NSTR DCVRPIVCILPLITIALKISA
6481	36849	B	6531	96	2524	
6482	36850	B	6532	61	2025	
6483	36851	A	6533	674	2913	
6484	36852	B	6534	120	1849	
6485	36853	A	6535	1	426	
6486	36854	A	6536	2	475	
6487	36855	A	6537	1	501	
6488	36856	A	6538	15	593	SMWWNSAREPCPWRIVDDCGG AFTMGVIGGGVFQAIKGFNRNAP VCRLLSEAPLFIYSCSRVSPTV NVSSERAESRPTLFMAVSLHMA WCLAHIGIRHRLRGSANAVRIR APQIGGSFAVWGGLFSTIDCGL VRLRGKEDPWNSITSGA/LTGA VLAAARSAPLAMI/VGSAMMGGI LL/ALIEGVSILL/TR*TATV
6489	36857	A	6539	2	557	RRFRASAMEEYAREPCPWRIVD DCGGAFTMGVIGGGVFQAIKIG FRNAPVGIRHRLRGSANAVRIR APQIGGSFAVWGGLFSTIDCGL VRLRGKEDPWNSITSGA/LTG A/VLAAAR/SGPLAMGGLQQ*WG GILFAPHLRAFGILLTRYTAQ/Q FRNAPPFLEDPSQLPPKDGTPA VTGYPSPYQYH
6490	36858	A	6540	223	2274	

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6491	36859	A	6541	2795	3762	FLHFHLRNAVPHQQWNKAGW RMTLRS*EKKASDDQITLSYGR TFKPK/DKEVENFEQNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERISV MED EMNEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DGENGTKLENTI.QHIIQENFPN LARQANVQIQEIQRTPQRYSSRI AIPRHIIIVRFTKVEMKEKMLRA AREKGRVTLKGKPIRLTADLSA ETLQARREWGPIFNILKENNFQ PRISYPAKLSFISEEEIKYLTQDK MVRDFVTTTRPALKELLKEALN MERNNRYQLLQNHAKF
6492	36860	A	6542	245	1293	TGAVPIRPSWQWGNRTEKL ETLKRRAPLLQRNAVPHQQQ NKAGWRMLTS*EKKASDDQIT LSYGRTFKPK/DKEVENFEKNL EECITRITNTEKCLKELMELKTK APELREECRSLRSRCDQLEERV SAMEDEMNMKREGKFREKRI KRNEQSLQEIWDYVKRPNLHLI GVPESDVENGTKLENTLQDIIQ ENFPNLRQANVQIQEIQRTPQ RYSSRRATPRHIIIVRFTKVEMK EKMLRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK YFIDKQMLRDFVTTTRPALKELL KEALNMERNNRYOPLQNHAK
6493	36861	C	6543	116	283	
6494	36862	A	6544	51	281	KSQNQLLSSKGEYADGQQDQV SIPAPSPYTLSPQTQSCVPVRPE LGL*GASSAVQAPAVRYLTRFL LFVMSNLHSP
6495	36863	B	6545	1	897	
6496	36864	B	6546	91	8030	
6497	36865	A	6547	126	362	

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6498	36866	A	6548	936	2064	ERADCLFKRKTNNQKGHLHRK PICTSPSSKTKSR*NHKDGEKTE QKNWKL*NAERLSSS/IRNAV HQQQNKAGWRMILTS*EKKAS DDQITLSYGRITFKPK/DKEVENF EKNLEECITRITNTEKCLKELME LKTARELHEECRLSRCDQL EERVSAMEDEMNMKREGKFR EKRIKRNEQSLQEIWVYKRPN LRLIGVPESDVENGTKLENTLQ DIIQENFPNLARQANVQIEIQR TPQRYSSRRATPRHIIVRFTKVE MKEKMLRAAREKGQVTLKGG PIRLTADLSAETLQARREWGPIF NILKEKNFQPKISYPAKLSFISEG EIKYFIDKQMLRDFVTTRPALK ELLKEELNMERNNRYQPLQNH
6499	36867	A	6549	1	767	MAGAPPPASLPPCSLILDCCASN QRDSVGVGPSEPGVGYSLVVR RFLSRSEKRNIRVGVTRFSSEM NPVPQMEMQKSPSSASLTGA VDRSCSYSAILAPPLGFCFYPLY ENSTLQSAKKRDAELANGALGI IELNNDYTLKKVMKPLITSNTV TDEIERANVFKMNGKWYLFDT SRGSKMTIDGINSNDIYMLGY/D IKLFNRPLQAAEQNRACAANGS *SKRCDIHLSLRSAASQRQQC GYHKLHDKQRLLRG
6500	36868	B	6550	50	327	
6501	36869	A	6551	333	1301	FLHFHLRNAVPHQQWNKAGW RMTLRS*EKKASDDQITLSYGR TFKPK/DKEVENFEQNLLECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERISV MED EMNMKREGKFREKRIKRNEQ SLQEIWVYKRPNLRLIGVPES DGENGTKLENTLQHIIQENFPN LARQANVQIEIQRTPQRYSSRI AIPRHIIVRFTKVEKMEKMLRA AREKGRVTLKGGPIRLTADLSA ETLQARREWGPIFNILKENNFQ PRISYPAKLSFISEEIKYLTOKQ MVRDFVTTRPALKELLKEALN MERNNRYQLLQNHAKF
6502	36870	A	6552	352	2304	
6503	36871	A	6553	1	1617	

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6504	36872	A	6554	1	257	MGPPIHKISHYVYANISKSEKVL KSEHFRSQAFQPGQSETVSEK KKKTRKKRKKRKKRKKKKK KKKKKKKKKKKKKKKKKKKK SE*DRLGKKKEDEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
6505	36873	A	6555	5	156	RKKGGG/EREEEGEGEEEEEE EEEEEEEEEEEEEEEEEEVVL LTPGTGAEDFKKH
6506	36874	A	6556	1	279	
6507	36875	A	6557	3	120	TEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
6508	36876	A	6558	3	123	
6509	36877	A	6559	239	432	CLWLFQEEEEEEEEEEED*EE EEE/EEEEEEEEEEEEEEEE EEEEEEEEEEKIFLGHVRGI
6510	36878	A	6560	1	588	
6511	36879	A	6561	1	204	
6512	36880	A	6562	75	234	
6513	36881	B	6563	100	2510	
6514	36882	A	6564	47	4976	
6515	36883	A	6565	3	4755	SCRCRRRRRGPAPAMAQILPVR FQEHFQLQNLGINPANIGFSTLT MESDKFICIREKVGEQAQVITI MSDPMPIRRPISAESAIMNPAS KVIALKAGKTLQIFNIEMKSKM KAHTMAEEVIFWKVWSVNTV ALVTETAVYHWSMEGDSQPM KMFRHTSLVGCQVIHYRTDE YQKWLLLVGISAQQRVVGGA MQLYSVDRKVSQPIEGHAAAF AEFKMEGNAKPATLFCFAVRN PTGGKLHIIIEVGQPAAGNQ
6516	36884	B	6566	47	482	
6517	36885	A	6567	1	555	MNARPHKVD/GRVVEPKRAV* EDSQRPAFVAGIKEDTEHHILR DYFQYQYGMVEIIMTDRGSG KKRGFAFVTFDNHDSVDKTVV QKYHTANDHNCEGRKALSKQE MASASSQRGHSSGNFRGGHG GGFGGNDIFGYGENFSOHGGFS GSCGGGGYGSSGGGYNEFGND GSNTGGGGSYNDFGN
6518	36886	A	6568	1	645	

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6519	36887	A	6569	2	944	GRGLRKLFIGLSF*FIDESLKS QVGEWGLTDCVVMRDPNTK RSRGFGFTYATVEEVDAAAMN ARPHKVDGRVVEPKRAVSRED SQRPGAHI/TLVKKIFVGGIKED TEEHHLRDYFEQYGKIEVIEIMT DRGSGKKRGFA/VTFDDHDSV DKIVIQKYHTVNGHNCEVRKA LSKQEMASASSSQRGRSGSGNF GGGRGGGFGGNDNFGRGNGFS GRGGGGSRRGGGYGSGDGY NGFGNDGSNFGGGGSYNDFGN YNNQASNFGPMKGGNFGGRSS GPYG/GGGQYFAKPR/NQGGY GSSSSSYGSGRRF
6520	36888	A	6570	1	1512	
6521	36889	A	6571	2864	3677	RCQLDHLPLCHLCCCHHR/CIPSL RDPQAPGSTRLSRAPHIESRV GRKPPEEPANPTMNSLTLRDKQ /HDASTC/DWKRAL*VPESGLPR ALLKYIRCPNMSSAQKPRELSK RRN*K*PCVKRTPFRPT*E/DLP YSGKKTGVKGLICPVPGTAVK APQRPPGPQQPHAPQASSETA WFPVADRRVFSENPGWTAAKT LGTLSPPCQAGAGVGRQDGP GQELTSQEKPWVGRKIPEHAV ADKGYRQCCGAGEARGGPVF WAAAPRTSWQQASYT
6522	36890	A	6572	1	666	
6523	36891	A	6573	2926	3304	EYSLGHRHYNWKC*ALGQKDQ VTFATKFAPTSHRTRKQPELWR /QDPGSYGEKQPAWCSVPPGRF SGGLVGLGFLDGGIVVQPLRRP CCQDCVCGFPLRSSTKTSTEL GPSFLPCERQGETISVT
6524	36892	A	6574	1	665	

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6525	36893	A	6575	3	1121	SSTFRMPWRLVTSWTAYIPEL EGSTSDPSPAVAQKGEKPVKL GNSLWGSHTPEVPRPGTGPRPL SFVHRLPTMDPHKVNALRAV KMCKQDLSVLHTKEMHFLRE WVESMGKLSPATQKVKSEEN TKEEKPDSSKKVEEDLKADEPSS EESNLLIDNEDVIEPDPAPQEM GDENAEITEEMMDQANHKKVA AIEALNDGELQKAIDLFTDAIKL NPQLAILYAKRASVFIKLQKPN AAIRDCDRAVEIYSAQPYKWR/ GKYEQKREEREIKERIERVKKA REEQERAQREEEARGQSAQY GSFPDGLPGGMLEMRGGMPGK PGITGLNEIFSDPEVLAQVQDPK VMV/AFQDVAQNPNANMSQYQ GNPKVM
6526	36894	A	6576	3	1351	PEAGGERERERAQREEDSTRQS RAQYGSFTGGFPGMPGNFPG GMPGMGGPSARSRAQRLSLE PDRSPSYAHHLPMTDPRVNE LRAFEKMKCKQDPSVLHTEEMR FLRECVESMCGKVPPATHKAM SEENTTEEKPDSEKAEDLQAD EPSSEESDLRKLKEGVIEPDT APQEMGDENAEIPEEIMMDQA NDKKVAAIEALNDGELQKAIDL FTDAIKLNPRLAILYAKRASV VKLQKPNAAIRDCDRAIEINPD SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDYDEASAML KEVQPRQAQIAEHRRKYERKR EEREIKERIERVKKAREEHERA QREEEARRQSGAQYGSFPGGFP GGMPGNFPGMPGMGGMPG MAGMPGLNEILSDPEVLAAMQ DPEVMVAFQDVAQNPNANMSK YQSNPKVMNLISKLSAKFGGQ
6527	36895	A	6577	2	433	GPPLNLSSPRGGILKTYGCELGG KRFLDSLRLRMHLLAHSAGAK AFVCDQCGAQFSKEDALETHR QTHGTDMAVFCLLCGRKFQA QSALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHGTGDH PYECEFCGSCFRDE
6528	36896	A	6578	1	687	
6529	36897	A	6579	2	449	

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6530	36898	A	6580	852	1084	TDAGCYAARQCGTAVPSRDV HIRHQGTVPVQF*TAPLRARS/E VSPARRRRARMLSSSASFASANIT TSSAWSDTLQP
6531	36899	A	6581	1	681	
6532	36900	A	6582	1	483	
6533	36901	A	6583	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG/SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS
6534	36902	A	6584	1	678	
6535	36903	A	6585	3	634	
6536	36904	A	6586	4	479	CSAKTAIRGVSECLIHGHGIPHS TASDQGTHTFAKEVWQWAYA HGIHWSYHVLHHPEEA/GKER WNLGKLSQLQCQLGDNLTQGG* GKVLQQAQVYVLN*HPIYGTVP IARIH/GSRNQG/VETELTPLTITP SDPLAKFLLPVPPTLHSAGLEIL VPEGEIR
6537	36905	A	6587	1	1539	MVGKAKWKPLELPLPRKMVSQ KQYRILGGTAEISVTIKDLKDA RVVIPSTSPFYSPWVQKIDGS WRMTEDYRKLNQVVTPTAAA VPDVVSLLEQINTSPGTRYAAID LTNAFFSIPFHKAHQKLFASF WQGGQYTTFTVLPWGDINSALCH NLIRRDPCFSLPQDITLVHHID DIMLTGSREQEVADTRDFLVKD KLLHLAPPTTKQAQHLVGLF GFWRQHIIPLGLLQPIYRVTQ KVASFWSQEQKTALQQVQAA VQAVLPLGPYNPADPMVLEVS VADRDVCSLWQAPIGESQWR PLGFWKALPSSADNYSPPFERQ LLA/CHKVGHAQQHSISKWK*Y IHDRAQADYHPWTQACLIHCQ GIPHSIASDKDAHFTTKEVWQW THAHEIHWCYHVLHHPEAAGL TERWNRLLKSQQLRQLGDNLT QSGGKVLQKAMYALNQHPYIG TISPIARIHGSSNQGVEVAPLTIT PSDPLAKFLLCVPTTLRSAGLD VLVPEGGMTQQQFH

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6538	36906	A	6588	1	566	MGRNQSRKAENSKNWSASSPP KDHSSLPAMEQSWMENDEF TEVGFRRSVITNFSELKEHVLTY CKEAKNVEKRIYRSRNQGMVEV KVAPLTITPSDPLANFFASVPAT LHSAGLEVLVPEGGTLPLGDTT MIPLNWKRLRLRTGYFGLLLRLS QQAQKKGAMVLA/GVVDPDYQ NEISLLHN*GKTHDH
6539	36907	A	6589	221	357	
6540	36908	C	6590	228	342	
6541	36909	A	6591	745	849	
6542	36910	A	6592	1	240	
6543	36911	A	6593	2	495	FVRLVGRGDCDPLLSVCLTTMP LYEGLSGGGEKTAVIDLGEA FTKCGFAGETGPRCIIPSGIKRA GMPKPVRRVVQYNINTEELYSYL KEFIHILYFRHLVLPNPRDRRVV IIESVLCPSIHFREDTHSCFFFKY FEVPSVLLA/PSHLMALLTLGI NSWHGPRL
6544	36912	A	6594	1	579	
6545	36913	A	6595	1	621	
6546	36914	A	6596	1	351	
6547	36915	A	6597	1	447	
6548	36916	A	6598	114	880	
6549	36917	A	6599	1	2625	
6550	36918	A	6600	1	1674	
6551	36919	A	6601	1035	2235	QTHSQYHTEWAKTGSIPFENW HKTGIPSLTTPIQHSVGSSGQGN QAGEGNKGYISIRKRGSIQVPC RRHD/VYI*KTPLSQPEISLS**A TSAKS/LGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKNNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPM PFFTELEKTTLKFIWNQKRARIT KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNILFDKPEK NKQWKGKDSLFNKWCWENWLA ICRKLKLDPLFTPYTKMNSRWI KDLNVRPKTIKLEENLGITIQD IGMGKDFMSKTPKAMATKAKI DKWDLIKLKSFTAKETTIRVN RQPTK

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6552	36920	A	6602	369	1917	AGEKNKGYSIRKRGSIQIVPVC RHD/VYI*KTPLSQPKISLS**AT SAKS/LGYKINVQKSQTFLYTN NRQTESQIMSELPFTIASKKIKY LGIQHTRDVKDLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKVITYRFNAIPIKLPM TFFTELEKTTSKFIWNQKRARITK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYLYQNRDIDQWN RTEPSEMTPHITYNYLIFDKPEK NKQWGKDSL FNKWCWENWLA ICRKLKLDPFLTPTKINSRWIK DLNVRPKTIKLEENLGITQDI GMGKDFMSKTPKAMATKDKID KWDLIKLSFCTAKETTIRVNR QPKKWEKIFATYSSDKGLISRIY NELKQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAHQKSGNNRCWRGCGEIGTL LHCWWDCKLQVHILTHRWE L NNEITWTQEGEYHTLGT VVGW GEGGGIALGDIPNAR
6553	36921	A	6603	1	2781	

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6554	36922	A	6604	1320	2403	LQTLQVYSNQNSMVLVPKQR YRSMQNRALRNNAATYQLSD L*QT*EKQAMGKGFI**MVLG KLASHM*KAETGSLPYTLKY QFKMD*RLKR*T*NSKKQSPSP PPKERSSPATEQSWTENDFDE LREEGFRSNYPFLREDIQTKG KEEIQTIREYYKHLANKLEN LEEMDKFLNTYTLPRLNQEEVE SLNRPTGSEIVAVINSLPTKKSP GPDGFTAEFHQRYKVELVPFLL KLFQSIEKEGILPNSFYEASIIIP KPGRDTIKKENFRPISLTNIDAKI LNKILANRIQQHIKKLIHYDQV GFIPGMQDWFNIRKSINVIQHIN RTKVKNHMIISIDA EKAFDKIQ QRFMLKTLNKL AQNLKLLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVGRLNIVK MAILPKVIYRFNAIPIKLPMTF TELEKT TVKFIWNQKRACITKSI LSQKNKAGGITLPDFKLYYKST VTKTAWY WYQNRDIDQWNRT EPSEIMPHIYNYLIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLD PFLTPYTKINSR WIKDL NVRPKTIKTEENLGITIQDIGV DKDFMTKTPKAMATPKPIDKW DLIKLKS FCTAKETTIRAFDELD DVHPHEEIEACRVWQNYGTHP
6555	36923	A	6605	2202	2515	KSLQCEHSSHQDLPLACLGLR KHYMVAQYL*HSHS/ASGGGSR YDVLKISVSCSSTIDI*LA FVSLG *DKRTS**TNLAESSPNFFHWV WIFLASKKFCSPAR
6556	36924	A	6606	1934	2077	AIPFRIQA WARTSCPKHKKQWQ QKPKLTNGI*FN* RASAQKKL PSE
6557	36925	B	6607	1	2325	

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6558	36926	A	6608	1524	2877	IRKRGSQIVPVCRRHD/VFV*KT PSSQPKISL**ATSAS/LGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASRKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPKLPMTFFTELEKTTL KFIWNQKRARIAKSILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQCNRTPESEIMPH IYNYLIFDKPERNKQWGKDSLF NKWCWENWLAICRKLKLDPF TPYTKINSRWIKDLNVRPKTIKT LEENLGITIQDIGVGKDFMSKTP KAMATKDKIDKWDLIKLSFC TAKETTIRVNRQPTTWKIFAT YSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSSSLAIRERQIKT TMRVHLTPVRMAIHKKSGNNR DMDEIGNHHSQ
6559	36927	A	6609	1	2226	
6560	36928	A	6610	1	674	MGKKQNRKGTNSKTSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRLRSR CDQLEERSAMEDEMNMENKRE GKFRKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQEN/CPQSSKAGQRSD SGNTENATKILLEKSNSKTHNC QIHQS
6561	36929	B	6611	1	5175	
6562	36930	A	6612	1666	2032	LQTLQGYSNQNSMVLVVKQR YRSMENQRALRNATY/LQLSD L*QT*EKQAMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKH*T*NHKNPRRKP RHYHSGHRHGGQLHV
6563	36931	A	6613	1596	2169	AGEGNKGYSIKRGSQIVPVC *HD/VYI*KTPLSQPKISL**ATS AKS/LGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASRKRIYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIM KMAILPKVIYRFNAIPKLPMTF FTELEKTKVHMEPKKCPHHQG NPKPKEQSWRHHTT

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6564	36932	A	6614	1667	3103	AGEGNKGYSIKRGSIQIVPVC *HD/VYI*KTPLSQPKISLS**ATS AKS/LGYINNVQKSQAFLYTNN RQTERQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLLQE IKEDTSK WKNVPCSWVGRINIV KMAILPKVIYRFNAIPIKLPMPP FTELEKTILKFIWDQKRARIAKS ILRQKNKAGGITLPDFKLYYKA TVTKTAWYWYQNRDIDQCNR TEPSEITPHIYNYLIFDKPEKNK QWGGKDSL FNKWCWENWLAIC RKLLDLPFLTPTKINSRWIKD LNIRPKTIKLEENLGITIQDIGM GKDFMSKTPKAMATNAIDK WDLIKLSFRTAKETTIRVNRQ PTKWQKIFATYSSDKGLMSRIY NELKQIYKKKTNNPIKKWAED MNRHFSKEDIYA AKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAHKKSGNNRLTLNNHNNPQ PLISIKEPREKEELNLQV
6565	36933	A	6615	3134	3288	
6566	36934	A	6616	1	2630	
6567	36935	B	6617	877	7936	
6568	36936	A	6618	2	1589	
6569	36937	A	6619	1	240	
6570	36938	A	6620	200	486	
6571	36939	A	6621	1	558	
6572	36940	A	6622	1	3885	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US/N 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6573	36941	A	6623	1	2302	KLPVTNRAAHGLCASLGPDFM TFKVPSSWRHSDSICREWFTLA GAPSRDVLVSAIITVLSLVTVV LCGLCHWCQRKLGKRYKNSLE TVGTDPDSGRGRSEKKAIVSRP CPPPAKASATHPTCKSPRSQEK VESPGDLDRDFWNNNESTVQQ KWSSYPPEFILNISPYAPYGDP RLSLNGLTLLSGAKVAAAAGLA VEREGRLGEKAPVPPPGEDAL RSGGAAPSEPGSGGKAGRGRW RTVQSHLAAGKLNLSNFEDSTL STATLESIPSTGEPKCQRPR LMRQQLSQQLSQHQRGRQPS QPTTSQSLGQLQAHMASAGP NPRAVGRGQARQGTSAISKYR AAGGRSRSPGSDWHVVGQIR NRGLDMKSFLTSSRAAKWNF TNSETVPALDLDSAVVLIPWISS KEDTGDSDHYGRVAIYHKGLSFS SDGLVYPGAKGREGRMVVLSL VLGLSEQDDFANIPDLQNPQTQ QNQNAQGDKRLPAGGKAVNT APVPGQTPHDESRRTEPRSSV SDLVNSLTSEMLMEDWPPAVF SSGWAIAHTAPASLHSPGYSF LAARGGLLFEADFCWCKRSG STFPDCDGVANLAATEMALSQ LRFKETAMRESLVMLSPGSEE DEAHEGCSRENLGRIQFSVGYN FQESTLTLKIMKAQELPAKDFS GTSDPFVKIYLLPDKKHKLKTK
6574	36942	A	6624	1	576	
6575	36943	A	6625	1	155	
6576	36944	A	6626	4746	5258	DAGAQPSPRYLIYHQPSRFFRI TSTVTPFSKPISLLWLV*/GLHG DILL/RLQS*RC*CRSHPEYHSG PPGRWQGPSPAPQKCSRRTSR RSSR*HPPPPRPGGSAPSPASYS WTPPRTVPGSWARRWRRHLSR PSWATQPSWTATLWSQPLWRL KWEDCLSPGRSRLQ
6577	36945	A	6627	1	588	

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6578	36946	A	6628	444	1056	GPLLREPHQLCHFPVAGFVLDA GLPEAAAAPHDRGP ELAGPQA AGQHPAQVAHQPRAAAQQRQ GRRAREEAGAAQEEPRGPQE RRRRLAEGLRRQCGHPAGRDG RGGYRRAAQGPARGGRTPEWQ QSGGARRTPSVGHPRRARADW CLTGANDALSCSSPTCGKFLKT VSKVPV/CRRLAVNRKEAEGR SSESPTSSATFQSPALSWMLVS QRLLLPHMIGAQSSPGKRPNG TLRKWLTPSVRRLSSGKADGH VKKLAHKHKSREVRKSADAG SQKDSDSAATPQDETVEEDTV AQPRGRREGAGRQSGSRAAGP GRRASAIRGGHARTDVGKRN GTRTRKELMPLHGKRDAAEH DEPTSASRPAGERPELTLAAVQ TEYNCSFPS
6579	36947	A	6629	128	1103	
6580	36948	A	6630	1	602	
6581	36949	A	6631	3	1618	
6582	36950	A	6632	1	602	
6583	36951	A	6633	3	1618	
6584	36952	A	6634	1	912	
6585	36953	A	6635	195	396	VLPLHRQI**LLH*SKKHNHYK GKQQDLR/CSSTVPRRPQILPII SFSNVVPGSRRLKAPLVFIGPG

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6586	36954	A	6636	2	1813	FNTPLSTLDRSSRQKVNKDIQD VISALHEAGLIDYRTLHPKSTE YTFFSAPHHTYYKIDHIVGSKA LLSKCKRTEITNCLSDDRAIKL ELRIKKLTQNYTTTWKLNLLLL SDYVWNEMKAEIKMFFETNE NKDTMYQNI.WDTFKAVCRGK FIAVNAYKRKQERSKIHTLTSTQ LKEPEKEQETHSKASRRQEITKI RAELKEIDTQKTLQKISVSRSW FSERINKIDRLIARLMKKKREK NQIDAINDKGDITIDPTMQTT IREYYKNLYANKLENLEEMDK FLDTYILPRLNQEEVELPNRPIT GSENEAIIINSLP/TKKSPGPDEFT AKFYQRYKGLARAIRQEKERE DTQLGKEEVKLLFAEDMIVYL ENPIVSAQNLLKLINNFskVSGY KINVQKSQAFLHTNNRQTESQI MSECPLTIASKRIKYLGIQLTRD VKDLFKENYKPLLNKIKEDTN KWKNIPIRSWLGRNNIVKMTILP KVI/YKKTTLNFIVNQERARIAK TILSKKNKAGGITLPDFKLYYK ATVTKTARYWTLTIKKGSVWPI SLKSEKRHRTRPLWKLCHND VQGELL.KTIQFLFGSPL.GHSSLD
6587	36955	A	6637	1	2988	MPPHSEQPHSPSTRQKRKVPLF VRQCPFSFVIQAPKAKMDTFDGR KKQFTRFLFLFSMDQLGQGRFS MQTLSFALAVYRKDPSLVACQ VQALGNLEPSSVEAHVSSHGIAI DRKGWHVSLFSIQPGDCFPKAL VEDSPDRARRQQSKEEGWC RDRRRLKFHSKKGAAAIIVVKS KKYESPSFGVCFESLNNPRLTS RREKTISSSKRCRQCHAEETT VFWAKESQTGEQTGRGAGQRR MGMIICKACSMPLPAE
6588	36956	B	6638	362	1463	
6589	36957	A	6639	1	1061	
6590	36958	A	6640	1	1581	

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6591	36959	A	6641	46	862	AAFPAPRTLFFLSRPLRPTACAA FRPEFWRLNMKLPARVFFTLGS RLPCGLAPRRFFSYGTKILYQN TEALQSKFFSPLQKAMLPNSF QGGKVAFITGGGTGLGKGM TTL LSSLGAQCVCVIA SRKMDVLKAT AEQISSQTGNKVHAIQCNVKYP DMVQNTVSELKVKQHPSTVIT N*STERSSISFLLPTIYA*DWFRF CSTQVLLPKQVWKPMKSLAA EWGKIWNAIQC
6592	36960	A	6642	1	2902	MVKGSLQQUELTILNIYAPNTE APRFKQVLRDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKINKD TQELNSALYQADLDIYGTLHP KSTLEYTFFSAPHHTYSQNWTT IVGSKALLSEHKRTEIITNYLSD VHSAVKLELRKKLTQNRSATW KLNNLLNDYWVHNDMKAEI KMFFETKVENKIDTTYQNLWDT FKAVCRGKFIAKNAHNRKQEV RSKIDTLTSQLELEKKEQTYL KASRRQEI
6593	36961	A	6643	1	5127	
6594	36962	B	6644	1	3570	
6595	36963	A	6645	1	3663	
6596	36964	B	6646	143	3122	
6597	36965	A	6647	1	3235	
6598	36966	A	6648	1	3249	
6599	36967	A	6649	1	3297	

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6600	36968	A	6650	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEVESLNRPIITGAEI GAIHNSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIIIPKPGRDITTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIIISIDAEKAFDQIQPFMLKTL NKLGDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTTRQGCPL SPLLNFNILLEVLARAIQEKEIK GIQLGKEEVKLSLFADDMMIVYL ENPIVSAQNLLKLISNFSKVSQY KINVQKSQAFLYTSNRQTESQI MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLLKD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITQDIGMGKDFMS RTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQPTTWKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKHKMKKCSSSLAIREMQI KTTMRYHLTPVRMAIHKKSGNN
6601	36969	A	6651	1	3402	
6602	36970	A	6652	1	3288	
6603	36971	A	6653	1	3168	
6604	36972	A	6654	1	3516	
6605	36973	A	6655	1	3693	

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6606	36974	A	6656	1577	3354	TEPKTKTT*LSQ*MQKRPLTKF NNLSC*KLSIN/IVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPVISAQNLKLLSNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSQWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELGKTALKFIWNQKRARITKSI LSQKNKAGGITLPDFQLYCKAT VTKTAWFPSPGDVGLEADFSPSH TLKTQFFSCLAEFAAASCFFQR MNGFGMAMTTTYSTGAESPL PSCSIDQGGDTKLHRRASPGRT FPAAAGIPAAAAADGPPSLLLH KLWFPVELGGRALPRAESHGHE VAALGVMVVAQGKNGQEEA RSTPWLRPTSHLPPCSSSAWW TEQTDHPLLLCLGIYLLNA LSNLSMVALVRS DGALRSPMY YFLGHLSLVDVCFCTTVTVPRLL AGLLHPGQAISQACFAEMYFF VALGITESYLPAAMSYDRATAA CRPLRYGALVTPWALRLAARY DRLASVVYAVITPTLNPFINSLR NKEVKGALKRGLRWRAAPQE
6607	36975	A	6657	1	3514	MELKTKARELREECRLSRSCD QLEERVSAEMEDEMNMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRIGVPESDVENGTKLEN TLQDIIQENFPNLRQANIQIEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFSPHIIITYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRJKNLTKSRSTTW KLNNLLNDYW
6608	36976	A	6658	3	3316	
6609	36977	A	6659	1	4794	
6610	36978	A	6660	1	3570	
6611	36979	B	6661	1	3384	
6612	36980	A	6662	1	3429	
6613	36981	A	6663	1	3780	
6614	36982	A	6664	1	3894	

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6615	36983	A	6665	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRLDLSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDFAKAVC RGKFIALNVYKRKQERSKIDTL TSQKLELEKQEQTHSKASRRQE ITKIRAELEKIETQ
6616	36984	B	6666	1	3145	
6617	36985	A	6667	1	4398	
6618	36986	A	6668	523	3852	
6619	36987	A	6669	1	3934	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRLSR CDQLEERVSADEDEMNEKRE GKFRKRIKNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMQRYSSRRATPRHIIVR FTKVEKMEKMLRAARQKAPH HTYSKIDHIVGSKAL
6620	36988	B	6670	1	5215	
6621	36989	A	6671	1	7171	
6622	36990	A	6672	3	493	
6623	36991	A	6673	1	729	
6624	36992	A	6674	3	800	
6625	36993	A	6675	1	327	
6626	36994	A	6676	2	462	KSSWLEEDDDPVVARVNRMQ HITGLTVKTAELLQVANYGVG GQYEPHFDFSRPFDSGLKTEG NRLATFLNYMSDVEAGGATVF PDLGAAIWPKKGTAVFWYNLL RTGEGDYR/TRHAACPVLVGCK WVSNKWFHES/GQFLRPGST EVD

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6627	36995	A	6677	3	717	RHRLRNRLKDVGGAEFYPLLE DDQSNLPHSNSNNELSAATLP LIIREKDTEYQLNRJILFDRLLKA YPYKKNQIWREARVDIPLIRG LTWAALLGVEGAHAKYDAID KDTPIPTDRT/QLKWDIPRCHSV R*TVIHAPEGHAKFRRLKAW VVSHPDLYVWQGLDSLCAPEL YLNNNEALVYACMSAFIPKYL YNFFLKDNSHVIQEYLTVFSQM IAFHDPELSNHLNEIGFIPD
6628	36996	A	6678	1	508	
6629	36997	A	6679	1	888	
6630	36998	A	6680	2	584	
6631	36999	A	6681	2	152	QVAKGMDALLQHLEDCGYR/S SKKKAQICRQQVTKWGDGSAL MGTSSTASL
6632	37000	A	6682	733	894	
6633	37001	B	6683	1	1626	
6634	37002	A	6684	1	1971	MAQVWANDNPPGLAVNQAPV LIDVKGPAQPIRQKQYPVPREA LKGIQPGTKDYQPQDRLRVN QATVTLHPTVPNPYTLGLLLA EDSWFTCLDLKDAFFSIRLAPES QKLFAFQWEDPQSDLGICLLLY VDDLLGHSTAVECAKGMVDL LQHLEDCRYKMSKKKAHICRQ QVRYLGFTIRKGRS/WEREKM AVGVLTQTVGPWPRPVAYLSK QLD/EVSKGWPLCLRTLAATAL LAQEADKLTGQNLNIKAPHA VVTLMITTEGHHWLTNARLTKY QSLPCENPHITIEVCNTLNPITL LPVSESPGEHNCVEVLDSVYSS RPDLRDQPWASSVDWELVMD GSSFINSQGERCAGYAVVTLDA VIKAKLWLQGTSAQKAELIALT RAVELSEGOESLEELLGRYFYV SHLPFAKAVAQ/CITCRQHNA RQSPVTSPIQAYGAAPFEDLQ VDFTEMPKCGGNKYLLVLTCT YSGWVEAYPTRTEKPYKKGKN DPSCTKGQCNPLELVITNPLNP HWKKGERTVLGIDRARLDPRV NILVRGGEVYERSPEPVFQTFY DELNVVPPEIPGKTRNLFQLA ECVAQPLNVTSCYVCGGTVTG YQWPWKARELVVPDVPDEFEL AQKNYPDNFWVLKPSITGQYCI
6635	37003	A	6685	1	1461	
6636	37004	A	6686	1	1005	

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6637	37005	A	6687	1	174	
6638	37006	A	6688	519	588	
6639	37007	A	6689	2	4527	GRAGLGWSSGGGRGRACSEGP AEARGREGDKGSAALSPPLPLT LGEEMAAERGARRLLSTPFWL YCLLLLGRRAPGAAAARSGSAP QSPGASIRTFTPFYFLVEPVDL SVRGSSVILNCSAYSESPKIEW KKDGTFLNLVSDRRQLLPDGS LFISNVVHSHKHNKPDGGYYQCV ATVESLGTIISRTAKLIVAGLPR FTSQPEPSSVYAGNNAILNCEV NADLVFVVRWEQNRQPLLLDD RVIKLPSGMLVI
6640	37008	A	6690	1	879	
6641	37009	A	6691	407	594	
6642	37010	A	6692	1	3621	
6643	37011	B	6693	1	609	
6644	37012	B	6694	1335	1599	
6645	37013	A	6695	1	354	
6646	37014	A	6696	181	683	SRYFILLRKPTFPAMALLPVLFL VTLLPSLPAGGKDPATALLT TQLQVQREIVNKHNELKAVSP PASNMLKMEWSREVTTNAQR WANK/CTLQHSDPEDRKTSTRC GENLYMSSDPTSSWSSAIQSWY DEILDVYGVGPKS/PQYCPAG NNMNRKNTPTYQQTGPCG
6647	37015	A	6697	199	969	
6648	37016	A	6698	1	564	
6649	37017	A	6699	153	427	
6650	37018	A	6700	1	978	
6651	37019	A	6701	3	419	
6652	37020	A	6702	9	255	VRAPAQGPLAGGRRRCGSGA SCTPSRGPASWSRSAAQVPRS SRWRAGSASS*/N/GRQAPPTSQ PPRAQFFAQPPGPWPLS
6653	37021	B	6703	96	283	
6654	37022	A	6704	172	365	PTYHLYPCHFYQHRTRRIPRK SERLFTPPQLSWKGTWDY*1 CLCCNDSEGRDVLVLRLVK
6655	37023	A	6705	3	1171	
6656	37024	A	6706	2	740	
6657	37025	A	6707	256	461	
6658	37026	A	6708	1	414	
6659	37027	A	6709	1330	1386	YIDSILPK*NHDTLSQYCRYMH SRQRAAS*PLSTGKLQCLGLD LVLC

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6660	37028	A	6710	207	1173	GGDRDRMTANHESYLLMASTQ NDMEDWVKSIRRVINGDLSCGG IFGQKLEDTVRYEKRYGNRLAP MLVEQCQDFIRQGLKEEGLFR LPQANLVKIELQDAFDCGEKP SFDSNTDVHTVASLLKLYLREL PEPVIPYAKYEDFLSCAKLLSKE EEAGVKELAKQVKSLPVVNYN LLKYICRFLDEVQSYSGVKNKMS VQNLA TVFGPNILRPKVEDPLTI MEGTVVVQQLMSVMISKHDCL FPKDAELQSKPDGVSNNNEIQ KKATMGQLQNKENNNTKDSPS RQCSWDKSESP/TEKQHEQWIP HSSIRQQNQPKQEQWSQAI
6661	37029	A	6711	173	881	
6662	37030	A	6712	1605	1844	
6663	37031	B	6713	123	699	
6664	37032	A	6714	1	462	
6665	37033	A	6715	1	2607	
6666	37034	A	6716	1	918	
6667	37035	A	6717	1	549	
6668	37036	A	6718	1	687	
6669	37037	A	6719	1	258	
6670	37038	A	6720	90	1621	HGLDLRTMNRSRQVTCVAWV RCGVAKETPDKVELSKGGVKR LIAEAEELQEEGGSDSEKGTG SPLEEGMQSARTQARP/REPLE/ DGDPE/DRTLDDDELA EYDLD KYDEEGDPDAETLGESLLGLT VYGSNDQDPYVTLKDTEQYER EDFLIKPSDNLIVCGRAEQDQC NLEVHVYNQEEDSFYVHHDILL SAYPLSVEWLNFPSPDDSTGN YIA VGNMTPVIEVWDLDIVDSL EPVFTLGSKLSKKKKKKGKSS SAEGHTDAVLDSLWNKLIRNV LASASADNTVILWDMSLGKPA ASLA VHTDKVQTLQFHPFEAQT LISGSYDKSVALYDCRSPDESH RMWRFSQGIERTVWNHFSPOCH FLASTDDGFVYNLDA RSDKPIF TLNAHNDEISGLDLSSQIKGCL VTASADKYVKIWDILGDRPSLV HSRDMKMGVLFCSGCCPDLPFI YAFGGQKEGLRVWDISTVSSV NEAFGRRERLVLGSARNSSISGP FGSRSSDTPMES
6671	37039	A	6721	1	549	

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6672	37040	A	6722	1	1318	AKQQLNLRTHMADENKNEYA AQLQNFNGEQHKHFYVVIPIQY KQLQEMDERRTIKLSECYRGFA DSERKVIPIISKCLEGMILAAKS VDERRDSQMVDVSFKSGFEPFG DFFPEDYSQHIYRTISDGTISAS KQESGKMDAKTTVGAKAGKL WLFGKKPKQSPPLTPTSLFTSS TPNGSQFLTFSIEPVHYCMNEIK TGKPRIPFSRSLKRGWSVKMG/ AALEDFSHLPPEQRRKKLQORI DELNRELQKESDQKDALNKMK DVYEKNPQMGPGLSQPKLAE TMNNIDRLRMEIHKNEAWLSE VEGKTGGRGDRRHSSDINHLVT QGRESPEGSYTDDANQEVRGPP QQHGHNEFDDEFEDDDPLPAI GHCKAIYPFDGHNEGTAMKE GEVLYIIEEDKGDGWTRARRQ NGEEGYVPTSVIDVTLEKNSKG
6673	37041	A	6723	1	741	
6674	37042	A	6724	1	1063	MPFYISDLICGDRILRALCPQD LPTYSLHSRGMKMRASCRRKFLD NNSSRLVSCNMGALISIWGTTT PPLHATILDSQPTVHPPLAKDCL PCGLQASASDLRALQRLCQ QLPWVGSQPHTRSPSPQRGGKT GLFAGLASSVSMRPASPPSPA DSCSACRFFARRPPLRVTWVKP SSALALCVSISDSPGNLKALPA ETRAQLHHAESLSQPPLQLRP FPKTSQAGDLQDLGPYVCVRK AVGKGDKQIRAVVKEHSVRSQ ERIWHPGITTANMPGHLGQNT ESGRDKLPMFGVWFPGRFWG LWVWRLP*LKLAAPCRPSRSLR SSPISRRASSTRCLTVSGCPAAP
6675	37043	A	6725	25	573	
6676	37044	A	6726	1	483	

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6677	37045	A	6727	1	996	MVGKAKWKPIELPLRRKIVNQ KQYHIPGGVAKISATIKDLKDV GVVPTTSPFNSPIWPVQKTDGS WRK WLS*QGQQT/FTVLPHG YINSLALCHNLIRRLDHFSLPQ DITLVHYIDDIVLTGSSEQEVAN TLDLLTSLDWALVETECLTMG HQVTMQPELTIMNWALSDPSN YKVGCAQQHSIIKWKWYIRDQ ARAGTTCKWTAALQPLSRTS LKDSGERKSSQWAELEAVHLI MHFAWKEKWPDVQLYTDSWA VANGSAGWSGTWKNHWDKIA TTVIAQWAHEQSSHSGSRNGGY TWAQQHGLPLTKADVATATDE CPICQQQRPTLSP
6678	37046	A	6728	2	1380	CLAGLFGFWSPCIPHLGLVLLQSI YLVTQKAA/SSEWGPEQEKALQ EVQAAVQAAALILEPYDPAGPVV LEVSLADRDVWSLWQAPIGE SQQRPLGFWSKALPSSA/DHKA CHAAQHSIIKWKWYIHDRARA GPEGTNSSARYAATM*KWITAS ALQPLSRKSLKDSSEKSSQWA ELRAVHLAVHVAWKEKWPDV RLDTSWAVANGLARWSGTW KEHDRKIGDKEVWGRGTRIELS EWSKTVTIFVSH/VLLPRLPSIRG LTECLIHQHGPHSIA SDQGTHTF TAKELQQWAHAHGIHWSYHVP HHPGWGWKVLQAVYALNQRPP IYEWKEESCLHTGVADALRGN WAEGRHREKALWGLWSTWS QHPLRSLKTRRHHPGLGVLS ICEAGGATELSRASGFATGYG KRKEDTKKHKQHSVSDIIEQQH SLGLTEKTVKGTPTQGISMRRP LYHKATEFQE
6679	37047	A	6729	1	2229	
6680	37048	A	6730	1	789	RDLQPFTSVTVHCRKGNDDTF GGPLDAGSELTLIPGDPKHHCG PPVKVGYAGGQVINGVLAHPL IWL VQKTDGS/WRMTVDYCKL NQVVIPIAAVSDVVSILEQINT SPGTWYAAIDLANAFFSIPVHK AQKQKFAFSWQGOQYTFVLPL QWYINSPALCHNLIRRLDCFS LPLDITLVHYIDIMLIGSSEQE VANTLDLFRHLRARGWEINPT KIQGPSTSVKFLGFQWCGACQA IPSKMRDKLLHLVPPPTTKKEAQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6681	37049	A	6731	1	553	MTVDYCKLNQVVIPIAAVSD VVSLLLEQINTSPGTWYAAIDL NAFFSIPVHKAQQQAFSWQG QQYTFTVLQWYINSALCHNL IRRDLDLDCFSLPLDITLVHYIDDI MLIGPRQLLACY/WALVETEHL TISHQVTMRPELPMNWVLFDP SSHKVGCAQQHSIIKWYVH DWARAGPEGT
6682	37050	A	6732	3	266	
6683	37051	A	6733	3	582	
6684	37052	A	6734	3	403	
6685	37053	A	6735	1	2712	
6686	37054	A	6736	875	1506	LSIYLVTVQKAA/SSEWGPQEKE ALQEVQAAVQAALILEPYDPA GPVVLEVSLADRDVWVSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQQHSIIKWYIHD RARAGPEGTNSSARYAATM*K WTASALQPLSRKSLKDSSEGK SSQWAE LRAVHLA VHVAVWKE KWPDVRLDTSWAV/ANGLAR WSGTWKEHDRKIGDKEVWGR GTRI
6687	37055	A	6737	1	633	MTVDYRKFNQVVTPTMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFALPLQ GYINFALCHNLIRRELDFFLLL QDITLVHYIDDIIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQLTPWEQVPSS GDIKEYFPNAFVLLTTASLQGG DNLSQLQLTWKAPEDIKMSKT DADADEEIEALRG
6688	37056	A	6738	2	1103	DLWPFTRVTLHRGKRNDQTQ GLLDGTGSELMIPEDTKHHCGP PVKVEAYGGQVINGVLAQIQLT VGPVGSNGTHPVVIYPVPECIIG GILSSWQNPHGSLTSRKTDGS WRMTVHYHKLNMVTPIAAAI PDVVSLLEQVNTSPGSWYAAID LANAFFSIPVHKAHQKQAFSW QQQYTFTVLQWYINSALCH NLIRRDLDLDCFSLPLDITLVHYID DIMIGSSEQEVANTLDLFRVRL LRARGWEINPTKIQGPSTSVKFL GFQWCGACQAIPSKMRDKLLH LVPTTTKKEAQCLQLLACY/W ALVETEHLTISHQVTMRPELPI MNWVLFDPSSHKVGCAQQHSII KWKYVVDHVARAGPEGT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6689	37057	A	6739	1	2058	
6690	37058	A	6740	2	1173	WEVRQYFTFTVPQGHINSLVLC HDVVRRLDGHFFLPQDITLVHY IDDIMLIGSTPPTKKKAQLVVG LFGFWRQLVPHLGVLLWPIYQ VTQQAASFEWGPEKEKALQQV QAAVQAALPLGPYDPADPMVL EVSVADRDVAVWSLWQDPGES QWRSLGFWSKALPSSADNYSPP ERQLLACYWVLVETERL/QWV TPAEEDFNNQVDRMTHSVDDTT QPLSPATHVITQWAHEQSGHG GRDGGYTRVQQHGLPLTKADL ATAGKVFFQKAV*ALN*HSIYGT LSLIARIHRSRQGVVEVAPLT ISPSDPPAKFLLPVPTLRSAGLE FLVPEEGMLPSGDTTVPLNWKL RLPPGHFGLLFLPHQQANKGVT VLVGVTDLQDEISLLPHNG
6691	37059	A	6741	823	2487	KELKLWKNRHKLLSYPTVGAA VTQLQNLTAMGVIGSHGARGQ VVALNRQRQGLDQPFTRVTVH WGKG/NMQIFGGLDGTSELTL IPGDPKHHCGRPPVKVGAFFGQ/ VINGALARVQLIVGPVGPWAHP VVISPVPECIIDISSLSSWQNPHIS SLTGRVRAIMVGKAKWKSLEL PLPRKIVNQKYHIPGGIVEISA TIKDLKDAGEVPIPTTFPLNSPI WPVRKTDGCRMTVDYCELN QVVTPTAATVPDVVSLLEQINT SPGTWYADIDLANAVFSIPVHK AHQKQFAFSWQQQQYFTVLP QEYINSLGLCHNLIQRDLDFSL LQDITLVHYIEDIMLIGSTEQEI NTLDLLFMAKEVWQWAHAHG IHWSYHVSHHPEAAGLIEWWK GLLKLQLQCQLGDNTLEGWGK VLQKTVYALNQHPYGTVSPIA RIHRSRNKGVVAPFTITPSDPL PQFLLPVPATLCSAGLEVLAP GGTLPPGDRTTPLNWKLRLPP EDFGLLPSLSQQAQKGYTVLAG VIHPDYQDEISLLHNGCKEDL
6692	37060	A	6742	3	350	
6693	37061	A	6743	1	3339	
6694	37062	A	6744	1	2271	

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6695	37063	A	6745	3	1377	AHLAADDFTK*GWVSGLPQG LDKL.TPGANLEMQPENLKED LVYLKKNHHEELSMAIKRNESM AKGLQRRLLQQQFEDDSKCFP RPQDLIRLYDIILQLTLEDREGK GLSFSFACVDKDVSVKMDTVP GVNLSCLINEMRDQDKKLVEK SCKDAQGWFFSLKALLEGLVE TEVCYRTQLAQLQGLIRSMEEQ LCELCCDAEHQDHEHQVLLDV KTQLEQEIATYSRLLEVEDAQL ATQYSLSLASQPTREDLEKAIL KFIWNQNRQAIAKTILSKSKA RGIMLPFSKIYYKTTVTKTAWC WYKNRHIDQWNRIENPEIRPHT YNHVIFDKPDKRKQWGKDSLF NKWCWENWLAICSKLTDPFL NPYTKVNSRWIKDLNLOPKTIK ILKENLGNAIQDTGKGKDFMTK MPKAIAATKAIKDWLIKLSKF CTALRNYQSKPTTYRMGENF
6696	37064	A	6746	1	882	
6697	37065	A	6747	13	1402	STGSTHACDLLFSPSPVCLPPAA ATMTTSIR/QFTSSS/SIKGSSGL GGG/SSRTSCLSGGLG/AGSCR LGSAGGLGSTLGG/SSYSYSCYSF GSGGGYSSFGGVDGLLA/GGE KA/TMQNL/ND/RLGSYLDKVP PWKEANTELEVK/IRD/LVTRGR APGPARDYSQYYRTIEELQNKI LTATVDNANILLQIDNARLAAD DFRTKFETEALRLSVEADING LRRVLDELTLARADLEMQIENL KEELAYLKKNHHEEMNALRGQ VGGEINVEMDAAPGVDLSRLN EMRDQYEKMAEKNRKAEDW FFSKTEELNREVAATNSELVQSG KSEISELRRTMQALEIELQSOLS MKASLEGNLAETENRYCVQLS QIQGLIGSVEEQLAQLRCEMEQ QNQEYKILLDVKTRLEQEIATY RRLLEGEAHLTQYKKKEPVTTT QVRTIVEEVQDGKVSSREQVH
6698	37066	A	6748	2	452	FLLPSSFCTHSLSPITITIVGPG DFNLASHIIPDTTPDPHDCISMIH LTFTFPFHISFFVPHPDHA*FID GSSTRPNRHTPAKAGYAIAQAT IPPLRTSHFLSIVEIYPQGNNSFV FHVLFYSSGHHQAPSLPYTLRR DRRPGTSRA
6699	37067	A	6749	1	1791	

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6700	37068	A	6750	1	219	
6701	37069	A	6751	2	528	TLTVESKSIKAYKLSLQFPHTC PKTGHALQVSSGFVESPTVITVP GLDINLASHTIPDNTPEPHDCIS LIHLTFTFPFHVSVFPVPHPDHT WFIDGSSSTRPNCHSPAKTGYAI VSSTLIIDATALPPSTTSQQAELI ALTRALTLAKGLPINIHTDSKY AFHILHHHAVI* AER
6702	37070	B	6752	1	1744	
6703	37071	A	6753	1	1376	MCKRMPGLQASQTVCPFYDKN YLDLKRKGTEIKRRERLKCGTK IERRKRLRDSERLEKRIKRGCLP DLKLSTEIQINRLRGLYTLLRKE RRFGLQETINYAEVTGIYVKELI EDREHLNSGKYIFNIFDIKVPV VFGLIDPYMLWEKKEGTKEGJK EGMKRESQKRIKWERSFITFIAL NTADRTLMSAGCYRKQVKIHI DALPPNSQTLKKRGGASLIISF RRQSGPSAAGLWEFARGPFQTL FAWLSPAAEAQORLLPASSAE SFIAEGDPPDAGQSSPPSSLHAA AATALMLEALKITNYAQLTLY SSPNFQNLFSSSHLLTHLSADWL LQLYSLFVESPTITIVPGPDFNPA FHFIPDTPDPHDCISLIHLTFTF FPHISFFPVPHPDHTWFIDGSS RPNRHTPAKAGYA/DGRNTSYC VLPVPGNSPLVPNPGSARCTEG GLLYARA
6704	37072	B	6754	400	820	
6705	37073	B	6755	1	1190	
6706	37074	A	6756	1	1002	
6707	37075	B	6757	1	3216	
6708	37076	A	6758	1	4020	
6709	37077	A	6759	1	1155	
6710	37078	A	6760	2	346	SSYLMHILSAPNLLQLYSLFVES PTITIVPGPDFNLASHIILDTTPD PHDYLSDDPDHIS/TFP/DISFFPV PHPGHTWFNDGSSSTRPNRHSPA KAGHAIVFSTSIIEATALPPSTT
6711	37079	A	6761	189	1201	
6712	37080	A	6762	1	231	
6713	37081	A	6763	1	834	
6714	37082	A	6764	470	479	PRNPSSFLQVQVQHRFLQLFVP FHFVFLLASLYVMVTLTTFWR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT
6715	37083	A	6765	21	706	
6716	37084	A	6766	1	158	

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6717	37085	C	6767	78	401	
6718	37086	A	6768	536	694	
6719	37087	C	6769	1	1410	
6720	37088	B	6770	1	1836	
6721	37089	A	6771	306	487	VGFLGILF/CFEAIVNVSSLMIW LSVCLLSVYKNACDFCTLILYP ETLLKLLJSSSLYLW
6722	37090	A	6772	714	1096	FFLPMSMECSSICLYPL/CISLRS GL*FSLKRSFTSLVSWIPRYFILC KSQGMRWLGLGSEA*YSCLLIL IRKITQNSVEVLGRKFLGGGM EREWVWFLRAASSGIRGSVGT NFKSESRIQISCASV
6723	37091	C	6773	1	2796	
6724	37092	A	6774	126	490	FFLPMSMECSSICLYPLFPAGAV VCSSP*RGPSHPL*VGFLGILF/C FEAIGNGSSLMIWLSVCLLLVY KNACDFCTLILYPETLLKLLISL RRFWAETMGFSRYIIMSSANRD NLTSSFPN
6725	37093	A	6775	1	550	
6726	37094	A	6776	578	865	MCPRDYGMLCLCSHCFKEHLY FCLHFVMPVVIQEQVVFQPCS *AVLSEFLNPEF*FDCTVV*ETV CYNF*SFTFAEKSFTSNVSVNFG IGVVWC
6727	37095	A	6777	1	2091	
6728	37096	C	6778	1	1458	
6729	37097	B	6779	1	504	
6730	37098	A	6780	70	511	NHASPGIRNLFHPRGLRAITIA VFCKQNTYIRLEPFKINVLEQIT KHIEKLQCGGVVKQLSRRGNN QHISSTYDINRADTQVRAVNN YDIIV*ATVSMASRSIRCGSVGS LPSSNLPIINSVIRCARQEGIM SSPGQQVGFA
6731	37099	A	6781	3	306	
6732	37100	A	6782	1	3567	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRSLRSCDQLEERVSV MEDEMNMKQEGKFREKRIRK NEQSLQEIWDYVKRPNLRIGV PESDGENGTCLKNTLQDIIQENF PNLARQAKVQIEIQRMPIQRYS LTRATPRHIIVRFTKVE
6733	37101	A	6783	386	550	
6734	37102	A	6784	1	594	

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6735	37103	A	6785	1	1324	MGKKQSRKTGNSKRQASPPK KERSSSPAMEQSWMENDFDEL REEGFRRTNYSLEQEGIQTKGK EVKNFEKNLDECITRITNTEKCL KELMELKAKARELREECRLRS RCDQLEERHHTTPIPKLTTYLE VKLSPANVKEQVITNCLSDHSA IKLELRIKKPTQNPSTTWKLN LLNDYVWNKEMKSEIKMFFE TNENKNTTYQNLWDAFKA VCRGKFIALNAHKGKQERSKIDTLT SQLRELEKQEQTHSKVSRQEI TKIRAEPKEIETQKTLQKINESR SWFFERINKIDRRRLRIKKKRE KNQRDAIKNDEGDITDPTIEQIT TIREYYKHLYANKLENLKEMD KFLNTYTLPRNLQEEAESLNRPI AGSEIVAIHNSLPTKKSPGPDGT AEFYQRYKEKLVFGAGYFGM WALAALPSNLLKLSQLCQEEA EVNVLVQFVCIC*SCLNSVRRQ
6736	37104	C	6786	1	1719	
6737	37105	B	6787	1	1098	
6738	37106	C	6788	1	1782	
6739	37107	A	6789	3095	3217	CRCLQMAM*WS*AIALSMKIS MSPRKPEV*IKVLGAGLCL
6740	37108	A	6790	1	5364	
6741	37109	C	6791	1	2505	
6742	37110	A	6792	37	1214	KLLQDLPFSSINSSAVEKISMSTT GQVIRCKAAIILWKPAGPFSIEEV EVAPPKAKEVRJKVATGLCGT EMKVLGSKHLDLLYPTILGHEG AGIVESIGEGVSTVKPGDKVITL FLPQCCECTSCNLSEGNFCIQFK QSKTQLMSDGTSRFTCKGKSIY HFGNTSTFCEYTVIKEISVAKID AVAPLEKVCISCGFSTFGAAI NTAKVTPGSTCAVFGLG/VGVL SVVMGCKAAGAARD/IIGVDVQ QGRKF*GRAQELGATEC/LNPQ ALKKPHFKEVLFDMDTDAIDFC FEAIGNLDVLAALASCNESYG VCVVGVLPASVQLKISGQLFF SGRSLKGSVFGGWKSRQHIPKL VADYMAEKLNDPLITHTLNL DKINEAVELMKTKW
6743	37111	B	6793	1	2280	
6744	37112	A	6794	1498	1764	LVLYKVMGRMEPSWKTLCRL SRRTSANLSKAGQCSDSNGTEN TTKILLKKSNSKTHNCQIHQS*N EGKNVKGSRQERSGYPRGRPS

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6745	37113	A	6795	3	640	
6746	37114	A	6796	1	996	
6747	37115	A	6797	1	933	
6748	37116	A	6798	74	1128	LLLDL*VD*SPSRPLEMRFRV*P MKRCTLKKNYLSFLVVISRNL *NRVKAIM/VGKAEWKIETPL PRKTVNQKQYRIPGGIAEISTTI KELNNAGMVIPTTSPFNSPIWP VQKIDGSRWMTVDYCKLNQV VTPIAATVPYVVSSELEQIN/TSPG T/WNRKRCNRSRLHKLCHL GHMTQOI*CFRLCQWHIGMLF GPEICGCTLSGQKL/WKIFVSH AASFWSPEQEKALQQVQAVV QAALPLGPYPDPADPVLLEMSV ADRDVAVWILWQAPISESQWRPP GFWSKALPSSADNYSFPERQLL ACYWTLVETERLTMGHQVTIPP ELPIMNWVFSDLSSPKMCHPQQ
6749	37117	A	6799	1	229	
6750	37118	A	6800	1	1011	MVSTPATLPSLPKALMASWG VPYDQLTKEEKTRVWFTDGS RYAGTTQKWTAAVALQPLSR LKDSEKSSQWAEQAVVYLV VHFAWKEKWPVGLYTDSSWA VANLAGWSETWEKQDWKIG DKEIWGRGMWMDLSEWSKAV KIFVSHVSAHQRVTSAEFEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYSWAQQTGLPFTKADL AMATAECPCQQRPTLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFVLTVIDTYSRYFAY PAHNASAKTTIHGLIECLIHCY GIPHSIASDQSIHF/TTKEVQ*WAH AHGIHWSYHVSHHPEAAGL
6751	37119	A	6801	2	739	HKMGHAQQHSIIKWK*YICDW ARAGPKGTTAPMASWGLVYD QLTEEEKTRWFTDGSARYAG TTQKWTAAALQPLSRSLKGS GEGKSSQWAEQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
6752	37120	A	6802	1	354	
6753	37121	A	6803	3	592	

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6754	37122	A	6804	126	365	QLAEPHWWLPD*KGAGFEWGP EQKKALQ*VQAAVQAAALPLGP YDPADPMVLVSVVADKDAVWI FHLGSDRWRRTRYRCL
6755	37123	A	6805	1	636	MEFNDSMHNTFDHIWRTKEYD EAGWLLSSLDKAMKENDEL DSNSQIQKQILSLQSSKILNLTE GTVVTLQNLNSVGIIGSQGGR GQVAALSLQRQAGFEWSPEQ EKALQQVQTAVQAAALPLGPYD PSDPMVFEVSADGNVWSLW QAPIGELQWRILEFWSKALPSS ADNYSFGRQLLACYWALVET EHLTVDHQVT/M*PELPI
6756	37124	A	6806	1	672	
6757	37125	A	6807	308	470	
6758	37126	A	6808	1	1908	
6759	37127	A	6809	1	1218	MGIIGSRGGRGQVAALKRQRQ VTKKAASFEWGPEEKALQQV QAAVQAAALPLGPYDPADPIVLE VSVADRGA VWSLWQVPIGESQ QRPLGFWSKALPSSADNDSPF RQLLACYCAI.VETERLDMGHQ VTMRPEVLIINCVLSDPSSH/QG WRLCMSATWTSTYQ/A*PGY GHC*VPLNPAETNTDPSIWHH S/YG*LASYLVIG*LHWTSIME GAEVCPHWNRLRLI*VCLST QCFCED/SHPWIHE/ASYLPSWH ST*HCL*SRHSPYS*RSVAVGSC SWNSLVLPSPSS*SSWINRMV EWPFEVTITMPTR*QYSAGLGK SSSEGCVCESASNIWYCFRSQ DSWVQESRGGSGSTIIHHF** PTSKIFASCFDLMFCWT*GCS/S *WRNAATTRHNNFI
6760	37128	A	6810	901	1142	GPEDLQGLFSLFQDPLL/SHPV CLEALAPFPSPVVPISFPHPVA GEFWLYPSGAA/RASSDAQSWT VIAVSPLRGLNSWG
6761	37129	B	6811	1	1452	
6762	37130	A	6812	122	1838	
6763	37131	A	6813	101	249	MTHVTALRTSSNLMRN*RKVG EAKSQEH*S*QACHL.KSRMSS SRLWIN
6764	37132	A	6814	1	1074	
6765	37133	A	6815	310	397	LTIWQDSNPGSCL*GCSVCAHA /CVGQGHMVC*PSYSLYLKSE PKEGTGRNKDPDLNSQNRKGF LEQIHQ
6766	37134	A	6816	1	583	

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6767	37135	A	6817	1	486	
6768	37136	A	6818	2	1001	
6769	37137	A	6819	1	2307	
6770	37138	A	6820	3	393	
6771	37139	A	6821	1	1776	
6772	37140	A	6822	1	1140	
6773	37141	A	6823	1	558	
6774	37142	A	6824	2	798	PRVRIFFSITWYSLRVLTEISLW GGLLLVVIITQYDMTRTRNKYL HTNSLVLANMSAQFRSLHQY AA\QRIIRLFSLLSKKHNVLEQ ATQSLRGSLSNDVPLPDYAQD LNVIEEVIRMMLEIHNSCLVTNS LHHNPNLGITPWLQ\RRSLWN NFRVTHPSFQINGKII\WVIF/LS /SRLQGLAGKLGAEISVERVLEI IKQGVRI\SLPKDRLLKFPPELKF YVEEEQPEEFFIPYV\SLVYNF SSRPVLGIPQDIPAVSPWVSD
6775	37143	A	6825	3	206	PSASRPWAHPALHPSVPVARG WQPP\TGLHPLREQRGLGQHM* QSSGQQPQGGVGPESHFPAL WAQL
6776	37144	A	6826	200	601	EMGSCDQWQRPCVPWEAVVM PRDP/LKMALAVVWPMMKAPR VTKRTP*LTSTHQLAGLTSSISE SLA*MRHSPGKTKMKQAARPP MTEITLPMGSMKS/VQQQGEQE PDQRLQHSPPPLPPHVLLHWWP LVAQFQA
6777	37145	B	6827	25	1407	
6778	37146	A	6828	1786	1795	HC*LNALPSGETWGQKRGPLG TQLPLPL/VPLRAPKGRSPKGSK GPTHHTWALSSFSLSPTSQVTVG TEDQATSASGRPWLRIGHTGPGG GRVWAGRDSIRGVPALTVLHV LSSLGRETP*RPCLRGPTAPAGP KRAPGKWLPWSQAPPCGCCPR *LSHVL*DRNRCAW*KGGGRG L/LRAPTPVPELAHPHCPGAPTL SKPLSSPNMPAQGLTQE*PGSV ANLPPYPGALLCLGRREWDER GQVG*VPTSEME*RRTEPLKT PGDCSAAASKIPSFSSNRTPFPPL CPHKNKLGKT
6779	37147	A	6829	1	311	
6780	37148	A	6830	1	402	
6781	37149	A	6831	1	750	
6782	37150	C	6832	130	450	

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6783	37151	A	6833	1	875	MRLRLRLKLVKEQHVELYQKYS NNSWRYLSNRLAPSDSPEWLS FDVTGVVRQW/VWSRGGEIEGF RLSAHCSCDSRDNTLQVDINGF TTGRRGDLATHGMNRPFLLFM ATPLERAQHLQSSRRHRLDTK YCFSSTEKNCCVRQLYIDFRKD LGWKWIHEAPKGYHANFCLGP CPYIWSLDTQYSKVLALYNQH NPGASAAPCCVPQALEPLPIVY YVGRKPKVEQLSNMIVRSCKC NLGPAPPRPAPAGPAPRPAPV ALPMGAVFKDTRAPSPPGAPLK MERGKKKKKK
6784	37152	B	6834	162	635	
6785	37153	A	6835	2	1846	
6786	37154	A	6836	322	2104	
6787	37155	A	6837	1	352	
6788	37156	B	6838	92	1774	
6789	37157	A	6839	260	1016	
6790	37158	A	6840	479	1937	DVEHVGMKRRRWRRRVVVAD GNVVKPMSCAGDLQ/PFTRVTV HWGKGNDQTFQDLDLTGSELT LIPGDPKRHCAPPVKIGAYGGQI INGVLAQVQLTVDAVGPWTHP VVIFPVPECIGIDMLSSRQNPHT GSLTGRVWTIMVRKAKWKPLE LPLPRKIVNQKYHIPEGIVEIS ATIKDLKDAGVVPTTSPFNPI WPVQKTGSGWRMTVGYCKLN QVVTPIAAAVPDVVSLEQINT PPGTWYAAIDLANDF
6791	37159	B	6841	20	26	
6792	37160	B	6842	2	207	
6793	37161	B	6843	187	405	
6794	37162	A	6844	451	770	LFLFLLSSHPRSSASWYRHRH PHHPAARLPVADSASSSSPSS SSPSPSSSSSSPSSSSSFVYPHC QPPAPHFPH*HSR*QGRLFHFLP LPQLPSSPLSPWW
6795	37163	A	6845	1	417	
6796	37164	A	6846	191	314	
6797	37165	A	6847	129	212	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6798	37166	A	6848	1	192	CALNAGL/IGENEAKRRRSKVT QEADFPMSMDGASNFVRGDAI AGILIMVINIVGGLLVGVLQHG MSMGHAAESYALLTIGDGLVA QIPALVISTAAGVIVTRVSTDQD VGEQMVNQLFSNPSVMLLSAA VLGLLGLVPGMPSLVLLFTAG LLGLAWWIRGREQKAPAEPPK VKMAENNTVVEATWNDVQLE DSLGMATGLLT*PIFRAQWTGQ VTLFAAMPSPGSSSWSLTSLAG CWSACCNMA
6799	37167	B	6849	65	1129	
6800	37168	B	6850	46	1038	
6801	37169	A	6851	2	413	PSFQGPVSLPSITVVSIDSQASKP LKTPTQLWCQLRQYSFKHSFLV VPTCPVPLLQ*DTLTKLSASLTI PGLQPHLIATHLNPQVEDTSIPS LATYHAPLTISLKPNIHPPSPQC QYPIQHALKGLKPVITHLLQH
6802	37170	C	6852	35	346	
6803	37171	C	6853	239	484	
6804	37172	A	6854	1	1020	
6805	37173	A	6855	3	131	
6806	37174	A	6856	1	956	MAGALPPASLPPCSLISDCCASN ERSSMGIGPSEPCAGYNLLVCR LTKKKRIRSTNKVWDYVVRPN LRHIGVPEEEENSKSCENILGEIIE ENFPSLATDLDIQIEAQRTPOK FITERSLPRYIVIRLSKVKTKEI LRAVRQKHQIFLTQRLKNTAQ SPQKLPGPSQTLVLTREITIVP GLDFNPASHIADTTPDPHDCIS LIHLTFIQPHISFFVPHPDHTW FINGSTRPNRHSPAKAGYAIVS STSHIETTLPSSTTSQAEFIAL TQALILAKGLCINIYADSKY/AF HILHHHAVIWAERDTFTG
6807	37175	A	6857	1	1269	
6808	37176	A	6858	1	741	
6809	37177	B	6859	411	1257	

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6810	37178	A	6860	438	3997	SPLPHSTPISHPAACFKKIKACY HLPATAWPKAYKLSLQFPHT CPKTRQGLQHNSHKNTALPD YRLRLISQTPIPSTKQQLSFLG MVSKVRILTQELGPRPIAFLSKQ LDLTVLTQPSCLHAAAAAAIL LKALKITKYAQLTLYSSHNFNQ LFSSSYLMHILSAPWLLQLYSLF VESPTITIVPGTDFNPASHIILD TPDPHDCISLIHLTTFPFRISFFP VPHPNHIWFDIGSSTRPKCHSPA KAGY
6811	37179	A	6861	245	505	
6812	37180	A	6862	346	522	PAPEFWVHG*NVSPLSL*SKEQ EDRGFISQGRSPDLSHGTFHV RPCEETTKQALCEQH
6813	37181	A	6863	3	879	SGDLPEINPSSYTLLCEKDPP TISGPQTNQPKHILTNFKSETK ETRFIRGPTTPAPVTDWEGSLPL VFNHSRDTSLIHPGFRGVRPRR DACLGPSLAASPTFLGKGPA PRQTELGPNSSASAPPPYNPFI ASPPHTWSGLQFPMSPTPPPA QQFTLKKVAGAKGIVKDLINLT FKVYNNRKKLQFLASTVRQTP ATSPAHKNFQTPELQQGPVPPE PPPRGACYKFQKSGHRAKECLQ PRIPPKPHPICVGPWHKSDCP THLAATPRAPGTLAGGSLTPSQIFL
6814	37182	A	6864	143	331	DTSTPSLVTDHASLTISLKPNIH YPD*CYPIPQHALKGLKPVITC LLQHGLLKPINSYPRA
6815	37183	A	6865	1	783	
6816	37184	A	6866	32	415	WRHALKGLKPVITRLLQHGLL RPINSYPNSPFLVLEPDKPYRK RK*ISPPNRHILASVEVLKNQVN SHEFERSALIHTLSGLAPCSLH KMCSKLPKRSFLSVGSGTGKEAR SKILTFRTASRHLVL

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6817	37185	A	6867	1	1374	MSELPTIASKRIKYLGIQLTRD VKDLFKENYKPLLEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTTFTELEKTT LKFIWNQKRARIASILSQKNK AGGITLPDFKLYYKPTETKTAW YWYLNRRDIDQWNRTEPSEITPH TYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPPF FTPYTKINSRWIKDLNVRPETIK TLEENLGITIQDIGVGKDFMSKT PKAMATKDKTGKWDLIKLSF CTAKETTIRVNRQVAALLNSA VFQNAVEVVVWPSSEVHVKFL FCKIISCAQKQPIKFDGSSLS GVATAMMSATIAHLKRIKACY RSPVTAWTFKAYKLSLQFPHFT CPKTGQALQ*HT*KGLKPVIAH LLQHGLLPINSYPNSLILPVQK PDKPYRKLESFTSKAIKWHQIPS VPGKHLC*GS*RSPVTAWTFKA YKLSLQFPHFTCPKTGQALQEA GVIHFGKHGMASDPITQGNTYA NKVAKEAASVLTSPVHGQFFSF SSVTPTYFPTIEDFTYMPQVRKL KHLMV
6818	37186	A	6868	122	281	
6819	37187	A	6869	2	2144	
6820	37188	A	6870	224	418	LSQWRHALKGLKSVITRL*HG LLKPINSYPNSPIVPVLKPKDKTY RKVESFTAKTIKRCQIPLL
6821	37189	A	6871	5	289	
6822	37190	A	6872	1	2205	
6823	37191	C	6873	1	2082	
6824	37192	B	6874	1	1614	
6825	37193	A	6875	1	2067	
6826	37194	A	6876	1	1152	
6827	37195	A	6877	1	798	
6828	37196	C	6878	488	788	
6829	37197	A	6879	90	765	NTVFLGVVLPLELKLRIFRLLD VRSVLSLSAVCRDLFTASNDPL LWRFLYLRDFRGRNDIYSWT TKDFEYYINLVDKTEARFEKVD SDFESFTVGKMPSNSIACTEKSF MKGRVSQCDKKPVITRLQLHG LLKPINSYPNSPILPVLPDKPY KLVDLHRINQVLPHPGCAQP HTLFCPQYLPQLTIPVPLKDA FFTIPLQPSQVPLFAFT*TPDPT

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6830	37198	A	6880	1824	2286	PRVLRPNSPRNISPISNRIFSD*R CPIASEASWTITDALG/RLQWR HGLLNPNISPYNSPILPVQKPKD PYRLVQALLSLPQLPLFLAWTSI WPPTLFRITLLNPMPTVSL*ST*H SLHFPMFPSFLFLTLITLGLLMA VPLGLIATHQQRAML
6831	37199	A	6881	930	1289	LSQWTDGLLKPMSNPYNPILP VLKPKDPYK*VQDLRLINQIVL PIHPVVNPYPYTLSSIPPSTTHY SVLDLKLAFFTIPLHPSSQPFFAF TWTDPDTHQAQQIT*AVLPQSF SDSPHE
6832	37200	A	6882	2	196	IHGCKFIQCKRILSNFTEVADHV HDQIRL*TGIRLLTQPQRLSCR HQVAQHSVCRYLCQLPLL
6833	37201	A	6883	2	1441	LNQEEGESLNRPTGSEIEAIINS LPTKKSPGPDGITAIFYQRYKE ELVPFLVKLFQSTEKEGILPNSF YEASIIIPKPRDRTTKKENFRPI SLMNIDAKILNKILANRIQQHIK KLIHNGQHINRTNOKSHIISIDA EKTFGKIQQPFMLKTLNKLIGID GTYLKIIIRAIYDKPTANIILTGQ KLEAFPMKTGTREGCPLSPLL NIVLEVLARAIQKEIKGIQLG KEEVKLSLFADDMIVYLENPV SAQNLLRLISTFSKVSGYKINVQ KSQAFLYTNNRQTESQILSELFF TIASKRIKYLGIQLTRDVKDLFK ENYKALLNEIKEDINKWKNIPC SWVGRINIVKMAILPKVIYRFN AIPIKLPMFTFTELEKTTLKFIW NQKSARIAKSILSQKNKAGGIM LPDFKLYYKATVTKTAWYWY QNRDIDQWNTTEPSEIMLHIYN Y/LIFNKPENKKKWKDLSLFNK WCWENWL

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6834	37202	A	6884	69	2415	DKTSRGTIRQQRLRFTNIRCSAA TAADIQANRVWRGPPANSNR AAVRVLTVRRKTNKQKGHPHQ KPICTSPSSNTKEIQTIREYYKH LYANKLENAEERDKFLNIYTL RLNQKEVESLNRPTGSEIEAIK SLPTKKSPGPDGFTAKFYQRYK EELVPFLKLFQSEIEGILPNSF YEASIIIPKPRDRTTKENFRPI SLMNIDARILNKILANLIQHHK KLIHHDQVGFIPGMQGFNICK SINIIQHMRNTKDKNHMISIDA EKPFDKIQPFMLKTLNKLDD GTYLKIVRAKYDKPTANIILNG QKLEAFPLKTGTROGCPLSPLL FNIVLEVLAREIRQEKEIKGIQL GKEEVKLSLFVDDMIYLENPIV SAQNLLKLISNFSKVSQYKISVQ KSQAFLYTNNRQTESQTMSELP FTIASKRIKYLGIQLTRDVKDRF KENYKSLSEIKEDTNKWKNI CSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI NQKRARIAKSLSQKNKAGGIT LLDFKLYYKATVTKTAWYWY QNRHVDQWNRTEPSEIMLHIY NYLIFEKPDINKQWGKDSL FNK WCWENWLAICRKLKLPFLTS YTKINSRWIKDLNVRPKTIKTLE ENLGNTIQDIGMGKDFMSKTPK AMATKAKLDKWDLIKLSFCT AKETTIRVNRQPTGWEIFATY
6835	37203	A	6885	1	2358	
6836	37204	B	6886	1	1443	

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6837	37205	A	6887	452	2913	KMGLAREWILRFLVLILQEIRS MRQKENKDIQDLNSALHQADL IDIYRTLHPKSTEYTFFSAPHC/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKTQ/NRS ATWKLN/MLLNDY/WVHNEMK AEIKMFFETNENKDTTYQNLW DTFKA VCRGKFIALNAHKRKQ ERSKIDTLMSQLEKEKQEQTTH SKVSRRPISSEIEAIIINSLPTKKS PGPDGFTA E FYQRYKEELVPFL LKLFSQIEKEGILPNSFYEASILI PKPGRDITTEKENFRPISLMNIDA KILNKILANRIQQHIKLLHHDQ VGFIPGMQGWFNICKSINVIQHI NRTSDKNHTIISIDA E KAFNKIQ QLFMLKTLNKLGTNGMYLKIV RAIYDKPTANIILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVLA RAIRQEKEIQGIQLGKEEVKLSL FADDMIVYLENPVISAQNLLKLI SNFSKVSGYKINLQKSQAFLYT NNRQTESQIMSELPFTTASKRIK YLGQLTRDVKDLFKENYKPLL NEIKEDTNKWRNIPCSWVGRIN IVKMAILPKVTYRFNAIPIKLPM TFFTELEKTILKFRWNQKRAHI AKTILSQKNKAGGIRLPDFKLF YKATVTKTARYWYENRDIDQ WNRTEPLEIMPHIYNHLIFDKPD KNKQWGKDSL F NKWCWENWL AICRKLKLDPFLTSTYTKINSRWI
6838	37206	A	6888	I	1677	

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6839	37207	A	6889	2	2400	SMRQKENKDIQDLNSALHQAD LIDYRTLHPKSTETFTFSAPHCI /RTYSKIDHTLGSKALLSKCKIT EIITDSQTTVLSELRIKKLTQINR SATWKLN/MLLNDYWVHNEM KAEIKMFFETNENKDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDTLMSQLKELEKQEQT HSKVSRPPIPSEIEAIINSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEAII LIPKPGRDTTEKENFRPISLMNI DAKILNKILANRQQHIKKLLIIII DQVGFIPGMQGWFNICKSINVI QHINRTSDKNHTIISIDAEKAFN KIQQLFMLKTLNKLGTNGMYL KIVRAIYDKPTANIILNGQKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIQEKEIQGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINLQKSQA FLYTNNRQTESQIMSELPFTTAS KRKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWRNIPCSWV GRINIVKMAILPKVTYRFNAIPI KLPMTFFTELEKTILKFRWNQK RAHIAKTILSQKNKAGGIRLPDF KLFYKATVTKTARYWYENRDI DQWNRTEPLEIMPHIYNHLIFD KPDKNKQWGKDSL FNKWCWE NWLAI CRKLKLD PFLTSYTKIN SRWIEDLNVRPKTIETLEENLG
6840	37208	A	6890	1	1515	
6841	37209	A	6891	1	1428	

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6842	37210	A	6892	150	1920	NYQCREVLKGPDGAENHGTRIT* RMHKLSSQFSQLEERVSGMEDQTNETKDT HRLKIKGWRKIYQANGKQKKA EAAILVLDKTDFKPTKIKGDKQGHYIMVKGSIQQ GQLTILNIYAPNTGASRLIKQVL RDLQRDLDSHTIIMGDFNTRLSTLDRSTRQRLNKDIQELNSALH QVDLIDIYRILHTKSTEYTFSSAPHITYSKIDHTVGSKALLSKGK RTEITNRLSDHSAIKLELRJIKELTQNRSTTWKLNLLNDYWNL WDTFKAVCRGKFIALNIQKRKQERSKIDTLTSQFKELEKQEQT HSKASRRQEITKIRAEKERETQKSLQKISESRSWFFEKINNIDTP LARLIKKKREKNQIDTIKNDKG DITTDPTETIQTTRQYYKHLIYANKQENLEEMNKFLDTYTLPRLN WEEAESLNRPTGSEFAIINSLPIKKSPPDGFTAKFYQSYKEEL VPFLKLKFQSIKEGILPNSFYEASIILIPKPGRDITTKDNFRPISL MNIDAKILNKILANKIQHSHKLLIHHNQVGFIPGMQGWFTNCKS INIHQHINRTKDKNHMISIDAEEKAFDKIQQPSC
6843	37211	A	6893	1	1797	

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6844	37212	A	6894	2	1880	APNTGAPRFIKQVLSLQRLD SHTIIMGDFNTPLSTLDRSMRQ KVNKDIQELNSALHQADLIDY RTLHPKSTEYTFSSATHHTYSKI DHIVGSKALLSKCKRTEITNCL SDHSAIKLELRJIKLTENRSTTW KLNLLNDYVWHNEMKAEIK MVFETNDTLPLRI.NQEEVESLNR PKTGSEIEAIINSLPTKKSPGPDG FTAEFYQRYKEELVPFLLKLFQ SIEKERILPNSFYEASILIPKPGR DTTKK/EENFRPISLMNIDAKIL NKILANRIQQHIKKLIHIDQLGF IPGMQGWFNICKSMNVQHINS PKDKNHMISVD AEAFDKIQQ PFMLKTLNKLIGDGYLKIRAI YDKPTASIIILNGQKLEAFTLKTG TRQGCPSPLLFNIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMI VYLENPIISAQNLLKLIGN FSKVSQYNTINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDFPKENYKPLLNE IKEDKNKWKNI PCSWVGRINIV KMAIPPKVIYRFNAIPKLPMTF FGMIFLSQKYGHVTLFRLLQW LLNVARNNKVFYKIYKVGHK LSSAYVCLCTCSHFSVSFL
6845	37213	B	6895	13	1506	
6846	37214	A	6896	1	6635	MTPESRDTTDLSPGGTQEMEGI VIVKVEEEDHDFQKERNKVE SSPQVLSRSTTMNERALLSSYL VAYRVAKKMAHTAAEKIILP ACMDMVRTIFDDKSADKLRTIP LSDNTISRRICTIAKHLEAMLIT RLQSGIDFAIQLDESTDIASCP LVYVRYIPLKRLGLI.QPEKPI VLKVESRDGTQYNSQQHINLS AAWLKTA VQGREAPGKQPSKQ QHSARKRTHRTQLKKESGDGP HPKFGGNNLASP
6847	37215	B	6897	1	3045	

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6848	37216	A	6898	1	2764	MARELHDKCTSFSSRFQLEES LSAMEDQMNMEMMRREEKFKREK RRKRNEQSLQEIWWDYVVRPNL HLIGVPESDRENGPKLENTLQDI IQENFPNLRQGNIQEIQRMP QRYSSRRATPRHIIVRFTKVEM KEKMLRAAREKEIQTTIREYYK HFYANELENLEEMDKFFETYTL PRLNQEEVESLNRPIITGSAIEAII NSLPTKKSPGPDGFTAEFYQRY KEELVPFLLKLQFSIEKEGILPNS FHEASILIP
6849	37217	B	6899	1	3549	
6850	37218	A	6900	387	541	
6851	37219	A	6901	1	545	
6852	37220	A	6902	71	370	RRCKVRPSARGVLRVAVCVCV CVCVYPCVHVCTCVRMCLCVC VCVC/CSVEIHCGGQGCARCIC LQPQEGGCTEQAAVALHCAAQL WRNRLKLMKQPVARV
6853	37221	A	6904	1	738	
6854	37222	A	6905	1	567	
6855	37223	A	6906	1	1416	
6856	37224	A	6907	3	1267	
6857	37225	A	6908	1	552	NALPGRKSRVFGVCSADTWK PPSSAKVTETKGASPAFLRAGQ PRLVPGETLEKSLGPKDPQVE PQHVPVHLPGISSEGFWDGFNE QTPKDLPNRDGGAWVLGYRA GPACPFLLHEEREKSNRSELYL DLHPDHSLTEQDDRTPGRIQA VWPPPKTKDTEEKVGLKYTEA EYQAAILHLKRE
6858	37226	A	6909	1	561	
6859	37227	A	6910	219	1343	RRLCHTQPTLGMRESELVNV CVHSVFSPLSPVQAMQEKDEAK AETIQALYHQTFLEALQTLKAL FIEDPTPAGLKSILEALGPWMNS GKAHERARAVNTNVSVLNMH LLTLFFMPLGFPALGLLRLI LHIGDPDEIGCEALDGIHILYTI LELQKRARDKEETNKKELYES NKHFLGYPYVSPCQNILRVIEE FGDFLGPQIKDLLLALEGLK GSSEAPGKDSREMMQLASEVM LSSVLEWYRHRALEVIPEIMQGI YMQLSHIQEPRAQVALLPVSL LASSFMTEVVALLMCPLPLNR QPAACASSCPSTAAWAV*GAST LSCSWPCFSRSTITTSASTCLAAW LLPRTPRRRVHSPSYLCAGW

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6860	37228	A	6911	3	730	
6861	37229	A	6912	2	1218	ERKCMQGGKYAGAMESEPCVCT EADFDCCDYG YERHSNGQCLPA FWFNPSLSKDCSLGQSYLNST GYRKVVSNNTDGVRE:QYTAK PQKCPGKAPRGLR/VVTDAGKL TAIEQGHNVLTLMVQLEFGDVQ RTLQVDFGDIASVYVNLSSM EDGIKHVYQNVGIFRVTVQALV RLPPHISQCDVFRFFEAPEDV NPPKDQALLGELGPAVELCLK EERFADAILAQAGGTDLLKQT QERYLAKKTKISSLLACVYVQK NWKDVVCTCSLKNWREALAL LLTYSGTEKFPELCDMLGTRME QEGSRALTSEARLCYVCSGSVE RLVECWAKCHQALSPMALQD MHVISTDENQVFAAVQEWQON DTYNLYISDTRGVYFTLALENV QSSRGPEGNIMIDLYEVTI
6862	37230	A	6913	1	1659	
6863	37231	A	6914	540	824	KPRLENYVKNAEASGADAINW KKGY/LVMEDEMNMKREGKF REKRIKRNEQSLQEIWDYVKDQ IYVRLVYLKVTGRMEPSWKT CRILSRRTSPI
6864	37232	A	6915	1	939	
6865	37233	A	6916	285	458	QVFSQLEGRIALGKFORPSSLPT GKWTQRCSWGAQWE*D*LFG LHGWWVRPIAGFP
6866	37234	A	6917	32	171	
6867	37235	A	6918	294	461	
6868	37236	A	6919	2	255	LIPCPATVNNVSDIMGMYMKE CSASLITREMQRITTMRHHLTS IGTEMIRK/SKNNECWSGRECQ TVGAGQCVRAPCASRSARH
6869	37237	A	6920	2	393	
6870	37238	B	6921	87	633	
6871	37239	A	6922	78	260	TQYLRWKCRNHLRLRRSCWEL *TRAVPIRPSWLQNR YOGTSRF CVCFEESGTPSTQLEI
6872	37240	A	6923	1	369	FVLHEKCLGPFITGNTNDEM VKKICAPT*TKHVW*LES*M WEEPRWPNGKAPVYSSQREQR RRRVISAFPPSEGVLPSTFKNKKF TVKQPQVGRSVGIPEGIVIGD GQLQGCLLPLKTF
6873	37241	A	6924	3	201	LKEMQINTTMRYS*TPSRTS* IKKTDNNKFWMRMTEKLETSY CWWECEMTQPRWKVSLQYLL PLI

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6874	37242	A	6925	1	2064	
6875	37243	A	6926	95	752	
6876	37244	A	6927	2237	5072	RAKSPANIHMTGNSNHSITLTNLVNLGNSPIKRRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDKPTKIKRDKEGHYMMV KGSIQQEELTLNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFSSAPHHYSKIDHILGSEA LLSKCKRTEITNYLSDHSAIKL ELRIKNLTSQR
6877	37245	A	6928	3	331	
6878	37246	A	6929	364	853	
6879	37247	A	6930	2	531	RPRVRELVGSAIQALKEWNTT GKLRINH*KRCGSTQHHGSKYA TDKEERPDACPLQPPQIQNG PMNGCEKDSSTDSANEKPALI PREKKISILEEPSKALRGVTPGNI EKSADLQRCVTSLTRYRVMIK EEDVSSVKKITAFAELHNCIID KEASLMAEMGTVNEQAMRC
6880	37248	A	6931	1	456	ISILEEPSKALRGVTEGNRLQ OKLSLDGNPKPIHGTTERSDGL QWSAEQPCNPSPKPAKTSPVKS NTPAAHLEIKPDELAKKRGPN EKSVDLQRCVTSLTRYRVMIK GEVDSSVKNKAACAEFPICIID KEVSLMAEMDKVKGRKPW
6881	37249	A	6932	333	964	
6882	37250	A	6933	240	691	
6883	37251	A	6934	1	2076	
6884	37252	A	6935	14	485	RRSLESVLSRKLNP*KATGTSR SESAVVAIIDA VSSPQKRLDSE FIDPLMNKKARISHLNRPVPTL NGHNLNPTSEKSAAGLPLPAAA AIPTPPPLPSTYLPISHPPQIADS HSPAAPVQGIQPFLLTADQYWLE NRYPSQHLSRVTSARARHQT
6885	37253	A	6936	1	643	
6886	37254	B	6937	1	408	
6887	37255	A	6938	2	197	
6888	37256	A	6939	103	298	CLWLFQEEEEEEEEEEEE*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEKI FLGHRVGI
6889	37257	A	6940	117	257	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6890	37258	A	6941	46	219	LKECNCIVCNSKNKCLKG*KKK EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEGRRRGRRRR RRRRRRKKK
6891	37259	A	6942	1	1314	MVSRISWISWIAQCPLCRPSGT YGPGEAALLWLCIEAAAAA AARSTTPIITNHQSNITAEQNP PRIHENGDPKTYIIHVLAEQVLE RLPHGVALRHDPLAPVVSRA GVGHQRCAADDALQPLLQGRP EPGLAERHGVQDNLILKVSHTH TQKSAEKRAVSDPSSTVHRPQP LPPSTVHQSTIPSNPDSSAYCL PSTRHGFSSYTDSFVPPSPSPNP MNPTIGNGLSPQRVHYQHLPTH AGGKRNAALEYGVPRKYHYM LKITASDYKTKPFQVGDVVM GSGWRKVGMMQT*FL*LKKEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEENSLSTE
6892	37260	A	6943	1	160	
6893	37261	A	6944	1	306	
6894	37262	A	6945	1	933	MWLARELEESLAVSLQGEPGL LAGAGRLQGSFSPHMEPGRQS ETLSQKKKKKKKKKKKKKK EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE DQLDTMFGTHQQTSPQRSAR RRPCSVOGPRS*SPFSHPMEPGR QSETLSQKKKKKKKKKKKK EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEDQLDTMLWDSSTNLNTAL SKEKTMFSSRAKIVKPNGEKPD EFESGISQALLEMLNLDLKAQ LWELNITAAKEIVGGGRKAIH FVPVPLKSFQKTQVQLRRILP KPTQKSCNTNNKQKLPRSCITLTA VHDAILEDLVFPSEIVGKRIHV LDGSHLIKIHLEAQQNNVEHK VEPFSGVYKMLMGKDVNFEP
6895	37263	A	6946	1	1365	
6896	37264	A	6947	416	610	EFKKPVLEGG*RGEGGSPCV WSFFDPVHFNYQAGLFRVALP GEQCRTGRLVARVYTGISGASF
6897	37265	A	6948	1	846	

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6898	37266	A	6949	3	620	HVTLLIVVTQSHLVIHNLFEGLMI WFIWPISCVICNDIMAYMFGFFF GRTPILKLSKKKTWEGFIGGFFA TVGFGLLLSYVMSGYRCVFCP VEYNNDTNSFTVDCEPSDLFRL QEYNIPGVQSAUGWKTVMY PFQIHSA/LSTFASLIGPFGGFF ASGFKRAFKIKDFANTIPGHGGI MDRFDCQYLMATFVNVYIACV LRPL
6899	37267	A	6950	50	554	
6900	37268	B	6951	446	625	
6901	37269	A	6952	1	2149	
6902	37270	A	6953	1	1704	
6903	37271	A	6954	1	1853	
6904	37272	A	6955	1	1305	MVKGSIQEEILTILNIYALNTGA PRFIKQVLRDLQRDLDSHTIIMG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADIIDIYRTLHPKST EYTFFSAPHHTYSKIDHIVGSKA LLSKCQRIEITNCLSDYSAIKLE LRIQKLTQNCSTIWKLNNLLN DYVWHKEMKAEIKMFFETNEN KDTTYHHLWDTFKA VCRGKFI ALNAHKRKQERFEMDTLTSQ KELKKQEQTTHSKASRRQEITKI RAERKEIETQKTLQKINESGSW FVEKINKIDRPLARLIKKKREKN QIDAINKDKGVITTDPTIEQTIRE EYKHLIYANKLENLEEMDKFL DTYNLRLNQGEVESLNRPIGT SEIEAIINSLP/TKKS PGPNGFTA KF*QEELTILNIYALNTGAPRFI KQVLRDLQRDLDSHTIIMGDFN TPLSTSDRSTRQKVNKDIQELN SALHQADIIDIYRTLHPKSTEY FFSAPHHTYSKIDHIVGSKALLS KCQRIEITNCLSDYSAIKLELRI QKLTQNCSTIWKLNNLLNDY WVHKEMKAEIKMFFETNENKD TTYHHLWDTFKA VCRGKFIAL NAHKRKQERFEMDTLTSQLE LKKQEQTTHSKASRRQEITKIRA ERKEIETQKTLQKINESGSWFV EKINKIDRPLARLIKKKREKNQI DAINKDKGVITTDPTIEQTIRE YYKHLIYANKLENLEEMDKFLD
6905	37273	A	6956	1	1926	

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6906	37274	A	6957	2	1025	WRRYQANGK*KNK/QKKAGV VILVSDKTDKPTKIKRDKEGH YIMVKGSIQEEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLNIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRKIKLTQNSSTTWK LNNLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCCKA VCREKFIALNAHKKQERSKID TLTSQLE/LEKQEQTHSKASRR NLEEMDKYLDYTYLPRLNQEE FESLNRPTGSEIEAIINSLPTKKS SGPDGFTAKFYQ
6907	37275	A	6958	1	1661	
6908	37276	A	6959	2	1632	WRKIYQANGK/HKKAGVAIRV SDKTDKPTKIKRDKEGHYLM VKGSIQEEELTVLNIYATNTGAP GFIKQVLSLQRLDSHTIIMED FNTPLSTLDSMRQKVNDQTQE LNSALHQEDLIDIRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRKLNLTQSRSTTWKLNLLN DYWVHKEMKADIKMFFETNES KDTTYQNLWDAPFAEELES LN RPITASEIVAIINSLPSKSPGPD GFTAKFYQRYKEELVPFLKLF QSIEKEGILPNSFDEASIIIPKLG RDTTKENFRPISLNMIDAKILN KILANQIQQHKKLIHHDQVGFI PGMQGWFNIHKSINVQHINRT KDKNHMIIISIDAEKAFDKIQSF MLKTRNKLGDGTLYLKIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRQ EKEIKGIQLGKEDVKLSLFADD MIVYLENPIVSAPNPLKLSNFS KVSQYKINVQKSQAFLYTNRR
6909	37277	A	6960	1	2169	

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6910	37278	A	6961	2	1255	EGKFRNRIKRNEQSLQEIWDY VKRTNLRLLIGVPESDWENGTKL ENTLQDIIQENFPNLR*AKIQRI RSQDPSTHLTSRDTHRLKIKGW RKIYQANGKQKKA AVTILVSD KTNFKPTKIKRDNEGHYIMVKG SNQQEELTILNIYAPNTGAPRFI KQVLRLDQRDLDSHTITGDINI PLSTLDRSTKQKVNKDTQELNS ALHQVDLIDYRTLHPKSIEYTF FSAPHHTYSKVDHILGSKALLS KCEIEIITNCLSDHSAIKLELRI KNLTQNHSTWKLNNLFLNDY WVHNEMKAEIKMFFETSENKD TTYQNLWDAFKAVCRGKFIAL NAHKRKQERSKIYTLTSQLKEL EKQEQTSHSKASRRQEIIRAEI KEIETQKTLQKLNESISHQLEW QSLKSQKTTGAGEDVEK
6911	37279	A	6962	1	1122	
6912	37280	A	6963	551	1536	EILSPPLPYKSS*KKH*TWKGT TGTSCC/INHAKIVTHRLKIKGW RKIYQANGKQKAGVANLVSD KTDFKPTKIKRDKEGHYIMVKG SIQQEELTTLNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLLTLDSTRQKVNKDTQELN SALHQADLIDYRTLHPKSTEYTF FFSAPHHIYSKTDHILGSKALLS KCKRTEIITNCLSDHSAIKLELRI KNLTKNRSTTWKLNNLFLNDY WVHNEMKAEIKMFFETNENK DTTYQNLWDTFKAMCRGKFIA VNAHKRKQERSKIDTLTSQLKE LEKQEQTSHSKASRRQEITKI
6913	37281	B	6964	28	1209	
6914	37282	A	6965	1	1284	
6915	37283	B	6966	1	1056	
6916	37284	B	6967	124	963	
6917	37285	A	6968	3	1162	
6918	37286	A	6969	1	1364	
6919	37287	A	6970	1	1003	
6920	37288	B	6971	1	1129	

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6921	37289	A	6972	1	1917	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIHTNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDDTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDLTSL KELEKQEQTTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLRLARLIKKKREKNQI DAIKNDKGDITTDPEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPTGAE IVAIHNSLPTKSPGPDGFTAKF YQRYKEELVPFLKLFQSIEKE GILPNSFYEASIIIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISDAEKAFDKIQPFMLK TLNKLGIKYLGIHLTRDVKDLF KENYKPLLKEIKEDTNKWNIP CSWVGRINIVKMAILPKMCL*R RWTPLCLLTAAASLNRE*ERLV QPLLWRQMYCGPRHCRQVPQH RRLNWSPSLRLS
6922	37290	A	6973	1	2673	

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6923	37291	A	6974	261	2667	TWCSGRYMVGCR/DWHLLLV/ KGLRKLTIVAEGEGGAGMSLG ESGNKKRKDEKGYIMVNGSIQ QEELTILNIYAPNTGAPRIKQV LRDLQRDLDSHTIIMRDFNTPLS ALERSTREKVNKDIQELNSALH QADLVDIYRTLHPKSTEYTFFS APHRTYSNIDHIVGSKALLSNC KRTEHTKCLSDHSTIKLELRKK LTQNRSTTWKLNLLNDYWV HNEMKAEJMMFFETIENKDDTY QNLWDTFKAECRGKFIALNAH KRKQERSKIDTLTSQKLELEKQ EQTHSKASRRQEITKIRAELEKET ETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNLIDAIGN DKGDITDPTEIQTIREYYKHL YANKLENLEEMDKFLDITYTLP RLNQEEVESLNRPTGSEIVAIIN SLPTKKSPPDGFTAIFYQRHT VSILISYCQGGSLMSQVYWNQQ EKPPSSSNAPPGLSVNKAQHRH VCCRGEMLKRQVYHYVRAGES DSASFHCVAQGPRAFGKPLILS KENHLLTVTAIAKLNHKLCEIK SMGVFINTEPLYDSCLEQKHAL FASPPATTHTTMISKAKVIPML SLTPGSFQTVESLAPSAGKFQG TETSSLKTLINLCCPKLPSPSPA HLGGLPGGSQERPSRQYLYESA RTTVLLGLGCPLKQIQLRSQHS SPLEYLESPLKKDRKKREKIQIN

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6924	37292	A	6975	1	1687	MLKGSIQQEELTVLNIYAPNTG APRCIKQVLSDVQRDLDSNTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLDIYRTLH PKSTEYTTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNSLSDHS AIKLELRKLNLTQNRSTTWKLN NLLNDYWVHNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQKLEKEKQEQTHSKEIQTIR EYYKHLTYTNKLENLEEMDKFL DYTYLPRLNQEEVESLNRPIIGS EIVAIHNSLPTKKSPGPDGTAEF YQRYKEEMHINRAKDKNHMIS IDA EKAFDKIQPFMLKTLNKL GIDGTYFKIIRAIYDKPTVNILN GQKLEAFPLKTGTRQGCP LSPL LFNIVLEV LARAI RQEKEIKGIQ LGKEEVKLSL FADDMIVYVEN PLPSQPQNLL*GWLSNFSK/MSS GYKIN VQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQFTR DVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILP
6925	37293	B	6976	1	2431	

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6926	37294	A	6977	1	1921	MGESVQSLTLAQRKSMMIQV AVAPRTPTLKKLYKEKASKTQ LKKVNLVVQDQGSLESIEVHD HEPADTYKLLSLVKEPAEEIPR VIQNVFGHRSKKENLKDSYGLR QSSTMVATTWNNVSLMQHHSL RRPNRHILTASYPHFHQEI PVNF FHSGRDSESGWNVQHIKKDKE GHHIMVKGSIQEEELTMLNIYA PNTGAPRFINQVLSIERDLDSH KIIMGDFNTPLSLDRSTRQKV NKDTQELNSALHQADLTDIYRT LHPKSTEYTLFSAPHHTYSKIDH IVGSKALLSKWKRTETITNCLSD PRAIKLELRKKLTQNRSSIWKL NNVLLNDYWVHNEMKAEIKIF FETNENKDTSCQNLWDTFKAV CRGKFIALNAHRRKQERSKIDT LTSQLEKEKQERTHSKASRRQ EITKIRAEMKEIETQKVLQKINE SRSWFFKINKIDRPLARLIKKE REKNQIDAIKNNKGDIITDPTET ETTIREYYKHLTYNKENLEEM DKFLDITYTLPRLNQEEVESLNR PITGSEVVAIINSLPTKKSPGPDG FTAEFHQRYKEKLISELLPMPN HTALKKQTQDLSCKAMFLYY QSVSVQTAIINYHRLRGLNRRN LFLTIVLEYSSLRSGCEHSRVL

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6927	37295	A	6978	1	1848	MSLTKMLICAALLGLFCMLLGL RWQVAELIGMTLALSSTAIA QAMNERNLMVTQMGRSAFAV LLFQDIAIPLVAMIPLLATSSA STTMGAFAALSALKVAGALVLLV VLLGRYVTRPALRFVARSGLRE VFSAAVALFLVFGFGLLLEEVGL SMAMGAFLAGVLLASSEYRHA LESDIEPFKGLLGAVFTPRVVV NIYSSSELRTAKNYQANGKQKK PGVAILVSDKTAF/KPTEIKRDK EGHYIMVKGSIQQEELTILNIY APNTGAPRFIKVLSLQRLDLD SHTLMMGDFNTPLSTLD\IRSTR QKVNKDTQELNSALHQADLIDI YRILHPKSTEYTFPSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKNTQSRSTT WKLNNLLNDYWVHNEMKAE IKMFFETNENKDMTYQNLWDT FKAVCRGKFIALNAHKRQERS KIDTLTSQLEKEQEQT\HKA SRRQEITKIRAELEIETQKAIQ KINESRSWGPPGNCQQNYRNSE SGEKSAPEGQAQHAQPTGKVV PTFLYVGKEKFPPSYLLTRKSSH LPTCGDPICGEKCRWVPTTSQG GNKADQWGGVGIGDTHDSDA
6928	37296	A	6979	1	2235	
6929	37297	A	6980	1	2955	

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6930	37298	A	6981	3	2156	KSLKDLMEIKMAQELCDEWT SLSSRCNQLLEERSVMEDEMN EMKDKHRPKIKIEWRKIYQANG QKKTRVANLVSDKTEFKPTKI KRDKEGHYIMVKGSIQQEELTI VNIYAPNTGAPRFIKVLSDLQ RALDSHTIMGDFNTPLSTLDRS TROKVNKDIQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHYTY PKIDHIVGSKALLSKCKRTEIT NCLSDHSAIKLELKIKKLTQNL STTWKLNLLKDYVVKEM KAEIKMFFETNKNKDDITYQNF WDTFKA VCRGKFIALNAHKRK QEGFKIDTLTLQLEKEQEQT HSKASRRINKIDRPLARLIKRR EKNQIDTIKNDKGIDITDPTEIQ TTIREYYKLYANKLENLEEM DKFLDITYTLPRLNQEEVESLNR PITGAIEIVAIHNSLPTKKSPGPDG FTAKFYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASILIPKPR DITKKENFRPISLMNDAIELNKI LASQMQQHKKLIYHNQVGFH GMQGWFNHKSINVIQHINRTK DKNHTIISLDAEKA FDKIQQPF MLKCLKTLNKLIGIDGMYLKIIRA IYDKPTANILHWQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLR AVRKEKEIKRTQIGREEIKLSLF ADDMIVYLENPIVSAQNLLKLIS NFTKVSQGYKINVKKSQAFLYN
6931	37299	A	6982	3721	8717	MLPIKRHRLANWIKSQDP/SVC CIEETHLCRDAHRHKIKGWR KIYQANGKQNKTKQQKKQGLQ ILVSDKRD FKPTKIKRDKEGHYI MVKGPQQEELTILNIYAP/NTG APRFIKQVLSDLQRLDSHTLA MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAP/HHTYSKIDHIL GSKALLSKCKRTEITNYLS/DH SAVKLKLRIKNLTQNHSTTWK LNNL

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6932	37300	A	6983	599	1074	NPRAWKQPPPTSPQEFCLVCF VVHLQKSTREALNNKNIKPLLS TFSQVPG/SINHSSCENVLAHSL AIGGVTEGICTASTPFVLLGDVL DCLPLDQCDTIFTFVEKNVATW KSGTASLPAAFMAQVEHLWLF QVNGANCQWYTPSGVVRTVAL FSQLH
6933	37301	A	6984	1	312	QSRALLWPMLVDVIQPKPWKA PGSLGLPSCISAITVQSSPGLRLC SCGQGPVNTPGTKLPQPNRPV SLSFQMKLLTSSHWSFHCPA *INPAQSSPGWP*PQLSGCPAF QFLSFG*KSLSSGNTASSPLW FLCWCFNLVLQAKLPDGFSPA HRV
6934	37302	A	6985	2	484	
6935	37303	A	6986	234	405	ELKICSCDPITVRYNADDSTVSL SFSQMKLLTSSHWSFHCPA* INPAQSSPGWP
6936	37304	A	6987	1	2021	PTRPAAQWRARAAEKMSPTP PLFSLPEARTRFTKSTREALNNK NIKPLLTSTFSQVPGSENEKKCTL DQAFRGILEEEIINHSSCENVLAI NSLAMGEVTEGICTASTHVFLL GDVLDCLPLDQCDTIFTFVEKN VATWKSNTFYSAGKNYLLRMC NDLLRRLSKSQNTVFCGRJQLF LARLFPLSEKSGNLQSQFNLE NVTVNTNEQESTLQKHTED REEGMDVEEGMGDEEAPTTC SIPIDYNLYRKFWSLQDYFRNP VQCYEKISWKTFLKYSEEVLA VFKSYKLLDDTQASRKKMEELKT GGEHVYFAKFLTSEKLMDLQL SDSNFRRHILLQYLIFQYLGQ VKFKSSNYVLTDEQSLWIEDTT KSVYQLLENPPDGERFSKMVE HILNTEENWNSWKNEGCPSFV KERTSDTKPTRIRKRTAPEDFL GKGPTKILTNGEELTRLWNLC PDNMEACKSETREHMPMLEEFF EEAIEQADPENMAENYKAMN NSNYGWRALKLLARRSPHFFQP TNQFQKSLQEYLENMVIKLAKE LPPPSEIKTGEDEDEEDNDALL KENESPDVRRDKPVTGEQIEVF ANKLGEQWKILAPYLEMKDSEI RQIECDSEDMKMRKQLLVAV QDQEGVHATPENLINALNKSGL SDLAESLTNDNETNS

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6937	37305	A	6988	155	811	EFYRTGKVHRA PGVQEVETDP RDPLAQLATDRKERRGSLDH LALRVREAQLDQLVPPEVAA KDLKAPRAKPAVVPPLGSPALR APVGTQAPRAHQAKRDSPALR ALLASRDFRAPLGLGCLDLGD CQACLG YQACQAPRAPALLA HQRWCPWPCRMSQPQHRRT MAARLTGRTSQTNA TIFQLRKK FLRMQSF SVKTS LHILFS*TLER NSNG
6938	37306	A	6989	91	918	
6939	37307	A	6990	199	380	CSTSSRTY*IPSRCSKG*HWRH TVNSNFGPMGNPSHPTSSAHH TVPLIESQPSSTSKK
6940	37308	A	6991	1	483	
6941	37309	A	6992	178	298	
6942	37310	A	6993	864	1298	RLQNRITLASDLSGSDRWRTY RCL*RHGPRFSSCRLSCRPFDK TCRLMCHQRLSGFPQEQTRDS RCIQLLFRQRFAAASCPTHQVH VHRWRKPMVFLILESDLKYTV LSLPEECHTGAHEQSSHCLLLSL ASVDVHCSQRP
6943	37311	A	6995	2	348	KKKRKKKIEEEEEEEEEEE\
						REEEGDEEQEEEEEEEEEE
						EEEEEEEEEDDDDNGLLQTL
						PGLHEMRVNLTRSDGIISVWHF
						PFWHFSFLMPYEEGALLRLHLP
6944	37312	A	6996	1	192	
6945	37313	A	6997	1	507	MEKNEKEQEEEEKEKNSKKK EEEEEEEGGEEEEEEEGEGEE EEEEEEEEEEEEEEEEEEEEEE EEE/DKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEK VVE EEDEFIWLGNLSYFPSHFHA WSQPSREDEGERRLRVNSMIM DFTSNTNHVQLIVAR
6946	37314	A	6998	1	257	MGPiHKISHYVYANISKSEKVL KSEHFRSQAFQPGQSQSETVSEK/ FREDEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEI
6947	37315	A	6999	1	156	
6948	37316	B	7000	1	757	
6949	37317	A	7001	1	279	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in U.S.S.N. 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6950	37318	A	7002	1	1226	MPSSKGVVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGDSDNFPELVLFEEFFALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYITLNQDAQNKSP SAVMSHESDAAHSDSARSSSSK LELSPDVNKRKSEAMVKEKKK ADKKGEKSARSPPSSLSNDLDFS KQDGNTTTQEMSPAGVPLLGM QLNEVKPKKDRQNVQQNE/GC HPIRRVHSDQTHSGKL*RGKGS W/DCMREKASQPFKAVVPIV*V /VPFENLQEGEEGRLECECPDEP RRVHVAGRSMYEGEVVNGMR NGFGMFKCSTQPVSYIGHWCN GKRHGKVGEVATWRAEKKKK EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKIRP
6951	37319	A	7003	3	123	
6952	37320	A	7004	2	458	
6953	37321	A	7005	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEE EEEEEEEEKIFLGHVRVGI
6954	37322	C	7006	7	162	
6955	37323	A	7007	39	2154	
6956	37324	A	7008	1	639	
6957	37325	A	7009	1	651	
6958	37326	B	7010	1	684	
6959	37327	A	7011	3	428	TRFQGVYLLWEQSF/CWKSPI ALGYTRGHFSALVAMENDGYG NRGAGANLNTDDDVTTITFLPV DSERKLLHVHFLSAQELGNEEQ QEKLLEWLDCCVTEGGVLVA MQKSSRRRNHPLVTQMVEKV LDYRQIRPCTSLF
6960	37328	A	7012	2	800	

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6961	37329	A	7013	1	930	DHNSSPAMEQNWMENAFDEL T EVGFRRWVITNFSKLEHVL TQ CKEAKKLEKRLLEELLTRITS LEK NINDLMELKNTSQELREAYT TE ERISEIEDQLNEIKHEDRI REK/R/ VKRNEQSLQEIWVYVKRPNLH LT/GVPESDGENGT KLENTLQDI IQENFPNLARQANI QIEIQRTP QRYSSRRATPRHIIIR FTKVEMK EKMLRAAREKGQVTHK GKPIR LTADPLAETLQARRE WGPINIL KEKNFQHRMSYP AKLSFISVGE IKYFTDKQMLRDFV TTRPALQE LLKDALNMERN NQNSQLQKHA KL
6962	37330	A	7014	1	870	
6963	37331	A	7015	1	585	
6964	37332	A	7016	1	1032	
6965	37333	A	7017	2	770	
6966	37334	A	7018	1	2910	
6967	37335	B	7019	239	462	
6968	37336	A	7020	3	694	
6969	37337	A	7021	1	1212	
6970	37338	A	7022	1	1140	
6971	37339	A	7023	1	570	
6972	37340	A	7024	1	486	
6973	37341	A	7025	1	1476	MEVNREKQNLNELE VIGSEEQNL EEEGLMIGGVA VRLVPDDIVIP GGVNATNGTEAR DALRVKVA MSVTLLSGIIQYLL SALGWSYY TVDGVSQKNPRAL GVTA DQLH AIFTMSDEQASFR FGFVAIYLT EPLVRGFTTAAAV HVFTSMLK YLFQVTKRYS GIFSVVYSTVA VLQNVKNLNVCSL GVGLMVFG LLLGKKEFNERF KEKLPAPIPLE FFADHNSSPAREQ KWMENED EWTEVSFRRWVIT NNSSELKEHI LTQCKEAKNLEK RLEELLTRITS LEKNINDLMELK NTAQEFHEA YTSINS/RNQTE ERVSEIEDQLN EI*CKDKIR/EK KRMKRNEQSLQ EIWDVCVKRPNL RLTGVPESDGE NGTKLENTLQDI IQENFHNLAR QANSQIEIQRTP QRYSSRRATP RHIIIRFTKVEM KEKMLRAARE KGRVTHKGNP IRLIADLSADTL QARRQWEPIFNIL KENFQTRISH
6974	37342	A	7026	1	1080	

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6975	37343	A	7027	1	3501	MIVYLENPIVSAQNLLKLISNFS KVSQYKIKYKIDVQKSQAFLYTN NRQTESQIMSELPFTIASKRKY PGIQLTRNVKDLFKENYKPLL EIKEDTNKWKNIPCSWIGRINIV KMAILPKVIYRFNAIPKLPMTS FTELEKTTLKFIWNQKGARIK TILSKKNKVGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEASEITPPYNNHLIFDKPDKN KKWGKDSLNFKNWCWENWLAI CRKLLDPFLTS
6976	37344	A	7028	164	714	IGVNRHLIQESPSWNLGAPLE QIFQRKEQAIFAILQPLLVISRQ TSGVDPPQQTADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTIINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
6977	37345	B	7029	1	579	
6978	37346	A	7030	1	927	
6979	37347	A	7031	1	1362	MAAGRHLPGVADRHLIQUESTG WHLAGAPLGWSFORKEQTAIF AVLQPLLVIPTQGYGVDLQ MPADLQQRFLTVRRKTNKQKG IVSTSTKRTSSEGHQHRKVD KFTEMGRNQHKKAENSKQN ASSP'PKDHNSLPAREQNWTE EFDELTEIDFRWVITNSSQTKG SMF*P'CKEAKNLEKRLDELLT RITSLEKNINDPMEKNTAREL REANKSINS*IDQGRKERVISEIE DQLNEIKREDKIREKRMQRNK QTLQEIWDYVVRPNLHLIGVPE SDRENGTKLENTLQDIIQENFP NLARQANIQIEIQRTPQRYSSR RATPRHIIVRFTK VEMKEKMLR AARKKGQVTHKGKSIRLSADFS AETLQARREWGPPIFNILKEKNF QPKISYPAKLSFISEEITSFTDK QTLRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKM
6980	37348	A	7032	1	598	
6981	37349	A	7033	3	787	
6982	37350	A	7034	61	284	RLEPQGPLRAGSSPAGK/IGGT LERRGMPWPGP/HSEGGLSPLL LGASLAAAPHGEMPSVRVHPV RPSSRDCSSRV
6983	37351	B	7035	743	1683	

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6984	37352	A	7036	1	1137	
6985	37353	A	7037	1	663	
6986	37354	A	7038	1	197	
6987	37355	A	7039	1	291	
6988	37356	A	7040	3	342	
6989	37357	A	7041	1	439	
6990	37358	A	7042	3	253	
6991	37359	C	7043	1	210	
6992	37360	A	7044	1	165	
6993	37361	A	7045	1	346	
6994	37362	A	7046	1	389	
6995	37363	C	7047	1	464	
6996	37364	A	7048	1	1806	
6997	37365	A	7049	491	1640	
6998	37366	A	7051	188	383	
6999	37367	A	7052	1	759	
7000	37368	A	7053	1	1683	
7001	37369	A	7054	1	972	
7002	37370	A	7055	1	429	
7003	37371	A	7056	3	753	DQTFWGLLETG/S/ELMLIPGDP KCHCGPPVKVGAYGGQEIKGV LAQVQITVGPVGTRTHPVPVIS VPCEIIGIDILSSWQNPHTGSLTG RVRVIMVEKAKWKPLELPLPR KIVNQKQYCIPGGIAEISATIKD LKDTGVMIPTTSPFNSPIWPVQ KTDGWSRITVDYQVVTPIAAA VPDVVSLLEQINTSPGTWQHIT HLDVLLWRIYQVTQKAASFWE GPEQEALQVQAAVQA\CH LGHMTQQIQWCL
7004	37372	A	7057	2	430	
7005	37373	A	7058	1	1515	

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7006	37374	A	7059	1	1523	MGEERRWRPSSNGKHGAFAEL DKGWL V WLEGGVIGARRSW RAHSALIKICVQQIKDSLPGKM SKGLLQQQKPKHLLHDLYKA MSTRWGVQKARL NCTALPPTG CVTLDPFSLTEPQFPRQLSEDL LTREALEKEVQLRRQIQEKEE LLYRVLGANASPAFPLAPVTPT EVEKERELERDLDEQQRVLE GKNEEALQDPRLVDPLTSTCTVH FEKPQMLNARLWKHAGREAV ACKVRGSELPKTMGTYP LHQH DLDRHGVKGDHFGALRFDCP AGFWTCMGLAPSFWPISPIWN GPPLDISGYPATSTQKSTMCLRI IDTRLHPESRLKQSNFALNAR EKALQQVQAAVQAALPLGPYD PADPMVLEVSLADRDVWVSL WQAPIGESQQRPLGFWGKALPS SADNNSPLERQLLARYWALVE TEYLTMGHQVTM*P/ELPIMNW VLSDPSSHKVYVAWQHSIKW KIDRA*AGLAGTSKLEHEVAQ MPIVSTPATLPSCRIL
7007	37375	A	7060	1	2190	
7008	37376	A	7061	286	430	
7009	37377	A	7062	205	514	LWSLCAVPLQVPCLRAPFVFT RRHAPSAGRGFTRSYVSAGSW TETQQGLWGLTKLGADGLLL GISKHLVEFLQIFQISGCWGHYC YLQILFFALNSISPSYHVLLFN VQFGFIFFMVLCP*AGTHIAPC KSSSRTRGMSSCENWKGCSKA RHLQYVSTKTPQSLSFCCGIH FVTAVCQP
7010	37378	A	7063	1	487	
7011	37379	A	7064	1	1212	
7012	37380	A	7066	140	453	
7013	37381	A	7067	1	3341	MGGKQNRKTGNSKNQSA PPP KERSSSPATEQSWMENDFDEL EEGFRLSNYSELPEDIQTGKGE VENFEKNLEECITRITNKRNFKP TKIKRDKEGHYIMVKGSIQQUE LTILNIYAPTGA PRFIKQVLSDR QRDLDFHTLIMGD FNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHKSSTEYRFFSA PH HTYSKIDHLLGSAFLSKCKRT EHTNYSLSHSAIKLELRINKLTQ NRSTTWKLNN
7014	37382	B	7068	1	1785	

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7015	37383	A	7069	I	1141	MVTWNFIQERNRSGMDQCDD GGGKILDPVYILTVELTGFAKG WKMFVSVDQSVNVLGFAGYPL ITQTARKGAGKIPTWASLRQYQ KGLGSKYQLRRALRPDCALGN GQGVRYCNSLDEEEKRELKLF SQRKRENLGRGNVRPFVPTMT GAICEQCGQINGGDIASFASR AGHGVCVHPPCFVCTVCNELL VDLIYFYQDGKIYCGRHHAECL KPRCAACDEIIFADECTEAEGR HWHMKHFCFECETVLGGQRY IMKEGRPYCCHCFESLYAEYCD TCAQHIGHAGSFIKEC/SRLLP GEAEI/SRRATVCLVRVSVRPE AASKSPNMRRKRKRKGACPLS SVGPVIPSVP*NTQRT*RPQSRP LGAPWNPWPCLMQ
7016	37384	A	7070	I	2388	VHQYYSCLPPEKVPYVNSPGEK LRIKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSSQRKRENLG RGNVRPFVPTMTGAICEQCGG QINGGDIASFASRAGHGVCVH PPCFVCTVCNELLVDLIYFYQD GKIYCGRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECETVLGGQRYIMKEGRPYC CHCFESLYAEYCDTCAQHIGID QQQMTYDQGHWHATETCFCC AHCKKSLGRPFPLPKQQQIFCS RACSAEDPNGSDSSDAFQNA VGRSPGAVPKLARTRARRGAH AEPAQPAASEF*PAVSRRRPPVT ADGHAQPVQPDTPQPGPHILE EPGRALPLWEQDGAEPDPEPSA APARQCNIRTSYSPGGQGAQAQ PEMWGKHFSNPKRSSSLAMTG HAGSFIKECREDYYPGRLLRSQ SYSDMSSQSFSSTRGSIQVPKY EEEEEEGLSTQQCRTRHPISSL KYTEDMTPTQTPRGSMSLAL SNATGLSADGGAKRQEHLSRFS MPDLKSDSGMNVSEKLSNMG LNSSMQFRSAESVRSLLSAQQY QEMEGNLHLQSLNPIGYRDLQSH GRMHQSFDFFDGGMAGSKLPQG EGVRIQPMSETRRRRATSRDDN RRFRPHRSRRRSRSDNALHL ASEREAISRLKDRPPLRAREDY DQFMRQRSFQESMGHGSRRDL
7017	37385	A	7071	I	807	

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7018	37386	A	7072	500	2666	YCLRLAQVGIFAPSRRAWVPDL DPESRLCCFPSSLGSLANPTAVG LEEDREQDVGTSSRGGAWDTRI KRELEKMSSEKCGGQINGGDIIV FASRAGHGVWCWHPFCVCTVC NELLVDLIYFYQDGKIYCGRRH AECLKPRCAACDEIIFADECTEA EGRHWHMKHFCCECTVLLGG QRYIMKEGRPYCCHCFESLYAE YCDTCAQHIGEAIFGSQLGPSV MRSPLFWGVGIAAALDAVLIR AHQRTQGCHELSALLAFEKG SEKKEEEGGQVSRSSSLKVQA QELSATEDKGHSPPFWAVYH YASGECRGP GPYPYSHSLRLYSQ QALPTGRGPSSSQPFQCFYCC YKKSLLCDCLSKSPALEKAMR GIDQGMITYDGGHWHATETCF CCAHCCKSLLGRPFLPKQGQIF CSRACSGEDPNGSDSSDAFQ NAIGPRSPGAVPKLARTRARRIG AHAEPAQPAASEF*PAVSRRRP PVTADGHAQVPQDTPQPGP HLEEPGRALPLWEQDGAEPDPE PSAAP/RQCNIRTSYSPGGQGAG AQPEMWGKHFSNPKRSSSLAM TGHAAGSFIKECREDYYPGRRLS QESYSDMSSQSFSETRGSIQVPK YEEEEEEGGLSTQQCRTRHPIS SLKYTEDMTPTETPRGSMESL ALSNAITGKTCSVTFAQETCR YQDAQFGKVKARVKERQSLWS
7019	37387	A	7073	1	2239	
7020	37388	A	7074	1	282	
7021	37389	A	7075	2	430	GFGAQDPKSLALRTHCQTSGW/ SLTEQDPYNNVIRTIEAALATL GGTQSLHTNVFDEALGLPTDFS ARIARNTQIIIQEESELCRTVDPL AGSYGGAIQQIDVAGGLAKRI EAGLSKRMIEASAREQALIDQ GKRIVVGV

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7022	37390	A	7076	1	1561	MVTLILYFRFYRLNGDTLRRRIQI HLLDKYRKVPPEPVHADIPVGA RRFSRPSWFLRITKRGYRRTV HAMAGQKEKLLGAGMSDYLA KPIEEERLHNLLRYKPGSGISS RVVTPEVNEIVNPNATLDWQ LALRQAAGKTDLARDMLQML LDLPEVRNKVEEQLVGENPEG LVDLIHLHGSCGYSGVPRMK NLCQLIEQQLRSGTKEEDLEPEL LELDDEMDNVAREASKILGDPK THLRRIRRDVLATDPRPARDRR KACLHACVLRTPPLGAARAIQ QIDEAGGMAKAI EAGLPKRMIE EASAREQSLIDQGRVIVGVNK YKLDHEDETDVLEIDNVMVNRN EQIASLERIRATRDDAAVTAAL NALTHAAQHNNENLAAAVNA ARVRATLGEISDALEVAFDRYL VPSQCVTGVI AQSYHQSEKSAS EFDAIVAQTEQFLADNGRRPRI LIAKMGQDGHDRGAKVIASAY SDLGFDVDLSPMFSTPEEJARLA VENDVHVVGAISSLAAGRSR
7023	37391	A	7077	1	354	
7024	37392	A	7078	1	1116	
7025	37393	A	7079	1	450	
7026	37394	A	7080	1	252	
7027	37395	A	7081	1	242	
7028	37396	A	7082	1	242	
7029	37397	A	7083	1	9228	
7030	37398	A	7084	3	664	
7031	37399	A	7085	3	718	
7032	37400	A	7086	380	1038	WTRWRASAADNLAHGRWGEQ KLVTGTGASGAPDRQAARCAA SAKISWYRSKSGSKIHLTPKEVE KTGWGLKIP/MGQQQLPERV KEAARILELDGLKRRPRELSG GQRQRVAMARAIVRDPVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVEVDGDDTLEIL GADNLAHDAAGRAEAGGDWRI RSARRSSTCAH

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7033	37401	A	7087	380	920	WTRWRASAADNLAHGRWGEQ KLVVTTGASGAPDRQAARCGC IWRKISWYRSKSGKHPLTPKEV EKTGWGLKIPG/MGQQQLPERV KEAARILELDGLLKRPRRELSG GQRQRVAMARAIVRDPVAVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVE
7034	37402	A	7088	1	258	
7035	37403	A	7089	3	208	
7036	37404	A	7090	34	125	
7037	37405	A	7091	1	393	
7038	37406	A	7092	1	690	MVAPVYIRDQYSALITNIGKGD HTTFVKPNIPATGEFGVGFLE APRGMLSHWMVIKDGHSNYQ AVVPSTWNSGPRNFNDVGPY EQSLVGTVPVADPNKPLEVVRTI HSFDPDMAWVGNILLTDEAIGV RIVEALEQRYILPDYVEILDGGT AGMELLGDMANRDHLIADAIV SKKNAPGTMMLRDEEVPALFT NKISPHQLGLADVLSDLRFTIGE FPKLPWVQA
7039	37407	A	7093	82	224	
7040	37408	A	7094	1	239	
7041	37409	A	7095	1	1062	
7042	37410	A	7096	1	221	
7043	37411	A	7097	1	1067	
7044	37412	A	7098	1	1545	
7045	37413	A	7099	1	2820	
7046	37414	A	7100	1	1223	
7047	37415	A	7101	1	3087	
7048	37416	A	7102	1	1182	MDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKKSPGPD GFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEAHILIPKG RDITTKENFRPISLMNIDAKILY KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSNVIQHINRA KDKNHMIIISDAEKAFDKIQPF MLKTLNKLQANLLKLISNFNKV SGYKINVQKSQAFLYTSNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWSVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRAHIAKSLSQ KNKAGGITLPDFKLYYKATVT KTAWYCYQNRHIDQWNRIPSEI TPHIYNYLIF

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7049	37417	B	7103	1	1722	
7050	37418	A	7104	1	3513	
7051	37419	A	7105	1	2546	MSELPFTIATKRKLYLGIQLKSD VKDLFKENYKPLLNEIREDTYK WKNTPCSWIGRINIMMAILPK VIYGFNAILIKLPLTFFTELEKTT LKFTQSLKRAHIAKTILSKKNK AGGIMLPDFKLYYKATVTKTA CTIHNSKDLEPTEMPSNDTLDK ENVAYIIHHGILCSHSGRVHIL CRDMDEAGNHHSRQNTGTEN QTLHLVTHKWELNDENTWTQ GGEHHISGPVRTNNKNHMIISIG AEKAFDIQPPMLKTLNLQGLI DGTYLKIIIRDIFDRPIANILLNGQ KREASPLKTGTROGCPLPPLLF NIVLEILARAIKQKEIKGIQLG KEEVKLSLFADDMIYLENPIVS AQNLLKLSISNFSKVSGYKINVQ KSQAFLYTNNRQTESQILSELPP TIASKRIKYLGLQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPC LSIGKINIMKMAILPKVIYRFNAI PIKLPMTFFTELEKTTLKFIWNQ KRARIAKTILSQKNKDDGGITLPD FKLYYKATVTKTAWYQYQNR DIDQWNRTEPSEIIPHVVYHILF DKPDKNKKWGKDSLFPKWCW ENWLAICGKLLDPFLTPTYTKI NSRWIKDLNVRPKTIKTEENL GNTIQDIGMGKDFMSKIPKAM ATKAKIDKWNLIELKSFACTAKE TTISVNRQPTWEKIFAICLSDK GLISRIYKELKQRHKKKTNNPIK
7052	37420	A	7106	1	2575	
7053	37421	A	7107	1	875	
7054	37422	B	7108	1	3421	
7055	37423	A	7109	1	3790	MELKTKARELREECRLSRRRN QLEERVSADEEMNEMKREG KFREKRIRKNEQSLQEIWDYVK RPNLRLJGVPESDAENGTKLEN LTQDIHQEDFPNLRQANVQIQE IQRTQRYSSRRATPRHIIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFKQVLSDL QRDLDSHTLMGDFNTPLSTLD RSTRQKVNKDQELNSALHQA DLIDIYRTLHPKSTE
7056	37424	A	7110	134	307	

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7057	37425	A	7111	2	173	RPPRSEVPGPLSPGRPPAAGLRGR*PAGVRGLREPRAFSGVRVER RSLFIGKDMFDS
7058	37426	A	7112	888	1016	VPGEIHALHSAADROQHENA*NAR TRWQHAQSGRSPLFLALSRE
7059	37427	A	7113	573	872	SPSLLPDPDAHVGC*SRSRKRPD RIRRFDSR*NLFCYCRKTS*PFH *G*MCQ*YQTDPRNSAQCHPV LRLWWPGDEYDFLCRSGSVGS VRQSGRASGL
7060	37428	A	7114	1	654	
7061	37429	A	7115	71	2776	
7062	37430	A	7116	31	1016	TVLPERPYNRKSSRRNRRCGNP PARSPCPSSGSRSSSPATGP/ HTAIAALPRIAFGKISDSTQH TGPQDMAKAAT*NSLRGSMRY SFKPMVGRWIKSCLRPVWC
7063	37431	A	7117	279	1243	SVLLMCAADYLPRPDPVQTCN AVRVLRYHRSNHGTPPDFSP GPVSAWYYAH/QPKIPIWSQ/QR GFTD/R*TRHKCPQRFVAPDK*I SSPD*AMNYRKHHRPAPRHTA PTQKARLMADKSSLRHRHNSA NKRRSASPLSSAGYP/GKRJRAQ NLIPASTTNGQLRIRQRRISQAR **TKRMARKGSIPISAVSNSLN SS*ASIVSSCIRCALSPLSNIHK S*TAGPWGASSRKTNIGLSRQJ FPAWQSPCSRRTVKSSRQCAVT AAISSSVAFRNAAFNPEGISVAS SNSLRGSMRYSFKPMVGRWIKS CLRVPWCIRPK
7064	37432	B	7118	1	726	
7065	37433	A	7119	1	138	
7066	37434	A	7120	56	133	
7067	37435	B	7121	1	1524	
7068	37436	B	7122	1	1521	
7069	37437	A	7123	1	1494	
7070	37438	B	7124	4	1698	

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7071	37439	A	7125	1	1725	MELKTKARELREECRSLSRSCD QLEERPNNRLIGVPESDGENGT KLENTLQDIIQENFPNLAKQVN VQIQEIQRTPQRYSLRRATPRHII VRFTKVEMKEKMLRAAREKGR VTLKGKPIRLTADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKSFIDKQMLRDFV TTRPALQELLKEALNMERNNRS WFFEKINKIDRPLARVIKKKRE KNQIDAINKDKEDITTNPTETIQT IREYYKHLYPNKLENLEEMDTF LDITYTFPRLNQEEVESLNTSITG SEIVAIISIAYPKKVQDQMDPQ PNSTRVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKCLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTDLEKTTL NFIWNQKRARITKSILSQKNKA GGITLPDFKLYYTATVTKTAW YWYQNRWYQYQNRDIDQWN RTEPSEITPHVYNYLIF
7072	37440	A	7126	1	2478	

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7073	37441	A	7127	1	1746	METQKTLQKINESRSWFFKEKIN KIDRPLARLIKKEKNQIDTIK NDKGDITTDPTIEIQTITREYYKH LYANKLENLEEMDKFLDITYTL PRLNQEEAESLNKPITGPEIEAII NSLPTKKIPGPDGFTAIFYQRY KEELQHKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMISIDAEEKSDKIQQPFMLK TLNKLIGDGYLKIIIRAIYDKPT ANIILNGQKLEAFPLKTGTROG CLLSPLLFNIVLEVLAIRQEK EKKCIRLGKEEVKLSLFADDMI VYLENPVSAQNLLKLISNFSKV SGYKINVQKSAFLYTNNRQIE SQIMSELPFTIASKRIQYLGQLT RDVKDLFKENYKPLLNEIKEDT NKWKNI PCSWIGRINIMKMAM LPKVIYRFDAIPKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPDKNKQWG KDSL FNKWCWEIWLAIGRKRK LDPFLTPTYTKINSRWIKDFNIRP KTIKTEESLGNIQDISMGKKFTS
7074	37442	A	7128	1	1908	
7075	37443	A	7129	1	1494	
7076	37444	A	7130	2	1562	
7077	37445	B	7131	1	1569	
7078	37446	A	7132	1	1593	
7079	37447	A	7133	1	1520	
7080	37448	B	7134	1	2796	

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7081	37449	A	7135	101	1686	SIAYQPKRVQDQMSQPNSTR ANIILNGQKLEAFPLKVTGTRQF SKENFEPVSPLLFNIVLEVLAARA IRQEKIKGIQLGKEEIKLSLFA DDMIYVLENPIVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKQNYKPRLKE IKEDTNKWKNI PCSWVERIYIV KMAILPKVIYRFSAIPIKLPMTFF TELEKTTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKDT VTKTAWYWYQNRDIDQWNRT EPSEIMPHIYNILFIDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLNPFILTPYTKINSRWIKDL NVRPQTIKTLEENLGITIDIGM GKDFRSKTPKAMATKAKSDK WDLIKLSFCTAKETTIRMNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDIN RHFSKEDIYAAKRHMKKCSSSL AIRQMOKITTMRYHLTPVRMAI IKKSGNNRDMDEIGNHPSQ
7082	37450	A	7136	1364	3024	TEPKTKTT*LSQ*MQKRPLTKF NNASC*KLSIN/IVLEVLARAIQ EKEIKGVQLGKEEVKLSLFADD MIIVYLENPIVSAQNLLNLISNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNER KEDTNKWKNI PCSWVERINIVK MAILPKVIYRFSAIPIKLPMTFF TELEKTTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYSYQNRDIDQWNRT PSEILPRIYNILFIDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFKLPYTKIKSGWIKDLNV RPKTIKLEENLGITIDIGMGK DFMSKTPKAMATKAKIDKWDL IKLSFCTAKETTIRVNRQPTER EKIFATYSSDKGLISRIYKELKQI YKKRTNNLIK VVKDMNRHFS KEDVYAAKKHMKCCSSSLAIR EMQIKTTMRYHLTPVRMAIHK SGNNRITIVLLPGSLIVRSFHVTL NAILLHPGLTLFSPSAGRRDIPR VAFSYLAFSAQPSHNTPVN
7083	37451	A	7137	1	2274	
7084	37452	A	7138	2	2348	

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7085	37453	A	7139	1	2202	
7086	37454	A	7140	1	2823	
7087	37455	A	7141	1052	3831	RHKKPFKKSMPGAGFFERINK IDRPLARLTKRKREKNQIHAIK NDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEIESLNRPIGTAEIVAIL NSLPTKKSPPGPDGFTAEFYQRY KEELVPFLKLFQSIEKEGILPNS FYEASINLIPKPGRDTTKKENFR PISLMNIDAKILSKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIC KSINVIQHINRTKDKNHMHISID
7088	37456	A	7142	1	327	
7089	37457	A	7143	1	446	
7090	37458	A	7144	382	1485	
7091	37459	A	7145	1	378	
7092	37460	A	7146	2	217	
7093	37461	A	7147	1	483	
7094	37462	A	7148	1	1260	
7095	37463	A	7149	1	891	
7096	37464	A	7150	5	182	RQGLLVSPRLVQKGEIRTPGLK RSSRLDLQKC*DYRHEPSSLAS EAPSVWVLLPPWRQS
7097	37465	A	7151	1	1914	

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7098	37466	A	7152	1	2200	MKLTTHRENMALTNFGCHHIA AQQLNYTNTLLAARIKQRLTEQ FELMLRQAQIDFAGKAHSLTEA QANTTQVSAERDRLFKNYQRY LKGSQAAVNPFSERDIDDARQN FLAQDALAQISQLDSL VNGEQ SQIVSLKAQLAEAKYNLEQTIV RAPSNGYVTQVLIRPGTYAASL PLRPVMVFIPDQKRQIVAFRQ NSLLRLAPGDDEEVFNALPG KVFSGLAAISPAVPGGAYQST GTLQTLNTAPGSDGVITIELDE HTDLSALPDGIYAQNPKNLKIV ELKAPQLPRSLDDAQIALAVIN TTYASQIGLTPAKDGIFVEDKES PYVNLIVTREDNKDAENVKKF VQAYQSDEIPCTRSKHCTPAE SGACKTESAARHAGPNLYQCR RIRSANRSAISVKGWRTPCIPDS LPAAEWLTYGSGYL AGMKLGD TPLVEYTRDRLHRETRLRSFGRY ELTTAYTPAGQLQSOHLNLLS DRDYTWNDNGELIRISSPRQTR SYSYSTTGRLTGVTHTAANLDI RIPYATDPAGNRLPDPELHPDST LSMWPDNRIARDDNLYLYRDR HGRLTEKTDLIEPEGVIRTDDET HRYHYDSQHRLVHYTRTQYEE PLVESRYLYDPLGRRVAKRVW RRERDLTGWMSLSRKPVQVWY GWDGDRLLTIQNDRTRIQTIVQ PGSFPLIRVETATGELAKTQRR
7099	37467	A	7153	719	1575	
7100	37468	A	7154	1	239	
7101	37469	A	7155	1	735	FNDSPSEARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHHP DMEIRGRVEQRVGYTIEQINH MRDVFGTLLRRAEDVFPVIGV AAHKELNNDYTSKKVMKPLIT SNTVTDEIERANVLKMNKGWY LFTDSRGSKMTIDGINSNDIYM LGYVSNLSLTPGYPLNKTGLVL QMALDPNDVTFYSHFAVPQT KGNVNVITSYMTNNGFFEDKK ATFAPSFLMNIKGKNTSVVKNS ILEQQQLT
7102	37470	A	7156	1	4368	
7103	37471	A	7157	1	1452	
7104	37472	A	7158	1	516	
7105	37473	A	7159	1	743	

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7106	37474	A	7160	3	1743	DSPEARKITRRWRIGEAADLV GVSSQAIRDAEKAGRLPHPDME IRGRVEQVRVGYTIEQNHMRDV FGTRLRRAEDVFPFVIGVAAHK GNDPQGTASMYHGWVPDLHIH AEDTLLPFYLGKEDDVTYAIKP TCWPGLDIIPSCALHRIETELM GKFDEAQPNLIGITINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFPDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVRETDEVGKGQIR MRTVFEQAIDQRSSTDLSLSTP AAPMVDSLIARVGVGMARGNAI TLPVCGRVDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG KYFLRWLMRKIFHIITRCINTAK LPKSVVALFSPHGELSARSQDA LQKAFDTKEELLKQASNLHE QKKAGVIFEAEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMVLNLDLRVPTECIEKI EAILKELEKAP
7107	37475	A	7161	1	438	
7108	37476	A	7162	1	3216	MKLMETLNQCNAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGRTRLRRAEDVFPFG FGDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLARQVSR/VKRAPTC WPGLDIIPSCALPRIETELMGK FDEGLPTDPHMLRLAIETVA HDYDVIVIDSAPNLG
7109	37477	A	7163	1	513	

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7110	37478	A	7164	1	2027	MRGHREKAAACKPRTRASEGT TPASTFILDFQPPNCNYITSGDNH TLRDPHYVEDKGHKYL VF EAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSACKRDA ELANGALGIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GK WYLF TDSRSGSKMTIDGINSN DIYMLGYVVSNSLTGPYKPLNKT GLVLQMGLDPNDVTFTYSHFA VPQAKGILCEEDNYTAGDNHM MRAPHCEEDRAHKFVVF DANA GTESGHQGESSLFNRACGGGGT FFFSKESQKLQQSACKRDCINA GHIENTKAIAIAQFNDDSP EARK ITRRWRIGEADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHM RDVFGTRLKR AEDVFPPIGVAAHKG VYKT SVSVHLAQDLALKGSLLLPKND FLFKLGLGLEHPLPGKIHSPTGA DVARGSSGLPKSELFLPERNTQ ELQQDSEEGPLALQVLQSNLM DFADFGTTIKQDFRLLGQTSVD RLQLSQGQAVKGNQLLPVSL VKRKTTLPNTQTASPRALADS LMQLARQVSRLESGQNN DGIC EIHVAKYVEIFGLTSAEASKDIR QALKSFAGKLVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQRAL CQTYQPIHSLLYRVTEPVYAV
7111	37479	A	7165	1	750	
7112	37480	A	7166	1	723	
7113	37481	B	7167	1	1156	
7114	37482	A	7168	1	999	
7115	37483	A	7169	1	529	MKLMETLNQCINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQ RVGYTIEQI NHMRDVFVAGDEKGYESFPWF IKTCA\HPSRGLYSVHINPYLIPS LSGYRTGLRSFGLVKQKKSPIR MPCVYTNPCVSIYSRMAQASSL
7116	37484	A	7170	1	1038	
7117	37485	A	7171	1	1098	

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7118	37486	A	7172	1	838	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLVVEGNDPQGTE TMYHGWVPDLHHIAEDTLLPF YLGEKDDVTYAIAKPTCWPGLDI IPSCIALHRIETELMGKFDEGSL PTDPHLMYYQAPCMKSNAL IVILGTVTLDVAGIGLVMPVICR ASCGISSIPTASPTMACC
7119	37487	B	7173	1	1212	
7120	37488	A	7174	1	738	
7121	37489	A	7175	1	654	
7122	37490	A	7176	1	448	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRRAEDVFPPVI GVAAHKAGNLSQCLH**IGQR AGRGGLRIGRQGGFSFHQ
7123	37491	B	7177	1	753	
7124	37492	A	7178	1	345	
7125	37493	A	7179	1	516	
7126	37494	A	7180	1	1989	
7127	37495	B	7181	1	1191	
7128	37496	A	7182	1	669	
7129	37497	A	7183	1	574	
7130	37498	A	7184	1	934	
7131	37499	A	7185	1	1281	
7132	37500	A	7186	1	324	
7133	37501	A	7187	3	817	
7134	37502	A	7188	1	587	
7135	37503	B	7189	1	610	
7136	37504	A	7190	1	882	
7137	37505	A	7191	1	1077	
7138	37506	A	7192	1	418	
7139	37507	A	7193	1	840	
7140	37508	A	7194	1	337	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRNVFGSLRRPTAELKCA SQT
7141	37509	A	7195	1	1142	
7142	37510	A	7196	1	1080	
7143	37511	A	7197	1	1170	
7144	37512	B	7198	1	1296	
7145	37513	A	7199	1	1179	

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7146	37514	A	7200	1	507	
7147	37515	A	7201	1	411	
7148	37516	A	7202	1	793	
7149	37517	B	7203	366	1502	
7150	37518	A	7204	1	1107	
7151	37519	A	7205	1	2388	
7152	37520	B	7206	1	2260	
7153	37521	A	7207	1	1067	
7154	37522	B	7208	563	1467	
7155	37523	B	7209	1	1272	
7156	37524	A	7210	1	1722	
7157	37525	B	7211	1	1917	
7158	37526	A	7212	1	2679	
7159	37527	A	7213	1	1207	MKLME TLNQINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRV EQRVGYTIEQI NHMRDVF GTRLRR AEDVFPPG FGDFAIHF GNHHQNRIFALLGQ TSVDRLLQLSQGQAVKGNQLL PVSLVKRKTT LAPNTQTASPR A LADSLMQLARQVSRL ESGQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMRDVF GTRLRR AEDVFPPVIGVA AHKGGVYKT SVSVHLAQDLAL KGLRVLLVE AARGLKKRGLAGTAQGPGE PG EAPKGGKKGKTEPGHERKGNWT GKGPQIREGTS PNP PREHGGE C APPPPSAKRKOPKAQKRKANSN AHPRQPKPKKRPRKRTNSRTN TRSGKRQNKQPEEPK
7160	37528	A	7214	1	2757	
7161	37529	A	7215	1	2984	

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7162	37530	A	7216	1	2387	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRD AEKAGR LPHDPMEIRGRVEQRVGYTIEQI NHMRDVFGRTRLRKAEDVFPPI GVA AHKAKGLTALSPQTDWNR KRNSKPLAQVQEEDSAWHPE CLQKTRQAWCDNLKTCHTSHG SVMETA VINHKKRKNSPRJVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNP LTQFRLSE TKEITNPYAMRLYESLCQYRK DGSIGVSLKIDWIER YQLPQSY QRMPDFRRRFLQCINAGHEMT KAIAIAQFNDDSPARKITRRW RIGEAADLVGVSSQAIRD AEKA GRLPHDPMEIRGRVEQRVGYTI EQINHMRDVFGRTRLRKAEDVFP PVI GVA AHKGGVYK/TLISVHL AQDLALKGLPGLLR/EGNDPQG /TTS MYHG WVPDLHIAEDTLL PFYLG EKDDVP/YAIKPTCWAG AWHFFLP CRALHRIETELMGKF DEGKLPTDPHMLRLAIETVAH DYDVIVIDSAPNLGIGTINVVCA ADV LIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFE PDVFIRD KLMERRNRRTGRTEKARIWEV
7163	37531	A	7217	1	917	

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7164	37532	A	7218	I	1862	MKLMETLNHCINAGHEMTKAV AIAQFNDDSPSEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVGFTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAY DLALKGLRVLVVEGNDPQGT SMYHGWVPDLHHIAEDTLLPF YLGEKDDVTYAIPKTCWPLDI IPSCALHRIETELWGK/FDEGR SFMPGPP/HHHPLGRSSQ*QVSN SLDRAAKGN*KPLCHCPCSGTT HATLRLIKEQRPYVPPYHLQQA VVDPRRGHMLV/LNVVRVTG DVGKGQIRMRTVVEQAIDQRSS TGAWRNALSIEWPVCNEIFYRL IKPRWEIRWGWKRAPIPKHTLN TQPVEDTSLSTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWWSGNE RDQELLTEDALDDLIPSLFTTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRLVVGELDDQ MAALSRLGNDYRPTSAYERQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGEAICPVRMFRMKLMTLN QCINAGHEMTKAI AIAQFNDD PGSEENNPALENR
7165	37533	A	7219	I	2724	
7166	37534	A	7220	I	3252	FNDDSPSEARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVGFTRLRRAEDVFPPFNDDSP EARKITRRWRIGEAADLVGVSS QAIRDAEKAGRSTATRILEIRGR VEQRVGYTIEQINHMRDVGFTGR LRAEDVFPPVIGVAAHKGGV YKTSVSVHLAQLALKGLRVL LVEGRSFPQTEACLLQYSSWDV SSEKPAALNKNKSEMGRGDFAD FGTITIKQDFRLLGQT
7167	37535	A	7221	I	465	
7168	37536	A	7222	I	291	

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7169	37537	A	7223	1	1710	MLCTKWDLGLEKNAGKNKN AYKWYGPANAPDEPHIEQLV GECRVMRQLKRLISRIAPSSV MVVGESGTAIPVVSHEAFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDDFGYLEFEGGANFSWGE YGFDFWENFYNGRHNKPGSEQ RYTFKNTNRIYLGDTGFNLYLH AYGTYGSANRVNFHDDMFLA GFGQF*PAGGW/WGSNPFFAK RYTRSKPYTGDNGYVAGWV AGYNFMLGSEKFTLTWNEYE FDRDATYAADFLPLYDVCQD NGNLEYDYSQPEWKHNFH YLAVLYRFKDESGKEQFSGAV VKTREATPGKIEAITRRMLDFS PRLKKLADCPSPRVFEALCICS MLDALLLCPLDYHASCNYS YALLDPQGFPLPHRRLLWGPYID VDVPMHLHIQHAWAQDALLSC LYSDLLYMSSFYPYPAGTLRLM GVTSYNHKNLTLLTYCITLMSTI RFAYDGDDEEIAMKYTDFLKGE LSMNIRPLHDRVIVKRKEVETK SAGGIVLTGSASAKSTRGEVLA VGNGRILENGEVKPLDVKIGDI VFFNDGYRGEI
7170	37538	A	7224	678	1588	RTQHKASLHGRASAFCPPLFA PQAPRLFDHRGFLTFSANFAA VAFCPPLFPPTGAAAVCPLPLF APRRFLPPPPRLFRCHGFFPPC LGFLTSAAFFLPPPLFALRRRG FLPFAAAAFPPTRLFAPPPTQL FAPSPWWLFAAAAFCPWWLAP TPPRLFVPAAAAFCCRDPLPSP PLFRHRDPLPPPRIFVPAAL RAGAADSAAGSTGVLGQDLWS RCVVGTMGEAPGSRGGGGGLR EDIPLPEFPSPGALSSCR*GNRR PEGEMTCQEPLLS/CSWIP*VKE FETNPNDIVRPH

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7171	37539	A	7225	1	1627	MTKQLELPQSPGEVPGSDYPLL IACAYIGFLTWGGGFGSGMPLL AATPGNPVEHIAGLIPVGDTLFS GFNIFITVALIVVMPFITRMMMP KPSDVVSIDPKLLMEEADFQKQ LPKDAPPSEERLEESRILTLIGAL GIAYLAMYSFSEHGFINITNTVNL MFMIAGLLLHKTPMAYMRAIS AAARSTAGILVQFPFYAGIQLM MEHSVTGIEAAMLDDLGGHLLG VNVASLLGDGQQRSEVEMLGY LFFVGNRKATPLPYQSQPDDSC DWYRLRHEEAMTPDAVVRLEAE AAYEKYGFNDFKLKGGLVAGE EEAESIVALAQRFPQARITLDPN GAWSLNEAIKIGKYLKGSLAY AEDPCGAEQGFSGREVMAEFR RATGLPTATNMIAATNWREMGH AVIAQSVSDIPLADPHFWTMQG SVRV AQMCHEGLTWGSHSNN HFDISLAMFTHVGAAAPGNPTA IDTHWVQEGDCRLTQNPLEIK KGKIAVPDAPGLGVELDEWQV QKAHEAYKRLPGGARNDAGP MQYLIPGWTFDRKRPFVGRH
7172	37540	A	7226	3	655	
7173	37541	A	7227	1	633	
7174	37542	A	7228	1	630	
7175	37543	A	7229	362	1491	PTLSVIHESMRFFIRHQPENLTL VVL SRNLPLALPICVFVINCW KLAVSNWHLPISTGC AVTKDG RWSPEFTITGQA/WDLPVVG YR NGVAQPLRLWQATHAHPDLT KFNDGDFLRAEQQGGINAEKLT VLYPNDNHTAGKKLRLMQQYF QCACSVADILRRHHLA GRKLLH ELADYEVIQLNDHTHTAIPELL RVLIDEHQMSWDDAWAITSKT FAYTNHTLMPEALERWDVKLV KGPLPRHMQIINEINTRFKTLDL QDAEHRPLKMRGCLLCQCHTL FQKGHRFFT GAGGNRQNNVIE HLVAASRYRFTTASRRPLFTAG FTLLTAFLFHSNFAEGVNSLMF MKNLTISGGFLLLAITGPGAYSI DRLLNKKW
7176	37544	A	7230	1	660	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,440,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7177	37545	A	7231	545	1322	KHAEHLGQATHAHPFILTKFNP GYFLRRQTTRGINAEK/LAKIFF \PKANHFAAGKKLRLMQQYFQC ACSVADILRRHHLAAGKRLHEL ADYEVIQLNDTHPTIAIPELLRV LIDEHQMSWDDAWAITSKTFA YTNHTLMPREALERWDVKLVKG LLPRHMQIINEINTRFKTLVEKT WPGDEKVWAKLAVVHDKQVH MANLCVVGGA VNGVAALHS DLVVKDLFPEYHQLWPNKEHN VTNGITPRRWIKQCNPALAALL
7178	37546	A	7232	641	874	KYPTPGRDLRMFITGLSERL*EI TSLLKRSITGDKYSLRPLTANSV TSVTHFSFGRVALKSLSSVRAV SLDLNRCFK
7179	37547	A	7233	1	693	
7180	37548	A	7234	980	1305	TWLKICIRHSHSLITSL/HVLH SDQGWQYRMRRYQNILKEHGI KQSMRKGNCCLDNAVVECFFG TLKSECFYLDEFNSISELKDAVT EYIEYNSRRISLKLKGSDSN
7181	37549	A	7235	1	3219	
7182	37550	C	7236	1	7521	
7183	37551	A	7237	1351	2117	CDRILCSACCAEPQPVSHLHRL RRSFSEKQPDNGSQNPASRDR/ DVVDVTVIAWIEHRGGHEAPS GPGEDGMDAPAIAAGTFSPREA STLPVQVS*VCLNCCSRDVPK ATRVPL/EKLAGPLRHPLFMLF QTCLHLSLFTHHFADDSRRLQIF SVGFVAGLKQYRRDLLQGDV NPRMATAVGNDQVWFQSGNG FQARLRARSDGLPRFQVRTHFG QDAFCIVIGNTDRDDVHGGQ RIGEREFQHINPLWRFEC
7184	37552	A	7238	690	868	

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7185	37553	A	7239	2607	3692	TWLRICSIHRSKSLILTSI/HVLHSDQGQWYRMRRYQNLKEHGIKQSMRSRKGNCLEDNAVVECFGTLKSECFYLDEFNSISELKDAVTEYIEYYNSRRISLKLGLTPIEYRNQTYMPRVNCPLFDTLRIPDIGGVVRARAIAKLLNDTDMAIIDKRRPRANVSQVMHIIGDVAGRDCVLVDDMIDTGGTLCKAAEALKERGAARVFAYATHPIFSGNAANNLRNSVIDEVVCDTIPLSD EIKSLPNVRTLTSEKYTAARFT RDLIAGITVGIIAIPALMALAIGSGVAPQYGLYTAAGVAGIVIALTG GSRFSVSGPTAAFFVILYPSVQ QFGLAGLLVATLLGLDFSDG
7186	37554	A	7240	1326	3930	NVLRGISAAFVG*AKAPRNGTQ
7187	37555	A	7241	3	195	RVDDFVGAGAPASPL*QCGQLQKLIGISIGSLRGLGTICAVSNDLTEQEIRLTLEHCPNSFF
7188	37556	B	7242	75	402	
7189	37557	A	7243	1	309	
7190	37558	A	7244	3	187	
7191	37559	A	7245	383	1778	
7192	37560	A	7246	2	447	IREKLIRLQHENKMLKLNQEGSDNEKIALQLSLDDANLRKNEL ETE/Q*VLVPINFPLTTAFVSH RFRLVNQRLLEVQSQVEELQKSLQDQGSKAEDSVLLKKLEEHLEKLHEANNEQLQKKRAIHEDLEPRFNNSSKIEELQEAIR
7193	37561	B	7247	80	1042	
7194	37562	A	7248	1	192	
7195	37563	A	7249	3	62	
7196	37564	B	7250	219	230	
7197	37565	A	7251	246	594	
7198	37566	A	7252	1	316	
7199	37567	A	7253	1	1059	
7200	37568	A	7254	1	516	EDALEQEKELQIQVEHYEFQTRQLELAKNYADQISRLERES EMKKEYNALHQRHTEMIQTYVEHIERSKMQQVGGNSQTESSLPGRSRKERPTSLNVFPLADGT/CTCTDRGQARACGGPLAPE*PRPA AVQLQLPGFVAVPWSERLLPVAGVPRSLGREPLQAALHGS
7201	37569	A	7255	1	1176	
7202	37570	A	7256	1	749	
7203	37571	A	7257	1	691	

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7204	37572	A	7258	2	810	VMMTGYNNGRCPRNSLYSDCII EEKTVVLQKKDNEGFVLRG AKADTPIEEFTPTPAFPALQYL ESVDEGGVAWQAGLRTGDFLI EVNNENVVKVGHQVVMNIR QGGNHFLKVVTVTRNLDPDD TARKKAPPPPKRAPTTALTLRS KSMTSLEELVDKASVRKKKD KPVEIVPASKPSRAAENMAVEP RVATIKQRPSSRCFPAGSDMNS VYERQGLA VMTPTVPGSPKAPF LGIPRGTMRRQKSIGKKCGTTP QKLPLGFQTQP
7205	37573	A	7259	1	1416	
7206	37574	A	7260	2	1142	
7207	37575	A	7261	1	576	
7208	37576	A	7262	21	289	
7209	37577	A	7263	2	372	
7210	37578	A	7264	170	655	VRRRLGALFTWICSVTRESTSK PLSSALLSAKLLHRARSRTGLS GRNPKTISQDLQFAAIGSPLTES LNLHSRQALRDCCWHTHTIPPNP *ICTHARR/WRDCCWHTHTIPPNP DTVWRFPPLSSPVSAPKQERAS SEPCSWSHWCRCSLSWLSIPT GCTPVCSSICLLMATFPMFSLIK IVR
7211	37579	A	7265	1	1725	
7212	37580	A	7266	307	686	PRRTPMKSKCIKEVPIFVPLRT TRENCLRPKGYAIYEKAPRSIL KDVHLTRNQCVPIPDTRYK WWS WQVCRPKQWGWTOGPVAPK RSAEFAAHA*KRRRVMLNLR GLDVDSLVIHQVNKAP
7213	37581	A	7267	1	276	
7214	37582	A	7268	1	726	
7215	37583	A	7269	3	231	
7216	37584	A	7270	1	217	
7217	37585	A	7271	3	283	KRKTEGDAKGDKAKVKDESRQ RSARLSAKPAPKPEPKPKAP AKKGEKVPKGGKKRKADAGKE REGYWRQVQKCIHFL*LYFW*L YSLKYYFI
7218	37586	A	7272	1	1188	
7219	37587	A	7273	5	365	
7220	37588	A	7274	1	453	

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7221	37589	A	7275	1	441	RQPAHPTGSSAAAAPKRKSA HAGVAVAASARLPPCAGCLR AAPPLASSARLRALRRP/GGL WAAGCAPAAGQLCTAAGSAAP GALQRCGGRHGIRPWCAEIAS AG*GSGSGRWGWCPCFLLR CTSHPLSSPLPTHGSLQASFS LTRDCVSSTKTLWVWLEVQR
7222	37590	A	7276	2	1957	
7223	37591	A	7277	1	678	
7224	37592	A	7278	1	720	
7225	37593	A	7279	190	2947	QALQRGLLSR/DRAPCSSKLSW RS/SPRRRAGTGPVQEEVALKP VLLRHPVQPVIRVKLPRI CLLEEAGQLRGVHRLESVEEY EADGAEWGPPDTAMLESLPE MAGKHSLSPLQLDSSASQPG AIQIISILYQIHLYLKHLLSS YWGASQWKHTRIHTHYFESLW *EHLPS*KYQKREKWADLTR SLENP/GQQPRDSWEP SGFWALPQAGDSCQTSQSP RKPTGPPKPSPPPEEGRLLR /CPTMPVMRKSLTE
7226	37594	A	7280	3	439	
7227	37595	A	7281	1	273	
7228	37596	A	7282	2	1664	
7229	37597	A	7283	1	7511	
7230	37598	A	7284	1	5046	
7231	37599	A	7285	42	8716	
7232	37600	A	7286	2	201	
7233	37601	A	7287	2	797	CS/GSPPTCRQAQTSLEVALYM FLQNPDTEAVLVAMSCFHLCE EADTQCGVDESVHNLNPN SNTFMEFACQCDVNSPPVGPVSE HKGSMISVMSSEGNADTPVSK YMDQLLSLMVCNLEKVG LQIP TNDKDLVLLTDINTQFVEQ TLDIMKNLLDNHTEGSP EHLQAS IETMMLNLVRNKMVEY LTDW VMGTSNQAADDDVKCL TSR/D HPGGTL*GQPRPELPA GLPRQ PASPGPRHPGASCGW PRAPDS APGGPGRER
7234	37602	A	7288	56	8669	
7235	37603	B	7289	278	2333	
7236	37604	A	7290	1	423	

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7237	37605	A	7291	2	1688	PLYFHSPPAWLCSPPPSARLYL ELRKLPA TL PWSSVTD TGSYS A GRRERGGEGEGRRVRVADH RSALPRTGPGQSEELANMQGL VERLERAVSRLESLSAESHRPP GNVCGEVNGVIA/GVAPSRGKPL HKLMDSMVAEFLKNSRLSGD VETLAEIVHSAFQAQRAFLMA SQYQQPHENDVAALLKPISEK I KEIQTQRE/RTRGSNMFNHL SA VSESIPALGWIAVSPKPGPYVK EMNDAA TFYTNRV LKDYKHSD LRHVDVWKS YLNIWSELQAYI KEIHHTTGLTWSKTGPVASTVS AFSVLSSGGLPPPPPLPPGPP PLFENEGKKESSPSRSALFAQL NQGEAITKGLRHVTDQKTYK NPSLRAQGGQTQSPTKSHTPSP TSPKSYPSQKHAPVLELEGKKW RVEYQEDRNDLVISETELKQVA YIFKCEKSTIQIKGVNSIINDNC KKLGLVFDNVV GIVEVINSQDI QIQVMGRVPTISINKTEGCHIYL SEDALDCEIVSAKSEMNILIPQ DGDYREFFPIPEQFKTAWDGSKL
7238	37606	B	7292	44	355	
7239	37607	A	7293	1	3623	SEKEKEELERLQKEEBEERKKRL QLYVFMRCIAYPFNAKQPTD MARRQKQKSKQQLQTVKDRFQ AFLNGETQIMADEAFMNAVQS YYEVFLKSDRVARMVQSGGCS ANDSREVFKKHIEKRVRLPEID GLSKETVLSSWMAKFDIYRG EEDPRKQQARMTASAASELILS KEQLYEMFQNLGIKKFEHQLL YNACQLDNPDEQAAQIRRELD GRLQMADQIARERKFPKFSVSK E MENMYIELKSSVNLLMA
7240	37608	B	7294	1	1555	
7241	37609	A	7295	1	1056	
7242	37610	B	7296	54	2173	
7243	37611	A	7297	1	984	
7244	37612	B	7298	95	1350	

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7245	37613	A	7299	1	2569	MDGAKAFFSAVAAGFVILTCQ LQWQWQHGGVHAHQWLWLA SGYRDACFCVSTYSSGPSEFP TLGLTNELAIDLLEERKRRKAK VWKGEGGGLRSPRQSLAFA VLASRGTRSCHVSPYLGVS SSPNPHPSTTGAGPIPPVQ PQINQKNREIAIPLTLGMST RGCKNMSRFSPLHCCTTPI FTDPGSHCKGAHGDI KGALPMSINRSYFNAHPL AVTFKDVAVVFTEELGLDPA QRKLYRDVMLENFRNLLSV QPFHQDTFHFLGKEFWKMK TSQREGNSGGKIQIEMETV GPHEEWSCQIWEQIASDL QNSIRNSSQFFKEGDVPCQ LSISHVQKPYRCNECKQSF VSVFDLHQQSHSGEKSHTC GKSFYCSPALHIHQRVHMG CYKCDVCGKEFNQSSHLQ RVHTGEKPFKCGQCGKGF ALNVHCKLHTGEKPYNC KAFIHDSQLQEHQRIHTG KCDICGKSFRVRSRLNRH TGEKAFRCDCGKNFRQ NSHSMVHIEEPYKCEQCGK ICRRDFCKHQMVTGEKPY KECGKTRWSSCLLNHQV GQKSFKECECGKGFYTN HQRSHNGEKPYNCECGK RRLDLEFHQRVHTGERPY
7246	37614	A	7300	2	326	
7247	37615	A	7301	166	443	

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7248	37616	A	7302	1	2692	MDPGTLQSASQGP TAINPCDYV LKRRNIQTWSQRLTPIKWHVYI LMIGPGEKEAGRN LGIFGK WTP FPKIPAKRLRESNCPVDAQEIW LPQAFREYLGRRGNFGPGRRTC EFWEVESICSVESWELWLRQA DSGDSGKCSPDACGHIDTSLR AGHCYLTRLWHVSGRIPPSFKL HHPGVCKFPKVGGKMTTFKEA VTFKDVA VVFTEELGLLDPAQ RKLYRDVMLENFRNLLSVGHQ PFHQDTCHFLREKFWMMGT ATQREGNSGGKIQTOMETVPE AGTHEEFSCQIWEQIASDLTR SQD TTISNSQLFEQDDNPSQIKA RLSIHVKTETSEGRCKKSFSD VSVLDLHQQLQSREKSHTCDEC GKSFYSSALRIHQRVHMGEL YNCDVCGKEFNQSSHQIQRI HTGEKPFKCEQCGKFSRRSGL YVHRKLHTGVKPHICEKCGKA FIHDSQLQEHRQHTGEKPFKC DICCKSFRSRANLNHRSMVHM REKPFRCDDTCGKSFLKSLNS HRMVHTGEKRYKCEECGKRFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVHSG ETTFKCECGKFYTNQRYSH QRAHSGEKPYRCEECGKG YKR RLDLDFHQRVHRGEKPYNCKE CGKSPGWASCLLNHQRIHSGEK PFKCEECGKRFTQNSQLYTHRR
7249	37617	A	7303	1	585	KRTAISPKDAFETRQDLNEEEA AQVHG VKDPAP/ASTQSVLADG TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYNNSSGGRG/RL MKTV/TQGSQQPSLADPASHLP VGDHLTYSNETEPVRALLPDEK KEVKPPALSMNLHEATMPVL LDHLRETRADKKRLRKALREFE EQFFKQTRSPQKEDRIPMADE YY
7250	37618	A	7304	1	366	

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7251	37619	A	7305	1	1265	R Y R P G I G S T I S S L V E E H A P P S W E P Q H Q N V E A T V L V D S V L R P S M G N F K S R K P K S I F K A E S G R S H G E S Q E T E H V V S S Q S E C Q V R A G T P A H E S P Q N N A F K C Q E T V R L Q P R I D Q R T A T S P K D A F E T R Q D L N E E E A A Q V H G V K D P A P A S T Q S V L A / D G T D S A D P S P V H K D G Q N E A D S A P E D L H S V G T S R L L L / Y H I T D G D N P L L S P R L F P L S G S Q R F N L D P E S A P S P P T Q Q F M M P R S S S R C S C G D G K E P Q T I T Q L T K H I Q S L K R K I R K F E E K F E Q E K Y R P S H G D K T S N P E V L K W M N D L A K G R K Q L K E L K L K L S E E Q G S A P K G P P R N L L C E Q P T V P R E N G K P E A A G P E P S S S G E E T P D A A L T C L K E R R E Q L P P Q E D S K V T K Q D K N L I K P L Y D R Y R I J K Q I L S T P S L I P T I V S Q D T C M L L L C
7252	37620	A	7306	797	1390	P R M G A R P R A P A Q P P P A A A Q R P P A R P A T P T A C G S S A H R A P S P A R S R R S P C T P R A A P A A P G P K A A R Q W A G T A T R S S R P Q R S A R R S P R D S S R C W A I S S R S K R A A T A C T P G A K R R V A T K A R G A L W S K P K S K A M R L W P W C L S G R L G S * K A Q E V A Q D P G S D E G R G R L V E S G L Q D E G W V P Q G G E G G V A G Q D A S H R G S F R G A L K
7253	37621	A	7307	605	697	
7254	37622	A	7308	1	1263	
7255	37623	A	7309	257	1190	
7256	37624	A	7310	394	485	
7257	37625	A	7311	21	674	
7258	37626	A	7312	277	396	G L L P G W K I * C S R V F V T S A I H V E V A E L E A N L P C T K V H F P D P N K L H C F Q L T V T P D E G Y Y Q G G K F Q F E T E V P D A Y N M V P P K V K C L T K I W H P N I T E T
7259	37627	C	7313	74	316	
7260	37628	C	7314	211	390	
7261	37629	A	7315	1	2601	
7262	37630	A	7316	1	1365	
7263	37631	A	7317	358	760	S I P L L F R K S S L S R K * C S A A S I F S G S S K F K R S V N K E F N P Q T T S F N V L V G A Q P V P S I E C S L N K L R H I S P V S V I V G V P D S L V Q A F H F G R H H V V R I R E L Q F Q T E I F H P G S N P H L G L L L A E N N E A C L D Q E N A L Y M Y K V
7264	37632	A	7318	1	1728	
7265	37633	A	7319	1	558	

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7266	37634	A	7320	2	1884	PAGAGPGQEAGAGPGGAVAY ATGAEEGEMKPVAAGAAVPPG EGISAAPTVEPSSGEAEGGEAN LVDVSGGLETESSNG\KDTLEG AGDTSEVMDTQAGSVDEENGR QLGEVELQCGICTKWFTADTFG IDTSSCLPFMTNYSFHCNVCHH SGNTYFLRKQANLKEMCLSAL ANLTWQFRTQEEHPKTMFSKD KDIIFFIDKYWECMTTRHRPGK TTWPNNIVKTMskerDVFLVK EHPDPGSKDPEEDYPKFGLLDQ DLNIGPAYDNQKQSSAVSTSG NLNGGIAAGSSGKGRGAKRKQ QDGGTTGTTKKARSDFLSAQOR LPPHGYPLEHPFNKDGYYILA EPDPQAPDPEKLEIDCWAGKPIS GDLYRACLYERVLLALHDRAP QLKISDDRLTVVGEKGYSMVR ASHGVRKGAWYFEITVDEMPP DTAARLGWSQPLGNLQAPLGY DKFSYSWRSKKGTKFHQSIGKH YSSGYGQGDVLFYINLPEDTE TAKSLPDTYKDKALIKFSYLY FEEKDFVDKAEKSLKQTPHSEI FYKNGVNVQGVAYKDIFEGVYF PAISLYKSCTVSINFGPCFKYPP KDLTYRPMDSMDGWGAVVEHT LADVLYHVETEVDGRRSPPWE
7267	37635	A	7321	1	267	
7268	37636	A	7322	60	888	RGAALARTLSVRVPGAGTRR SHALGPRPGARSSFLRCELRR CMCGNNMSTPLPAIVPAARKA TA AVIFLHGLDGTGHGWAEAF AGIRSSHIIYICPHAPVRPVTLN MNVAMPWF\DIIGLSPDSQED ESGIKQAAENIKALIDQEVKNGI PSNRILG/GFSQGGALSLYTALT TQQLAGVTALSCWLPLRASFP QGPIGGANRDISILQCHGDCDPL VPLMFGSLTVEKCLKLVNPNAN VTFKTYEGMMHSSCQEQEMMD VKQFIDKLLPPID
7269	37637	A	7323	1	1182	

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7270	37638	A	7324	1	2469	MVDRARPTVLVTEVPLSKHT AQMGVLVTANESQPLVHETAL KNKKPQSWFNPFCVSYNRKPG LQD*GRAERPELGEQATEAALL KAPAESVRQEHRSNT/PQTRSC CPQYFPRAGCLPSRGHDVEPQH EAGDGPCRGIRNG*KLLSSFFG QQVRT**R/CSELTPEKQEFFKGS ESSNRTSGGLFGVVPGA AETGD VCVYTFKELEGQTSDEEGSRLE NDFLEITDEDKKKSTKDRYDKY KEVGEHPPLSSSPVEHEGVKLG QKSYRCDECGKAFNRSSHLIGH QRIHTGEKPYECNECGKTRFQT SQLIVHLRTHTEKPYECSECG KAYRHSSHLIQHQLHNKEKPY KCNECAKAFQSSRLTDHQT HTGEKPYECNECGEAFIRSKSL ARHQVLHTGKKPYKCNECGRA FCSNRNLIDHQRIHTGEKPYECS ECGKAFSRSSGLISHHRVHTGE KPYSCIECGKAFNQNSQLIEHQ RMHRGKKVYKCECGKAFGLS KCLIRHQRLHTGEKPYKCNECG KSFNQNSHLIHHQRIHTGEKPYE CNECGKVFSYSSSLMVHQRT TGEKPYKCNDCKGAFSDSSQLI VHQRVHTGEKPYECSECGKAF SQRSTFNHHQRTHTGEKSSGLA CQEGNKEISKGPQKPPGYRLCP LQAVGGGEFGPTRVHISFSLSD LKQIKVFFPGGLMLEKQKKKS
7271	37639	A	7325	1	1596	
7272	37640	A	7326	2	3394	MAHAGGGSGGSGAGGAPAGR LSGARWGRSGSAGHEKLPVHV EDALTYLDQVKIRFGSDPATYN GFLEIMKEFKSQSIDTPGVIRRV SQLFHEHPDLIVGFNAFLPLGY RIDIPKNGKLNQSPQTSQENSH NHGDGAEDFKQQVPYKEDKPK VPLESDSVFNNNAISYVVKIKTR FLDHPEIYRSFLEIHTYQKEQL NTRGRPRFRGMEEEVFTEVANL FRGQEDLLSEFGQFLPEAKRSLF TGNGPCMHSHVQ
7273	37641	A	7327	1	738	
7274	37642	A	7328	1	399	
7275	37643	A	7329	3	223	
7276	37644	A	7330	1	1040	
7277	37645	A	7331	1	465	
7278	37646	A	7332	1	288	

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7279	37647	A	7333	109	4770	
7280	37648	A	7334	109	4687	
7281	37649	A	7335	109	4860	
7282	37650	A	7336	1	336	
7283	37651	A	7337	1	441	
7284	37652	A	7338	305	446	
7285	37653	A	7339	2	461	
7286	37654	A	7340	59	620	FQKIGL**/FIDLKDLFTIPLAE QDCEWFATIPVNNLQPAKRF HCFDTGSGNNGKASYSGSKNV FQMSYTSAQKAEVAVIELIEN AQLRFHTDEQLMTLFTQLQTA VRSRMHPFYITHIRAHPLPGPL TEGNQMADRLVANAISSARHF QQHLL/THSHPPGDRSRSCRHW RKKLEESGTSSHE
7287	37655	A	7341	1	1410	
7288	37656	A	7342	1	1740	MGQVWALVHSTLETFTDEEE GEYNEVTEQVCLPAKAGSAAV DLCTKA VSLLPGESPPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQVITS TSVPWKA KPGDHIAQLLVIPKK FIEGLKEPLQVERQSSCQGLGY/ PFLMAAIVKPEPIPLKWLTDKP IWTEQWPLSKEKLEALEDLITQ QLKKGHIAPTFSPWNSPVFIKK KSAEQDCEWVFVITLAVNNLQL KPAKRFHWKVLPGPNQPIWI PSRYLKYHKPDACEEIEPGSQ GFPVAAMSRLTLRRTPTVTSNT HRTQPPTWGQIEKLPMQAEENL RKAGQPVITISNWILPRITKFKPI EGAENVFTDGSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIHQRCPTQVMLSAEE QHLQKSAAKTEAEKLVVWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKIPGESRGPPVAAMSRLTLR RMPTVMSNTHRTQPPTWGQIK KLSQMAEENLRKAGQPVTMNN LMIAVITTA FNKG
7289	37657	A	7343	1	1239	

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7290	37658	A	7344	1	777	MPQNSLEECALGLGKKSLQEN VNNFPKTKLQFLKLTNWLPKI TKFKPIEGAENVFDGSSNGKA SYFGLKGKVFQTPYTAAQKVE LVAVIEVLTAFDMPVMSIDST YVVHSTQLTENAQLRLHTDEQ LMTLSQLQTAVR/CFAVMGIP ASTTT/DNAPGYTSQALATFFS MWNIKRITGIPYNSQQAIVER MNLCLKQQLQKQTEGDREYGT PQMQLNLALLTLNLSLPGQG MLSAAEQHLQKPAVKTEAEQLI
7291	37659	A	7345	1	1307	
7292	37660	A	7346	1	2040	
7293	37661	A	7347	1	1898	MAGAPPPAWLPHCSSISDCCAR NERGSGVGVPASKPARSAAVDL CCTKAVSLLPGEPPQKVPARVC GPLPAGTVGLLGRSSLKKEV QIHTGVISDYSKVEIQVVSSTV PWKAEPGERIAQLLVPPYVGT GKSEIKQTEGFGSTNKQGKAAY WVNOITDKHLTCEITQGGKFK GLVDTGADVSIISLQHWPSMW IQSTQFNIVGVDGSSNGKASYF GSKCKVFQMPYTSQKVELVA IIEVLTTFDMPINVISDSSYVVHS TQLIENALQFHTDEQLMTLFT QLQTAVRSRMHPFYITHIRAR/H TPLPGPLTEGNQMADCLVATA VSNARHFHNLTHVNASGLKCR YSNTWKAAKAIQRRPTCQMV HSSSFTGGVNPQGLEPNSLWQ MDVTHVPSFGRLAYVHVCVDT FSHFVWATCQSGESSACVKHH LLQGFVVMGIPASIKTDNVPGY TSQALATFFSMLNKRITDIPYN SQDVEADANADVGVDVDADA DVEDAEVEVFTDADADAEDVDV EDADAERLCNADNEDSLDL VDAEMDADVDTNLDVDAADV VDVDADADVDADIDVDVDTG LNLEADLDDVDADVDTDADV DRDADVEVADADATVNADV DYVDVDTDS
7294	37662	A	7348	2	565	
7295	37663	A	7349	1	996	
7296	37664	A	7350	18	260	
7297	37665	A	7351	1	594	
7298	37666	C	7352	232	603	
7299	37667	A	7353	1	1236	
7300	37668	A	7354	568	1370	

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7301	37669	A	7355	1	1800	
7302	37670	A	7356	1	498	
7303	37671	A	7357	1	3400	MDCSEKWRDPLDAVCVLPATE EPVVQGSALYLVAHDDYCV WYSLQRTSPEKNERVRQMRPV CDCQAHLLWNRPRFGEINDQD RTDRYVQALRTEIPLTLKGAKL QREEKEGDMPCRANILVTELF TELIGEGALPSYEAHRHLVET SLGEQVIVPPVDVESC PGAPSV CDIQLNQVSPADFTVLS DVLPM FSIDFSKQVSSAACHSRREPEL TSGRAQVVLVSWDIEDMPEGK IKCTMAPFWAHSDEEMQ
7304	37672	A	7358	1	687	
7305	37673	A	7359	1	660	
7306	37674	A	7360	112	474	
7307	37675	A	7361	352	441	
7308	37676	B	7362	1	831	
7309	37677	A	7363	460	612	
7310	37678	A	7364	251	496	LFVSI/VQVFH*GRRGFLVRN DCVQIWCEMISHSGFDLHFS DGQ*/WMSISSC/DFLAA*MSSFEK CLFMSFAHFLMGLVFVFL
7311	37679	B	7365	1	729	
7312	37680	A	7366	1	774	
7313	37681	B	7367	1	516	
7314	37682	A	7368	10	504	
7315	37683	C	7369	520	1656	
7316	37684	B	7370	1	1206	
7317	37685	A	7371	677	1126	AVTLTTKVCSTPEASETTNPPG GTNNSRRTALRAVALTAKVRS FTPRGSAASFLKSVRPRTHQFRT Q*HVHQIEFSPGGLWESCPRAS SSTGDPGRPPERRGAAARKTVG VQGVGYSLPRKLCPLFSRTTYP HTSLRKDCLESDDTAE
7318	37686	A	7372	2	394	HLFIYLLVLLWCPGWQPTAG LKGSCLLSSNWNYPPL*AL LLGTQKLPRVWNFIMVRRIQDG VKPSVIAEREMSKRKAASLL SQRDHEPTRRKKLRTHPNIRRN KLQTRHLKSCNTHCEGPWRHS
7319	37687	A	7373	1	204	
7320	37688	A	7374	1	879	
7321	37689	A	7375	139	4488	
7322	37690	A	7376	1	933	
7323	37691	A	7377	335	582	VLQLLRQHVVSCSFLLVGSWS HWLQERSCRSSQ*VLQLIKAV WTQRTQEPSWLHLVDPAPGLQ VELPASPTRYAHTPQLGG

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7324	37692	B	7378	1	3101	
7325	37693	A	7379	365	625	VAKIFSHVVGCLFTLMVVSFAV QKLFSLIRSHLSILAFVIAAFGLV DMKSLPTMS*MVMPRFSSRVF MVLGLKFKSLIHLELIFV
7326	37694	A	7380	994	1167	NKGGHKQMEEHSMMLMDRKNQ YRENGHTAQGNL*IQCHPHQAT NDFLHRJGKNKLASNM
7327	37695	C	7381	143	3529	
7328	37696	B	7382	54	1158	
7329	37697	A	7383	1662	1919	LLNVFALAFVLLEMLGCQFW IFPAFSCRHLVL*ISLYTLL*MRP RDSGMWCLCSRWFQRTSLFLA SFERYVPSHSGAGCSVSM
7330	37698	A	7384	63	1650	SPGHI*SSV*REIYSTKCPQEA GKI*NSHPNITIKRTGEARANTF KS*QKARNN*DQSRTEGDRDT KNPSKNQ/CNPGAGFLKRSTKLI DR*QD*RRK*RRIK*T**KMIK GI/VTDPTEIQTITREFYKHFYA NRLKNLEEMDEFLETYTLPLRN QEEVESLNRPTGSEIAIINSLP TKKSPGPDGFTAIEYQRTNDKN HMIISIDEKAFDKIQPFMLEM LNKLGIYGYMIKIIRTIYDKSTA NIILNVQKLEAFPLKTGTTRQGPC LSPLLFNIVLEVLARAIRQEKEI KGIRLRKEVFKMFLFADDMIVY LENPIISAPNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQI MSELPFTIATKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPKLPMTFFTELEKTTL KFIWNQKRALNAKTILSQKNK AGGIMLPDFKLPYKATWYWNQ NTEIDQWNKTEASEITPHIYNHL VFDNPDKNKK
7331	37699	A	7385	392	493	
7332	37700	A	7386	1	1223	
7333	37701	A	7387	386	553	KMIKGISLIPQRYKLPSSENTINT STQIN*KI*KKWHHSHTHTPSQD* TRKKLNL
7334	37702	B	7388	285	1581	
7335	37703	A	7389	1	1473	
7336	37704	A	7390	755	1042	SSYATKKEPALPSQSEAKKTKL ETSCYLTSNYTRTLQ*PKQHG GTKEI*ANGTEQSPQ*YHTA TTIWSLTNLTKTRNGERIPYLN GVGKTG
7337	37705	C	7391	1	2334	

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7338	37706	A	7392	1	1539	
7339	37707	B	7393	1	2361	
7340	37708	A	7394	5071	5535	GTAFLWRRRGALRFRVSSFSVL FFPHLCGFYFWSLMMVMYRC VFGVDVLVVC*FSF*QTGPSAA GLLEYPAV*GVSVPLLGGASQL GCSGVRGQGP*GGSPLVLRSP AACWENHCSLQSCQTGTFKSA EVTAVFLVFCALPPEVEPTEAG
7341	37709	A	7395	1	459	
7342	37710	A	7396	3	1063	
7343	37711	A	7397	39	895	
7344	37712	A	7398	2	277	
7345	37713	A	7399	34	845	
7346	37714	A	7400	1	3399	
7347	37715	A	7401	1	3126	
7348	37716	A	7402	1	387	
7349	37717	A	7403	1	3578	RDLVVGCGGFVKSDVEINYSLI EIKLYTKHGTLKYQTDCAPN GYFMIPLYDKGDFILKIEPLGW SFEPTTVELHVDGVSDICTKGG DINFVFTGFSVNGKVLKSGQPL GPAGVQVSLRNTGTAKIQSTV TQPGGKFAFFKVLPGDYELAT HPTWALKEASTTVSVTNSNAN AASPLIVAGYNVSGSVRSDEP MKGVKFLFSSLVTKEDVLGC NVSPVPGFPQDESLEYLYCYTV SREDGFSFYSLPSG
7350	37718	A	7404	34	460	
7351	37719	A	7405	105	245	VSSEKVLGVPCPAASAAASGD ASR*MATGRGGGGGVAALPE SAP
7352	37720	A	7406	1	1289	
7353	37721	A	7407	462	5250	
7354	37722	A	7408	714	887	
7355	37723	A	7409	1	109	PLRQLLCVKRGFC*HH*HEGCQ SRLLRLCLLCSTAI
7356	37724	A	7410	1	1845	
7357	37725	A	7411	192	1507	
7358	37726	A	7412	2	688	
7359	37727	A	7413	1	518	
7360	37728	A	7414	1	276	

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7361	37729	A	7415	984	3112	MWQETFFRMENLQLIILILGSP SQLHFPVIRNNQGWTLYHQWP HFLNRFSSRLSNSLLNLQKFTC ANCKKPLQKGQTAYQRKGS LFCSTTCLSSFHKKPAKPKLCV MCKKDITTMKGTT/VLAQVDSS ESFQEFCSVTSCLISL/YEEQQNP TKGALNKSRTCICGKLTEIRHE VSFKNMTHKLCSDHCFNRYRM ANGLIMNCCEQCCEYLPSKGA GNNVLVIDGQQKRFFCCQSCVSE YKQVGSHPFLKEVRDHMQDS FLMQPEKYGKLTCTGCRTOC RFFDMTQCIGPNGYMEPYCSTA CMNSHKTKYAKSQLGIIHCF KRNSLPQYQATMPDGKLYNFC NSSCAKQFALSMQSSPNGQFV APSDIQLKCNKYCKNSFCCKPEIL EWENKVHQFCKTCSDDYKKL HCIVTYCEYQEEKTLHETVNF SGVKRPFCEGCKLLYKQDFAR RLGLRCVTCNYSQCLCKGGAT KELDGVVRDFCSEDCCKKQFD WYYKAARCDCKSQGTLKERV QWRGEMKHFCQDQCLLRFYCQ QNEPNMTTQKGPENLHYDQGC QTSRTKMTGSAPPPSPTPNKEM KNKAVLCKPLMTKATYCKPH MQTKSCQTDDBTWRTYVVPVPI VPVPIVPMHMYSQNPVPTTV PVPVVPVFLPAPLDSSEKIPAAI EELKSKVSSDALDTELLTMTD
7362	37730	A	7416	1	1071	
7363	37731	A	7417	88	2118	
7364	37732	A	7418	2	2930	
7365	37733	A	7419	1	1677	
7366	37734	A	7420	172	13329	
7367	37735	A	7421	2	946	
7368	37736	A	7422	255	933	WIEAAPQAQEVQGDGLWLPCG AAGAGGLQSARSYGTVGEASY AEHPW/CAPGGCMAGCGSLAA AASPLGVPGHLP/QPTAAPSHPH RASLRVALLSGQWGLTCGQLL ASAPLLQSWAWDTRLLMCRRLL SCSSEEGERIAQLLLPYLKLGS STVKRTGGFGNTNPAGKAVYW VNQVSKDRPICTVAIQGKDFEG LVDTEADVSIHAIHQWPHWPK QKASIGIVGVGAA
7369	37737	A	7423	718	2385	
7370	37738	A	7424	1	180	

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7371	37739	A	7425	1	1713	
7372	37740	A	7426	1	774	
7373	37741	A	7427	2	158	
7374	37742	A	7428	1	174	
7375	37743	A	7429	252	1245	ELGECGCRQGSVSHCGRGRPL LPRVRGKRHLPRARLARCQEAL SPWGFRCRFRNHHQTGFSLAGA NQRGPLAATLSGPGGEGQSAV ARLMGEKKNHPGAQYATRLSP RVGRFINAAGTTGFTGKRAPT CWPGADNIPSCCLALPRIETELM GKFDEGKLPDTPHMLGLAIET VAHDYDVVIDSAPNLGIGTINV VCAADVLIIVPTPAELFDYTSAL QFFDMLRDLKKNVDLKGFEPP VRILLTKYSNSNGSQSPWMEEQ IRDAWGSMLVKNVRETDEVG KGQIRMRTVFEQAIDQRSSTGA WRNALSIEWPVCNEIFDRLIKPR
7376	37744	A	7430	1	1113	
7377	37745	B	7431	56	1234	
7378	37746	A	7432	667	1048	LLLFRDLGIGTINVCAADVLI PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPPDVRILLTKYSN SNSQSPWMEEQIRDAARFPV GKPVVPAALMNRPTRRGEAVC VLGARVVFLFTSETGNS
7379	37747	A	7433	1	1428	
7380	37748	A	7434	1	1125	
7381	37749	A	7435	1	756	SDRRYEWDRGPSLIIRPTIRVGP WSQTNNQTDTSGTVV/RRFPF PVIGVVFHKGGVYKTSVSVHL AQDLALKGLRVLLVEGNDPQG TASMYHGWPDLHIHAEDTLL PFYDPLMLRLAIETVAHDYD VVIDSAPNLGIGTINVCAADV LIIVPTPAELFDYTSALQFFDMLR DLKKNVDLKGFEPPDVRILLTKY SNSNGSQSPWMEEQISDALRIS QRRNISSKFIQSACITLTFIST CWAIIVTQSG
7382	37750	A	7436	1	1329	
7383	37751	A	7437	1	1185	
7384	37752	A	7438	1	1065	
7385	37753	B	7439	67	1033	
7386	37754	A	7440	1	1192	
7387	37755	A	7441	1	1413	
7388	37756	A	7442	1	1176	
7389	37757	A	7443	1	1302	
7390	37758	B	7444	1169	3356	
7391	37759	A	7445	14	3974	

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7392	37760	A	7446	677	1033	RATASSISTTRPCESTSNAPSCN SPIRSRSPLIPIRPASITLILVSM MRMVRAATISCAILVSRCPAISP PLCTAFFRPICAAAGVPVFTLFTT TP*SLPLLLISAPSMPLKMELES T
7393	37761	A	7447	1558	1748	CSNASARFFAAVNPSSGLGMILM *SRFIVFTKLSAIPPLSGLRTAVF FGSSPNIRANWRVSLAR
7394	37762	A	7448	1	595	LKNSKPQVVMMAAGIFLIMCG VWLFGGGVLDPTKSSGYLIVDI YNEIICMLSNRIAGLGLSIMAVG GYARYMEGTPASRAMVSLLSR PLKLIRSPYIILSAT*VIGQIMP/Q FITSASGLGMLLMVPLFPTLVSL GVSRLSAVAVIATTTMSIEWGIL ETNSIFAAQVAGMKIATFFCHA HNPVASRVILSVAISGTRAR
7395	37763	A	7449	1	978	
7396	37764	C	7450	32	316	
7397	37765	A	7451	1	2465	
7398	37766	A	7452	1	1416	MIILIDAEKAFDKIQPFMLKTL SKLGTDTGYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNIGLEDLARAIRQKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQI MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNQWKGDSLFFHKWC WENWLA VCRKLKLDPLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKCCSSSLAIREMDIKTTMR YHLTPVRMAILKKSGNNRCWR GCGEIGTL

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7399	37767	A	7453	3	2272	RSTRQKVNKIDTQELNSALHQA DLIDIYRTLHLKSTEYTFSSAPH HTYSKIDHILGSKALLSKCKRTE IITNYLSDHSAIKLELRKINLTQ NRSTTWKLNLLNDYVWHN KMKAEIKMFFETNENKDTTYQ NLWDTFKAVCRGFIALNAHK RKQERSKIDTLTSQLEKEKQE QTHSKASRRQEITKIRAELEKE TQKTLQKINESRSWFFERINKID RPLARLIKKKREKNLIDAIKND KGDITDPTETIQTIREYYKHL TNKLENLEEMDKFLDITYLPR NEEEVESLNRPTGAIEIVAINSL PTKKSFGPDGFTAIFYQRYKEE LVPFLLKLFQSIEKEGILPNSCY EASILIPKPGRDITKKENFRPIS LMNIDAKILNKILAKRIQHHKK LIHHDQVGFIPGMQGWFNIRKS INVIQHINRAKDKNHMISIDAE KAFDKIQQFFMLKTLNKL/DIGR NYCKVHMEPKKSPHRQVNPKE KEQSWRHHTT*LTQILQGSYNQ NSMVLVPKQRYRSMQNRALR NNAAYLQLSDL*QT*EKQAMG NGFPI**MVLGKLASHM*KAET GSLPYTYLKNQFKMD*RLKR*T *NHKNPRKPRHYHSGHRHGG GLHV*NTKSNNGNKSQN*QMG N*TKELLHSKRNYHQSEQATY KMGENFHNLLI*QRANIQLQ* TQTNLQEKKNQPHQKVGKGHE
7400	37768	A	7454	1	3020	
7401	37769	A	7455	1	3046	MVKGSIQEEILTINLIYAPNTG ALRFIKQVLRDLQRDLDSHTIM GDFHTPLSTLDRSTQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRKINLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQ LEKEKQEQTHSKASRRQEITKIR AELEKEITQ
7402	37770	B	7456	197	1917	
7403	37771	B	7457	1	1954	

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7404	37772	A	7458	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLIGDGT FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIQEKEIKGIQLGKEEV KLSLFADDMIVYLENPVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMITFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTPQSEITPHIYNILIFD KPDKNKQWKGSLFNKWCWE NWLAIKRLKLDPLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGDMFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFTTYSDDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAARKH MKKCSPLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGC GEIGTLLHCWWINWMKKTWH IYTMEYYASIKKNEFMSFAGA* MKLETII
7405	37773	A	7459	1	1713	

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7406	37774	A	7460	281	2882	KPRLNMYMKNAEASRADAINW KKGGY/LVMEDKMNMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIHQENFPNLRQANIQIEIQ RTIPQRYSSRRATPRHIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHYRANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTA EYY QRYKEELVPFLKLQFSIEKEGI LPNSFYEASIIIPKGRDITTKKE NFRITSLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPMGQ WFNIRKSINVIQHINRTKDKNH VIISIDAEKAFDKIQQLFLLKTL NKLIGIDGTYLKIKRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLARAIRQEKEI KGIQLGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVS YKINVQKSQAFLYTNNRQTETQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIMKMAILHK VIYRFNAIPIKLPMTFFTELEKTT LKFTWNQKRARIAKSILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNILIFDKPEKNKQWGKDS LFNKWCWENWLAIRWKLKLD PFPTPYTKINSRWIKLDNVRPKT
7407	37775	B	7461	1	2633	
7408	37776	A	7462	3	1336	

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7409	37777	A	7463	2	2458	SWFFEKINKIDRPQARLIKKKRE KNQIDITIKNDKGDIITDPTIEQIT IREYYKHL YANKLENLEEMDK FLDITYTL PRLNQEEVESVNRPT GSEIEAITNSLPTKKSPGPDGFT AEFYQRYKEELVPFLKLFQPIE KEGILPNSFYEAIIIPKGRDT TKKGNFRPISLMNIDAKILNKIL ANQIQHHIKLIIHHDQVGFIP MQGWLEVLARA/IRQEKEIKGI QLGKEEVKLSLFADDMMIVYLEN PTVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLNEIKEDTNKW KNIPCSWIGRINIVKMAILPKVI YTFNAIPIKLPMTFFTELEKTTL KFIWKQKRSHIAKSILSQNKKA GDITLPDFKLHYKATVYKTAW YWYQNRDIDQWNTTEPSEIML HIYNHLIFDKPKNKQWGNDS LFNKWCWENWLAICRKLKLD FLTSTYTKINSRWIKDLNVRPKTI KTL EENLGNTIQDIGMKDFMS KTPKAVATKAKIDKWDVIKLE SFCTAKETTIRVNRQPTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSLAIREMQI KTTMRYHLTPIRMVIAKSGNN RAPGGRGGCGCSFGRLKRSVCP ALKRVADLPAQRSSSAKGETAS
7410	37778	A	7464	2	2101	
7411	37779	A	7465	196	792	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSLAIREMQIKTTMR YHLTPVRMAIKKSGNNRCWR GCGEIGTLLHCWL DCKLVQPL WKS VWRFLRDLELEIPFDPAIL LGIYPNEYKSCCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVQ SLVG/TWVNWETTFSVTIAVQK PTRLSH
7412	37780	A	7466	3	610	
7413	37781	A	7467	1	1986	

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7414	37782	A	7468	965	4421	TWKGITTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEYTFSSAPHTYSKI DHILGSKALLSKCKRIEITNYLS DHSIAIKLELRIKNLTQSRSTTW KLNNLLNDYWVHNEMKTEIK MFFETNENKDTTYQNLWDAFK AVCRGKFIALNAYKRKEERSKI DTLTSQLKELEKQEQRHSPSR RQEITKMRAELKEIETQKTLQKI NESSWFFERINKIDRPLARLIK KKREKNQIDT
7415	37783	A	7469	1	1674	MGQLQRNARDLQESVMSIRM MPMEYVFSRYPRLVRLAGLK GKQVELTLVGSSTELDKSLIERI IDPLTHLVNRNSLDHGIELPEKRL AAGKNSVGNLILSAEHQGGNIC IEVTDDGAGLNRERILAKAASQ GLTVSENMSDDEVAMLIFAPGF STAEQVTDVSGRGVGMDEVVKR NIQKMGGHVEIQSKQVTGTTIRI LLPLTLAILDGMSSLLTHGIGQF ADVACAGPLLAELDALGKAL KEPARPMVAIVGSKSVSTKLTV LDLSKSIADQLIVGGGIANTFIA AQGHVDVGSLYEADLVDEAKR LLTTCNIPVPSDVRVATEFSETA PATLKS VNDVKADEQILDIGDA SAQELAEILKNAKTILWNGPVG VFEFPNFRKGTEIVANAIDSEA FSIAGGGDTLAAIDLFRIADKNS YISTGGGAFLEFVERLTTLTQLL HDQGYVTQAIGKWHMRETTPEP QPQNVGFDDFRGFNSVSDMYT AWRDVHVNPEVALSPDRPAYI NQSPLSKDDVHALRGDQQA ADITPKYMA LDLQRC TEYGAQ LLDKMAKSA
7416	37784	A	7470	1	3360	
7417	37785	A	7471	2	543	
7418	37786	A	7472	1387	1805	QAIAFDVQPGRGDYAGNQRHH NQYNQHQAHS*SWQRCGIGDGL ARFARHNATKANKPGETGDR FNHQKNHGGQDPVLHQLIEV MLVGRGGDQAVGQATLGIDTN VGLHAKV/LTDCLSWSDASPD VAALCSWSSWVPO
7419	37787	A	7473	4088	4228	SPPSA*VKALPGPKHHGGLKPV HPIPGASLVLARRWSMFRRWG LIT
7420	37788	A	7474	332	538	

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7421	37789	A	7475	1	1983	
7422	37790	A	7476	856	964	
7423	37791	A	7477	1	1563	
7424	37792	B	7478	1	1086	
7425	37793	A	7479	372	886	
7426	37794	A	7480	2028	2368	RPPGNSLNVSRMGTRSSYSCRR HSPAFLSWGKGRCHLCNK AHL LAGA*HYSFLSGSAPY*N*VNG QI**R*TAHRSTPDAPIGH*NCC S*L*CHSY*QRA*PGYRHD*CR MCC
7427	37795	A	7481	146	402	LGFLRLLEMPRKQGDYRTR/C EIRGRVEQRVGYTIEQINHM RD VFDRRYEWDHGPRLIRPTIRVG PWSQSDYQTDDTSGTVVVD
7428	37796	A	7482	3	149	
7429	37797	A	7483	5	753	ARKVVVAARHKCPA/CISFSA SHRLYRYWEEEMNPAPVEAMR TFQFIDEGNYTSGDTHTLRDP HYVEDKAHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQA SAKKRDAELANG ALGIHLENNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDGINSNDIYML GYVSNSLTGPYKPLNKTGLVLQ MGLDPNTNIQTDDTSGTVVQT NNQTADTSGTMVVD
7430	37798	C	7484	182	709	
7431	37799	B	7485	1	1488	
7432	37800	A	7486	2	1034	YLIQSRGLIRRSKISLQTGSQIER AFLQAPVEER*SMACSK/YSSH DLTFTNFIRFTYNIF*NHASP GIP NLLHLPRGLRAITIAVFGKQNT YIRLEPFKINVLEQITKHIEKLQC G/ECSQTTOQAWEQSAHQH HIR H*SCRYPG*ARCQ*VHQARTL* DQRS*ADHEAYRKTA VRRC SQ TTQQAWEQSAHQH HIRH*SCR YPG*ARCQ*L*IIHSHEQ QFQWP VG/CIRCGSVGSLPSSICPLTQF QYGAEPDRKE*QCAPASK WAL LHK*HRFPQDRKAGECL LHEY EDLVPIRDLRLFPGGRYL PRA KHVAPSEPDPTIRVG PWSQSDY QTDDTSGTVVVD
7433	37801	A	7487	2	426	
7434	37802	A	7488	138	346	RWRLQNLSCSSC/SRIWL*RGY VFCSWKPREQSSQSP LACSAAC LTLRTQSC LGTAGQTDDTSGT MVQY

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7435	37803	C	7489	1	1290	
7436	37804	A	7490	48	439	HHHSGGLDD/HRRKILNTAYRSR KLQASC*KSAERA WKTKASLT VNGWMKKIRCKTPMCRPTVR* SIRILIIITPLPRVPSRS*LKPPTS CT*CIPTQPTRC*KMITCWRCRS TSRKSSGHVCVSPGSVAVTI
7437	37805	A	7491	1126	1340	KARWMLQTRKRAVRRSNWRK RNIWCAPAAICKRSTLTITSF*K PVKMACPFICAMLRRLARRC AGALPN
7438	37806	A	7492	12	960	
7439	37807	A	7493	1	1806	
7440	37808	B	7494	1	1318	
7441	37809	A	7495	1	1385	MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNISIDS WKNAGR VFKDSKFDANDPIL KDQTQEWSSGATFTSDGKIRLF YTDYSGKHYGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGE RKTYQNVQQFIDEGNYTSGDN HTLRDPHYQNTYIRLEPFKINV EQITKHIEKLQCGGVVKQLSRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQV WIDRKAGECLLHEYEDLVPIRD TLRLFPGGRYLPRAKHVAPSEP DPEQDEQKLSCTYRKRYRVL VGELGDEQMAALSRLGNDYRP TSAYERGQRYASLLQNEFAGNI SALADAENISRKIITRCINTAKLP KSVVALFSPHGELSARSGDALQ KAF*SASPD RADSSPG*EK RATT D/SRQFGGVDTAGNNLT*NIFRI SQRRNISSKFILQ*ACITLTTFIST CWAIIVTQSG/LMQPSAHPAR QPEHDIAFGKCSSSVSVHLA/LG SGEGATCFARGR*RPNGNSLN VSRMGTRSSYSCRRHSPAFHRS TPDAPTH*NCSS*L*CHSY*QR A*PGYRHD*CRMCC
7442	37810	B	7496	1	3597	
7443	37811	A	7497	1	666	
7444	37812	A	7498	1	738	

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7445	37813	A	7499	1	727	MKVLIVESEFLHQDTWVGNAV ERLADALSQNNVTVIKSTSFDD GFALLSSNEAIDCLMFYSQMEH PDEHQNVRLQIGKLHERQLNVP VFLGDRKALAAAMDRDLLEL VDEFAWILEDTADFYRRTAPVA RE*TRYPPGSCWPLF/TAPLMK YS/DIHEYSWAAPGHQGGVGF TKTPAGRFYHDYYGENLFRTD MGIERSTAVSLDHSAGFGQS EKYAARVFGADRSWSVVVGT GSRNTI
7446	37814	A	7500	1	744	
7447	37815	A	7501	1	250	
7448	37816	A	7502	1	850	
7449	37817	A	7503	1	1085	GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQKEEDVLK FLAAGTHLGGTNLDFQMEQYI YKRKSDGIYIINLKRTWEELLR QPRA/MVPIENPAD/VSVISR/N TGQVCQGTVA/VLRLAATGAT PIGGIRFTPGFT/IN/QIQASLPGS PRAFLWVT*PPGAEPPLSRAS LC*PFLPLALVNP/SPLRRYV AIPCNNKGAHSVGLMWWM AREV/LRMRTISRHPW/EVM PDLYFYRDPREEIEKEEQAAAEK AVTKEEFQGEWTAPAPEF/TLA TQPEVADWSEGVQGAFLVPIQ QFP/TEWWSAQPA/EDWS*A/P LAQATEWVGATTDWS
7450	37818	A	7504	1	1053	
7451	37819	A	7505	2	654	
7452	37820	A	7506	674	805	TLMQKSSIKYWQTESSSTSKSL STMIKWASSL*REIYSTKCPQEK AGKIQN*HPNITIKRTRARANT FKS*QKARNN*NQSRTEGNRDT KNPSKN**/MPGAGFLKGGTKLI DR*QD**RKKERRIK*/IAKNDK GDITNPTIEIQTIREYYKHLA NKLLENLEEMHKFLDTYTLPRLN QEEVESLNRPTGAIEIVE*SIAY QPKKVQDQMDSQANSTRGTRR NWWYHSF*TIPINKRGNP*TLM QKSSIKYWQTESSSTSKSLSTMI KWASSLGGKAGSIYANQ

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7453	37821	A	7507	1	1577	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDYRNLHP ESTEYTFPSAPHHTYSKIDHILG SKAPLSKYRSEIKINCLSDHSA IKLELRIKLLTQNRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYQNLWDTLKAVCR GKFIALNAHKRQKERSKIDTLT SQLKELEKQEQTHSKASRRQE SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLARLIKRR EKNQIHAIKNDKGDMSNHTTE QTTIREYYKHLYANKLENLKEI DKFLETYSPLRLNQEEVESLNR PITGSEIEAIINSLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNIPCSWVGRINIVKMAIL PKNWKKTTLKFIWNQKRARIA KSLSQTEQSWRHAT*LTQILQ GYNNNSMVLVSKQRYRSMEO NRALRNATYLPQSD
7454	37822	A	7508	58	330	FTENDDFQFHPCPYKGHLEIIFY GCIVFHGVVYPHFLNPVYHCW TFGLVPSLCYCE*CRNKHTCAC VFIAA*FIVIWVYTQ*WDGWVK WYF
7455	37823	A	7509	1246	1522	DCLGNAGSLFVPELGHYGHF HNIDSSYQ*AWMFFHLFVSFFI SLSSGL*FSLKRSFTSLVSWIPR YFILFEAIVNGSSLMIWLSVCLL
7456	37824	A	7510	140	577	YSMVYMHIFLIQSIIVGHLGW FQVFAIVNNVTINIRVHVS*QH DL*SFGYIPSNWMAGSNGISSR SLRNRHTVFHNG*TSLSQSHQOC KSPVISPPLQHLFPDFLMIAIL TGVRYLIVVLICISLMADE HFFMCLAA
7457	37825	A	7511	399	677	NQREQRHNPESLGRIQSSV*RE IYSTKCPQEKAGKIQN*HPNITI KRTRKARANTFKS*QKARNN* NQSRTTEGNRDTKNPSKNQ*IQE LVF
7458	37826	A	7512	1446	1855	IYKLPWAVWPFS*Y*FFLPMS/G GVFFHLFVSSFMSLSSGL*FSLK RSFTSLVSCIPRYFILSEAVNGS SLMIWLSVCLLVYKNACDFCT LILYPETLLKLSLRRFWAETM GFSRCTIMSSANRDLISSFRN

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7459	37827	A	7513	1	2982	
7460	37828	A	7514	5202	5430	
7461	37829	A	7515	2	454	
7462	37830	A	7516	2	744	
7463	37831	A	7517	1	2422	MCPILREHRGSTEGRKRQKRLP LELTLKDEEVLAHRQIEIVAKA SPSKGNIIHFGYKGVEYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKLELTKA EK HVHNFMMDTQLTKRHCPWAA TIQPKLSFLISLPgcdYRGESAR ARPLSHIPPLQLGLGKDARYLRI CDRSLLCVCAAAGNAGLRPRD SPHTLLHWRSPYFFSPKPVPP QLLGGQPAHRRDDLGEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPAPGGDVMPIVLVRPT NRTRRLDSTGAGMGPSHHQQQ ESPLPTITHCAGCTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPPP RSSHLHCQQQQSQDKPCPPFA PLPHPHHHPHLAHQQPASGGSS PCLRCNSCASSGAPAAAGADNL SLLRLTSSPGGAFRTTSSPLSG SSCCCCCSSRRGSQLNSELTP SSHASALRQQYAQQSAQQAAS ASQYHQCHSLQPAASPTGSLGS LSGGPPLSHHHHHHPAHHQH HQPQARRESNPFEIAMSSCRY NGGVMRPLSNLSASRRNLHEM DSEAQPLQPPASVGGGGGASSP SAAAAAAAAVSSSAPEIVVSKP EHNNNSNNLALYGTGGGGSTGG GGGGGSGHGSSSGTKSSKKK NQNIQYKLGHRRALFEKRRKLS
7464	37832	A	7518	1	579	

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7465	37833	A	7519	1	1184	MSSANRSILEVPHLDILLQELPG VSKVVTVVEVRGNWQRWLKVR DLTKGVTFYFRVQARTITYGPE LQANITAGPAEGSPGSPRDVLV TKSASELTQWTEGHSQDTPIT GYVIEARPSVFGNGSFQVSKEE NQYFSEGLTSIEVPSQQVQKEG AVAMALMVPDEGLWDMFVKD IPRSATSYTLSDKLRQGVTYEF RVVAVNEAGYGEPSPSTAVS AQVEAPFYEEWWFLLVMAISS LIVILLVVFALVLHGQNKKYK NCSTRQISTMEESVTLNNGGF AALELSSRHLNVKSTFSKKNGT RSPRPSPGGLHYSEDEDICNKY NGAVLTESVSLKEKSADASESE VSVGAYFRAVTISPYFCKDAGF AVRTIALGLAETAGSKADARK
7466	37834	A	7520	1	1347	
7467	37835	A	7521	512	1051	MAYCKSTPAVGLRVTV*SLRRL SLICYTFCIGAPSHLSVGSIIAT SFIVSNRPCRAPYVDITYRLPSP LRLAGHRTLPLKPSFPRRSPLL YYPSRPPAHYPLSPSSEPNRRY TMALTAVPPYPTSPLQAFPFLLH SRIPQLQLFLTNSFTSRTPVEP VQVLEILSQWKATTKWHYG
7468	37836	A	7522	352	546	
7469	37837	A	7523	1	360	
7470	37838	A	7524	3	349	
7471	37839	A	7525	1077	2142	SAVRYSVAITTADRRTAAGAIS YPTK*S*SEPIQEGQPEEQ/RAN YPNGTYPTSLRHLERLWLSAL SVKARF/YHQQYSLKKYRYKHI ADNVQQWLDEVFLRPKEMSDI HKLTFFIEKRERLKNVSFKSLHD VRTVEDPSGTQLEVVSNNPWD PKRQLLKWDGKTWGTWDIPD YSAAPPEAVPSLNNPQTFSEQK LDEALYHGAVLRVRPKAMTVA VIIAGLLPILWGTGAGSEVMSRI AAPMIGGMITAPLLSLFIIPAAY KLMWLHRRHWLKCKSARRPQ YQSGYTDHRHSRVKASPTAG LPSLTHEQQQKAVRIQELMAQ GMSSGQAIALVAEELRANHSGE RVARFDEDE

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7472	37840	A	7526	116	191	RLKFTETNLTYNIYVGSIIHLN LEIIHMSLH**MDRTNINIRVQIC FCEFKSLVLLDKPGRQELIDDL NKRTDNFLTDSGISVSDWIDAA TWEVFSSRLRELLGIKINRLAS QDLHGVLSSSETVAEDIWCRILD TVTRKGEHSRRIHSAADKSYLR PDLEWFKQRVEDDQSRSGRKI YVKRDLPHILTPFRAPMASVCA KRKGQVLHQYSLKKYRYKHI ADNVQWLVDEVFLRPKEMSDI HKLTFIEKRERLKNVFKSLHD VSEFLGRVLLHATDPAAPRPPA YSLHAIRGKSRGRKNS
7473	37841	A	7527	1	177	
7474	37842	A	7528	1	399	
7475	37843	A	7529	3	209	
7476	37844	A	7530	1	288	
7477	37845	A	7531	2	256	
7478	37846	A	7532	414	1188	TSFLTGGKKGSKKKVVDPFS KKD/WL*YVKHPAMFNIRNIGK DVGSPTQTGTIASIDGLKGRV FEVSLADLQHDEVAFRKFCLIT VEDVQGNCLTNFHGMDLTRD KIMCSMVKKWQTMIEAHVD VKTTDGYLLRLFCVGFATKKR NNQIGKPF*AQHHRVRQIGKK MMEIMTREVQTNDLKEVVNKL IPDSIGKDIEKACQSIYPLHDVF VRKVKMLKKPKFELGKLMELH GEGSSSGKATGDETGAKVERA
7479	37847	A	7533	1	1140	
7480	37848	A	7534	131	410	
7481	37849	A	7535	1	861	
7482	37850	A	7536	1	406	MWEILELPRDLLNGFAQNADS NMDNKVQAEVALDNGNELVG YYSKASAGDTQANRVWSGPPA NSNRPAEGERNTININKKIDIN TKTPSVGHRHRQRPVKDTTKT RKTAEKLKILKTRVPLIFQRT AALRQR
7483	37851	A	7537	1366	1629	TQSPVQTKPTPITTRGGGFLPTQ PFPVILQRQFCPE*LVAFMGS*E DVP*GSFRVSAESSIL*RAP*GA QSTCKPVNRNEKISKRIHV
7484	37852	A	7538	502	648	

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7485	37853	A	7539	I	1169	PPLLIPRQTGSGVDLQQTPTDLQ LRVLTVRRKTNKQKGPHQNSI CTSPSSKTKDFKPTKIKRDKEG HYIMVKGSIQEEELTILNIYTPN TGAPRFIKQVLRDLQDRLDSHT IIVGDFNTPLSTLDSKRQK VDK DIQELNSALYQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCNRTEIITNCLSDHS AIRLELRIKKLTENRSTTWKLN NLLKDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDTGKAAC RGFIATNAHKRNQKRKMDTL TSQLEKEKQEQRHKSASRRNL QEEVESLNKPRTGSEIEAIINSLP TKKSPGADGFTAIFYQRYKEE/ PGTIPSETIPINRKRGNTP*LIL*G QHHPDTKA
7486	37854	A	7540	I	404	MDEFNLNTYTLPRNLQEEVESLN RPITGSEIVAINSLPRKKSPPGD GFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEAISILIPKPG RDTTIKENFRPISLNMIDAKILN KIILANRIQQHIKLIHHDQVGF PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAADKIQQP FMLKTLKFGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKWKNIPCSWVGRINIM KMAILPKVIYRFNAIPKLPMTF LTELEKTLKFIWNQKRARIK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYWKQRDIHQWN TTEPSEITPHIYNHIFDKPEKNK QWGDLSLFNKWCWENWLAIW RKLLKLPFLTPYTKINSRWIKD LNVRPKTIKLEENLGITIQDIG MGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQ PTKWEKIFTTSSDKGLISRIYN ELKQIYKKKSDNPIKKVVKDM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRVHLTPPSLL IPRQTGSGVDLQQTPTDLQLKV LTVRRKTNKQKVHPPHONPCTS PSSKTKELEKQEQTSHKASRRQ EITKIRAELEKETQKNLQKINES RSWFLEKVNKIDRLRLARLIK REKQIDAIAKNDKGDITDPTEI QATIREHYKHLVANKLENLEE

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7487	37855	A	7541	3	1284	SAADTQANRVWSVPPTNSNRP AAEGPDC*KEN*QKGHPHQNP CQSPSSK\PKVDKTTKMGKKQN RKTGNSKNQSTSPPPQEHSSPA MEQRITNAEKYLKDLMLKTT AQELHDECTSLSSPFDQLEERV SVMEDQMNMKREKFKREKRI KRNEQSLKEIWDYVKRPNPLPI GVPESDRENGNKLENTLQDIIQ ENFPNLRHANIQQEIQRMPQ RYSSKRATPRIYIIVRFTKVEMK EKMLRAARDKSLVTHKGKLIJR LTAGKFIALIAHKGNQERSKIDT LTSQLEKEKQEQTHSKPSRRQ EITKIRAELEKETQTTLQKINES RSWFFEKINKIDRLARLIKKKR EKNQIDAINKDKGDITDPTIEI TTIREYYKHHYANKLENLKEM NKFLDYTLPLRKQEEVELSNR PIKALKLRQ
7488	37856	A	7542	1	1082	MLSSVGLLTHRRKKKSTDTIN DESLNKERDMTGNPHIFPYQE IWQVFVSSGNNYITATGPTAV PPLLIPRQTGSGVDLQQTPTDLQ LRLLTVGRKTNKQKGHPHQNP CTSPSSKTKEIRTTIREYYKHL YANKLENLEEMDKF/H*HIHPPKT KPGRS*ISA*TNNRL*N*GNN** LTNQKKSRTRWIHSRILPEVQ GADKQRAKHE*PIHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQM/DRTFHAHG*E ESIS*KWPYCPR*FIDSPSSSYQ *LSSQNGKNYFKVHMEPKKSP YCQVNPKPKEQSWRHHA*TLQ TILQGSYNSQNSMVLVPKQRYRP MEQSPQK
7489	37857	A	7543	1	2012	MNLSRHLNEVKGELLWSLEWR DPDGGSSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFLGLQQKKMDLKGVFCSFKI YCSSKHLLKTGFISEAVLCYGE GGEGDVTLMKERWPHECIVLI QC�KGRLTPTHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQPKMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQQEELTILNIY

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7490	37858	A	7544	402	675	QGYPGTELSAPSGPNRHLQNF PPOINRIYILLSTTSHLFQN*PHS WK*STPQQM*KRRNRYKNQIL ELRIKKQTQNRSTTWKLNLL NDY
7491	37859	A	7545	21	428	DKTSRGRTIRQQHLLFTNIRCSAA SAADTQANRVWSGPPANSRDP AAEGPDC*KEN*QTERSTSPKS HLYVTIHKDQRNKIPKNPTYKG CEGPLQGELOTTAQQNKRRYK QMGEHMLMGRKNQYHENGH TAQGNL
7492	37860	B	7546	1	1650	
7493	37861	A	7547	1	946	MAMPPLLIPTQTGSGVDHQQTP TDPQLRLTVRRKTNTQKGIPIH QNPNCSTPSSKTKELKEEVGTQ RKEVKNLEKRLDEWLTRIANA EKSLKDLMLQKTMAQELQLDK TTLNFIWNQKACIATILSKK NKAGGIRLPDFKLYYKATVTKT AWYWHQNRVIDQWNRTEASEI MPHIYNHLIFDKPDKKKQWGN DSL/K*MVLGKLASHMQKTEI GPLPYNFYKN*LKMD*RLKGG T*NHRNHRKPKQYHSGHRHG QRLHD*NTKSNNGKGN*QMG SN*TKELL/RQKKLPSE*TRNL QNGRKFVQSIYLTGG
7494	37862	A	7548	189	380	QTERSTQNPICSTPSSKTKGR* NHKDGEKTEQKNWKL*KAERL SSSKGMQLLSNGTKLDGE
7495	37863	C	7549	1	2805	
7496	37864	A	7550	535	696	
7497	37865	A	7551	214	363	LLEGKLTNRKE*HQHQKQGH HQNPICTSPSSKTKVT*NHKDG EKT*QKS
7498	37866	A	7552	787	1056	GQKKKLMIGINSRNHHGPQ*P ALQKMPAS*VTEIMNNHFLFCF RKKGRIKLVNSRVEHQAGSW GPWFQSLVAGQYFWTCSPDGP SPLP

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7499	37867	A	7553	1	4560	MKHTLIPRIKNAQLQMSSLAVP VNSLVCLGKILEYLDKWLVL D GILPFLQIPSKESA VLMGILGIY KCTFTHKLGITKEQLTGKVLPH LIPLSIENNLNQFNSFISIKEML NRLESEHKTKLEQLHIMQEQQK SLDIGNQMNVSEE:TKVTNIGNQ QIDKVFSHIGADLLTGSDSENK EDGALNVPPAGAKPTQQRPTD MSALNNLFGPPQPKVSMNQLS * QOKPNQWLNQFVPPQVSPATG SSVMGTQMNMIQG
7500	37868	C	7554	1	1359	
7501	37869	A	7555	272	915	YPGKQGLEWTSKKLQQTCC*GS *LLEGKRTNRKDINTKNPSVRH HHQRPKMGKEKTEQKNRKLKIR APLLLRNTAPH/HAMEQSWM ENDFDELREEGFRRSNYSELKE EVRTNAKEVKNFEEKLDEWIT RITNAEKSLKDLMEKTTA:EN YVTNAQAPVANATN*KKGYQR WKT*K*MK*SEKRSLEKKE*KEK KQSLQEIWDYVKRPNCLIGVP
7502	37870	A	7556	196	494	HTDGVSVVWMSFLFVSFSPNSQD PQLQVCWSLLEVHSRPLPGYQ QQRIRLEPFKINV/T*ADHEAYR KTAVRRCSQTTQQAWEQSAHQ QHIRH*SCRYPG
7503	37871	B	7557	28	303	
7504	37872	A	7558	1216	1863	HPDITIKRTREARANTFKS*QKA RNN*DERRTEGNRDTKNPSKKS VNRRS WFFEFKNKIDRRLARLI KKKREKNQIDA:KNDKRDITTD PTEIQTIREHYKHLKYANKLEN LEEMDKFLDITYLPRLNQEEVE SLNRPITGSEIAHINSLP TKKSP GPDGLTAKFYQRYKEE/PGTIPS ETIPINRKRGNPP*LIL*GLHHPD TKAWQRHYKKREF
7505	37873	A	7559	166	785	FRATSAADTQANRVWSGPPAN SNRSAEDPDC*KEN*PTKGGHP HQNPICTSPSSKTKARQANIQIQ EIQRMPQRYSSRRATPRCIIVRF TKVEMKEKMLRAAREKGGVTV HKGNPIRLTADLLVKTQLARRE WGPIFNILKEKNFQPRISYPAKL SFISEGEIKSFTDKQMLRDFGTT RPALKELLKEALNMERNNQYQ PLQKHVRL
7506	37874	A	7560	1	1164	

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7507	37875	A	7561	770	2670	RRARCSCAPSSSTTLGRTGPSLA RRRACPSSAGRSRW*ARTTPR GGRPSESGTPTFEPASSPPGRSR RDFQEGQSWVRGWQL/WTSTV GCSPHIFWCVDCECDCEGYLK GHYVAGLRRSFRLLGCRERLGG QEGKMSSGAESPPELLTYEEVAR YQHOPGERPRLVVLIGSLGARL HELKQKVVAENPQHFGVAVPR APWDVKLQWAEDPGSECDKE DEEEENEGARFLEHGEYKENLY GTSLEAIQAVMAKNKVCVLDV EPEALKQLRTSEFKPYIIFVKPAI QEKRRTPPMSPACEDTAAPFDE QQQEMAASAAFIIDRHYGHLVD AVLVKEDLQGAYSQKVVLEK LSKDDTHWPPLVIPRTGSGVDL QQTPTDLQLRVLTVRRKTKKQ KGHPHQNTCTSPSSKTKVGER VSVIEDQMKEMKREKKFREKR VKRNEQSLQEIWDYVVRPNLR LIGVPESDGENGTKLENTLQDI MRENFPNRRARQANIQIEIQRM PQRYSSRRATPRHIIIRFTKVEM KEKMLRAAREKGWVTHKGKPI RLTADLLAETLQARREWEPIFNI LKGNFQPRISYPAKLNFISEGE IKSFTDKQMLRDFVITRPAQL LKEALNLERNNWYQPLQKHAK
7508	37876	A	7562	181	690	OHAIVTGDVGMDDIPQEARQ YRHNQAYAYSIGDGAEDDDE RIVRFHTRCLNGRVLL*DK/IF RNDQAATFAAHQYPLFCSLHC* YPGTQGLEWTSSKHQQTCS*GS *LLWPGDERLWPSWEEQKLS LPTDPDTWL*GSPQAAQGPRCV PPGAQPLSSVTASLCHCA

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7509	37877	A	7563	2	2233	SSENILTVHEQANVESLKETKQ NCKDLDEDANGITDEGKEINEK SSQLKNLSELQDTSI.QHDEEE STVISVSEDMNSEGNVDFECDT KLYTFLSSDESQQSENSENEED TLCFVENSQGRESLSGDTGSL CDNALFVIDTTPGMSADKNFY EEEDKASEVAIEEEKEEEDEKS EEDSSDHEDENEDEFSDEEDFLN STKAKLGRLLTPHMAGYSSETKL PEERPGSNICCSPISAVLQPPLLI PRQTGSGVDLQQTPTDLQLRVL TVIKKTNKQKGHPHONPICTSP SSKTKDRSTRQKVNKDQIELNS ALHQADLIDYRTLHPKSTEYTF FAAPHCTYSKIDHIVGSKALLS KCKRTEHTNCLLDHSAIKLELRI KKFTQNCSTTWKLNLLNDY WAHNEIKAIEKMFETNENKDT TYQNFWDTFKAVCRGKFIALN AHKRKQERSKIDTLTSQLEKE KQEQTHSKASRRQETKITAEL KEIETQKTLQKINESRSWFFEKI NKIETASKTNKKREKNPIDAIK NDKGDITTNPTIEIQTITREYYKH LYANKLENLEEMNKFLDTNTIP RLNQEEVESLNRPIITGSEIAIIN SLPTKKSPGPHGFTARFYQEQYK EE/PGTIPSETIPINRKRGNPP*LI L*GQHHPDTKAWQRHNKKREF *TNIPDDHQCCKNPQ*NTGKPNP AAHQEAYPP*SSGLHPWDARL
7510	37878	A	7564	3	377	DHNCATVLQPG*QSEIL*KEERE REREKKERKKERKKERKKERK KEGKQ*RGGRKKERKEKEIK KERRKGKKEKKEEKRRKERK KERERKKRRKEGRKKEYTRKA KRIHRPFEGNGSPLPAP
7511	37879	B	7565	1	834	
7512	37880	B	7566	1	915	
7513	37881	B	7567	1	666	
7514	37882	A	7568	330	793	SCWLCPGPCCPAQPQNTAPFIPE A*TPAMAERGPATAAGQLEFT GGALQTLFAWVSAAAAAEQWI LVNRKCCCLIVPLEVLSQRSTW PCIGLVMPVLPGLLRDIVHSDSI ASHYGVLLALYALMQFLCAPV LGALSDRFGRRLPGLLASLLGAT

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7515	37883	A	7569	991	1842	IQCHPHQATKNFLHRIGKNYFK VHMEPKKGPHCQVNPKEQS WRYVKQSKKIAVYAERSRCS GTEFAGTLILDFFSSRTAPSSRG R/P/GRLTRPGTPLRQSFQNDQ AATFAVQQYSLFCSLCC*YPGK QGLEWTSSKLQ/QY/LQLRERSS SPATEQSWMENDFDELREGFR RSNYSKLKEEVQTHCKEAKNL EKRLDEWITRITNVEKSLNDLM ELKNMAKELRDERTSFSSEFNQ LEERSVNIENQMNMKREEKFR EKRVKRNEQSLQEIWDYVKRP
7516	37884	B	7570	1	2448	
7517	37885	B	7571	2379	4476	
7518	37886	A	7572	1	570	
7519	37887	A	7573	1	1404	
7520	37888	A	7574	1	474	
7521	37889	A	7575	746	1215	PNINRFLKHYREPVPKKRERNY STLWPLCPSTLNKIYTIMSYLSP ATKEYPPFLLLLFQEC*AE*LLA LAVSQPLLSTTNCNKN*MVTW NGSLIPWSPCKINLTP*/PAVVL QNRRALDLLTAESGGTFLFLEE KCCCYVNQSGIITEKVKIEQGRI
7522	37890	A	7576	1	1178	MPESPTLLGRDILAKAGAIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFYQRYPLRPEAQQLGQ KIVKDLKVQGLVKTCSNCPDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPVNPYTLSSQIPEEA ELFTVLCLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPGQ FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQEQECHQATQV LLNVLATCGYKVSQKQAQLCS QQVKYLGVKLSKGTRAL/QQ*R TDRT*LSTSNCSNLRHSRGPSRG SLD*SQQLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIIRRRKKGL IRIYMLPLILSAPYDHLH
7523	37891	A	7577	1	1338	
7524	37892	C	7578	109	231	
7525	37893	A	7579	279	346	LLRLALLQ*QKEEWVLFCCGA
7526	37894	A	7580	260	393	VEVVILMPVVPNLPSIPARITKG RMGTLLRLRLGTT*LYKSCSV

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7527	37895	A	7581	3	2677	TKETCFIRGPKTPVPVTDWEGS LPLVFNHCRDTSVIIHPRFKGVR PRRDACLGPSPLAASPAFLGKG QAE LGPNSSSSASAPPPYNLFIA PPHTWSGLQFRSVTSPPPAQQF TLKKVAGAKGIVKRLKTD TAR SPWKTPRPSRTSPFRKAERTKG LLKIH LTKLSHQLKKDWITLLP LSLLRIQACPRNATRLATGQLG YPFISQSYVLVNGFQTVEDLCE AADLRVSVADLRVSVTALKVA RLELFVPPGGLVVS LASAVKLQ TFAVLQLIKAKRWDWGTLEQG AALIGEARD AQEPTGVGGSG MAGCRSRDLPRGKA AKARREI ERSAGLTIKKERCIRNGYSKEK MKLIVVSHGLHVNDLQHKLT FTKETYYTLARDSEKQKQGYL AGLEGAHANRVNQISDNLVV KTGALPPPYRTKGEKLYFYMSR QNCLFSVSGQLLQGFPPNGGQA APNPYALLSQIP EAEWFTVLD LKDDFFCIPVHPDSQFFAFEDP SNPTSQLTWTVLPQGFRIHLFG QALAQDLSQFSYLDLTVLCGVL KSPHIVWELNQIDTIKNDKGDIT TDPTEIQTITIREYYKHLTYNKL NLEEMDKFLNTYTLPRLNQEEV ESLNRPTGAIEAIINSLPTKKS PGPDGFTAEFYQRVADV KREE KDNEMLLVPLSDLLYQVHAPIP QLPEVLAANSPTCHLDPTTITES
7528	37896	A	7582	1	459	MAVRYTDENVLRKGTREAGT MMRLRGTTTECCADFAAWDVT HDALRATGGELPGAQVMLTTT ECGRHVD FCDRAVWVLP RMWG YPLALPGEMRKLYTVRMAGRD ILAKAGAIHNLNIGEGTPVRCP L/EGINPEVWKTEGGYRQAKNA RPVQVKL

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7529	37897	A	7583	3	910	YFSQPLSYDWDGALFFSHAFILM LESPTTLLGRDILAKAGAIHLNI GEGTPVCCPLLEEGINPEVWAT EGQYGRAKINARPVQVKLKDS ASFPYQRQYPLRPEA/LTKGFQ KIVKDLKAQGLVKPCNSPCSTPI LGVQKPNGQWRLVQDLRIIDE AIVPLYPAPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPGQ FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNRQQECHQATQV LLNVLATCGYKVSQKQAQLCS QQVKYLGVKLSKGTRAL
7530	37898	A	7584	158	1272	NPAARTPFVVIKKGKGRGRDIL AKAGAIHLNIG/GTPVCCPLLE EGINLEDWATEGQYGRAKNAR PVQVKLKDSASFPHQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGVQKPSGQWRLV QDLRIINEVTPLYLAVPNPYIL LSQIPEEAWEFTDLDLKDAFFCI PVHPDSQFLFAFEDPSNPMSQL TWTVSPQGRDSPHLFGQALA QDLSRFSYLGTLVLWPCIS/LCT *TMEQLQHRNKHHRFSRTSCF QSGNNPYLKPHLCKI*QYCRHN QLPMHQCPHDHLH*TRFI/PIML YLSPTTKEYSFFLLSEQEC*VD *VLALAVPOPLLSSTTNYLKNS MVTWNGLPPTWSPCKINLTS

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7531	37899	A	7585	1	2083	MPLLLQMIATPLQQSLISTEDEM DELTEVGFERWVITNFTTEEPSA LGFTPEHKGNGVHAGKGPLESS SPDPFLCGQEKQEKAGLLHRQ YPLRLAEAKQGLKIVKDLKAQ GLVTPCSPCNTPTLA VQKPNG QWRLVQDLRIINEAVVPLYPAV PNPYILLSQIPEEAEWFTVLDLK DAFFCIPVHPDSQFLFAFEDPSN PMSQLTWTVLPQGFRLSLHLFG QALAQDLSQFSYLDLTVLQYM DLLLLVTHSETLCHQATQALFN FLATCGYMYSKPKAQLCSQQ/R YLGKLKSGTRALSEEHIQPIIA YPHPKTLKQLRGFLGVIGFCRK WIPRYGEIARSLNTLIKETQKAN THLVRWTTVEVAFQALTQAP VLSLPTGQDFCSYVTEKTGIAL GVLTQIRGMSLQPV AHLTK EID VVAKG*PHCLRVVVAVAVLVS EAVKIIQGRDLTVWTS HDVNGI I.TAKGDLWLSNDCLLKCAQLL LEGPVLR LCTCATLNPATFLPD NEEKIKHNCQQVISQTYATRGD LLEVPLTDPDLNLYTDGSSFVE KGLRKVG YAVVSDNGILESNPL TPGTS AQLAELIALTWALELGE EK RANIY TDSKYAYLV LHAHA AIWKEREFLTSE RTPIKHQEAIR KLLLA VQKPREVA V LHCGRHH K GKEREIQENCQAYIEAKRAAR
7532	37900	A	7586	80	678	LCCNMPAAQHRERASNESRHG GCCPP/PWLLSS/APPHDAFTTPQ EAVLSAPSALPSSAATSLLSLT PQQMFCSKTAGPKFSSNPPIPR LKAPTSSC/PL*PQAAPSGNAHC Y*GHRRGRTVPEDPGCLSPRAR PHRTSGTSSPPLQPSRTIPPASS APKQGDAGSPPYQAVPEKNKP GATPRTCAESPKRLPRPGPKSFL

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7533	37901	A	7587	3	804	GLLQATALQPAQI*IFL*KKEE EEEEGGGEGEEKKKKKKTEEE EEEEERKK/EEEEGEEEEEEEE EEEEKEERTGAGDSSEDEGFDEI PSPGDSRQKTEGNAANIISGCD QRYEESMDLGRGIVSGHRYI FTRVSPLEAIGELLFPFSVAPA QGGGLGRRVDQLALPMGAQSL ERPFCVDGGSRPPLNYAVSSVE DLLNGNNFKCPTTLRTIEITVGN LIISPRQKQLNANIGKNFNAAEN HENAKTTTTSSTVGDATHLTA
7534	37902	A	7588	3	191	SSHPVFSRWWLSPHQSQCYT* GSGAQNLTAASPPFCVCRGDRGN HLRKDTKVEVKRKTCLW
7535	37903	A	7589	1	1899	HVGASDPDAGPGWGLTSRPR LVTPRSAPRGAFOGATVGLAP VEGMCRAESSGGVSTDHSELPI GAAATMAHEIGHSLGSHDPD GCCVEAAAESGGCVMAAAT/G VRGWGVGAAAGRLVLGTSSA AFLWSSLFLCKMGIMIIVSAS GWFMRLLKGGKLRQSGFTV*R LFSE*PGEVTPTPGGAPSGRST LGPGLLTIGASSSPVPLVV*LCA GYFPSLGSARLAAVAKPRGGD QRSAGVGGLSLHAQCPPRAGR HPFPRVFSACSRRLRAFFRKG GGACLSNAPDGPLVPVPPALCGN GFVEAGEECYCVS/GQECRDLC CFAHNCSLRPGAQCAHGDCCV RCLLKPGALCRQAMGDCDLP EFTGTSSHCPDVPVLLDGSPC ARGSGYCWGACPTLEQQCQ LWGPESHAPAEAFQVVSAG DAHNGCGQDSEGHFLPCAGRD ALCGKLQCGGKPSLLAPHMV PVDSTVHLDGQEVTCRGAAL PSAQLDLLGLLVEPGTQCQPR MVCNSNHNCHCAPGWAPPFCD KPGFGSGMDSGPVQAENHDTF LLAMLLSVLLPLLPAGLAWC CYRLPGAHLQRCSWGCRQGPC VQWPQRWPTQGPVPPGRRSPHG VGPHSHWTALAPGP
7536	37904	A	7590	2	280	
7537	37905	A	7591	1	1266	

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7538	37906	A	7592	1	458	LQSQSFIHISQKTIKKCLDLFLFLAEKENYKNFFFAFSKNLAKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGSPCWCLVFFSLSCPCVEGSKLRVSSPIPSLLLTAGLDVVYCGLFYFLHFVCLKLYAK
7539	37907	A	7593	1	862	
7540	37908	A	7594	3	437	IPEF/LNF/IRGVVTLGLPLNISREMLQSKILKVIKKNIV*EC/LFELLSLEAEDKENYKFFYEAFSKNLKLGIEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANSFAFVERVPLSHLAPPAGV
7541	37909	B	7595	106	1966	
7542	37910	A	7596	453	719	ARGSKHTGLIAQWAHEQSGHGGRAGGYAWAQHGLPLTKADLPAMATAECPIQQRPTLSPRYGTIPW/WAWDAPGGRGCWRLQKAGE
7543	37911	A	7597	3	837	PECVIGIDILSSWQNPHTGLTRVRAIMVGGAKWKPLELPLPRKIVNQKQYHILGGTVEISATIKDLKDTEAVTPTTSPFNSPIWPVQKTDGSRWMTVDYCKLNQVVTPIAAAVPDV/VSLLEQINTSPGTWFEWSPK/KALQQVQAAVQAA LPFGPYDPADPMVLEVSVA DRDAIWSLWNAIGESQRRPLGFWSKALLSSADNYSFPERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSQAQQRSIIKWKYIHDWVRAGPEGT
7544	37912	A	7598	1	399	
7545	37913	A	7599	126	392	ARGSKHTGLIAQWAHEQSGHGGRAGGYAWAQHGLPLTKADLPAMATAECPIQQRPTLSPRYGTIPW/WAWDAPGGRGCWRLQKAGE
7546	37914	A	7600	1	1677	
7547	37915	C	7601	37	465	
7548	37916	B	7602	1805	2542	

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7549	37917	A	7603	3	865	VIPTTISQNFPIWPVQKTDGSGW RMTVDYCKLNQEENFNQVDR MTHSVDTTQPLSPA THVITQWA HEQSGHGGRDGGYTRVQQHGL PLTKADLATAGKVFQKAV*AL N*HSIYGTLSLARIHRSRNQGV EVEVAPLTISPDPAPAKFLLPVP PTLRSGALEFLVPEEGMLPSGD TTVPLNWKRLRPPGHFGLLFPL HQQANKGRLSPHSRERGTSVFA SSNSQPVTALNNEPAGPNKRDI GKAKGLKFHHGPHRQERDML E/SML*PWGYPVGKQWNHLIK KQGRH
7550	37918	A	7604	3	857	VTASLSPVVATSPQPMPLPSDFP PLSEINPMLEATVIASPKIAR QDNVDSQEPPTTPQFSSRPITR LKSQWAPRGPECVIGIDILSSW QNPHTIGSLTGRVREGYMVGKA KWKPLELPLPRKIVNQKQYCIP GEIAEISTTIRDLKDTGVVPTTS PFNSSIWPVQKTDGSWRMTVD YCKLDQVVTPIAAVPMVSL VKQINTSPGTWQHITHLDVLLW RIYQVTQKAASFEGWQEKEA LQQVQAQVAILCHLGHMTQQ IQWCLRRNGEMCDYILYGL
7551	37919	A	7605	1	608	MAPGMVPIPPPGKYHSPKKLIY STPPKPGTYGISDSLSQYPTSAK AEPVPTHKNPRRESPIHSSPSSF TDG/PSNPSFGDARPHQNKTS RGRPAQRVPTTTTTPAPPARS PNSAHSPAFRDLPFRAEKGTA ARVPREPHSPAPKNGSLQPP AGELLQRGARTTLPRILGTAPG PHLPGCSAPPAP*RPAAPIGL
7552	37920	A	7606	179	544	HTRLHSHPLRGFPWSLHFSVSI RSPASGHLEFPFARSSGSGSTS PLSFGAMITTEKQALGGRAAFPP KYYK*AQGRAACFVLTSQQQPS WQ*GVTVTATGSPMHRGTFWH SCTGTPGSGDR
7553	37921	A	7607	90	653	VPGERPRGSGSPQVLPYGPTWC SSNTPEPQSLRAPQ*LQVPPVLQ SRGQR*QPQMP/VRSPKAP*V QMPPTPSSAKGPHLDGVRVPA ANPE*PTAGPTRAAILRATPAPS LPMPGTNRPSRGNLSQDSAPA SDAGWPPTEAVTCTP/PWSREN PQRNL*AHPRQGRPVPGTERR NRRGGAGCRQL

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7554	37922	A	7608	1	804	
7555	37923	A	7609	28	682	TTCEMSDLEDDDETQLSAHG/T LAALQEFYAEQKQIEPGEDDK YNIGIIEENWQLSQFWYSQETA LQLAQEAIAAVGEGGRIACVGS P*CLPET/HESCAEKTFSIYFEY DKRFAME*KEILIFYDYNPLD LPERIAAHSFDIVIAADFPFYL ECLRKTSSETVQVLTGRKILL/CT GAHHGRTGSRTPLE*RCARLFP RHRTRNFGKWSFRLVYVNL
7556	37924	A	7610	1	611	MAPKAKMEAPAPPEAEAKVKA LKAKKVVVLKGVHSH/KKKKKKI RTSPTR*/PLRLRRQPKYPWES VPRRTSTQISSGERPLENKQPRY PRESSPPPGEQAPKYVPEERSPG ETRLDHLCLSIKFP/LTH*VLP MKIEDNNTLVPLVNVKANKH QIKQAVKKLYDI/DVAKVNTLI RPDGEKNGICSDLAPDYDALG CLPTKFGII
7557	37925	A	7611	1	1035	DKDSLDCSCKTSCSYNCSKPRS SWQDQDISSGTGLHSRLTANT GKESKTVQASLDQQLGRLLSVS LRLGVEPSLQSSGNLLVSLLSR FITYKVTIVEWVKTYALGLDLK KSERPGFESELHSHNSCECAVS HLKPVHLRVSPMGHSEYYLV TADYSEANGSQSAGDEFFQTQS FPSRQQALFRPKIQTIREYYKH LYANKLENLEEMDKFLNTCTL QRLNQEEVESLNRPIGSEIEAI NSLPTKKRPGDGTAKFNQRY KEELVIYKKFQIPCIPELNSTIS ANSTNADTCTPKYVTFNSKGT AQNADSDSAGLE/CEPDVLIH** SLRLGVEPSLQSSGNLLVSLLS RFITYKVTIVEWVKTYALGLDL KKSERPGFESELHSHNSCECAV SHLKPVHLRVSPMGHSEYYLV TTADYSEANGSQSAGDEFFQTQ SFPSRQQALFRPKIQTIREYYK HLYANKLENLEEMDKFLNTCT LQRLNQEEVESLNRPIGSEIEAI INSLPTKKRPGDGTAKFNQRY YKEELVIYKKFQIPCIPELNSTI SANSTNADTCTPKYVTFNSKGT AQNADSDSAGLEWSLMFCISD KVSDDDDADA VDS

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7558	37926	A	7612	3	573	KEETFSAWYVDGRVLVVIVTF GIILPLCLLKNLGYLGVTSGFSL SCMVFLIVVIYKKFQIPCIPEL NSTISANSTNADTCTPKYVTFN SKTVYALPTIAFAFVCHPSVLP YSELKDPSQKKMQMVSNISFF AMFVMYFLTAFGYLTIFYDNV QSDLLHKYQSKDDILITVRLA VIVAVILTVPLV
7559	37927	A	7613	1	831	MSELEDRLFENTQSEESKGKRI KKNEVCLQDLKYSCLKRANLRD TGLKEEVIYKKFQIPCIPELNS TISANSTNADTCTPKYVTFNSK KKMQMVSNISFFAMFVMYFLT AIFGYLTIFYDNVQSDLLHKYQS KDDILITVRLAVIVAVILTVPV LFFTVRSSLFELGLRKQRFNLW PSIPVVTICILLVVINLVGDLHTP P*RIFFGVVGSYILLNMLFILP/S IFFILKITDQDQDKGTQRIWAAL FLGLGVLFSLVSIPLVIYDWACS SSSDEGH
7560	37928	A	7614	1	1118	FNCEIFYF/SYGDEEISKTALN ERRGEIKIRKLDFEKIVSYQVDI KASDGAAGLSGKCTVIIQVVDIN DNAPELTMASFTSPIRENSPETV AALFSIQDRDS/FALRSLDYEAL QEFEFRVGASDPGF/PALSSEAL VRVLVLDANDSSLFVLPPLQN GSAPECTEL/IPGRAAEPGYLVTK QLLKATEPGLFGVVAHNGEVR TARLLSERDATKHRLVVLVKD NGEPPRSATATLHVLLVDGFSQ PYLPLPEAAPAQAEADLLTV YLVVALASVSSLFLLSVLLFVA VRLCRRSRAASVGRCSVPEGPF PGHLVDVSDTRTLQRYKYEVF LTRGSGTNEFKFLKSVIP/QASG RCE*WEEKSNFVNGFGFN
7561	37929	A	7615	1	764	TRPGAHGASLTDLANLSEGVSL AERGSFGAMDDPFKNKALLFS NNTQELHPDPFQTEDPFKSDPF KGADPFKGDPPFQNDPFAEQQT STDPPGGDPFKESDPFRGSATD DFFKKQTKNDPFTSDPFTKNPS LPSKLPFESSDPFSSSSVSSKGS DPFGTLDPPFGSGSFNSAEGFAD FSQMS/KGKSTPVSQLGSADFPE APDPFQPLGADSGDPFQSKKGF GDPFSGKDPFVPSSAAKPSKAS ASGFADFTSVS

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7562	37930	A	7616	1	817	MGFCHVQASLKLLASDPFGTLDPFSGSGFNSAEGFADFQMSKTDPPQRSELKVGTAARLVTRLDPVSGPHVTR*PELTVLVPSDSCRASPDAGSVVGAHL*GLGTTGAADGGTPNSNRSFVLGVIIIVVWSMCQLYLVP PPPSGPFTSSLGAGGFSDDPFKSKQDTPALPPKKPAPPRPKPPS/GHRLPVPDGGGPGPPCSP/DPE*QQMPWDVPVWGA RGSPPSPCPGPRKCRMCVVP RV IQHPSLLLPSLVGRRSQQIWRSHMPMAAPP
7563	37931	A	7617	3	1039	GSMLFQQVPMVEIDGMKLVQTRAILNYIASKYNLYGKDIKERALYAMTHDDEAELRTPAACCKL*SECQFRTRVDAVRTMMIP/AFTQVLKSHRQDYL VG NKLSWADIHLVELFYVVEELDSSLISFP LLKVKLLASSVKPVPLPSALRWPAHAVAQNI VTSWLTGGRFIELKT VQILDRLELEKPCIDAEDECFT EWSTFTLLKAWDEY LKAWFALHLL EAMFQPSDSGKSFIFNMS VGYNLEGQPLNPKNYSQGVPRVLKSHRQDYL VG NKLSWADIHLVELFYVVEELDSSLISFP LLKPHTHVDNTKKGSHPHMCAITDYVNNPNDRMPQREITFVS
7564	37932	A	7618	2	698	NQKTVTMAGKPKLHYFNGRGRMEPIRWLLAAAGVEFEKFIGS AEDLGKLRNDGSLMFQQVPMVEIDGMKLVQTRAILNYIASKYNLYGKDIKERALIDMYTEGMADLNEMILLPLCPAAEEDAKIALI KEKIKSRYFPAFEKVLQSHGQDYL VG NKLSRADISLVELLYVVEELDSSLISNFP LLKALKTQNPATLPHG*RSFLQPGSPRKP PADAKALEEARKIFRF
7565	37933	A	7619	102	825	RNLQETA IMAEKP KKLHYFNARGRMEPPRWLLAAAGVEFEKFIKSAEDL DKLRNDGYLMFQQVPMVEIDGMKLVQTKAILNLHLP ANYNLLMGKDIKGREP*FDYVF*EGFSQILGLN*SSFLPVC/PPELEKDAQALPLIQEKTKNRYFAFEKVLKSHGQDYL VG P TSLSRGWTFIWWELLYYVEGA WTPRLISSP LLKALKTRISNLPTVKKFLQPGSPRKPMPDEKSLEEARKIFRF

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7566	37934	A	7620	2	1256	CHCGPP/VKVEAYGSQVLKGVLAQVQLTVGPVGRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNPIWPVQK TDGSWRMTVGYCKLNQVVTP AAAVPDVVSLLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEI NMTKIQQPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHPIHLPIYRV SRKAANFEWSPEQEKALQVVQ AAVQAAWPLGPYDPADPMVLE VSVADRDAWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGRWWQLAE RQDSRDREAAIGERQETA VGKT ARDGEAVCD
7567	37935	A	7621	1	518	MTVDYCKLNQVVIPIAAAVSD VVSLLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLQWYINSALCHNL IRRDLDGSLPLDITLVHYIDDI MLIGSTIKWVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG
7568	37936	A	7622	1	696	
7569	37937	B	7623	1	1014	
7570	37938	B	7624	1	837	

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7571	37939	A	7625	1	2592	MVRKAKWKPLQLPLPRKIVNQ KQHRIPGGTVEISAITKDLKDA GVVIPTTSPFNSPIWSVQKTDGC WRMTVDYCKLTQVMTPIAAV VPDVSLLKQINTYPGTCKIFLG VQWCGACRDI/PSKVKDKLLHL APPTTKKEAQLVGLFGFWRE IIIPHGLVLLQPMYQVTRKAASF EWGLEQEALQQVQAAVQAA LPFGPYDSADPTVLEMSVADRV AVWSLWQAPIGESQWRPLGLW SKALPFSADNYS PFERRLLACY WALMETEGLTMGHQVTMQPE LPIMNWVLS DPSRHKVGHAQQ HSIIKLKWIYICQARAVPEGTC\
7572	37940	A	7626	20	238	*LNKEVAQMP/MGTTTRKWTAA ALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGT WKKHDWKTGDNEIWGRGIWM DCSEWSKTVKIFVSHAHEPSGH GGRDGGYAWAQEHELSTKAD LATGIVEPCICQQRPRLSPRYG TIPQGGTFILTGINTYSIYGFAYP AHNASAKITIRGLTECLIHHGI PHS/IVSD*GTHFAKDVETRIH RPRNQGVVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLE GGTLPPGDPTTIPLNWKRLRPR GHFGLPLPLSQQAKKGVSULA GVTDLDYQDEFSLLLHNRVTA AFPSLLHSSFAYLDNMIEKANK CHVEGDVHVS DPAQRRECDRH
7573	37941	A	7627	3	229	
7574	37942	A	7628	1086	1369	ETGMLPLRLLPFLSDFAGPLH TSIMPTRRFCSKSPT*HTLATAL SQGLS*GT*NEASLTKEKVGKN RCRYSYSPPSGIREGKAQLCFY THWK

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7575	37943	A	7629	1	1805	MSGRSRGRKSSRAKNRGKGRA KARVVRPAPDDAPRDPDPSPQVS LGEDTQAAQVQAGAGWGGLE AAASAQLLRLGEEAACRLPLDC GLALRARAAGDHGQAAARP GP GKAASLSERLAADS VFVGTAG TVGRPKNAPRVGNRRGPAGKK APETCSTAGRGPQVIAGGRQKK GAAGENTSVSAGEEKKERDA GSGPPATEGSMDTLENVQLKLE NMNAQADRAYRLRSRKFGQLR LQHLERRNHLIQNIPGFSGQAF *NHVLLASFLNSQKEVLSYLN SLEVEELGLARLGYYKIFYFDR NPYFQNKVLIKEYGCGPSGQVV SRSTPIQWLPGHDLQSLSGQNP ENNRSFFGWFSNHSSIESDKIVE IINEELWPNPLQFYLLSEGARVE KGKEKEGRQGPQPMETTQP GPLSFVWVAVSPSWLPGQQGP QELPVDRLPLVHETHYTPPQL SRNPTGCQTDGRAGLPVTPCDK KALPCAQCFSHLLYCMGLQP RQKEKINPEVSSITNVPK DME KVHAGALDKPMCGRQGKESQ GATHHATPSAISPAPSHPLGSSE TLIDGLAHFLEHSQINPSLLSR VLIQRQHLRHVAVTNG
7576	37944	C	7630	66	206	

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7577	37945	A	7631	3	1643	VQASQAEADQQQCTCLKQLQ/S\ QLSRL*KQAIELREAVEQHKVK NNDLREKNWKAMEALATAEQ \ACKEKLHSWTQAKEES/ERNQ LCLIEAQTMALLALLP\ELSVL AQQMYTEWLQDLKEKGPTL/L KHPPAPAEPSFGTWAFQV*GEA E\ETQSTICRAEF\DQYRSILGGD GRALLRDLQKSVEEEEQ\W/R AKVGAAEEELQKSRVTVKHLE EIVEKLGGELES\SD\QVREHTL HLEAELEKHMAAASAEQNYA LLEVAG\LRQLLE\SQSRLRPP KNRNPQKTEPMSFALGQASS*V KLKSHVED\GDIAGAPA\SSPEA APQPSRDPRSA*RTQLELDQKPI PWRMRQTTSRQKLHGSPFEAE SDLRACSVYKEGFWEKLPHSA APPRSFFRNRRRAFTA*RRDLEK RGRSLTSD\LGARPRRLQELSE RRTQEQLGKGRRTRVKKLQEI/Q L\EKAEDGSS\SKEGTSVL.SFLFG KKKLLFQLYQNALTHSFTIKPT NLHSVYPGPNFV\LREKAHEET SLFRRPQEVRTFPGGPILLNGTC
7578	37946	A	7632	3	247	
7579	37947	A	7633	3	389	GQEFSPKVY/FVNQTMGN/SCG PIGLFINAVANNQDKLGFY\GP LLNQFLF*NR*KCPPKDRAKCF ER\NEAIRAAH\DAVDKEG\QCR VDDQGEFFFLFCLQNVDPSPM NLDG\RMPPFRGPMAPSFRTP

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7580	37948	A	7634	1506	3135	RGLGGGLAEQELQPWSPERSPV HNN/RM/QEKS LKDL MEL KTM AQELRDECTSLSSRFQLEEKV SVMEDEFINEMKQEEKVREKRIK RNEQSLQEIWVYVVRPNLHLIG VPESDRENGTKLENTLQDIQEN FPNLRQANIQIEIQRMFPQYS SRRA TP RHIVRFTKVEMKEKM LRAAREKEIQTTIREYYKHLYT NKLLENLEEMDKFLDTYSLPRLN QEEVESLKRPTGSEIGAINSLP TKKSPGPDGFTAIFYQRYKKEL VPFLLLKFQSTEKERILPNSFYE ASIIIPKPGRDITTKENFRPISL MNINAKILNKILANQIQQHIEKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTNEKNHMIISIDAEK AFDKIQQPFMLKTLNKLGDGT YLKIVRAIYDKLTANIILNGQKL EAFPLKTGTROGCPLSPLLFNIV LEVLAIRAIQEIKGIQLGKEQ VKLSLFADDIMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI
7581	37949	B	7635	1	594	
7582	37950	A	7636	434	744	TLACLARLGKFSWHISCRVFSNL VPFSPSLSGTPIRRRFGLNVRVT ATRILRFSDRLKRRRTTRLYPPT GSEGPTPTESR*LLAQQSEIKLQ GGSEAGGGAPA
7583	37951	A	7637	1	1077	
7584	37952	A	7638	1	348	
7585	37953	A	7639	1	831	
7586	37954	A	7640	275	457	LIAYQPK*AQDYMDSQLNSTRG TKKSC*GRL*GSGVIHIGSMVPV TRTAGLPFFAGPCR
7587	37955	A	7641	341	504	ILRFSDRLKRRRTTRLYPPTGSG GPTPRESR*LLAQQSEIKLQGGN EAGGGAPA
7588	37956	B	7642	1	627	
7589	37957	A	7643	121	375	DGQQIALHRLALRELQQAVH AGLPQQA KILFDGGSEIGIKH*L RCAHCPLSSRETCRASCINESAT RGERPFAYWAPGWFFHHQ
7590	37958	A	7644	3	479	
7591	37959	A	7645	382	642	
7592	37960	A	7646	273	1464	

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7593	37961	A	7647	76	1763	IFGITRFLPFIYQKIHIFSKEQLPD LHSHFSDLNLEAHMYASQWFL TLFTA KFP LCMVFHII D L L L C E G LNIIFHV ALAL LKTSKEDLLQA DFEGAL KFFRVQLPKRYRAEEN ARRLMEQACNIKVG VYTGT E L Q*DFSLDSLVSWSWDS S C C G K ASWQDDGRNLHYGSL*RPCFQ PAAR*RLPH*SGGHQQAQVYG TNK K L K K Y E K E Y Q T M R E S Q L Q Q E D P M D R Y K F V Y L * V T P A V A F I L G I F I R S * E K E R G K R K W L S T F K N E T K R K N G K V L F * L C M S Y P Q R L L A G E L F Q D * H K D V S N L P L S V E N V K N T N S L G R K N K N H K \ R E N R R L Q E A S M R L E Q E N D D L A H E L V T S K I A L R N D L D Q A E D K A D V L N K E L L L T K Q R L V E T E E E K R K Q E E E T A Q L K E V F R K Q L E K A E Y E I K K T T A I I A E Y K Q I C S Q L S T R L E K Q Q A A S K E E L E V V K G K M M A C K H C S D I F S K E G A L K L A A T G R E D Q G I E T D D E K D S L K Q L R E M E L E L A Q T K L Q L V E A K C K I Q E L E H Q R G A L M N E I Q A A K N S W F S K T L N S I K T A T G T Q P L Q P A P V T Q P P K E S T
7594	37962	B	7648	1	618	

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7595	37963	A	7649	1	2375	MAGAPPPASLPCCSLISDCCAIN QRDSVGVVRPSKPGAGYNLVVR RFLSLLEKRSIPVGVTRFSRCRP SPLSLTRKGNSLTPCASRIINMH FQAFWLCLGLLFISINAEFMDD DVETEDFEENSEEIDVNESELSS EIKYKTPQPIGEVYFAETFDSSGR LAGWVLSKAKKDDMDEEISIV DGRWEIEELKENQVPGDRGLV LKSRKHHHAISAVLAKPFIFAD KPLIVQYEVNFQDGDCCGAYI KLLADTDDLLENFYDKTSYIIM FGPDKCGEDYKLHIFRHKHPK TGVFEKHAKPPVDLKKFFTD RKTHLYTLVMNPDDTFEVLVD QTVVNGGSLLDVPPIKPPKEI EDPNKKPEEWDERAKIPDPSA VKPEDCALGLELWSMTSDIYFD NFIICSEKEVADHWADGWRW KIMIANANKKKHKDTEYKKTDI CIPQTKGVLEQEEKEEKALEK PMDLEEEKKQNDGEMLEKEEE SEPEEKSEEEIEIIEGQESNQSN KSGSEDEALAEQPREGPGVPGP IPPKRPSRSPPEPRAAKRLPTQE LRGESYTSASGTARGSPKER LGLTTKTGEKVAQGFCREPGL RRPPNAQARDRSSRAPATHRKE LKPEREHISCSRSHIRYQEWVSL RDTVHRNLVLDTKRHPALILVE YKERTSSPATEQSCMENDFDEL REEGFRRSVITNFSEKEDVQT
7596	37964	A	7650	914	2786	
7597	37965	B	7651	1	2369	
7598	37966	A	7652	333	752	MSYVSRVYCGGRKNVATVSKG WAGSLA WPGGFPKVKGGGS WRPSGGV/DVAA PVRARLALL SGPIASESPLTTNPHSHSARRPR TYI/GHAPALRVTN/PESFSYWG TRGPSATMACDGLTRTGHSPPS RARSPLLCARSL
7599	37967	A	7653	1	177	RPLPSRPHAAPPGHHTISSGPCG HRKFSPKAGDSNTPRTSRPRV SCALPPDVRGWSLS*KWNQIW YHTLPQPQENTPKSQENKPKSK PQPTQR*TRGPW/PSSRCRVRSG /THRRPGLFSL*KQ/PSESIHRSR ALSAFTPAEMISTLPPPTTSKSPL AARAAPPNG*SPKAGDSNTPR TRSRPRVSCALPPDVRGWSLS

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7600	37968	A	7654	1	1430	MQDTCSEIISPADFTPTFSSSLKIR FSTDSPSQIFKKKHCIQKIVLILLP KNSYTRRLVSNQMYLESFEH QCRKTHILCKRTAGSGPFCSCPT GQPRHNSSASKCPASERGLCLK/ PKSKREKREPVPVAPAPLHAAP SSPGLGAPQLR*PGRTRSGFRD HVGSGPPRAGPRLFAPRPVLS RCSANPSGSPHTQSPKQSSGTQI SGRADQVCGCWIRKRGVPGAA RGSPGCARTCHSRGHPHAAPFP QCNSLAPSAAGLWRTQNAGP SG/HAQPSCPPVPPL*PPHPH*G LSFSSCSRSWVPNTTP/EPREGE GQVPGRRASAPGASFSAPGT/P RAPQLPHFPVPAQSPAAVAA SSECKREARRSPGASALHLP KSARPRQAPCPTLTDGGHIFPAS AARP*HKGHQTAEGKNPGRAD TSTSPFATFFISGGEKSRSPVL PERTRQREEAPGPPSSPLRGLW LTFWVFL
7601	37969	A	7655	1	609	
7602	37970	A	7656	3	649	AKD/ELHIVEQGHDIRGRSIKIT/ LATLKMS/VQPTFS/LGGFEIQPT VV*GLKCVSGPCHISGQHLVA/ VEEDAEESEDEEEENVKLLSISER RSAPGVVSMVPQKKVK/LAAD EDDDDDDEDDDDDDDDDDDFD DEEAEEKAPVKKSIRDTPAKNA QKSNQNGK\DSNPYSHPRSQG/ QDPFRKQKTPKTPKGPSSVE DIKAKMQASIGKKRIEVLGTy
7603	37971	A	7657	1	1013	PWCDSVLRGCSLEQRFSFISVRL SYLSACRHPMEDSMMDMSPL RPQNYLFGCELKADKDYHFKV DNDENEHQLSLRTVSLGAGAK DELHIVEAEAMNYEGSPIKVT\A ATLKMSVQPTVSLGG/FEITPPV V/LRLKCGSGPVHISGQHLVA/ EEDAEESEDEEEDVK\LLSISGK RSAPGGG\SKVPQKKSKTCML MKDDDD\DEED\DDDD\DDD DF\DEE\AEKAPSERNL\YRDT PS\AKNAQKSNQNGK\DSKPS TPRSKGTIPSKKQKTPKTPK\ GPSSVEDIKAKMQASIEK\GGSL PKVETKFINYVK\NCSRM\TDQE A\AQDLWQW\RKSL

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7604	37972	A	7658	9	271	GRVCKALWHSDWHTARVLCIN STTTITASCNP/RHTARRSI.TTPT *MCRLENWTKNLLFNGPVPVVL VMSSLFIASVFMHLHIWKGK YTRS
7605	37973	C	7659	189	500	
7606	37974	A	7660	5	291	ATPSPSPPG/VPT*RPELLGP RR ERLLGPEGS/PGGGALPGVPPSR FVRTASSTLFLPPSRPAFPSSIP LVPSPPRHCARSRETWPRTLRI G SAP
7607	37975	A	7661	1	431	LALQFSFLQN RQGLNLLIAEKG RLCIFLNEECFCYLNQSGLVYD NIKKLKDRVQKLANQANNYAE PPWALSINWMSWVLPILSPLIPV FLLLLFGPCVFCLVSQFIQNR IQ AIANN SI*QMLLLTTPQYQPLPQ NLSSVESLPL
7608	37976	B	7662	41	1547	
7609	37977	B	7663	74	298	
7610	37978	A	7664	3	647	ELWTRGPRKRQNGSSKPLWLL YGESGAQKSVVEVT KPRLLWP QWQHRRARRPCLQQAPCSSRPH APASLPSSSPTARDTKHRAQV KTTDSGARRRDGRVLGVLEVS RSIADGQYKRCGVTSVPD IRR C/QLTPQ*PGSILLACDGLFKVF TPEEAVNFIL/SCLEDEKIQTR EG KSAADVRYEAA/CNMLANKA VAAGARPDNVTVMVVRUGH
7611	37979	B	7665	1	1302	
7612	37980	A	7666	3	1268	SCARVAAWGGKLRRLGLAVSRQ AVRSPGPLAAAVAGAA LAGAG AAWHHSRVSAARDGSFTVSA QKNVEHGIIYIGKPSLRKQRFM QFSLEHEGEYYMTPRD/FLFSV MFEQMERKUQSRS*QKRFIEDT LSGIPTAGCGSFFQRPWAIKGL ISYNRVIFFALQSSLNPIPGFH VAFKMLD TDGNEMIEKK/ENFL SCRRS*VNKMT*LT VKTNETWI SGSNK*KNLKL/DTLQMRFFG KRGPRKLHYKEFRRFWENLQT EIQGN/VEFLQFSKGLSFMKR RR TLQSGYFFSTNTENKDIYWK NV REKLSAGESISLDEVKAFCHCT RQIGTL CY/SAMQMFTLAHRPV RLAEFKRAVKVATGQELSN NIL DTVFKIFDLGDDECLSHEEFLG VLKNRMHRGLVGTTTSEYTRIL EVCEERKH

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7613	37981	A	7667	2	342	QNRGPGRT*DFLPNS/VGEKILS FCNCSLGSIGALGPACCRVLSEL SEEQVFHVNYLDVEELSLRLC QCLVELSFQLATAYHGSATTRE AARGEAAACRAHLMFWCLCIWQ FCRL
7614	37982	A	7668	1	1166	VGCVLGRVEAAVTVPAGTTEE GMSEEEQSGSTTTGCGLPSIEQ MLAANPGKTPISLLQEYGTIRIG KTPVYDLLKAEGQAHQPNFTF RVTVGDTSCGTGQGPSKKAACH KAAEVALKHLKGGSMLEPALE DSSSFPLDSSLPE DIPVFTAAA AATPVPSVVLTRSPAMELQPPV SPQQSECNVPVQALQELVVQKG WRLPEYTVTQESGPAHRKEFT MTCRVERFIEIGSGTSKKLAKR NAAAKMLLRVHTVPLDARDG NEVEPDDHFSIGVGFRL/DVL QNRGPGCTWDSLNRNSVGEKILS LRSCSLGSLGALGPACCRVLSE LSEEQAFHVSYLDIEELSLGLC QCLVELSTQPATVCHGSATTRE AARGEAAARRALQYLKIMAGSK
7615	37983	A	7669	2	328	
7616	37984	A	7670	181	1271	LEASLDQH*ASVHSFRSHIHVIS RTHRKISQRPSELDAEHAQKV LEMEHTQQMKLKERQKFFEEA FQQDMEQQYLSTGYLQIAERR GEWGLGLLVWGLTGACGCHD SSWGLVRWYKCYSFKFVDEPC LQFERNCKPIGSMSSMEVNVND MLEQMDLMDISDQEALDVFLN SGGEENTVLSPALGRVDKLALA EPGQYRCHSPPKLQQWCGSVM NSSQRFDMLHSGNFEIHLSELL VVKDWRLQGGADSPAGLTGNS SLFVRQAFRGVPAMGKAMGSS QVLQAPGPESSTCQNEITLQVP NPSELRAKPPSSSTCTDSATRD ISEGGESPVVQSDEEEVQVDTA LATSHTDREATPDGGEDSDS

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7617	37985	A	7671	60	965	QRGVGGVGRGRQRQQPEA* GEETAAAAMLETLRRLRLSVQ QDFTSGLKTLSDKSREAKVKSK PRTVPFLPKYSAGLELLSRYED TWAALHRRRAKDCASAGELVDS EVMMLSAHWEKKKTSLSVELQE QLQQLPALIADLESMTANLTHL EASFEEVENNLLHLEDLCGQCE LKRCKHMQSQLENYKKNKR KELETFKAELEDAEHAQKVLEM EHTQQMKLKERQKFFEEAFQQ DMEQYLSTGYLQIAERREPIGS MSSMEVNVDMLEQMDLMDIS DQEALDGLPELWRRREHCAVP
7618	37986	A	7672	1	124	
7619	37987	A	7673	3416	3920	CCLIKNDIKEKLHYSDCRLNVG QPCILPRNAFEFDLLIFYLGNLH FYISEIGLLGYCTFFFFFEMESC SLTQAGVQ*CNLGPLQLPPGL E*F/SCLSLPSSWDYRHHVPPHWL IFVFLVEMGFCYVQGAGLEFLT SGDPPTSASQARITGVSHHAQ PGYCILILGFC
7620	37988	A	7674	1	387	

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7621	37989	A	7675	1	1827	MKKVGGRVFWAKERASAEAL RHELAGLLKCKKGSAADADQG GLGQGCRRRHRSRWEFGTRGAS RAARLGNEEQDAASAGPGPNG CGHLGAEEPSAAASGMDQCVT VERELEKVLHKFSGYGQLCER GLEELIDYTGGLKHEILQSHETC LSVLLSLPMVMAGSGLNKVL QLCRFLHMKTTGEMNYGFHLA HHMALGTSIFGEEGRYSLSTS NSSIAALLCALYPHFGFTALD NRYHLQVALR/HLVVLAAEPRA FLVPVCGGTQTRPCYALLGSLP YKGTQWYEQTKEDLMAPTLL PELHLLKQIKVKGPRYWELLID LSKGTQHLKSILSKDGVLYVK LRAGQLSYKEDPMGWQSLLAQ TVANRNSEARAFKPTISAFSTSD PALLSFAEYFCKPTVNMGQKQ EVLDFSSVLVECVYPRETPAE MLPAYIAMDQLIRRLGEREMS ETSELWQIKLVLEFFSSRSHQE RLQNPPPLKRGALLMELGNSPPF CKCTNNNTLDTWLQVRGDIC VNAYLTGQPLAEESSQDMLACF LVFHFVPSSTALPTL*D*KGSTS FAVELLKFKAISKMPSAELCLR LAPLPSLEIPQNGDVTYSGGEP
7622	37990	B	7676	374	515	
7623	37991	A	7677	102	1237	HSRAACPDNTNRLVPGASR*HY LHRCRSRHSS/NIGKNI/HSRA GAVNNQSRPQSHSSGEFSLHD HEAWSSSGSSPIQYLKRQTRSSP VLQHKISETLESRRHKIKTGSPG SEVVTLQQFLEESNKLTSVQIKS SSQENLLDEVMSKLSVSSDFLG KDKPVSCGLARSVSGKTPGDFY DRRTTKPEFLRPGPRKTEDTYFI SSAGKPTPGTGKIKLVKESSL RQSKDSNPYATLPRASSVISTAE GTTRRTSIHDFLTKDSRLPISVD SPAAADSNNTTAAASSEYHLHQ WSSHLDIPTHTIGSCAQNDLAI DMPEPLYAQARNSTRGRSHFL NQTFATIRMPSDAFGLAKDK HRTIYCGPFISAILPEYRIS

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7624	37992	A	7678	1256	1971	HNCALHADSTMRGKAPLFRPT YKLEMEQLLLRIFRWISQKQCNV EVTSLICWF/CTCTYSGWVEAYP TRTEKPYKKGKNDPSTKGQC NPLELVITNPLNPHWKKGERVT LGIDRARLDPRVNILVRGGEVY ERSPEPVFQTFYDELNVVPVEIP GKTRNLFQLAECAQPLNVTS CYVCGGTVTGYQWPWKAREL VPVDPVPDEFQAQKNYPDNFW VLKPSITGQYCIAREGKKFTHP
7625	37993	A	7679	1	1710	
7626	37994	A	7680	1	561	
7627	37995	B	7681	1	642	
7628	37996	A	7682	2	611	
7629	37997	A	7683	1	1718	MLSIQSTHAEKELENNFFQNTED WYFHTSHHLSLRFFSARESN SMKLYEEAYMERYRDFLPATM WSAHEVDVPGQATWIKQKSE KDPVHLQKGKNGPSTKGQC PLELVITNPLDPCWCKEERVTL GIDGAGLDQVHILVRGEVYKH SPEPVFQTFCEDELNVVPVEIPGK TRNLFQLAWHVAQCLNVTS YVCGRTIIGDQWPQEAQELVPT DPVPDEFQAQKNHPDNFWVLK A/IIHQYCIAREGKEFTHPIG*L SCRRQKLYNGTTKTIT/WRGSS NHTERNPFSKFPKLQTVWTHLG VPRAWEQPPLGFLGYVRAW LLTGLLDHWAGSCCLLGT/KPS FFPTAP*KQGKLLGFPVYASRE KRHAIENWKDDEWPPERIIQY YGPVTWAQDGLWGYQTPYVVL NRHRLQAALHITDKISRALTIL AWQETQMRNAISQNRALDYL LAAEGGVYGKFNLTNCLHVD DQGGVVEDIVRDRTKLAHVPV QVWHEFDPGAMFGKWFPA GFKTLIIGVLIIGTCLLPCLLP VLLQMIKSFIALTVHQNASAQV
7630	37998	A	7684	3	406	TLISFIYPAQNPELLNKLQSKRT TVLAMDQVPRVTIAQGYDALS SMANIAQ/YLIVGGGVAGLASA GAAKSMGAIVRGFDTRAALAE QFKSLGAEPLEVDLKESEGEGG GYAKEMSKFIEAEMKLAFAQ CKEVDI
7631	37999	A	7685	1	236	
7632	38000	A	7686	1	978	
7633	38001	C	7687	415	453	

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7634	38002	A	7688	3	408	
7635	38003	B	7689	1	2137	
7636	38004	A	7690	112	3688	GNWGARKLGTHINMANLLKTV ATGCSCPLI.NNLGSCKGLRVK KDFLRTFYTHQELWCKAPVKP GIPYKQLTVGVPKEIFQNEKRV ALSPAGVQNLVKQGFNVVVES GAGEASKFSDDHYRVAGAQIQ GAKEVLASDLVVKVRAPMVNP TLGVHEADLLKTSGTLISFIYPA QNPELLNKLSQLKTTVLAMDQ VPRVTIAQGYDALSSMANIAGY KAVVLAANHFGRFTGQITAA GKVPAPKILIVGGGVAGLAS
7637	38005	A	7691	2	288	EFPATIQSNRARGAKPGRRVDR GPQARCFDVGCGPRSPAPSNGLR NSEPSP*GR/CGRSPVSPALSSSR DVNL.PCMLSSGTDGACSEVLV GTLYRPL
7638	38006	A	7692	54	522	RFHMSSLSASPPRRLWTQMNT QCLVFSASHLPRCQEMLFQGT *EKPHSPRCFSPAKKPRPAGAPA ASHKCR/CT*PGPPSEPTV/PSD KAPLVGNAESQRVASPSGPPAP CSPVAGWPGTYKAIPASGTVAP TPLSAGTTDMTRLCLPSLEFL ND
7639	38007	A	7693	3	57	RAGAGRSERAVAEES*GGLSGS CGRHNPQSQRLQRRPSQDVELE DCCRCG*SGSLW/LRTLPRKRA PFGGFSVPASSAASIPTGSAVVQ PGPLPGPTGKSPPVFAGSGPSSN PQPAFS\NMRTDGSKPGSA/SF APLTPPLEPAGLAPSSGVSPL LPATIQSNRARARSPGDA*AAP PRPGVLTSAVPLPRRV/CLRNS RAFAPAVRTNAVTP*PGGVSGP SQRRAEAA
7640	38008	A	7694	3	237	
7641	38009	A	7695	114	186	

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7642	38010	A	7696	73	904	FGGFLANLSYQEALSDTQVAIV NILSSTSGFLTLLAAVFPSSNSGD RFTLS*ELLAVILSIGGVGLVNL AGSEKPAGRDVTGSIWSLAGA MLYAVYIVMIKRKVDREDKLD IPMFVGFAGLFNLLLLWPGFFL LHYTGFEDEFPPNKVVLMIHIN GLIGTVLSEFLWLWGCFLTSSL IGTLALSLTIPLSIADMCQMKV QFSWLFAGAI PVFFSFFIVTLL CHYNNWDPVVMGIRIFAFICR KHRIQRVPEDSEQCESLIMHSV SQEDGAS
7643	38011	A	7697	1	308	
7644	38012	A	7698	3	397	
7645	38013	B	7699	1	963	
7646	38014	A	7700	3	1433	KIRVTSKALELGKAQGGTGTG GSGRGWGRPNSSGKKEGHFYNN ISE*VGGGASRSAGAPRRWRRG PRMLQITNASLGLRFRRLLYW FL*GPSTLRGVESGSGGLEVLW GSRDPAGRMKVSNNVSCQASVS RMHAAFGGTFK*APAPTAHPF RAPQLICLAQVWAATGRRVAR VGMLSL*EGPGELVAGESGCA AVMQHLRAGPFRALLFTSNLD MDFRVSCLGWCMTSDFLTRPL SLLSLQEERMVYVAFSEFFD SAMESYFRAGALQLLLVGDKV CHGLFVGWAREGL*QSSLPHC AGGGRDRATCTPVRPRRGAIAIK PSGTTISVTASVTIALVPPDQPE VQLSMTMVRVPEWGGLLAGG QGKMGCGLLSR*AGALPCTSVI GGQSHLSTGMGWAGFVRS*PS PSPRKA/RGVMEERIGVNWNA GPD*ATNHAVSGGRMGKEGGP SPLSIAPQCHRPADVRASATPTP
7647	38015	A	7701	2	391	MALRGKALRTTSDLRFRRIYSN HSATWKSAL/L*IPLQAPLK/IM LPELG*MPQCSNERTWRGVQ DPHYPEGIKLCAMKVVTNPGCI PSPIGA*SPTFAKGLREVIEKNR PADVRAS/ATPTPSHSSCLSP
7648	38016	A	7702	1	189	
7649	38017	A	7703	202	455	KCDILPTALDSIHH/SSHRVHLA HSPHSLQ**HPHPLAQPSQQRDP SVPL**MSLADPESHSSESHF HL*PACRV*AYDLLPL
7650	38018	A	7704	313	378	

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7651	38019	A	7705	126	1246	PNGLRPPCPSAETPGNAPVCD PGSSSQGAQGKLNAAWAPGM A/ASRSLHSLHPVR/RACALPAQ SLLGPLRSFRCHLSDPVFRTGAP PGQGSWQYKVLVHAQERELTQ LREKLREGRDASRLNEHLQAL LTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLSPENDNDDED VQVELAEKVQKSSAPREMOKA EEKEVPEDSQEECAITYSNSHGP YDSNQPHRKTKITFEEDKVDST LIGSSSHVWEDAV/HHYSRK* K***GRGRKRASVSQKPEETPS\ PRPEPPPRGSGEAERSVGSWDA SSRSLRRLHPLREPVTPLPSRFR GRCGASAAIFGSCVPHGGSTRA GMMGSKEVGKGGDPGEETSPV ALFS
7652	38020	A	7706	3	5665	LLEKLQRRIHDKAVALERAIDE KFSALEEKEKELRQLRLAVRER DHDLERLRDVLSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ WLKEEMETKFSRWQKEQESIQQ QLQTSLHDRNKEVEDLSATLLC KLGPQGSEIAEELCQRLQRKER MLQDLLSDRNKQVLEHEMEIQ GLLQSVSTREQESQAAAEKLVQ ALMERNSELQALRQYLGGRDS LMSQAPISNQAEVPTGRLGK QTDQGSQMIPSRDDST
7653	38021	B	7707	1	1098	
7654	38022	A	7708	193	5850	HCQRNTTGEHCEKCLDGYMIK S*DSLFGDVWN*LPIFASNFSFA EL*K*GFVRDYHK*TFVCS/CLL NP*GPEFVGKKIKRKKNHDAK YLNV*YS/CFRCAPGYGYNPLLI GSTCKKCDCSGNSDPNLFEDC DEVTGQCRNCLRNTPGKYCHIL SIKKCISRLFLFPTVCNCGGGP CELH*EQNFWFKNYFNRSRHPLP QTDVSWCSAKTACL*HAFDL*F *RNVSPPGCDKCVWDLTDALR LAALSIEEGKSG

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7655	38023	A	7709	1	713	TPCFESPN/ETGTYFSTKAGYVL LN/ESSN/GIEFEIAFKVPRSSS GTLVHGHSVNGEYLVNVMKN GQVIVKVNNGIRDISTSVTPKQ SLCDGRWHRITVIRDSNVVQL DVDSEVNVHVVGPLGIQKPIDH REFVLVGGVPRILY*HPRFCPP QNPFTG/CIR/HFVIDGPPQWSFQ VKAAPGQAGARKASNSLSQQP GHGQKHSCKYKVPRLALEKE HKASPGGTVTLSPFGVGSFSS
7656	38024	A	7710	3	322	DGVSHCRPGWSAVA*SQLTAT STSWVQMIACFTLPSSWDYRCT PPCLTNFCVCFISDRDVMWMLA GW/LKNS*PQAIRPPQPPKVLGI TGHEPRAPGQKILTFHILT
7657	38025	A	7711	2	480	YSPPECPCFCGKIEHSEDMETH VKTKHANLLDIPLEDCCQPLDYD CPMCGLICITNYHILQEHVDLHL EENVTFSKAWIESSVLVIYNWLT SFSKKKTERGD/PESRQEIEEF QKLQRQYGLDNSGGYKQQQLR NMEIEVNRGRMPSEFHRKA DMMESLA
7658	38026	A	7712	187	468	
7659	38027	A	7713	1	1110	MHCIETGVERRILGLLLFRGSLA SVIRPGEVLDAAHALVCQRGPK GKPSGAQCQSCWPLGRPKALT QLVPASFVCLACAFGAERLGDS ALRSSDLTHLLVNTMLSCNIC GETVTSEPMKAHLIVHMESEII CPFCKLSGVNYDEMCFHIETAH FEQNTLERNFERINTVQYGTSD NKKDNTLQCGMEVNSSLGSC ASNHPKNSAQNLT KDSTLKHE GFYSENLTESRKFLKREKQSSSL TEIKGSVYETTYSPPECPCFCGKI EEHSEDMETHVKT KHANLLDIP LEGMDRVQCSGDLQLAHQLQQ EEDRKRSEESRQEIEEFQKLQR QYGLDNSGGYKQNNYEIWR* K*IGEECLHLNFGEKLI
7660	38028	A	7714	2	303	
7661	38029	A	7715	97	233	RTVTCYHRNSRACHPQQITSCP *HRALPCLPLWSPKCPSRW PWF G
7662	38030	A	7716	229	359	MKVVVYCSVTGMGKGQHRMP/ SKG*GWVQRYNRDGPSPRVLE LF

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7663	38031	A	7717	1	1185	MSTIDDPRLQGRMCLMLRGT PEQKALVIGGEACMWGEYVDN TNLVPRLWLCPPSTQDLANE REMTILHRHIPDRGKGVMRSCS FRTPRPFTLACGPEKSLMDPQS QSNSEGASSSLVVKLADTDRE ALRRMQQMAGHLGAFHPAPLP LGACGAYTTAILQHQAALLAA AQGPGLGPVAAVAAQMQHVA AFSLVAAPLLPAANAAPP PGTLPGLPAPGVNFGPLTPQT NGQPAPTRSTITGSP/L/SGWSQ SRPILRIMKYAEQRIPTLNEYCV VCDEQHVFNQSGMLKIQPTII QVWREDIPVNYMKELELVTKA GFRALLSAPWYLNRSYGPDW KDFYIVEPLSFEPTPEQKALVIG GEACMWGEYVDNTNLVPRLW AHRQL
7664	38032	B	7718	1	1196	
7665	38033	B	7719	184	1689	
7666	38034	A	7720	228	407	
7667	38035	A	7721	1	725	MQRGALSPVLMLSAAPEPPRP PPGLSPGSGPGSGSRHGSARPG PTPEPSGSLGAALDSSLRAAVA FKAEGQRCYREKKFREAGKY HRALLQLKAA/LGGP*RPARP RPPGPTSSPGPARLSEEQRRIVE STEVECYDSSPA/CLLQSELVNY ERVREYCLKVLEKQGNFRFP YRAGIAFYPLGDYARALRFLQ EAPSRPPDNTNVLRYIQLTLK MNRCSLQREDSGAGSQTRDVI
7668	38036	A	7722	1	262	NGKEPGRYTFEDAQEHYKLM KSDSYPRFIRTSAYQELLQAKK KGRNIPFPCHKNCTPTLRASTN LL*KEGKSLTSKRLTSLAQS
7669	38037	A	7723	1	1392	

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7670	38038	A	7724	1	1544	MAQGNNGYQTSNGVADESPN MLVYRKMEDVIARMQDEKNGI PIRTVKSFLSKIPSVFSGSDIVQ WLIKNTIEDPVEALHLGTLMA AHGYFFPISDHVLTLDKDDGTFF RFQTPYFWPNCWEPENTDYA VYLCKRTMQNKVARLLEADYE AESWA/RGLQRAFAFKWIEFIF MQAGAAQAKVDKKRDKIERKIL DSQERAFWDVHRPVPVCVNTT EVDIKSSRMNRPHKTRKSVY GLQNDIRSHSPHTHTPTETKPPT EDELQQQIKYWQIQDLRHLK MSKVADSLLSYTEQYLEYDPFL LPPDPSNPWALSDDTTFWLEVA SKEPSQQRVVRWGFVAWDEGI GKTQLGRRNSFLKIF*EFRISGS GNFKVLGWASGRTLKKRPFKE VPSRVQEIWQFLAPGAPSAINL DSKSYDKTTQNVKEPGRYTFE DAQEHYIKLMKSDSYPRFIRSS AYQELLQAKKKGKSLTSKRLTS LAQSYLNGSSCSMNADWSHCT HFVAQCDCLEQRTLEQDVA
7671	38039	C	7725	81	439	
7672	38040	A	7726	531	686	GWQWLHRRPPGATQHCNGNLP AEESLPARATN*ARPAAHTRGG RGQDLPPGG
7673	38041	A	7727	93	428	LHCQVHLSLIDLPLLSFLLLLF *D*VSLLLPRLECSGAISSHCSL H/LGPGSRDSPASAS*VAGITGT CHHVQLIFVFLLETGFHRVSQD GLDLI/NLVIRLPRPPKVLGLQA
7674	38042	B	7728	99	425	
7675	38043	A	7729	35	861	
7676	38044	B	7730	141	586	
7677	38045	A	7731	116	926	AEIVAQEVSEEGGKSRKGPQFG KSQYQELIRRSECGLNREGESI KANMQQVIYIPITLAEVVLRP HSYPSKKTGLTLAAASIAIYISR *EWLYFETGTWVYPVFAKLSLL GLAAFFLSLYVFIASIVLLGEKL NHWKWVSVRNSTLILYIRMAK SHITQSPSLAHMPCSIKIEMAE VPSSAQSMNWCEKLLVFPPR*C CFLRPRDSVSPVFAWFLMHF NTRLFQEAFFGQPOLQRWRLE SVGICFQWPDWKSPAKHQLVK

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7678	38046	A	7732	32	394	GKAVLPIMRETLDGFHYQHCC PDLPGTDLGHPGSPDLGEVKFL SQT*EVTSLVQSGKVWR*WTAI CTHTSQLSISLLAFCLRSASATS LTLSHCVNVVKGGLDFKRRRG HSIGGAPEQR
7679	38047	A	7733	1	765	
7680	38048	A	7734	3	1295	QARVSQELKKAARKRTVSISEGP DTLGDGMRERRETLALAPEPEP LEKEACEKWKRFPSASATSLT LSHCVDVVKAILDFKRRRHSI GGAPEQRYQIIPVCVAARLPTR AQDVLDAHLSEVQCCSFIPNS SLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDPDF G/SNQVLAATYNQAAQLWKVG EAQSKETLSGHKDKVTAAKFK LTRHQAVTGSRDRTVKEWDL GRAYFSRTIQCSFSYCNVDVCG DHIISGHNDQKIRFWDNRGPHC TQVIPVQGRVTSLSLSDQLHL LSCSRDNTLKVIDLRVSNITARG FRADGFKCSDWTKAVFSPDR SYALATLPVMGPF*IWECGTPG KNWKKQELGTPIALPVQTPW PWCLLPSPHGETWTQGRKGC AFGSAHDLPALGWRLLEA
7681	38049	A	7735	123	463	DVEVGLISQLQDCELGCGIPLK VFPAVFRPLPLSLHTFLPLPLSRT LASGGDGA TSACCRCPGAVSI S*L*QTVASP*VLVFVHSRKEVT GKTARAI RDMCLEKDTLGLFLR
7682	38050	A	7736	1	489	
7683	38051	A	7737	1	423	
7684	38052	B	7738	1	900	
7685	38053	A	7739	1	1824	
7686	38054	B	7740	400	969	
7687	38055	A	7741	3	4781	EISATQII VCTPEKWDIITRKGG RTYTQLVRLIIDEIHLHDDR PVLEALVARARNIEMTQEDVR LIGLSATLPNYEDVATFLRVDP AKVLFYFDNSFRPVPLEQTYVG ITEKKAIKRFQIMNEIYVEKIME HAGKINQVLVVFVHSRKETGKT ARAI RDMCLEKDTLGLFLREGS ASTFVLRTEAEQCKNL*LKDLL PYGFAIHHAGMTRVDRTLVED LFAIDKHIQVLVSTATLAWGVN LP*HTALFK
7688	38056	A	7742	2	518	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \=possible nucleotide insertion)
7689	38057	A	7743	18	1108	CSGIPRFRDSQSTRAACFFPAWT RMRAPSMDDRAAVARVGAVAS ASVCALVAGVVLAQYIFTLKR KTGRKTKIIEMMPEFQKSSVRIK NPTRVEIICGLIKGGAALKQIIT DFDMTLSTRFSYKGRCPCTCHNI IDNCKRLQMNVEKSYCQLKEK YYAIEVDPVLTVEEKYPYPMVE WYTKSHGLLVQALPKAKLKE IVAESDVMLKEGYENFFDKLQ QHSIPVFIASAGIDVLEEVRQA GVYHPNVKVVSNFMDDETGV LKGFKGELIHVFNKHGALRN TEYFQSN*KTNSNIILLGDSQG DLRMADGVANVEHILKIGYLN DRSGMSF*EKYMDSYDIVLVQ DESLEVANSILQKIL
7690	38058	A	7744	105	548	PQTPRLKQSYHVSLPSSWWHDHP VAGKRA*HAH*FYIMAQLFLPA ASPGPTPASQQLVLTQCLPISW RPWSAHSFLKSSSPGPGPTPASQ QGLWTQLPRSFQRPWPKSSSSR PGNGPGRAASRPRAQLRLGG LSRFNDGHGNFLAQ
7691	38059	A	7745	186	650	RCPGCPTTASARESREAESRGR GSSGASWGAVQWEEPQPRLL RGTDDCMIFWAPHGSSTWRRR CVHSRSTAADPVLTPSPA/STPS SNCSGSGTSLAALPLPLPQTLGP *QPGWKGTPOCLNTWGVSITS TGRWATPKIPGLTVPPENMDS MWG
7692	38060	C	7746	212	556	
7693	38061	A	7747	2	312	PDLK*STCLGLPKCDYRW/RA TMPGWENIFSSMNHITLNLGT AVTSTRDNS*LHRVSCISSPWCC CLSPCPCRVSA GTGRVPSC LCH SGAWNRLDQDINRNNSC
7694	38062	A	7748	2	366	FLHTKYLFCGKIAHPHYFIRSH FFFLLRQS/LYSIAQGGVQWGN LGSLQPPSPGFKQLSCLSLPSSW NYRCAPPCPANFVFLVEMGFH WIKPG*SRN*PRDPPASASQAG ITGVSHHAQP
7695	38063	A	7749	1	446	MPILFTTVSSALSGAQHADAQ CDRKGHRTTIQGSRVNLVQPSV GPKVEETQCWGPGRGMPGAPE APRERRVRSGRSQDPGVA/PR AASGVGGRYAITRGRASAAVP CRSGGARRGGAGQAADCGPG H*KESESRGPEGPAEGSQPL

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7696	38064	A	7750	1	744	GGLIPRAQRESKRRSRGRARAA SGV/VWALCYHPRQSECCGTL* KWRSSPRRCWRTSGDCGPGH* KESESRGPEGPAEGISASLKM* WFASGTCLSRCLTLRQRK*LKK IKIWIWK/SEK/PAEAT*SEGQPP F*GPRQTGAEGF*LEPPQPGMSL KLFKVILKG*DSRTKMGDQQPP RVHGRTHGPLQLTPVKQGQS CPVKGPSPSGIWP*KPLL*CLAT L*WQEGTFLSGLLGPPTPGAS VGHKIY
7697	38065	A	7751	316	650	SYNTHGTFHVPTANVLVVDL MCHLEKLAKYDDIKKMKVQKA LEGPL/KGILDYTEQQVSSNFT SDTHSFTFDAGAGTAFNNHFFK LIF*YDNEFGYSNRVVELMFHP ASKG
7698	38066	A	7752	2	775	QARRARSRNSRGLSQSAAARPLA AKTAWRTVAPQPWAAAPR*R SSCPHSSCSATSPGARACQSSA HSPSPRLQAPPPPTSSSGSVPE AATAPLAASARRGTPRPTGRP SWAGTRQGSWAGTORPWVWA PAPAGPPRAAAAAAR*GRDKS QLTCPPRHSTPPGSAAGASRHR RRGLAGPAPSPGCRAARPPWP SAAAAALGLGGRGPDVLVHCEI HWPLEFQSLCCCLLTSRGGEAS CHPEFHLFMHDFLPGSF
7699	38067	A	7753	1	552	MQTLFTLLQPSSQTGPQPVIC CVYAESGARDSGQP/PSKVPVPS FCTPAATQRG*REPGCSHPAGD CSAPQQCS*PGQ/RIS/RGDKVL ASNTYLPGPGLPGGQGPPTW MKVETITQ/TNTGTENRVFSL LYMTISKQYLSEEGSHWLSCL INALQAFFSNAAIWLVTWFELS RVLGGAEND
7700	38068	A	7754	2	538	LGYITGDKVLASNTYLPGP LPGGQGPSPGPKGSPGFPRY A/GLGQPGSRGSGTHGTIS*/ G/LPTKQGRRGVPGPPGPPERD GSKGERGAPGRGSPGPPGSD FLLLMLADIRNDITELQEKVFG HRTHSSAEFPLPQEFPSYPETM DLGSGDDHPRRTETRDLRAPRD
7701	38069	A	7755	146	373	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7702	38070	A	7756	678	1582	CQGNLSLGGVWPSGDWEDKHS Q*CPVVCSPQNLSQTSRHINDR DYRLPRAETHSSSYAQYSTPSN LVVHPTATPSTVPSSPFTLQSD/ YQPKKSFDDANGASTLSKLPPT SSVPAQKTERKESTSGDKPVSH SCTTPSTSSASATE/S/TTSAPPTS ASAGPCFSCSTARQYLPYFRDP NLLRTIAVLLKATVAALINS*C GTYLKIK*SSYSSCDTSLTAVYN S*VSYCWITCFQHNVSDFFSSCSA /PTQAQPSNQSPMSLTSDASSPR IICFSKE*GTPQTNTVPIQTFGFS TPPVSSQAKG
7703	38071	A	7757	1	1365	MHLIPATNCDTLVECLPGKL TRDLVCTAFTFGTSSYPQENS HNHSAHSSNSHSSNPSNNPSK TSDANILSQTSRHINDRDYRLPR AETHSSSTPVQHPPIKPVVHPTAT PSTVPSSPFTLQSDHQPCKSFDA NGASTLSKLPPTTSSVPAQKTE RKVLQQLSKHNKVMIRALIT SHLDLLYIEKDLRYQKNIESTSG DKPVSHSCTTPSTSSASGLNPTS APPTSASAVPVSPVQSP/PSLT SGPKSS*TIA/PALQATLQLNNS NVDISKINEAQPSNQSPMSLTSD ASSPRSYVSPRJSTPQNTVPIKP LISTPPCFITAKG*LLQ*LSQGTS VHSQPHTAACNC*/PSSK/SHEP VSPRSLQRSSQSPSPGSGFILL NSSNGIQMATVVPQEFFLARFH VFHLTPGTRRPPQWKISLKHV SRDGPADSWQEGRASRFTAE GRRH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7704	38072	A	7758	2	1256	CHCGPPV/KVEAYGSQVLKGVL AQVQLTVGVPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWVPVQK TDGSRWMTVGVCCKLNQVVTP AAAVPDVVSLLQEINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHLPIYRV SRKAAANFEWSPEQEKALQVQV AAVQAAWPLGPDADPMVLE VSVADRDADWSCWQAS/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQQRWWQLAE RQDSRDREAIGERQETA VGKT ARDGEAVCD
7705	38073	B	7759	56	3476	
7706	38074	A	7760	3	591	DPADPMVLEVSEADRDVPI ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVVLVEIEHLM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEKSSQW
7707	38075	A	7761	1	558	
7708	38076	B	7762	1	1189	
7709	38077	A	7763	604	1760	NSWCRWFNFRY*YPTFYWES* NT*IPLEWFG*NHDASCP*TLD SKSFSFETRTGSPCSSLQTAYC GTLWIVQGV
7710	38078	B	7764	1	474	
7711	38079	C	7765	1	3384	
7712	38080	C	7766	1	333	
7713	38081	A	7767	1	390	
7714	38082	A	7768	3	728	
7715	38083	C	7769	184	529	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7716	38084	A	7770	2	837	CHCGPP/VKVEAYGSQVILKGVL AQVQLTVGVPVGRTHPVVIFPV PECIHGIDMLSSRQNPHTGSLTG RVWITMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSRWMTVGVCCKLNQVVTPI AAAVPDVVSLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL
7717	38085	A	7771	2	469	
7718	38086	A	7772	3	587	YPASAGLMLQNFVGVLGRYHF AIHSPAAGGLDGLHAVAAIQG ITKIETTPNHQRAPAHWLLTQ QAHLPSPHLFNLPLTCLMHC PTAIPHCFADARTVWNLPTSSLI GHKKENLKEFISGLIVHEILEE VLQAEQDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVGYAGYGAQLL
7719	38087	A	7773	1	633	MTVDYRKFNQVVTPTMAA/AVP DAVSLEQINTFPGTWYAAIDL ANAFSIPVHEAHQKQFAPLPQ GYINFALCHNLIRRELDFLLLL QDITLVHYIDDILLGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPSS GDIKEYFPNAFVLLTTASLQGG DNTSQLQLTWKAPEDIKMSKT DADADEIEIALRG
7720	38088	B	7774	1	1431	
7721	38089	B	7775	75	947	
7722	38090	A	7776	6107	6706	MVVVFLHKCLHYFHSTQLVISR YNSPTSEYFQALDLTWALGT VGSAPPILPDLGGTNRQPPFIL SHSGLHRNVLPETDSQSEDRL PVTWLAVSACCCQQMVGGNP TRSKL*RTGSHYHLPG/WEP*RP HFPHAGSLAQWLLCSSLEHSF GA*ELPCNPCKGWCLCPCHFI YIFFNSFLSNCPQLCNWHSSYFI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7723	38091	A	7777	1	3179	MAEGKEEQVLSYTDGSRQREN EEDAKAETPDKTIRSHETYS.LPR EWYEGNRPHDSITTSQWVPPTTR GNYGSTIQDEIWVGDSGYVVRP VPVPRSLNSDISYFGVGGKQAV FFVQGSARMISKPADSQDVHEL VLSKEDFEKKEKNKEAIYSGYI RNRKDDYDNHTGIDLVTGIIATII KGSNEEDTDPLFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP
7724	38092	A	7778	281	1531	VRVLSPEVKELKLWKNTHKLL SYPTVGAAVTLQNLMTAGVI GSHGARQQVVALNRQRQGD QPFTRTVTVHWGKG/NMQIFGGL LDTGSELTLIPGDPKHHCAPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKYCIP GGTEEISATIKELKDAGEVPIPT TFPLNSPIWPVRKTDGCWRMT VDYCELNQVVTPTAATVPD VSLLEQINTSPGTWYADIDLANA VFSIPVHKAHQKQFAFSWQGP QYTFTVLPQEYINSLGLCHNLI WRDLDGFLLLQNITLLVHYVD DIMLIGSSEQEVANALDLLVSM ASSRVPYDQLTEEEKARFTDGS ARYAGTTRKWTAAALQPLSRIS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
7725	38093	A	7779	332	2159	RGYVFCSWKKTGDS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLNAFFSI PVHKAQKKQAFSWQGGQYTF TVLPQWYINSPALCHNLIRRD DCFSLPLDITLVHYIDIMLIGP RQLLACYWALVETECLTLGHQ VTI*PELPIMNWVLSDPSSHKVG HEQQHSIIKWKWYVHDWARA GPEGTTTTVISQWPHEQCCHGG RDGGYAWAQQCRLPLTKADL NTATAKRPIQQQRPTLSPQYG TIPQGDQPATWWVVDYMGSL PSWKGQRFVLTGIDTYSYGFGA YPACNASAKTAICGLTECLIHH HDIPHISASDQGTHTMAKEVVRQ WAHDHGIHWSYHVSHHPEAA GLIEWWNGLLKSQLCQCLGDN TWQGWGKVLQKVYVYALNQIIP IYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLPPFATLQSA GLEVLVPEEGLPPGDTMIPLN WKLRLPPRHFGLLPLNQAK KGVTVLAGVTDLDYKDEITLLL HNGGKEEYAWNTGDPLGLLLI LPCPMIKVNGKLQKLKPEALVP KGVVFPFGDTMLSLSWKRLP SGHVGLLMPLSQQVQKGVTVL
7726	38094	A	7780	84	202	
7727	38095	A	7781	1	551	RWGSHTVAQAGVQCDHGS QPRSPGVK*SSHLSLLGSWNHR HATITPG*FCFFSRIRSHCAQA GL*LLTNSHPPALASQT.VGITG VSHWTWPNTGFSVLATNKNL KFFHYAISKCLVRKLSRLKI EERNKALSAPVVSIFDRVLR LLGYSASDWQPEFVETAVSNFV IYGFIRGQ
7728	38096	A	7782	1	678	MPACRLGLLATALIISLLFGFTI VSGTGAETGVCPELQADQNC TQECVSDSECADNLKCCSAGC ATFCSLPNGQLAE*FESEESSL DTVSPFVVFSISSTLRIE*ARA GDSSQDKEGSCPPGVTI*LPFSS GLCRDQVPGGTAQCPGQIMK CCRINGCGKVSCVTAQFLSSSH HQAQVRRDSFLPGPASGFQAIH LPSPFFGTLYSLFGLTTSFSLSQP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7729	38097	A	7783	1	1972	MAVNGCLEGPSSNFLSCLFIVA LVGSESTHPLCLEQPATQETRY QLQLRPAQRASWIGYAIAYHL LEDYEMAAKILEEFRTQQTSP DKVDYEYSELLYQNQVLREA GLYREALEHLCTYEKQICDKLA VEETKGELLQLCLREDAADV YRGLQERNPENWAYYKGLEKA LKPANMLERLKIYEEAWTKYP RGLVPRRLPLNFLSGEKFKECL DKFLRMNFSKGCPPVFNTRLRL YQDKEKCAIIEKL VVGYESLTK SCRLFNPNDDGKEEPPPTLLWV QYYLAQHDKIGQPSIALEYIN TAIESTPTLIELFLVKAIYKHA GNIKEAARWMDEAQAALDTAD RFINSQCAKYMLKANLIKEAD MSSKFTRGGTSAVENLNEIQCM WFHTECAQAYKAMNKFGEAL QKCHEIERHFIEITDDQDFHTY CMRKITLRSYVDLLKLEDVLRQ HPFYFK/EQARIAIEIYLKAS*QP PYR*GIGKTRRLDTAKLSDKEL KKLRNKORRAQKKAQIEEEKK NAEKEKQQRNQKKKDDDDDE EIGGPKEELIPEKLAKVETPLEE AIKFLTPLKNLVKNIETHLFAF EIYFRKAAMVYYLDPSSQKR AIELATTLDESLTNRNLQTCME VLEALYDGLGDCKEAAEIYRA
7730	38098	A	7784	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEETLFSN
7731	38099	A	7785	1	681	
7732	38100	A	7786	415	692	
7733	38101	B	7787	1	2204	
7734	38102	A	7788	1	615	MPVDHPPIKAFSEKRTSQSVNM LAKTHPYNPLWAQLEWFKLLEI SPKSPINTDKFLLKRLSVPGSDS CRVRMENVLASQVLHPGQLM M*EGSGWAEART/V/CS*AANP *KWHPASLPLPW*CRVRMENV LASQVLHPGHADVDVGGKWLG RSKDHRAPEQQTRESGIRLPSLF PGSAEQPWRGNAQWHLWSKA LRGVFGMIPDSLLYEFHQSAKK SSHFKPPQPLLYWTLVNFLLPFS LHSSWFMWSSNQGMCKEEV

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7735	38103	A	7789	3129	3197	TQNRACSPDTEQLARQSGTYP VSLGQATVLEDSKAALPGLGPT LMAVTVVTTEAAVAIGCEAAH SSREDFTNHQLWRRITVEGKKG EGKNKFMGGVNTTVPLKTS RKGSPPSPHLREKPSLEKVTFOI GSFASPESEFESRMKKMEERVK ACGPSLEASEAADVAQDPQVS RSPFKPGFQENVCPCQNLSEG DEGESDKGFAEDRGSNDMAA DIAGQLSHAADLTGASHDDVT YAIKPTCWPGLDIIPCL
7736	38104	A	7790	1	1069	MAEKEAGMSYMAEVLGFVA VIIIEAELKRIFENFTVAEERS TDETFSLAETCSSNPAMVRRK KIAISIIIFSLCEKEEAQRNFQDF FSHFPLFESHMNRKSAIEKAMI SCRKIAESSLRVQFYVSRLEMA LGEFRGTIWNLYSVPRIAEPVW LTMMSGTLEKNQLCQRFLKEF TLLIEQINKNQFAALLTAVLTY HLAWVPTVMVDPHPPIKAFSEK RTSQSVNMLAKTHPYNPLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTIFYLRCELQ E/IPADLEWQSW*R*PAMVRRK KIAISIIIFSLCEKEEAQRNFQDF FSHFPLFESHMNRKSAIEKAMI SCRKIAESSLRVQFYVSRLEMA LGEFRGTIWNLYSVPRIAEPVW LTMMSGTLEKNQLCQRFLKEF TLLIEQINKNQFAALLTAVLTY HLAWVPTVMVDPHPPIKAFSEK RTSQSVNMLAKTHPYNPLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTIFYLRCELQ ENQLTWSGNHGEQDQVLNGSK IITALEKGEVESEYVITVRNE PALVPPHPTTNSRETQPLADR
7737	38105	A	7791	118	273	FSLSNLVQFFRVCDNHLTKLH FCFLQAEVKASNFCYDSLGH LGSHTTVECIATDEHTLHLTSP MG*SQGKQFLHRLFSWACPGIP PHS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
7738	38106	A	7792	1	551	MQPELPIMNWVLSEPSHHKVG HGQQHSIIKWRWYICDWAVVG RESTTNGLAIGWSIGTWKKHD WKJNDNEIWGKISMWIDLSEW SKTVKIFVSHESAHHIT*KSSAE EDFNNQWDGMCSDVTTHPLS LTTSVIAKWAHEQSDHGGRYG GYAGAQQHGLPLTKADLAMTT AECPICQQRPPLSP
7739	38107	A	7793	1	782	MTKIQEPSTSVKFLGVQWSGA YQDIPSKVKDKLLHLAPPTTTK EAYLGL/FGFWRQHPIH/LGTEQ EKTQHVVQAQVQVAFLEPYD PADPMVLEVSVAADRDAIWSLW QAPISESQWRPQGFWSKALPSS AANYSPFERQLLAYWALVET EHLTMGHQVTKQPELPIMNWV LSDPSSHKVGCAQQHSIIKWKW YICDRARAGPEGTTTPVITQWA HEQSGHGGRDGGYTWAQQQG LPLTKADLATATAECPICQQQR PTLSP
7740	38108	A	7794	65	230	
7741	38109	B	7795	1	2115	
7742	38110	A	7796	1	246	
7743	38111	A	7797	1	1293	MAAAACLDASGEARPLRPPW SQQGRKQAGALPPTKLAGLLA QLQPAEAPDLGIPVLSATREDPL SPQARKCLLPLPGLSPCSQHLL WCRASCGRWGWPSRPSRVCTG LDTAVTPAPCRLSPLWTSADK RGREASRGEGSSKWACRHPSA QTAWAVEGDRHFLSRKQGIT GKTPPSSQGQPEAWGLSCSPH TLHTSFFLDTGPLNGGTEKAVT QTGPKHAPCSPGCQGGGKGC GPSGTPDLGALRARAVTVGLCS SWHLQASGHHCIPQYLQKLL VVHLVQPQCTKPPVVPSPRLQ MTIENMNHKLFIPHKDYTANRL VSGLLQLPSNTSLVIDETLLEQ GQLDTPGVHNVATLSNLITWQ KVDYDFSYHQMEFFCNKVFIT SEGRSLLPADVPDSLTA PANST KHGGST*TAFSQRCLLPC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7744	38112	A	7798	1	2555	MPShLNQHqIHtKEkSYKCEE CGKsFRkSSNCTThKRiHTGek PYrCEEgGKAfRWpSNLTrHk RiHTGekPYtCEEgGQAFrSS TLtNHKRiHTGERPYkCEEgGK AFsVSSTLNDHKRiHTGekPYt CEEgGrafNCsSTLkThKRiHT GEkPYkCEECDkAFKRHSSLA KHKiHTGekPYkTGSiLLQR YCWSTT*TiHfKk*S*EN/PGSC DLNtLRLKKDYQRvGNCKGQK SSyNGiHQCLsATRSKtCQYNK CGKAfGLCSiFTEHKKiFSREKc YKCEEgGKDCRLSDFTiQKRiH TADRSYKCEEgGKACKkFSNL TEHNRVHTGkKPYkCEEgGKT FTCSSALtKHkRNHTGDRPYkC EECHKAfRWCSDLtKHkRiHT GEkPYkCKECHKAfRCCSDLT KHKRiHTGekPYkCNEgGKAf MWISALSQHNRiHTGekPYICE ECGKAFTYsSTLISHKRiHMeLR PYkCEEgGKTFkWFSDLTNHK RiHTGekPYkCEEgGKSFTCSs NLIKHkRiHMEVRPYkCEEgGK TFKWFPDLtNHKRiHTGekPYk CEEgGKTFTCSsSLiKHkRSHTG DR/PYkCKEEGKAfRWFSALL NISKHKRiHTGekPYICEEGKA FIRSSTLTSHKRiHMEERPYKCE ECGKTCiIHIGekPYkCNEGK GFMWISALRKHkRiHTGETPYI
7745	38113	A	7799	212	461	TEeHLYSPHWKGCGRkVKRLf QVRGRGWiQTRQPGSMVKEP PLSEAGAEshVSC/RQGDcSRPP SFPLSPERVTPWLpDSiITW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7746	38114	A	7800	1	1398	AAAERELELLRASLEHQGVSE LLRGRLRELEEAEEAAEAAAG ARAQLREVAITQTPWSCAEKAA QTESPAE/GPP*LRARPDPWTE TRAVAPAGILKSIMKKRDGTP GAQPSSGPKSLQFVGVNLGEYE SSSSEDTNDSGDSENGGAEP GSSSGSGDDSGGGSDSGTPGPP SGGDIRDPEPEAEAEPPQVAQG RCELSPLREACVALQRQLSRP RGVADGGAVRLVAQEWFRVS SQRRSQAEFVARMLEGVRLG PELLAHVVNLADGNGNTALHY SVSHGNLAIASLLDTGACEVN RQNRAGYSALMLAALTSVRQE EEDMAVVQRLFCMGDVNAKA SQTGQTALMLAISHGRQDMVA TLLACGADVNAQDADGATAL MCASEYGRDLTVRLLLTQPG/C DPSILDNEGTSALVALE/AETG MKVAALLHAHLSSGHPDTQSG VTPLAPQTANTW
7747	38115	A	7801	3	408	
7748	38116	C	7802	141	251	
7749	38117	A	7803	1	1173	
7750	38118	A	7804	451	853	LQMHRLCGHSLSGCGWHTAR GQELVGCFL*GGGQLLGLOH PL/AENPTFQEYSLITSEAGLLEG RKKKNKTSRGPSPATCPLGLP RTSPGATRPGPVS/HAIAISQRD SSRTRFSSSLDAIARPYTTPSA
7751	38119	A	7805	1	2950	MAASRLELNLVRLLSRCEAMA AEKRPDDEWRLEKVGVTYSVA SGRVLFQDFTEQFQVLLPKDAQ PCREVISTLLEKMKIDKRNQIG KTKVEPGV/EA/WPLRRVRRQPD QRQGLGAHRAGEAPGTRGDAR PVHRGPLQVGCQPHSGAPAG AADRPSSQAGELPHPRHHRGA EAVAAGAAARAPHDLRTVRRLP PSRRAAGEAGAAGCH/RMPSW STFKQPTTTTPWRDSSSTLSSNHP LTASGCAGWPCSRMST
7752	38120	C	7806	398	415	
7753	38121	C	7807	13	81	
7754	38122	B	7808	1	972	
7755	38123	B	7809	1	1803	

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7756	38124	A	7810	1	929	IAAAPELLERSGSPGGGGGAEE EAGGGPGGSPDGDARPGPSREL AVVARPRAAPTGPSSAAAMAR PLVPSSHKALLLELKLQEEPV EGFRVTLVDEGDLYNWEVAIF GPPNTYYEGGYFKARLKFPIDY PYSPPAFRFLATKMWHPNITYETG YVCISILHPPV/DTDPQSGELPSE RWNPVTQNVDRHSS*V*SSLLE RRPNTFLRPANVGRLPWMLQG SWEREQGGRIRELHRTSFRKQV LGTKVDAERDGVKVPITTLPEY CVKDQGRAPDEGSDLFYDDY YEADARVEEADSCFGDEDDDS
7757	38125	A	7811	2	296	LSLSFFVVKAHFYVKSMLHSHKD ASGISGMDFFYVQ*FSWQTAY AGEVGRWLSPALTERGSGQTL* TWCWRVFCVCLIGHMWVTEA YVTVKH*NYSKVK
7758	38126	A	7812	397	410	SPGEI*G*VPPLLG*GVLLYQPP LFKIWEAPLLPDLLQQ*KLYSL WLNKALGK
7759	38127	A	7813	2	739	ELCALVFGVNTFFATIVKTIITFI VSDVRGLGLPVRKQDSVVVFL DCPSIW*LRVIDLLILRVHLQIH LWGLRGRRAEFKHI/RSAAEKK LTRIPSVNGE*TGKSPAPANS/PP RGARDMWRTGRAPAPRPLVGG PSPSDRGPASTTSPELAVGAVN GGPSSANISRFGWQQSFHGNMC WFCAEPGVAGVPFTANIAGTPE GGLGQGRQCSLATQCHKPELK LQAKPAFFSFLSLFFFLKHIL

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7760	38128	A	7814	594	2868	CWTSRNRRLPIPGSCHPMELPRPF RGKAKVQNHQLVHVNKALIN RGSLSFWLDDGAIAQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSWLNEDPFVCEYQ GQSSDLQPVPVNAAGGSGGGS GGGSEGGGSEGGGSEGGGSE GGSEGGGSGGSGSGDFDYK MANANKGAMTENADENALQS DAKGKLDVATDYGAIDGFIG DVSGLANGNGATGDFAGSNSQ MAQVGDGDNPLMNNFRQYLP SLPQSVCECRPYVLSAGSEIGAA CASRSGYDNKGVRDIGYTDC RSEDLDPLRHQILGGKKA/QFTL QGFPTLPEGAPAGNSGSLAVHK TAQSSYRHHALLITPMSGTRF PPIPGPVVNIIRVFPAPSECRIC YSWSWVPGSPVHCQSDGVSPI SYAPLASQYSSSLFRRNRQPYA PYDYSVMTSPRTLREQIRIRYA PSAPRLPPPEVYCSNSTITVYVRN NPSGPTPGFAGGTLLEGRSGGP FRFYAKRAKGDVLPFSLNLPL QTLIRFMVDIACGMEYLSRNFI HRDLAARKCMYEFWRTRGWE TAAAYYGGGTTFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFDTDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTLGLVLQMGDPND
7761	38129	A	7815	2	474	RRFVSADNCRSLRWKSLYTPLD ADASVLSTGIDATQTNHGRQH LDETQVRVFGQHLMQGSYTTQ DGRSDVAISCCKLEMAQQSY DQLLAASTENWRQWWQKRRT VNGG/GSSPASDADQTPAPGFR RDVGDRDWFAWRQCLLKALT RRRPVAYIVISSAMSGLPKQS D
7762	38130	A	7816	302	409	
7763	38131	A	7817	199	359	ARRQQVSVKSYRWEEDQHCG ELQGS*VSDGLFKPP*S*HGW VEEERQEQN
7764	38132	A	7818	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLSILVLIRIVMMVMMLP QLALSGWGRFRVLPG

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7765	38133	A	7819	118	445	AAGGEPGDAPWVPGVWEPPE VCRGPPPSSTFHPVLSTFGASG PENSRDCSWLSPPQH*AA*VASG NNGPQAAQGSLSGIPDAA TLSG I*RASILHVSVVETIISPPGFR
7766	38134	A	7820	1	770	MRVLGIETSCDETGAIVDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCKIPAPNFR CALLGSAA YAVNHGTGLSKKP TTLGSDHSKTPAQLAKRAGEA RRNGWQGFPPWESARSGE TP/VICRH*HSHRAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVL
7767	38135	A	7821	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRRPFRGKAKVQNH QLVHLQSSHQPWLPHPFLAG* WGDSSLGGGSIEGGSEGGGSE GGGSEGGGSGGSGSGDFDY KMANANKGAMTENADENALQ SDAKGKLDVATDYGAAIDGFI GDVSGLANGATGDFAGSNS QMAQVGDGDN SPLMNNFRQY LPSPQSVVECRPYVFGAVRHDV RRIRVTGVTRVTPPEEVDTSVH SRGAHRIRSGFAPKRSVRVTTD TCIKRNSCTGVKSLSLWDGGGF
7768	38136	A	7822	1	1044	

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7769	38137	A	7823	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRVPVPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCRITSGSVYITLKKCKQREGS RAMLPGFYPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQGQSSDLPQPPVNAAGGSG GGSGGGSEGGGSEGGGSEGGG SEGDSSEGGGSGGSGSGDFF YEKMANANKGAMTENADENA LQSDAKGKLDSVATDYGAID GFIGDVSGLANGGATGDFAG SNSQMAQVGDGDNPLMNNFR QYLPSPQSVCECRPYVFGAGKP YEFSDCDKIKILRGVFAFLLYV ATFMLPVIANIAPQKRPFMQQT RCEVQCREIDIEVQKLKSYDKLL ASINKKPGVNGWQKRRTVNA GEAHDQALDYALYHLRIMTP AHDERSIAAKGLTGEGYKGH VFWDETVFLFPFLHSDPTVAR SLRLRYRWHNLPGRARRKRDN GWAGGAPISVGKARAAAKK
7770	38138	A	7824	601	853	
7771	38139	A	7825	2	644	MAQQQ/RKFAHKPAKSKTAA/ A/ASEKNRGPGRGVRVAPKKA RVVQQQKLKKVSLCCSGWS*T PGLKASSRLCLPKCWDYRRDTL WLFLSATFICRWNLKRSSEGGK IEHDVVMKA/SSSLPRLKALLK APSPRRNGAAAA/TSSTPPLRT AGPQLQGQHPTPLPSIWGPLQV NSHRLSLFRMRTLSPSDWASPR HSSGGPKGAENPGNDQGRYSH
7772	38140	A	7826	1	2616	
7773	38141	A	7827	1	504	

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7774	38142	A	7828	1	1068	MAEIQHKTRIFLLEGRDLLAAV KTGSGKTLAVLPAJELVVKLK MPRNGTGVLLSPTRQLAMQTF GVLEKELMTHHVHTYGLIIGSN RSAAEQKLANGINIIIVVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPKKEPLVYGVDEDKANATVD GLEQGHFVCPSEKRYLLFTFL KKNQKKKLMVFFSACMSVKYYP YGLLKYYDL/PVLAIHGKQKQN KHTTTFF*YCNADSGTLFQLE KLIEKNYFLHKSQETYKSYIR AYDSYSLKQIFNINNLPHIAL SFGFKLPFVDLNMNSNEGKQK KQGGFGYQTKKVEKSIIFKHS KSSAAGSSLTQEMPVILNNF
7775	38143	A	7829	3	1851	
7776	38144	A	7830	1	905	MVFDAKYLTGWRFEDTVVQSN MKHOPFIVVNKHNVQVEYKGE TKSFYPEEVFMVLKMKELAET YLGKTVTNAVVTVPAYFNDSQ HQATKDAGTIVSLNVLRIISKPT AAATAYRQKGIDFNTSIFHALF EELNAVLFHGTLDSEKALGN AKLDSQIHDIVL/GPFEQGRH* MYGPGS*EQS*R*EAEGQDVIQ EFS*KLCIRYESSC*R*ETSRQD* R*GQTEDS**GY*NYQLAG*ES DSEEGRISTSKSGESLQPHNYQP VPEYRRHTRRNAWGIP*WWSS LCWSFPRAPIEAD
7777	38145	A	7831	2	886	ARGACSSWVFCGLRYWSQAY TPATMSKGPVAGIDLTTTYSKV GVFQHGKVEIIANDQGNRTTPS YVAFDTDERLIGDAAKNQVAM NPTNTVFDKRLIGR/RFDDAV VQSDMKHWPFMVVNDAGRPK VQVEYKGETKSFYDDEVSSMV LTKMKEIAEAYLGKTVTNA/V VTVPSYFNDSQRQATKDAGTI AGLNVLRINEPTAAAIAYGLD KKVGAERNVLIFDLGGGTFDVS ILTIEDGIFEVKSTAGDTHLGGE DFDNRMVNHFIAEFKRKHKKDI SENKRAVRRLRTTK
7778	38146	A	7832	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTLDPVEKALRDA KLDKSQIHDIVLVGGSTRIPKIQ KLLQDFYEAVAYGAAVQAAIL SGDKSIENVQDLLSLDVT/PPF LGIEATAGVMTVPH

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7779	38147	A	7833	1	218	
7780	38148	A	7834	508	883	YYHSYQADT/IILGGEDFDNRM VNHFAIEYKRKKHKKDISENKRA VRRIR.TACERAKSTVSSSTHAS TEIDSLSEGDIYTSSTCASFEEL NADLFLSLDLPVEKALRDAKLD KSQIHDIASINPDEAVAYGAA VQAAILSGDKSENVQDLLLDV TPLSLGIETAGRVITDLIKHNTTI PTKQTQTFTTYSDNQPGVLIQL YEGEHTMTKDDNLLDKFELTGI PPAPRGVPQIEVTFDTNSNGILN VSAVDKSTRKKNKITITNDKGGH LSKEDIEYMVQEAKEYKAEDQ KQR/D/KVSSKNSL
7781	38149	A	7835	1	194	
7782	38150	A	7836	1	1482	MVFDKRLIAHRFDDAVVQSE MKHWPFMVVNDAGRPKVQVE YKGESKSFYPEKVSSMVLTNM KEIAEAYLGKTVTHAVVAVPA YFNDSQRQATKDAGTIIVGLNV LRIINEPTAAAYGLDKRHRSSLP ILTASLGGAGSL*STQA/SIEIDC LYEGINFCTSITHARFEELNADL FRGTLDPVEKALRDAKFDKSQI HDIVLAGGSTRIPIKQLLQDFF NGKELNKGINAEAVAYGIAV QAAILSGDKSENVQDLLLFDVT PLSLGIETAGGTQILTTYSDSQP GVLIIQAYEGKHAMTKDNNLLG KFELMGIPAPRGVPQTEVTFD SDANGILNVSAVDKSTGKENKI TITNDKGCLSKEDIERMVQEA KYKAEDEKQRDKVSSKNSLES YAFNMKATVEDEKLQGGKINDE DKEKILDKCNEIIWLNENETAK KEEFEHQQKELEKVCNPIITKLY QSAGGMPGRMPGGFPGGGAPP SGGASSGPTIEEVD

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7783	38151	A	7837	2	2221	PRVPRVRSAPALGFFVASFVIG ARPTQQPWSKGA V GIDLGTT YSCVGVFQHGKVEIIAN\DQGN RTTPSYVAFTD\TERLIGDAAKN \QVAMNPTNTVFD CQT V*LDGR FDDAVVQSDMKHWPFMVVND AGRPKVQVEYKGETKSL\YPEE\ VSSMVLTKMK\EICRSLTLGKT VTNA\VTVP\SYFND\SRQAT KDAGTIAGLNVLR\INE\PTAAA IALQKFRQKRFGAERNVLIIDL GGGTDFVSILTIEDGIFEVKSTA GDTHLGGEDFDNRMVNHFAE FKRKHKKDISE\NKRAVRRLRT ACERAKRTLSSSTQG\SIKIDSL* EGIDFYTSITRARFEELNADLFR G\TLDPGEKAL\DAKLDKSQIS *YLSWVGGSYSYPRLQKSCCQ DFFQWEKELELRSINPGWKAV/ AFIGAAVPGQPFLSGRQVLENV/ QDLLLLADVTP\SPWVLKTAGG VHDCPPSKRNTIPTKTQTFTT YFWTTQPGCGLFRFYEGRALP WTKDNQPALASFELTGIPPA PR GV\PQ\EVTFDIDANGYTPWSL AVDKKYGKKRTKITITN*QGPF *AREDIGTYGSEAEVTKLEG GGRQEGTRVSSNDFT*GPM PFN MKSTLLKDEKL\QGRINDEGQ NRRFLDQV*KLKSNWL**ESRL LEKEEFEHQ\KELE*VCNP\IIT QAGTQSARRHCQGGNPWGAF L
7784	38152	A	7838	3	757	PPFGGRVVR\HPVILASTVDSY ERRNKGAARVIGITLLGT V NKH SVEVTSCFVS SHNESDEVAVDM EFAKNMYEL/H*KVSPNELILG WHDITEHSLVLIHEYYSREAPNP IHLTVDTSLQNGHMSIKAYYST LMGVPGRIVGVFTPLTVKYAFY DTECIRVDLIMKTCFSPNRVVG LSSDLQQVGGASARIQD\TSLIVL QYAE DILSGKVSADNTIRKVGH FLMSLVNQVPKIVPDDFETMLH SNINDLLMVT
7785	38153	A	7839	1	1821	
7786	38154	B	7840	16	1305	
7787	38155	A	7841	1	359	

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7788	38156	A	7842	2	1085	GVAPWGRGRAAPRCASATVGG SGIGRLR/GITSSGLKMDNKKR LAYAIIQFLHDQLRHGGLSSDA QESLAEVAIQCLETAFGVTVEDS DLALPQTLPEIFEAAATGK/EMP QDLRSPARTPPSEEDSAEAERL KTEGKPKQMKIVENF/EAAVHF LTEKPFELNPSQRPSYFCNRAA AYSKLGNAGAVQDCERAICID PAYSKAYGRMGLALSSLQQLH EAVAYYKKALELDPDNETYKS NLKIAELK/LREAPSTGGVGSF DIAGLNNPGVMSMASNLMNN PQIQQLMSG/MISGNNPLETP GTSPSQNDLASLIQAGQQFAQ QMQSVGIPRVV**SAQESSIRSR TPSASNDQOE
7789	38157	A	7843	225	398	FIIDYTNSCIFHQNICLICSNRNF RQSNVVMICHY*TLQEIETFC* MNSSLWSIIIF
7790	38158	C	7844	162	269	
7791	38159	A	7845	273	501	HKDQPIQTENDHPSTNFSVLK LHDPLLNEMDLIVWVSF*Q*SC FYLVHPNCCSPLV*HP*SENPKF SNEYFLRVS
7792	38160	A	7846	1	867	
7793	38161	A	7847	185	1325	EEQQTNLASKKKSCIMLEKTEN KIRLVIVSEEEKKKVLKRP**K MTVRAHHGSRTPHSWVESNY YWDICDQWMS/EPVGYMPCQH CQVAKNTVIVAPKQHLQGGKI PWSLVTVDLMGAFSYKPKQS/N VYAIIMTDLFTKWIVILPLCDVS ASEVSKAIINIFFLYGPPQKJMD QRDEFIQQINIELYRLFQIKQIVI SHTSGTVNPTSTNTIKAFLSK HCADHPNNWDDHLSAVSFAN VTHLEPTKNTPYFQMFVKNP LYYLPETSDSLHEVDGDNSTMF AKILDIAIKEADKIMENKTTSLG QMENNLDLDELNKSIIIVKKKPK QLNPFHLKVGHGSEFKTEKLV GRMVVFQSWNGVGPLCHRLY YRKWMCCP
7794	38162	A	7848	2	455	MADRLTQLQDAVNSLADQFC NAIGVLQQCVPASPNNIQTAI NKDQPANPTEEYALFAA/LIA/ RTAKDIDVLIDSLPSEESTAAALQ AASLYKL/EEENH/EAATCLGG MLFIEGDMLLGGRYKGA/LDI/ AQSQLEGGQSGYP*ASLFPDS

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7795	38163	A	7849	229	560	
7796	38164	A	7850	1	1077	
7797	38165	A	7851	25	690	WPSDEAEGYSEIHFEVFKDVR KRFPQHTIMAGNVVTGEMVEE LILSGADIHKVIGIPGSVCTTRK KTGVGYPQLSAVMECANAAH GLKGHIISDGGCSCPGDVAKAF GAGADFVMLGGMLAGHSESG GELIERDGKKYKLFYGMSSSEM AMEEVLGGVAEYRTSEKGT VEVPF*REMLEHTIPRHP*GGIR STCTYVGA\AKLRRR*ARTNYL HPEVHPAR
7798	38166	A	7852	768	1857	EGGHHFGGQGDASAPFGSASI LPIKLDVHPHDGRRRAEKSXPG GNPQRQLYCQPPAGCLPGAVY RPRRSRGARMYSRYSPAERNRP DQRAGYCAQPDRLRFSRADD RSRWRHVHFGTSRHCAGDRAY RPPPHSAAEALPVLPVFQ*PTA DQVLFPSLIAACYNHNQNKIL EQEMSCVLLATFIQTRAQQRKY KRRNNRGIPRESTAREQARHNA NKAQQPRKHARNGASPAQQRK NRAAARDKDEKPAQQKDKAR QSAPEKKNRAIRGTNSREQAAK AERNRRQRGGQKGAQQGQHR EEAGEPTYVDEKAQAATSPPPQ TPHPAPDHDDAEDHRTDTRNR NAHQPKVYTHKDTPTNESR
7799	38167	A	7853	1403	2028	RRIQTNGRTFHAHGGPSRGLPE ELGKDHRKETSSRTL*QFQPN AKSPGQNLRESMNPVC/MTQQ ARRLQRLAKDLLKQVQVQDSG SWANNKVSALDRTLGEITRILE KERSRRGKGPSKEDLEGAAN/G VRRTM/WMSGNLVKESQPHPT HRPNILT*YPSIFP*RTLLTLWL KVQLQQLK*KMEKSGKKIKKK PKR*KPG*TSGLTNL
7800	38168	A	7854	1	675	

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7801	38169	A	7855	2	1110	AQEEEAKEVNEIAFINTLEAQNKRHDVLSKLLKEYEQLNELQEERQRRQEEKQARDEAVQERKRALFAERQARVEELLMKRKEQEARIEQQRQEKEKAREGAARERARDREERLAALTAQPRSYGRVTEKNSAQA**KYSKAH/RNRLNKEKKKLLS*AVGDMQILIMPPN*PLYERKKQCSLCNVLISSEVYLFSHVKGRKHQQAVRENTSIQGRELSDEEVEHLSKKYIIDIVVESTAPAEALKDGEERQKNKKKAKKIKARMNFRakeYESLMETKNSGSDSPYKAKLQRLAKDLLKQVQVQDSGSWANNKVSALDRTLGEITRILEKENVADQIAFQAAGGLTALEHILQAVVPATNVNTVLRN
7802	38170	C	7856	65	425	
7803	38171	A	7857	1	1131	
7804	38172	A	7858	953	1311	FLFFIFNFYFFFGGRKCPLLVAPRLEVQMAVILGSLQPSPPGFK)*FSLPQSPSSWDYRHAPTHAQPNFVFLVETGFHHIGQAGLELQTSGDPPTSASQTAGITGVSHRAWPGTILFLK
7805	38173	A	7859	2	857	FVDIFQRWKECRGKSPAQAELS YLNKAKWLEMYGVDMMHVVRGRDGCCEYSLGLTPTGILIFEGANKIGLFFWPKITKMDFKKSKLLTVVVEDDDQGREQHTFVFRLLDSARTCKHLWKCAVEHHAFRLRTPGNSKSNRSDFIRLGSRFKFSGRTEYQATHGSRLRRTSTFERKP**TSLSIPETFNVSQSKQPSDSSPALLKQIQKSNNYQPPISILISIPSPAPGGILTTPQMSGHPFQDDRSHWKASASGDDSHFELCPTTQNPEGTLGGMKPYDVSEINVM TAL

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7806	38174	A	7860	1	936	MELTHLQHPHEQEDVHAVGLL LGLREQHHMVSEGPQQSWQE ERTELAASVRLLFNMYPLLIHK NHASPGIPNLLHPRGLRAITIA VFGKQNTYIRLEPFKINVLEQIT KHIEKLQCGEHNFPQEIQEGK SHQNQHEAHFVVELCKYFLCQ EYLPSTITILTTYTQGLFCLRLK MPAKTFAGVRVHVVDKYQGE ENDIILLSLISNRICVALSRAKKG MYCIGNMQMLAKVSLWSKIIH TLRENNQIGPMLRLCCQNH PET HTLVSKASDFQKVTEEGC/MLP CEFRLCGCHVCTRAWHPYDSS
7807	38175	A	7861	218	580	
7808	38176	A	7862	3	1636	
7809	38177	A	7864	24	386	
7810	38178	A	7865	2	999	GRVGGFFAGNPGSDSFGGLLLG LTPVLRWVADGGTIPKRHEL KGPKEKVEKDKETELVAQWN YCTLSQEKLRRIVAL/CNFAD FYNKIEPVIEFLDKSAEKGSG RQASHIKTH*RIVDRAESFPDNP CPGKGIKGN/D*KVDKHDDIQA GASSSSPVGGPGRWNGRHRFL PSGGCGLCCFS*AEPWKEIKAG VCHTCGAGLSRRMMIIVLNGT KEDVDLLKTMMEERRL*SEAG KENKENPRQSLFQNDVSERS PRAIKS*DRGSLKKPAFDSREK KTNLAPKSTAMNESSGKAGK PPCGATKRSIADSESEAYKSLF ITHSSAKR
7811	38179	A	7866	1	559	MGCDGGTIPKRHELKVGPKKV EKVDKDAELVAQWNYCTLSQE ILRRPIVACELGRLYNKDAVIEF LLDKSAEKALGKAASHIKSN VTELKLSERALKKAEVCHTC GAAFQEDDVIMLNGTKEDVDV LKTRWRREG*ERRGKKTKKP KAAEVCFQNPVDSGRKPQGPS KVKTREALKKPS
7812	38180	A	7867	188	368	YVACMPAWPNVTVANQLFNV YFPARDMTVPSSPG/QPVVDQL STQGQARRDALEVVGYES
7813	38181	A	7868	179	554	LRPADPRSLVPGWALGLGPGAI LGPGRVTFPGGRPPPTHPPLSF PPGGRQPLWVPALPAEEGRE/R LGREREGRGKAGAGMA*AGL VL*CLQLQVQGGPLGGSWLST RLRSPRCHPWLLRRHLP

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7814	38182	A	7869	2	131	YKSELEEQLTSVAEEMRARLSK ELQA*KDRLGENMEKVRGRVLV KYRGEVQAMLGESIEELRVRLA LYLRLKLTGFLRDADHL* RPA GREYGESKRTL
7815	38183	B	7870	1	3639	
7816	38184	A	7871	279	1077	IQHPRLSADDFRNCETEPAM/* HAVENDIHLGCELETEIQAF KEELL/FMKKNHEEEVKGLQAQ IASSGLTVVVDAPISQDFAKIMA DIWAQYDEVAQKNREELDNNR SQQIEESTTVTTQSTEVGA AK AMLTELTRTVQFLEINLDSMRN LKASLENSLREVARYALQME QLNGILLHLESELAQTWAEQQC QAQEQALLNIKVKLEAAIATY RRLEEDGKDFNLGDTLDCSNS MQTIQKTTTRQRMQDGKVLSET NDTKLRH
7817	38185	A	7872	712	855	
7818	38186	B	7873	50	788	
7819	38187	A	7874	201	372	ICQMILKRRVLS* TQKHQATHG WNSAYSLTAPFPVSCQDHL C* P L* AEAQISKEEP
7820	38188	A	7875	3	323	FFFETEFHSAVQTGVQWHD PSS PQPPPPRFK* LSRPSLPSSWDYR HVPSPHGPFLHFQ* KRGSTNQA GLELPTSGDLAAFA\SPSARITG VSHCARPNYQCFLFKY
7821	38189	A	7876	1	911	MLLTLAGGALFFPGLFALCTW ALRRSQPGWSRTDCVMISTR LV SSVHAVLATGSGIVIRSCDDVI TGRHWLAREYVWFLIPYMIYD SYAMYLCEWCRTRDQNRAPSL TLRNFLSRNRLMITHHAVILFVL VPVAQRLRGDLGDDFFVGCIFTA ELSTPFVSLGRVLIQACNM EMT ESLKQQTLLYKVNIGLTLGNF FPCRUILLFPFMVWSYGRKKGL SLVPSTLQHPILTATWANA FPR* APQIYWFCLLLQKAVRLF DTP QAKKDG* MLLGVRRLTPAAS STQHSMQIVPWWASDFGY
7822	38190	A	7877	2	283	SCHCTPAWILALSPRL ECSGAIL AHCNLHLWG* SDSPASASRVA GTAGACRAWLIFCVL VEMGF HRVA/PGLVLNS* AQTIRLPRP KVLGLQA

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7823	38191	A	7878	1	1042	PKVRSPIRKRLAPAPAFVRKQE LKKIVDPALL*KKS*EFGHLDRDI QPQKRPPPLL*KWPRIYIRV/QG RRAILYKURLKGPFCDDYPGFTQG PGTPQTS*SSLKLVAHKYRPRD KAQRSKQRLLA\RAEKAAAK GAVPQERAHVPVLRAGV\NPVSP PLVGEQEKLSLVVIA\HDRGSPS ELVVFLPALG/RVKMGVPYCIHK GKGKTGDGLVHQKALHPLSAF TQVNSIEDKGA/ALKLVGSYQ GPNYNDRYDEVGRSFTQNTVIH KFSQITGWLNL*EVLSDDLG TAKQN*RN**PKSQKTVSQAN CLFLSFQIRRHGGNVLGPCKSV ARIAKLEKAKAKELATKLG
7824	38192	A	7879	3	472	GRGVAYRGPSPRGTGPRGDE RLQHGGG/SREGPPAAPAAAA GYGQSCCLIEDGERCVRPAGNA SFSKR/VKKSISQKKLLDIDKSV DLFQLQVNTLRRYKRHYKLQT RPGFNKAQLAETVSRHFRNIPV NEKETLAYFIYIMVKSNSKRLDQ
7825	38193	A	7880	3	638	GRGVAYRGPSPRGTGPRVR*T ASARRRTAAKGPPPPQLPPRA TAKSCCLNIEDGERCVRPAGNA SFSKR/VKKSISQKKLLDIDKSV VRHLVNCDFHK\NFIQ/SVRNKR KKEDQVYDGRENS/SPSTDTDIP EVDLFPACQVNTLRLRYKRH* QVARPRPGFNKAPVSRQL*VDT FRNIPVD*KETLALLSSSMVKSN KSLDQKSGGWQA
7826	38194	A	7881	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITHFSPKISDLILCLKKIM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRCRRGCGEIGTLLH CWWDCKLVPQLCKSMWRFLR DL/DPAIPLLGYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
7827	38195	B	7882	446	625	
7828	38196	A	7883	1	1875	

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7829	38197	A	7884	31	809	KPRLENYVKNAAEASGADAINW KKGY/LVMEDEMNMKREGKF REKRIKRNEQSLQEIWDYVYKRP TLHLIDVPETLNAHKRQERSK TDTLTSQI.KEL.EKQEQTSHSKAS RRQEITKIRAE.LKEIETEKTLQKI NESRSWFFERINKIDRPLARLIK KKREKNQIDAINKNDKGDISDP TEIQTITIREYYKHLIYANKLENL EEMDKFLDYYTLPLRLNQEEVES LNRPIITGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
7830	38198	A	7885	1	2142	MIILIDAEKAFDKIQPFMLKTL NKLIGIDGYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSNVSKVSG YKINVQKSAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPVNDKL MVLEVLAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLE KENYKPLLKEIREDTNKWNIP CSRIGRINIMKMAILPKVIYRFN DPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKAWYWYQ NRDIDQWNRTEASEVTSIYNH LIFYKPKDNKKWGNDSL FNKW CWENWLAICRKLKLDPLTPYT KIHSRWIKDLNVRPKTIKLTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVVIKLSFCTA KETTRIVSRQPTIEWEKIFAIYPS DKGLISRIYKELKQIYRKKVTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM

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7831	38199	A	7886	209	3816	QGRPTFRFRKYREHHKDPREE QLQDT*SSDSPKLG*KKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTETITIREYYKHLVANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPTGSEIEAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDITTKGNFRPISLMNI DAKIL
7832	38200	B	7887	1	3570	
7833	38201	A	7888	2	1624	
7834	38202	B	7889	67	3156	
7835	38203	A	7890	1	1416	MIILIDAEKAFDKIQPFMLKTL SKLGTDTGYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSQY KINVQKSQAFLYTNNRQTESQI MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFFHKWC WENWLAVCRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLTLEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSLAIREMDIKTTMR YHLTPVRMAIHKSGNNRCWR GCGEIGTL
7836	38204	A	7891	1	1932	

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7837	38205	A	7892	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNMNLP TK KSPGPDGFTAIFYQRYKEELVP FLCLKFSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIIKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTDKDNHMIISIDA EKAF DKIQQHFMKLTKLNKLVLEVA RAIRQEKEIKGIQKGEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSQYKINVSQAFLY TNNRQTERQIMSELPFTIA SKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTKLFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSL FKNWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKHKMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCTCRVAKEIQSL*RRI/W KRLQRTLSIPVLDAV*PPMF*AS
7838	38206	B	7893	1	1710	
7839	38207	B	7894	1	2265	
7840	38208	B	7895	1	2142	
7841	38209	A	7896	1	1791	
7842	38210	A	7897	1	1878	
7843	38211	A	7898	1	2091	

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7844	38212	A	7899	1	1751	MIISIDA EKAFDKIQQPFMLKTL NKLGDGTYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNI PCSWYGRINIMKMAILP KVIYRFNAIPKLPMPFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPTYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK IFTTYSNDGLISRIYNELKQIYK KKTNNPIQWAKDMNRHFSIE DIYAAKKHMKKCSSSLAIREM QIKTTMYHLTPVRMAIHKKSG NNRNHLDFKHIRILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA

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7845	38213	A	7900	1	2540	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLDIDYGLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITSYLSHSAI KLELRIONLTQNHSTTWKLNLL LLNDYWLHNEMKAEIKMFET NENKDTTYQNLWDFAKAVCR GKFIALNAHKRKQERSKTNTLT SINKIDRPLARLIKKKREKTQID AIKNDKGDITTDPTMQTTIRE YYKHLANKLENLEEMDKFLN TYTLPRLNQEEVESLNRPIGAE IVAIINSLPTKKSPGPDGFTAIFY /HEL/LKENKIPRNPTY/RGCEGP LQGELQTTAQ*NRGKQEMEE HSMMLMDRKNQYRENGHTAQG NLQIQCHPHKATNDFLHRSGKN YFKVHMEPKKSPHRQVNPQPK EQSWRHAI*IQTLQGYSNQN SMVLVPKQRYRSMKKNRRLRN NAAYLQLSNL*QT*EKQAMGK GFLI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RLKH*T* NHKNPRRKPRHYHSGHRHGQG LHV*NTKSNNGKSN*QMGSN *TKELLHSKRNYHQSEQATYKL GENFCNLPI*PRANNQNLQ*TQ TNLQEKKNQPHQKVGKGHEQT LLKRRHLCSQKTHEKMLSITGH QRNANQNHNHIPSHTS*NGNH* KVRK*QVLNGLDDVQLFR*NK QPCSHKACLVVSSYRRA*SLV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7846	38214	A	7901	1	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSLEQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAAMEDEMNEMK REGKFREKRIKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIQENFPNLRINKI DRPLARLIKKKREKNQIDTIKN DKGDITTNPTEIQTITREYYKHL YANKLENLEEMDTFLDITYTLPR LNQEEVESLNRPTITGAIEIVAINS LPTKKSPGPDGSIAEFYQRYKE E/PADKQLQQSLSIQNQCTKITSI LIHQQTNRPNHE*TPHNCFK ENKIPRNPITYKGCEGLLPGLQ TTAQGNKRGYKQTEEHSMLM GRKNQYRENGHTAQGNF*IQ HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKEQSWR HHTT*LQTLQGYSNQNSMVLV PKQGYRSMQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
7847	38215	B	7902	1	2337	
7848	38216	B	7903	1	1677	

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7849	38217	A	7904	1	1722	MAGYPSEMKLPEELSGSNICCS AVFTVLQPLLPRTQSGVDL RQPTDLQLRVLTVRRKNKQ KRTSTPKPHLYVTIHKDQSKKL TQNHSTTWKLNLLNDYVW NNEMKAEIKMFFETSENKGTIY QNLWDTFKA VCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAIAKN DKGDITADPTEIQSTIREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEDESLNRPITGSEIEAIINS LPAKKSPGPDRTAEFYQRYKE ELHINRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLVLA RAIRQEKEIKGQLGKQEVKLSL FADDVIVYLENPIVSAQNLLKLI SNFSKVSGYKINVOKSQAFLYS NNRQTESQIMNELSFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKDDTNKWKNNIPCSWVGRIN IVKMGLPKVVYRFPNAIPKLP TFFTELEK\ITLKFIWNQKRARI AMTILS*KNKAGGITLP
7850	38218	A	7905	1	2310	
7851	38219	A	7906	195	791	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMR YHLTPVRMAIIKSGNNRCWR GCGEIGTLLHCWLDCKLVQPL WKSVMWRFLRDLLEIPDPAIPL LGIPNEYKSCCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVQ SLVG/TWVNWETTFSTVIAVQK PTRLSH
7852	38220	A	7907	1	984	
7853	38221	A	7908	1	2076	
7854	38222	A	7909	1	1872	
7855	38223	B	7910	1	3309	
7856	38224	B	7911	133	3213	
7857	38225	A	7912	1	1364	
7858	38226	A	7913	1	3249	
7859	38227	A	7914	1	2757	

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7860	38228	A	7915	1	2268	MAGYPSETKPPEERSDSNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDLQLRLVLTVKRKTNKQKG HPHQNPRTSPSSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFKEVLKDLQ RDLDSTHIMGEFNTRLSTLDRS MRQKVNKDIQELNSALHQADL IDISRNLIHPKSTEYTFPSAPHRT YSKIDHIVGSKALLSKCKRTEII TKCLSDHSAIKLELRINKLTQNC STTWKLNLLNDYVWHNEM KAEIKMFFETSENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKTDLTSLKELEKQEQT HSKASRRQEITKIRAELEQIETQ RTLQKISESRSWFEKINKIDRS LARLIKKKREKNQIEAIKNDKG DITTNPTETQTTIKEYYKHLVK NKLLENLEMDKFLNTYTLPRLN QEEVESLNRPTGSEIVAIINSLP TKKSPGPDGFTAIFYQRCKEEL VTFLLKLFQSIEKEGILPNSFYE ASINLIPIKPGRDTTKKENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSIQVPCVCR*H DCVSRKPHHLSPOSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE*TPIHNCFKENKIPRNP YKGCCEGPLQGEQTATAQ*NRK GHKQMEEHSMMDRKNQHRE NRHTAQGNL*IQCHSHQATNDF
7861	38229	A	7916	1	4729	

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7862	38230	A	7917	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFSSAPHHTYSKTDHIL GSKALLSECKRTEIHTNYLSDDS AIKLELRKLNLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDFAKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELEKETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPEIQ TTIREYYKHL YANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPPDG FTAEFYQRAIRQEKIKGQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGDLSFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD
7863	38231	A	7918	1	1205	
7864	38232	A	7919	1	2274	
7865	38233	A	7920	1	2307	

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7866	38234	A	7921	569	3030	RKH*TWKRTSSTSHHKNNPN* LEKQEQTTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKKKREKNQI DTIKNDEGDITTHPTIEHTIIREY YKHLANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLKLFQSIEKIGLPNSF YEASIIIPKPRDRTTKKENFRPI SLLNINAKILNKILANRIQQHIK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIIISID AEKAFDKIQPFMLKTLNKLGI DGYHKIIRANYDKPTANIILNG QKLEAFPLKTGTROGCPPLSLL FNIVLEVLARAIQKETEIGQL GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKIN VQKSQVFLYTDNRQTESQIISEL PFTIASKRIKYLGIQLTRYVKDL FKER/YNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIWNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPDKNKQWGNDSLFNKWC WENWLAICKKLKLDPFLLPYT KINSRWIKDLNVRPKTIKTLLEN LGNNIQDIDGMGKDFTSKTPKA MATKDKIDKWDLMLKLSFCTA
7867	38235	B	7922	1	3171	
7868	38236	A	7923	1	2646	

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7869	38237	A	7924	321	2211	CCQFSMARRGHLPRSVQVSIPIG QSPVPRAAYQDSGRVKEPTAD C/VGPRQT*CMAPHCHLGGWH MLALSLGKGAGAGGKESTWEP SPGIRMTKTYSTRREQSHPTI/ KGQIKQMNLRETCSWTFHKKF LKTVAQFISHPHKNTCLAMAVS ANRSMRQKFNKDTQELNSALH QVDLDIYRTLHPKSTEYTFESA PHHTYSKIDHILGSKALLSKCK RTEITNYLSDHSAIKLELRINKL TQNRSTTWKLNKLLNDYVW HNEMKAEIKMFFETNENKDTIY QNLWDAFKAVCRGKFIALNAH KRKQERSKIDTLTSQKLEKQ EQTHSKASRRQEITKIRAEKKEI ETQKTRQKINESSSWFFEGINKI DRPLARLIKKREKNQIDTIKN YKGDITTDPTIEQTTIREYYKHL YANKLENLEEMDKFLDYTLPL RLNQEEVECLNRPITGAEIVAI NTLPTTKSPGPDGFTAIFYQRC SRWIKDLNVRPKTIKLTLENLGI TIQDIGTGKDIMSKTPKAMATK DKIDKWDLIKLSFCTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKSNPIKKW AKDMNRHFSKEDIYAACKHMH KKRSSLAIREMQKTTMR
7870	38238	A	7925	1	3057	
7871	38239	A	7926	1	1830	
7872	38240	B	7927	1	3192	
7873	38241	A	7928	1	3484	MGTSVQNGEERAGTSGQGSV EQLSGSSVQLPPGLKLCFEPYFS SCASDCILHASPLSLMAASGSQ NPNLWASWLCKWVQCPEQ LGCHLTSSVIYGLRYYPQAKRS ELELRDCEGLCNQTSPLSSLDG MGWKAEEESNSGIRNIWIPI AFATHKQYNVRQVISPSPPYWS HRGNGNNSLCVTRLSSGLKQP VAGTGRGLEGGSGTRDLMPPFL SAAPKEQPILAPARRSWFFEKI NKIDRLRLARLIKKRE

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7874	38242	A	7929	I	1946	NLTQNRSTTWKLNLLNDYW VHNKMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRRQERSKIDTLTSQLKELE KQEQTHSKASRRQEITKIRAE KEIETQKTFQKVNESSWFFERI NKIDRPLARLIKKEKNQIDAI KNDKGYITDPTIEHTTIREYYK HLYANKLENLEEMDKFVGTYT LPRLNQEEVESLNRPIITGSEIVAI INSLPTKKSPGPDGFTAIFYQRY KEELAGRDTTKEENFRPISLMN IDAKILNKILANRIQQHIKKLIH HDQVGFIPGMQGWFNICKSINV IQHINRTKDKNHMISIDA EKAF DKIQPFMLKTLNKLVLVFLAR AISQEKEIKGIQLGKEEVKLSLF ADDMIYVLENPIVSAQNLLKLIS NFSKVSQYKINVQKSAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKLLSK EIKEDTNKWNIPCSWVGRI VKMAILPKVIYRFNAIPIKLPM FFTELEKATLKFIWNQKRARIA KSILSQKNKAGGITLPDFELY KTTVTKTAWYSYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGDLSFNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK
7875	38243	A	7930	I	4801	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYWVNNEMKAEIKMFF ETK\ENK\DTTYQNLWDFAKAV CRGKFIALNAHKRRQERSKIDT LTSQLEKEKQEQTHSKASRRQ EITKIRAELEIETQKTLQKINES RSWFFERINKIDRPLARLIKKE EKNQIDTIKN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7876	38244	A	7931	1	3146	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRRIKLTQNRSTTWKLN NLLNDYVWVHNKMAEIKMFF ETNENKDDTTYQNLWDTFKAVS RGKFIALNAHKRQKRCRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAEKIEITQKTLQKINES RSWFLERINKIDRPLARLIKRR EKNQIDVIKNDK
7877	38245	A	7932	1	2669	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTPLGTQSKT VVAKRNRHGGKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTGKEVENFEKNLE ECTRITNTEKCLKELMELKTK ARELREECRLSRCDQLEERR KQERSKIDTLTSQLEKEKQEQ THSKAGRRQETKIRAEKIEIT QKTLQKINESRSWFFERINKIDR PLARLIKRRKREKNQIDTIKNDK GNITTDPTIEQTIREHYKHLA NKLENLEGMDKFLDITYTLPLRL NQKEVESLNRPTGSEIVAINS PTKKSPGPDGFTAIFYQRYKEE LHINRAKDKNHMISDAEKAF DKIQQPFMLKTLNKLVLVFLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLL SNFSKVSQYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGILQTRDVKHLFKENYKPLL KEIKEDTNKWKNI PCSWVERIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYSYQNRDIDQW NRTEPSEILPRIYNYLIFDKPEKN KQWGKDSL FNKWCWENWLAI CRKLKLDPLKPYTKIKSGWIK DLNVRPKTIKTEENLGITIQDI GMGKDFMSKTPKAMATKAKID

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7878	38246	A	7933	1	2962	MNNSIKEKVKLSLTQWEMQTK PNNNTVDLKDQAEVNLSTDY RKQHVMLPTEINSDDSLKIGVI RLANWIKSQDPSVCCNQETHLT CRDTHRLKIKGWRKIYQANGK QKKAGVAILVSDKTDKPTKIK RDKEGHYIMVKGSIQEEELTIL NTYAPNTGAPRFIKQVLSDLQR DLDSYTLIMGDFNTPLSTLDRS TRQKVNKDTQELNSALHQVDL IDYRTLHPKSTETYFFSAPHHT YSKIDHILGSKALLS
7879	38247	A	7934	1	4220	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTETYFFSAPHRTYSKIDHLV GSKALLRCKCRTEIITNCLSDHS AIKLELRKKLTQNHSTTWQLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKTSRRQETIKRAELKEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKRE
7880	38248	A	7935	1	3229	MGKKQNRKTGNSKTQASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSADEMEMNEMKRE GKFKREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLRDIIQENFPNLARQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKDRSTRQ KVNKDTQELNSA
7881	38249	A	7936	1	3227	MGDFNTPLSTLDRSTRQKANK DTQELNSALHQVDLIDYRTLH PKSTEYFFSAPHHTYSTTDDHIL GSKALLSKCRRTETITNYLSDHS AIKLELRKKNLTQNRSTTWKLN NLLNDYGVHNEKAEIKMFF ETNENKDTTYQNLWDAFKAV CRGKFIALNAHKRQERSKIDT LTSQLEKEKQEQTHSKASRRQ ETIKRAELKEIETQKSLQKINE SRSWFFERINKIDRPLARLIKKK REKNQIDTIKN
7882	38250	B	7937	1	2089	

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7883	38251	A	7938	1	3527	MELKTKARELREECRLSRSPCN QLEERVSAEMEDEMNMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTKLEN TLQDIIQENFPNLRQANIQIQEI QRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSDHSAIKLELRJKNLTQNHST TWKLNLLNDYVWHNEMKA EIKMFFETNENKDTTYQNLWD TFKAVCRGKFIALN
7884	38252	B	7939	1	5238	
7885	38253	A	7940	1	3587	MENDFDELREEGFRRSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRLSRSCDQLEERVSAM EDEMNEMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLRQANVQIQEIQRMPQRYSS RRATPRHIIVRFTK VEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDIDIYRTLHPKS TNEYFFSAPHHT
7886	38254	A	7941	1	6202	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH LKSTEYFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSHDS AIKLELRJKNLTQNRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAV CRGKFIALYAHWRKQERSKM DTLTSQLEELEKLEQTHSKASR RHEIAKIRAELEIE
7887	38255	A	7942	2	3134	WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPT QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSHSAIKLELM IKNLTQNHSTTWKLNLLNDY VWHKEMKAEIKMFFETNENK DTTYQNLWDTFKAVCRGKFIAK NAHKRRKQERS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, **Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7888	38256	A	7943	1	4455	MELKTKARELREECRLSRRRN QLEERSVAMEDEMNMKREG KFREKRIKRNQSLQEIWDYVK RPNLRLLIGVPESDAENGTKLEN TLQDIHQEDFPNLAQANVQIQE IQRTQRYSSRRATPRHIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQEEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKIS
7889	38257	A	7944	1	6108	MTGNSHITILTILNINGLNSAIK RHRLASWIKSQDPSVVCIQETH LTCRDTHRLEIKGWRNIYQANG KQKKAGVAILVSDKTDKPTKI KRDKEGHYIMAKGSIQEEELTI LNIYAPNTGAPRFIKQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR STRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFSSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRKIKTLTQN RSTTWKLN
7890	38258	A	7945	2	788	CGLAIYNCTIVDLHFPLALYKK LLKKKPSLDDKELMPDVGRS MQQLLDYPEDDIEETFCLNFTIT VENFGATEVKELVLNGADTAV NKQNRQEFVDAVVDYIFNTSV ASLFRCSFSGFGKVCGGKGLAR LFQPNELQAMVIGNTHF*WKG TGKDYRNTKGNIAEHPITKIF WEVFHLEPLEKKK/RFLFLTG SDRIPILGMSK/LVQSTGGG EEYLPVSHTCFNLADLPKYTK KETLRS*TSQAIDHNEGFSLI
7891	38259	A	7946	1	1647	
7892	38260	B	7947	363	550	
7893	38261	B	7948	1	1123	
7894	38262	A	7949	1	3136	MVTHQQPAARKPNMTSKPKP MGPKAHGIFSGTRKNNLEIYMD QTRTGIAKTKLSKNNKSGGMT LPDFKLYYKAIKACGGSY NSDTEDEETEPSSSQQIENSI TMNKMMLLKAKMKNMNLSSK HITQVSEDEEDDDGCDLFADSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDVAVRVDDEPTT VSYEDDRRGKNQDAYTEGGLS TIKTVNCSSSLTLRRSKTSEDITQ EKKERRTPSDEED

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, v=possible nucleotide insertion)
7895	38263	B	7950	303	1010	
7896	38264	A	7951	3	280	
7897	38265	A	7952	3	514	FYLKELDPAEHSYVLIRKIDPAL VWGLTGDDGTPKTRLLMITLD SIFMQASCVPPEEVVWEVLRVLE AHVSSKKHFVFGESMKLITKAS VQQEYL VHK*VSHSNPTLYVFL WGLSKETRQMEVPEFVAKVND THPSSFSVSGK*GI*EKEGGRYP VPMEGSCRLVTVTASV
7898	38266	A	7953	2	351	
7899	38267	A	7954	2	529	EKGERPHWSNKPNSNLRKTHEL DIDENPASDFDDSGSLGFKYG SGQKYGGIPYFSHRQVR**EKN VKLKAKYLNMRGQIKMKNKIH FFTKETEPFFKKSKILSKVEKF LTWVYNKPMDEEASQESSHDN GHDASTCDSEEQDMSVKKGD DLLETNNPEPEKQCSVSSAGEL
7900	38268	A	7955	1	1370	MPVGTSNFLLGLLENPNLPLT RPSFPFSQREASWGQKATTGP GEGETRLGFSLLLDVFCALHG PREKCVIELRSGHLLAISPGGVR EALISDETYNIVWGHRRGFAQV AIDAKVVEKFLTWNKPMDEE ASQESSHDNVHDASTSSDSEE QDMSVKKGGDLEETNNPEPEK QCSVSSAGELETENYERDSLLA TVPDEQDCVTQEVPSRQAETE AEVKKKKKKKKKKVNGLPPE IAAVPELAKYWAQRYRLFSRFD DGIKLDREGWFSVTPEKIAEHIA GRVSQSFKCDVVDAFCGVGG NTIQFALTGMRVIAIDIPVKIA LARNNAEVYGIADKIEFICGDFL LLASF*KADVFLSPPWGGPDY ATAETFDIRTMMSPDGFELRSL KKITKNIVYFLPRNADIDQVAS LAGPGGQVEIQNFLNNKLTI TAYFGDLIRRPASET
7901	38269	A	7956	3	560	RIHTGEKPYDCKDCGKAFGRTS ELILHQLRHTGVKPYECKCGK TFRQHSQILHQRTHTGEKPYV CKDCGKAFIRGLQLTVHRIHT GARPYGVLEKCGESLLDSTHS* LLHQRRIHTGVEEPYECKEKGK FIHSSEVTRHQRIHSGEKPYECK ECGKAFRQHAQLTRHQRVHTG DRPYESAED

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7902	38270	A	7957	155	1288	HTTASQTTMSQAVR/RRRSDYL SSARR/RRDPARSKPTQGGPPPN PPPTRQGRPTALTNPSPQRPRHR AHPHQHATPKPRTNEEQEGRR HTKQPNPTRTTEPRPPNRRGRPN PQTRRTKQQNTTTPQAHTSTRKN ARTPGLCP*CVKGKTEGGYDA RASARGPYMAGVSWPGEHEDP GAPEARRGRRALPG/GSAFPEM STHTESTPKTTAHTSNDRRNRE QRVKKKTYKTTRSGANRNST ERHEDGYFYGSLTTGPLPWHSA IHSVSAGQPWSLKFTVGLQQAS EGYFSQSQERSLPNRKSSVPRLR LLFLQQASRLSELPLGTGPGSL LLRPRELACTGKRRKTGGAIM GEVSVCELSLPAPAFQSPVQLC GCQPEKA
7903	38271	A	7958	1	2045	REAAAAATSPFPSSSVRPSVRAS VRSARSGPKHGRRQLQRPPGA /RWRLTRR*SERRARPTGLCTH MKMAPMTSSLQHGEKGACRSF RDTLRTTR*CTASAVSRTPKIRS AKIRAHQLGGRRC*A*CPQVRLC QPRG*GGRVLPGCRDRERQQ RGRHRRGCHRAAAL*AGATL QPCAAPTAAARG*ER/SSPWAPP TRRRMQLWK*SGLTESSSGSRP RRKKSCGRRRSGRPPWMRGSG SSRSQWSRSGRSKRSASGATGS GSSRSRSTGNSRL*KRRRPRG G*RSSLVLTIGMRKRPT*RSQ SRRWRRQQLLPSGLTTQSSSS SSRKESHRLRAAVMYPRPSTI DQAATWTATGGWRPLSPRGA RLTPAPPPPLSLSR*SGPWMRSP P/PQPPPLPPPPPPKRPRSPAPS* TVRRPEQQPLRPGPAPWRSPLR HRRLPGGQAALQRT*CSWSLQS RLSWLLPWSLPQLTPRRSTMQL TPLKLTPLPLPTTYPPPPPA SLTYGLATGKGPPHSRVSPGPP RHPRVLRSWPQRCPWWRWL RSHCCQQAQAVPPFSTLMSCLS RQPPSVTQRKWKGPWLP RPQ LCQPQLRSWSKSRSRPTC*PM ARPPRRRRGPRPSEGYFSQSQEEE FAQSEELCAKAPPPVFYNKASE NVIHMLGCRPSSRRGGGLRGW
7904	38272	A	7959	3	174	

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7905	38273	A	7960	3	862	GVMASRTLLLLLGALALLET WAGTHSIRYFSTAVSRPGREP RYIAGVGYDDTQFIDAATPRM* PQSPWLEQEGPEYWDSTRNIR PAHRLTRVNLMPRRYYHQS* AGTGIFHGIRRYIPDTCVQTHM IHHSVSDYKATLRCWALGFYP VEITLAWQ/QDEEDQTRDHE/L VETRPAGDGTQKWAADVVP GQEQRYTCHVQHEGLPKPLTL RWEPSSTPIPIVGIAGLVLFGA VITGA VVAAM/WQEEELRTFS SHR*SELTSERASSDHAQGS DV SLTACKV
7906	38274	A	7961	1	591	MVTDYAIELFLQASLILLSSTLP YNEREMGLSIFALLTLTVFLLL ADKVPETSLSPVPIIKYLMFTMV LVTFSVILSVVVLTLHHRSPHTH QMPLLVPSDLHSQTSAPVASKK AQTRERPDAGAPSLFFSRKWLG YIARQLQE QEDHD/VAEGGLAV CGHSGPPLPVDFHHLHQRWD PSHLPRGHVPLAPSRPLSL
7907	38275	A	7962	1519	1888	ILKHPTLDKELITYLFIYLFIL RRNFTLV A*ARVQWCDLAPPQ PLSPGFKPFSCLRFPSSWDYRYA PPYLANFVFLVGTGFSMLVRL VSNSRPQ/CDPPASASQSGITG VNHHARITFNF
7908	38276	B	7963	280	1977	
7909	38277	A	7964	994	1651	CRGSQAPAPLTPHPNAPLGP SD LHSQTSAPVASKKAQTR/GDLM PEPPHCSSPGSGWGRGTDEYFIR KPPSDFLFPKPNRFQPELSAPDL RRFID/VSKPGCPASGATGGV SSISYIARQLQE QEDHD/VAEGG LAVCGHSGPPLPVDFHHLHQ RWDPRSSWSHVPLAPSRPLSL KTGGLRPGPLPVEVREPGDTPK PYPPLPNSFTNLGLLFRSG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /-possible nucleotide deletion, ▽possible nucleotide insertion)
7910	38278	A	7965	10	533	DEVSLCCQAGVQLHDVQSLQT ASQVQAILLPQPPVEAIEISGACH HACLIFVFLVEMGFHHIGQAGL KLPTSGDLPASASQSAGITGVS HRARPASSYLFFF*DEVSLCCQ AGVQLHDVQSLQLPPRFKRFS C/PASRSS*DFRRLPPRLPNFCIF/ M*RWGFTILARLVNSRPQ/CD LPASASQSAGITGVSHRARPASS Y/CIFFLRWRLTIAQAGV**CNL SSLQPPTPGFKWVSCSLPSSW DYRSLPPLPANFCIFSRDGVSLC SLSWSRTPDFK
7911	38279	C	7966	312	467	
7912	38280	A	7967	31	678	TGLYFLFLFCLRRSLA/SVAQPG VQWRDLGSLQAPPGLRRFSFL SLQSSWEYRCPLRPADFLYF*S RRGFSTLVRI.VSNSRPQ/CDPPA SASQSAGITGVSHCAR/LFFSFE MEFRSVAQAGVQWRDLDSLQ PLPPGLT*FSCLSLPRLGAA/WD YRRVPPCPAIFC/IFFFSRDRVS PCWSGWSQTPDPQVIRPPPSQ SAGITGVSHRARPISHS
7913	38281	A	7968	23	99	YTMTPGPCWRPL*TGPHPPHT WPGGSSSHQIPHRPPCVFG
7914	38282	A	7969	144	1239	ERTEPDH/TTTLT*P/ELPADTTA TVEDMLPSVTSVTNSDTITETF ATAQYILTSETTTLTSSIAPPAT ATPDSNSVPAQATPSKGPSAS APSPAPASAPKVAPLVDSLDT TSTPAASNLSSSVLANQGAVLS PSAPAGVGEASKAPPASKPTPA PVPTPTGAASPLAAAAAPATEA PQAKQEA PSTKGPDPPTQPGA AKSPAEEAATALASPKSEAAVS TTNPSQGEDFKMDEGNFKTPDI DLAKDVFAALGSPAPAAGASG QAPELAPSTADSSVSPAPAKTE YGLSLSAVIGLCPVVS GWEDSG LPSIKWLLGLKVQEKGLNLSGK NTASGINLGL EEERTRSSDSVLL NYGCTLES LGCF
7915	38283	A	7970	3	375	ARQAMKSLHQCFLLTRQAL EASSCNSTGWGEGTGKSGLQ RGP*NCQWEPSPAQA AFTSS* AVATAAGQGEELPLLPSTTP GKNTASGINLWLEERTRSSDS VLLNYGCTLKSLACF

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7916	38284	A	7971	1	2230	MFEASVGFWMRLREERTRLDHI QAQDEAVTADLEAAAGYPDLA KIIDEGGYTKQIFSVDDTAFS WKKMTLRTFIAKEGTNTDGAS SATSSLVSLCLELCLRAHHDV GFYCDLDVYQSAVYAPCTPTG YSLPQAKEESDFIPLEYEKGRIT STAGQQQDVPEMEQLEKGSIK GVTETRTGPLGCSNYDNLDSVS SVLVQSPENKVQLLGLQVLLPE YLRERFVAAALSYITCSSEGL VCKENDCWCKCSPTFPECNCPD ADIQAMEDSLLIQDSWATHN RQFESEEFQALLKRLPDDRFL NSTAISQFWAMDTSLQHRYQQ LGSWL*KVLFKKTHRILRRLFN LCKRCHRQPRFLPKERSLSYW WNRIQSLLYCGESTFPGTFLEQS HSCTCPYDQSSCQGIPCALGE GPACAHCAPDNSTRCGSCNPG YVLAQGLCRPEVAESLENFLGL ETDLQDELKYLKQKQDSRIEV HSIFISNDMLGWSWFDPSWRKR MLLTLKSNKYKPLVHVMLAL SLQICLTKNSTLVEPVMAIYVNP FGGISHSESWFMPVNEGQFSL TWIERTNVDAQA/QCQNWMT HLGGIRWKTFFETVHVYLRSR IKSLDDSSNETYYEPLEDDWIP LRNLGYMKINTLQVFGYSLPF DPDAIRDILQLDYPTYTQGSQD SALLQLIELDRVNQLSPPGKV
7917	38285	B	7972	62	232	
7918	38286	A	7973	3	258	KLSPPPPPLPPSPPLPRPGPA/GPP SRLPSP/PASASPOGVP*LGPA AELPGIRSR*PQVAAPAEATH WCCC*RSSPQQQRISH

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7919	38287	A	7974	1	1048	MAHSQNSLELPININATQITTAY GHRALPKLKEELQSEDQTRQK ALMALCDLMHDPECIYKAMNI GCMENLKALKDSNSMVRICK TEVLHITASHSVGRYAFLHDI VLALSFLNDPSPVCRGNLYKA YMQLVQVPRGAQEIIISKGLISSL VWKLVQVEVEEEEFQEFILDTLV LCLQEDATEALGSNNVVLVKQ KLLSANQNIIRSKAARALLNVSI SREGKKQVCHFDPVILVHLK DPVEHVKSNAAGALMFATVIT EGKYAALEAQAIIGLLELLHSP MTIARLNATKALTMLAEAPEG RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7920	38288	A	7975	1	782	MAVTAAACWSLRPLARRDVCV GVALASFPVKPTHWFCKTLLEP CRPTGMGAQEIIISKGLISSLVW KLQVEVEEEEFQEFILDTLVCL QEDATEALGSNNVVLVKQKLL SANQNIIRSKAARALLNVISIRE GKKQVCVHFDVIPNPWSHLLKD PVEHVKV*RCRLPLMFAITVIT EGKYAALEAQAIIGLLELLHSP MTIARLNATKALTMLAEAPEG RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7921	38289	A	7976	1	300	VEQTGRGE/RAYDIYSRLRNA FLCVMGPIDDSVASLVIAQLLFL QSESNKKPIHMYINSPGGVVT GLAIYDTMQYILNPICLTLPRTVR MSPRWCRRSL
7922	38290	A	7977	2	470	RPPQRTLQNGLALQRCLHATAT RALPLPIVVEQTGRGEASYDIY SRLLRERIVCVMGPIDDSVASL VIAQLLFLQSESNKKPIHMYI/N QPSGGARGQATDIAIAEEIMK LKKQLYNIYAKHTKQSLQVIES AMERDRYMSPMEAQEFGLDK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7923	38291	A	7978	3	864	SCRYPALGPRLAAHFPAQRPPQ RRPPRTACSLQRCLHA/TATRAL PLIPVVEQTGRGERAYDIYSRL LRERIVCVMGPIDD/SVA/SLVI AQLLF/LQSR/SMKPIHMYIN/S PGVWVVTAGLGH/LDTIAVTF LQPDFTW/CSLGPGAASMSGSL AFFAAGTPGMRHFAQPLPVFMI QPALQEGAGGQSPPD/AIQAE NP*KL/KKQ/LYNI*QRRTQTRS LQGDRVPPMAEGTA*HEAPME GPQEFGLKTRFLVPPSPQDGE/ DEAPRLVQKEPVEAAPAEVP
7924	38292	B	7979	1	2088	
7925	38293	A	7980	412	812	FQSLFTCVLFHFKFSLTIHHMNS QPF*RIRSTFFFLKQSL/DSVTQA GVQWRDLGSLQPPPPGFKQFSC LSLPSSWDYRRAPHPANFFYF F**QTG/FTHVGRMVPI*PRDPP ALASQSPGITGMSHCTRPRJR
7926	38294	A	7981	2	178	
7927	38295	C	7982	279	322	
7928	38296	A	7983	2	760	GVRSSGGGR/GRPGGGPRKARR GKAEDKE*MPVTKLGH/LVKDM KIKYLEDV/YFSLPIKESETIDFF LGSS/LKEEGLKIMPVQKQTRAG QRTRFKA/VATG/DYNGH/VGLC VKCSKEVATAIRGSV/LTKHSIV PVRRGY/WGNKMDK/PHTVPCK VTGRGCSVLVHLIVSAPVPKLL LMMAGIDDCHTSARGCTAT/LG NFAKATFDTISKY/SYLTLDLW KETIFTKSPYQEFTHDLVKHTH RVSVQRTRAPAVATT
7929	38297	B	7984	318	406	
7930	38298	C	7985	333	439	
7931	38299	A	7986	2	171	
7932	38300	A	7987	1	668	MGGLFWRSALRGLRCGPAPG PSLLVRHGS GTIMGVFVAVGTI VPVSRVPCIEADTLKPGGSPWT REKTLVA VKPDGVQRR/LVGDV IQRFERRGFTL/VGMKMLQAPE SVLAEHYQDLRRKPFPPCPSSR YMSSGPVVAMVWEGYNVVR SRAMIGHTDS/AEAPG/TIKGV DFSVHISRNVHASDSV/EGAQR RIQLWFQEQ*SWVSWA/DIGGO HSSIHPA
7933	38301	A	7988	1	897	

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7934	38302	A	7989	1	142	MEYYAATKNDEVMFSV/GT/W MKLETILSKLTQEOKTKHHMF SLISGS
7935	38303	A	7990	287	1086	EPWREMFISVYTLQKLGAFTI AKTWNQPKCPSMIDWIKKMW H/YTMEYYAAIKKDEFMSFER TWMKLETILSNLTQEOKTKHR MFSLSISGSRMRIHGHRGNITC QGLLGGEVCVHTVATRGSPSATE DESCRMNVNDYGGNSPSTLQV KTSPPQRAEKGNNVRTWLYSN LVCWPSLGSMLMGKLRDRVIKR VIYTHTAGDVSMEHEGFQFPLK QVSLLLCAIAFQPSLVVAAALV HITMEAYTYLEVTLTLLQIHSPLFC FLPKCHF
7936	38304	A	7991	1550	1835	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKKMW HIHTMEYYAAIKRNEFMSFAGT WMKLETILSKLTQEOKTKVHH MFSLSIRGS
7937	38305	A	7992	164	647	DLPVEPHIGKMILFEALVL/HCL DPVL TIAASLSFKDP/FVPLGKE KIADARRKELAKDTRSDHLTV VNAFEGWEEARRRGFRYEKDY CWEYFLSSNTLQIM/MKIHKAVI CAGLYPKVAKIRLNLGKKKKK/K VKVYTKTDGLVAVHPKSVNVE QTDHFHYNWLI
7938	38306	A	7993	66	345	

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7939	38307	A	7994	1	2367	HRVTVISGETGCGKTTQVTQFI LDNYIERGKGSACRIVCTOPRRI SAHSSCGKSSCRKGQNLVASGN STGYQIRLPESVAQGNRVLSYT VPTRNHPSSGSDPYLSSVSHI VLDEIHERNLQSDVLMTVVKD LLNFRSDLKVLMSATLNAEF SEYFGNCMPHIHPGTFPPVVEYL LEDVIEKIRYVPEQKEHRCQFK RGFMQGHVNSQEKEEKEAIYK ERWPDYVRELRRRYASTVDVI EMMEDDKVDLNLIVALIRYIVL EEEDGAILVFLPGWDNISTLHD LLMSQVMFKSDKFLIPLHSLM PTVNQTQVFKRTPPGVRKIVIA TNIAETISITDDVVYVIDGGKIK ETHFDTQNNISTMSAEWVSKA NAKQRKGGRGRVQPGSLLFICI NGS*EASLLGWITQLPEIFEIPF WEGTLFTK*RFLRLGEIAYFLSR *MDPPSNEPVLLSIRHLRSLNA LDKQEELTPLGSHLARLPVEPH IGKMILFAGLFCCLDPVLTAAS LKFO*SPFVPLGKEKIADARRK ELAKDTRSDHLTVVNAFEGWE EARRRGFRYEKDFCWEYFLSS NTLQMLHNMKGQFAEHLGA GFVSSRNPKDPESINSNDNEKII KAVICAGLYPKVAKIRLNLGKK RKMVKVYTKDGLVAVHPKS VNVEQTDHFHYNWLIYHLKMR TSSIYLVADCTEVSPYCLLFFGVG
7940	38308	A	7995	25	312	WLIVITDARMYRQGRYYFL VSSSLDKVLMISFLLGWRRSSR RLRAFLVLHLRASPWAPRSFVR PVSAFSVGMCHMKTRVFENTF PFTLGHTVRYVGREIF/CRRVFT RYRESIKISLPTYLTVCPRVKGN VFSNTRVFMWHIPTLKADTGRT KLLGAQGEARRCKTKKARKRR EERLQPNKKEIKLTSKEEETKK
7941	38309	A	7996	2	417	QQIRKLIKVLIIHKPVIVHSQV GCQKSTFS/RTRKGRHMG TG*R KSTANFQMPKEVVTWMRRMRIL HWFGRYHESKKT DHHMYHSL YLKVQGNMFTNKQILMEHNNHK LKADKAHKFLADQAEARSSK TNKASKLREER
7942	38310	A	7997	3	124	KKRPELRDLLNQARKETU/ARK EDRSASSGAEGDVSSSEREP

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7943	38311	A	7998	911	1497	SQRKARDQRRKRNRKASSIAK HKEPKRPLPSGKNSQEGVATH TKPLAQGGKVLDP/NETNEIPN ANFRQQIRKLIKDGILRHRKPV TVHSRAQGWKSLTARRKGRHL GIESKKIDRHMVHSLYLKLGKN VFKHKRILTEHSHKLDKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEIHKLSQEEKAK
7944	38312	A	7999	34	279	EVIHAAIGEEKGSY/NA**PWVE EQLTRQPLIHHPASLHVSYY/RC RYHSLYLKVGKGVFNKRLIM EHIHLKADKARKKLLA
7945	38313	C	8000	351	530	
7946	38314	A	8001	356	921	WRATACTYPSWAPPRILVATGP AAVSAGLPSLHGTRAGPQAPCT AAVPPAPLPPHRPAS*G/MPAGP VQKGAPT/AAAAG*RLKKGQS RRQGRGGAERTEGCQHAVTFQ DCFLRCFFG*C*CLSG/ERAIALE QGASHAAEQLPRLQAFKRPGL /QVNPDAQKSAASSSLKVLGS LPKHQRPRRFCQNTGS*SGP**T TGRRSAAGAA/GKPNPGSPPA PHNFKSGTNPVATTHHPVGSKP RPEPHGNSEA
7947	38315	A	8002	495	653	MTLTSIDPVLTTFFNLECLP/VFT ATASSGLGEVE*AIALN
7948	38316	A	8003	1	1433	MPESNCSLTWRHVS GRAVAAQ GGEHSSQGASLV/GEPRGGSS WLLGLEGDTGLWGGLLKEGRL TDGKGKTIDCKDAIFIMTSNVA SDEIAQHALQLRQEALEMSRNR IAENLGDVQISDKITISKNFEN VIRPILKVRGLSWHFLLEPKAHF RRDEFLGRNGEIVYFLPFCHSEL IQLVNKELNFWAKRAKQRHNI TLLWDIREVADVLVDG\YNVH YGARSIKHEVER/RVNNQLAA AL*SRTLPPGGCTLRITVEDSD KQLLKSPPELSPQAEKRLPKLR LEIIDKDSKTRRLDIRAPLHPEK GRLTDGKGKTIDCKDAIFIMTS NVA SDEIAQHALQLRQEALEM SRNRIAENLGDVQISDKITISKN FKENVIRPILKVRGLSWHFLLEP KVLTTFFNLSVLYLHGNSIQR GEVNKLA VLPRLRSLTLHGPN MEEKGYRRARGHSLHQIEK YICESDDIFRKYCNNOFL
7949	38317	A	8004	1	789	

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7950	38318	A	8005	1	409	LRLELSFCSSCLLEPPWS/TTVV CLYCRPATDTHPSGSGRVS AVLIQ*G/RPLPLRLKACHCSHTA KCPGSSPSSMSPTAEEQKSGTA EERREGASEHGEFEFGWGRLE RS AVEWPNSRGSSSHSIPFPAPRP
7951	38319	A	8006	1	1787	MSKGESRKCNEENVSKSSKV V KVFI ¹ LT ² PQFLSRDKDQLTKEL QKHV ³ KSVTV ⁴ SKSPRKLLSHIT RLHPPSKGQGENLTHLVDSIKA TTWCQPPVWETVEGQRRRVGNC IDFTNGCDLVGSSSLHNMLVCS SYDINRQDTFQKDRTSEKHLID SVFTALQDSAGQWP ⁵ ARLHPQ RGEEVADPRGAPSRHVEPENSS PCQGNGEQAGKAGARALCGQ ARRSPATMPPPLT ⁶ TRSLCEFAVF LLHWLFP ⁷ ELFHYRKLGEQDSCY GDGGKQELDPQRLQIICNFTEV YFPHMQE ⁸ EEAWRQAGGPAAEA AD/TSATSR ⁹ RSTSPTCRRRRPGC SGAPAS ¹⁰ TTSFRAWGWTQA AK ASPPRDNCYNSSSLPDDISLFT H DNLHKQHSCDS ¹¹ LGKKQLDPS CIKLIRH*VHLLYLCTKN ¹² NRVW TLEFMGNLHWNRRGAPTSS ARSTC ¹³ WPRV*RHEELCNQ S*EV QRGV*GSPAAPERSSKDFCKIPL DEVVVP ¹⁴ H*/DFPVRSPYLLSDKE VKIVQ ¹⁵ QSLSVGNFAAGLL/LPP RTSSCSTTIFGL/DNKKQLDPTQ LRLICH*VEAVYPVEKVEEVWH CECIPSNDEQCHCPNKKCNIL

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7952	38320	A	8007	1	1475	MAVDFSLAVLMIVSSYDINRQD TFQKDRITSEKHL LDSVFTALQD SAGQQWPARLHPQRGEEVADP RGAPSRHVPEPENS SPQGGGEQ AGKAGARALCGQARRSPA TMP PPLTTRSLCEFAVLLH WLFPEL FHYRKLGEQDSCYGDGGKQEL DPQRLQIICNFTVEYFPHMQEEE AWRQAGPGPAEAA/TSATSRR STSPTRRRRPG LQRCACQIND KLQGLGLDAGSEGEPPTRQLLQ LLQPAR*HLSNQQGG*LQGRAL FTHDNLHKQHSCSDSLGKKQL DPSCIKLIRH*VHLLYLCTKNNR VWTLFEMGNLIHWNRRGAPT SSSARSTCWPRV*RHEELCNQS *EVQRGV*GSPAAPERSSKDFC KIPLDEVVVP H*/DFPVRSPYLL SDKEVKIVQQSLSVGNFAAGL L/LPRTSSCSTTIFGL/DNKKQL DPTQLRLICH*VEAVYPVEKVE EVWHCECPSNDEQCHCPNRKK CNILKKA KKEK
7953	38321	A	8008	1	3524	MCNNLIHLSLANNKITTINGLN KLPIKILCLSNQIEMITGLEDL KALQNLDLSHNQISSLQGLNH DLLEVINLEDNKIAELREIEYIK NLPILRVLNLENPIQEKSEYWF FVIFMLRLTEL DQKKIKVEEK VSAVNKYDPPPEVVAQDHLT HVVNSVMQQRIFDRYLLLEIQ PEFRLVLKLVGNESLPIASADSL ALTSDMVRNGLDGLFYDFRAC HTRTPPYFGEGRVDYHFISQD VFDEMVMNMGKF
7954	38322	A	8009	258	719	MTPPSVLP*PSLSY*HPDYSLPF PFSPPVLCFPHVPQGLYSVLVFN TAAEPREKSAMAILPLSGHACS HVCLGSHQSLFQRACGRCPRL SGSLRSHCHWLLILGVKKCSPP EAGKAILTTDRTETMNIWSKP RNPSHTVPHPHHICCHWRI
7955	38323	B	8010	1	1953	
7956	38324	A	8011	32	533	GRERPLLSPYMETLYRVPFLVL ECPNLKLLKPPWLHMP SAMTV YALVVVS YFLITGGIYDVIVPE PSVGSMTDEHGHQRPVAFGL QSKMDNNINGKGLCIQAS*FTM GGFRFS*ILDPIECTKYPKTSIDS FFCSIGISSVVLLEFFPWARSNS MRNNGCPGLI

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7957	38325	A	8012	670	1052	TRDRSRCKGTWLLSVKTLAISA VKSQSKASECRFTNRSSSTAVI RVLLPGILLSKLRCSMVLATA LERDDSDVGVTISSINPQDSHFS CLLLLRISNSC*IC/CNFAIRV HLAEVCI*QTSLLL
7958	38326	C	8013	40	186	
7959	38327	A	8014	1	1216	
7960	38328	B	8015	1	1032	
7961	38329	B	8016	1	1761	
7962	38330	A	8017	108	708	LTNQKKSRTRRIHSRILPEVQGG AAADRHCPIDRLGSLQDHHRRS RLLSQWSP*KSTHD*HGFSYQS AEDIRRLQQAFAAGMNTSEL LQIANQAFVNRDAVSRKENHR DNERQAQRNTDLLAAAIRGVPP KRQGGGPGKETQPGCQSLQR NQCAYPEIGHWKNKCPQLKR KPGDSEAEAPDKDEGALLNLA EGLLD
7963	38331	A	8018	1	512	LSRSSPLLPLVWHQAMVGSM VEPAAWVLMTFCWDTPRQSGV PRERMPHTGTWRTVGIRCPKK KLRSANSSMMRGKVQPFPR/DI QAYGAAPFEDLQVDFREMPKC GGNKYVLVLGRITYSGWVEAYP TRTEKTREVTPLVLRDLIRFRP PLWIGSDNGPAFLAALVQKTA
7964	38332	A	8019	3	764	KQVLVNGDAVSREEKRKENER QARRNADLLVSCSNQSGPPKEA REELWTKDYRPGQDLRLLSQA TLTFHPTVPSPTLLGLLPAEDS WFTCLDLKDAFFPIRSAPESQK LFAFQWEDPESALAKTVRQRC VSCRQHHAGKVQPFPR/DIAY GAAAFEDLQVDFTEMEPCGGN KYLPLVLRITYSGWVETYPTRA EKAREVTRVLLRDLIPRLPFR IGSDNGPAFVADLLQKTATVLG ITRKLHAASRPQSSGK

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7965	38333	A	8020	19	1548	CIYGAQLCTGPSAPVWYCYPLGT MAPTGLPGHPAVATATEPHRE RGSPL/IDSTVLVPPQDKHILRPP TVDKRGGEASGETPPLAARLRH KTGIQMPLREQQYTGIDEYGHV VERRVFGYQPFSAHLNWKWS NTPSYTEKQALIDLLQTHIQTH NPTRADCHQLLMFLFNTDERR RVLQAATKWLEEHAPTDYKNP QEDVRTQLLGTYPQWDPNERQ DMQRLNRYREALLEGLKRGAG KATNINKVSEVIQRKEESPAQF YERLCEAYRMYTPFDPNSPENQ CMINMALVIQSTEDIRRLQKQ AGFARMNTSOLLEIANQVFN RDVSRKENQKENGWPPCLR ALAATALLVQEAANKLTLGQNL NIKASRAVVTLMTKGHHWLT DARLTKYQTLLENPRITTEVC NTLHPATLLPVSESPVEPDCVE VLDSVDSSRPDLRDQAWASVD WELYVDGSSFFNPQGERGAGY AVVTLDTVVEARSLPQATSAQ KAELVAFIRALELSE
7966	38334	A	8021	1	895	MDGAGICYLHQTNAGTEIQTPH VLTYKRELNNENMWHRGDN THWGPEGSTNSPASASGVADV SRVGSLLQWVLGLADFKNEAKE LRLYKQEKREKAKRWKETEKG FNGDYGVTMTPGKWRTYFEID WSKLEVGWPSSEGNLERSLVSK VWHKVTGKSGHSDQFPYIATW LQLVLDPQWLRGQAAAFLVA KGQINPRKDPPTPPGRGKSTPEVL FDPTSEDP/QEME/PSDPSGALP LPGKDAPHSAHSPCASTRQTY P*ATRSRQERR*SLERNPYIGSS FKTQNWDTNAPERAVVYWDR

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7967	38335	A	8022	1	1959	MLKNFKKGFNGDYGVTMTPG KLRLTCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPSTDDPLQEMAKVIPVVP SPYQGERLPTEFSTVLVPPQDK HIPRPPRVDRKGGEASGETPPL AARLRPKTGQIMPLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWNKNTPSCTEKPQALIDLL QTHQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGHEHAP ADYQNPQEYKGESPAQFYER LCEAYHMYTPFDPDSPENQRM NMALVSQSAEDIRRLKQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHSVVTGPVAPLSK KTIDHIGAMGVSAAQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPVILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTV LPQGFKNSTPFGEALARDLQK FPTRODLCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSCKKVAQICQQQVRYLGFIT RQAERTLGSGRKQVICNLPEPK TRRQVREFLGAAGFCRLWIPNF AVLAKPLYEVTK*GDREPFWE
7968	38336	A	8023	2	367	
7969	38337	A	8024	3	687	GRRQRRSKVTSTWWQARESS CRGTLLYKTIKSCDYSLSQEQ HGNLHLIGVPESDQNGTKL ENTLQDIIQENFPNLARQANIQI QEIQMRPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKGRVT HKGKPIRLPADLLVETLQARRE WGPINFILKEKNFQPRISYPAKL SFISEGEIKYFTDKQMLRDFVTT RPALQELLKEALNMERNWYQ PLQNHAKL
7970	38338	A	8025	1	993	

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7971	38339	A	8026	1	842	MAEQEQLQSAVPSPLLVIPRQK GSQVDFQSQPTDLQLRDLTDOR KTNKQKGIASLTLRKSTPKPH LYVTNIKDQRPNRLIGVPESD GEKGTLENTLQDIIQENFPNL ARQANIQIREIQRTQRYSSRRA TPRHLIVRFTKVEMKEKILRA AAREKGRVTHKGKPIRLTTADL SAETSTSQKTEWGPFIENILKEK NFQPRISVPAK\LSFFISEGEIK\ YFTDKQMLRDFCHHQTCLP*K TRPALKELLERKHLNM/EGGNN WYQPLQ\NHAQICKDH
7972	38340	C	8027	320	433	
7973	38341	A	8028	9	189	
7974	38342	A	8029	26	738	VAASSFDTCADHLCALHLLQV LHYLAIQKPADLARHLLPCVIH AAVLKVKEESELENISSVKKIHK QIISHSSKVLHFPNPEDKKLEEII HQITNVEALIAARSLKAKFGT EKCEQEEEEKEDLERFVSCLEEQ PEVLVTGAGRGHAGRIIHKLFV NAQNVA\AMTPP\EEELKRMGS PEER\RQNSVSDFP\PPAGREFIL RTTVPRPAPYSKALPQRMYSVL TKEDFRLAVKIIDGDV
7975	38343	A	8030	3	2961	MAADSEPESEVFEITDFTTASE WERFISKVEEVLNDWKLIGNSL GKPLEKGIFTSGTWEEKSDEISF ADFKFSVTHHYLVQESTDKEG KDELLEDVVPQSMQDLLGMNN DFPPRAHCLVRWYGLREFVIA PAAHSDA VLSESKCNLLSSVSI ALGNTGCQVPLFVQIHHKWRR MYVGECQGPVVRTDFEMVHLR KVPNQYTHLSGLLDIFKSKIGCP LTPLPPVSIARFTYVLQDWQQ YFWPQQPPDIALV

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7976	38344	A	8031	1	1688	MREKPCQSNCEGKAFNYSSLLR RHHIHTSREREYKCDVCGKIFN QKQYIVYHHRCHTGEKTYKCN ECGKFTQMSSLVCHRRLLHTGE KPYKCNCEGKFTSEKSSLRCHR RLHTGEKPYKCNCEGKFTGRN SALVIHKAHTGEKPYKCNCEG KTFQKSSLQCHHILHTGEKPY KCEECDNVYIRRSILHRHRKI TGEQSYKCKVCDKVFSDSYL AEHQRVHTGEKPYKCNCKGRS FSRKSSLQYHHTLHTGEKPYTC NECGKVFSRRLENLARHHRLHA GEKPYKCECDKVFSRRSHLER HRRHTGEKPYKCKVCDKAFRS DSCLANHTESSILGEKPYKCYK CCGGFLIQGSLPQHQRVHTGE KPYECNECGKVFNQKASLAKH QRVHTAKPYKCNDCGKPLPD QSTLFHHQSNPIGVGKRYQCN DCHKVFSNATTIANHYRIHIE/ KIYKCNCKGFFRRHS*LVVHQ *THTGEKPYKYHDCDKVFSQA SSYAKHRIHTGEKPHKCDDCG KAFTSCSHLRHQRIHTGQMPY KCKGGKVFTLWSFHAHQKIH
7977	38345	A	8032	25	1091	IHIYSDSCSLSLQDSGDEKEFNL DDNVSFRAFLWDLAAGPGQGG GGGREKWRVVISRTMNRKMG KMMVKALSEEMVRPADIGDGV SRGPGDRSGRM*AEKMALAFS EQEEHELPLVLSRQASTGE*GMR GTPAESGGKDWVTAVLVAGPF CGRARVHTDFTSPYDHDLSKL QVRSASGLLWSLAGCAQKGSW TEPVGSFKFIYDVLPPEAVGH ARPSRRQSKGRPKPKTLHELL ERIGLEV*AWSSLVSSIREAQLP QGWGPGHNLNIMDPQHRAK LLTAAELLDDYDSEWL*ERPGE GAESSQEPGGEACPKVDIPRDS GCFEGSESGRDDAELAGTEEQ LQGLSLAGAP
7978	38346	A	8033	35	437	
7979	38347	A	8034	1	1845	
7980	38348	A	8035	1	212	
7981	38349	A	8036	371	915	
7982	38350	A	8037	1	2460	
7983	38351	B	8038	10	1510	

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7984	38352	A	8039	1	188	SASTTLWGLLFLIHLRLGTALRA VSSWGTIILTAKEVQWGH/DCG THWSYHHLHQPRAAHGKEC
7985	38353	A	8040	3	2332	FFFMWDPQHFTFI/VLPQQYYN SPGLYSTVLRLDENLDIL*NIKF LYFIDNIMLTGMDE*EEDGTLE ALVKHLLSRGVKINKPYRDSEV ATAVK/FLQV*WLGASRG/VPS NVKDKLLHLC/PCKGREAHCL G*ALF*VS*HHNPTCKVVS GFDP HF*VT*EECPAFEWSL/QQERTL QQIPGHGAVTILQDPLVLKVPV GGVRFGVELNQAPVGESQWKG LGIWSKAMSSTAQKYAP/FQSR EICWKQLLACY/W*ALI/EIECLT MGHKTTM*FQ/MPLRN*HLCNS *SHTLDMPQQHPIMRWKSFL*/ D*A*IPMLTSPRKHPNLKWP*TT KQKH/WKL/GQSPSPWVSPGRVG WVHKWSKHSGRD/GGYLWVQ QY*LPPTKVDPTATSKCPTHQ HLNPMIFP/R*GSISLGDQPDPK* GVDYIALFPS*KGQRFMFTGIGT YSIVGFSCRVPVPSVSTTFWGLL IFVIHRLGTASPCSSSWGTHLT AKEVQWGH/DCGTHWSYHHL HQPRAPGP*RMLKRASIGTAQR QLAGST/LCGWEGAIQDMVHF KNQRHLYSSVISVGRTRGSRYQ GVEVDVAPYPIPSHTLSWDFAL LSQNHHSAG*KVLDSKGGYP*K ETNECPLNYTLQLP/PGE/FGQY VSRDQVRVRGVPSSPGTVIDPD PQEEAWLLSHN/GG*EEFVWNP /GDPLGGLLV/LPCPIVSVRRIQ
7986	38354	A	8041	1	1296	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7987	38355	A	8042	498	2219	KSVKTS*DTLRTKAKTGQGHITGLQPLGLRIRQEP/SAKTEKAAAIQAKAGAEREATGVVVRPVAKTRAKAKAKTGSKTDAVAEMKAVSKNKVVAETKEGALSEP KTLGKAMGDFTPKAGNESTSTCKNEAGTDWFWWAGEEATINSWFWNGEEAGNSFSTKNDKPEIGAQVCAEELEPAAGADCKPRS GAEEEEENVIGNWFWEGDDT SFDPNPKPVSRIVKPPQVYEINEKNRPKDWSEVTIWPNAVTPAVLGFRRSQAPSEASP/LFIYCSGLR*RKCLFFACGNSLPFF*E/PRSCSQPIPECRFDSDPICQITIDEIRQIRIREVNGIKPFACPCCKMECYMDSEEFKLVSLKSTTDPLIHKIARIAMGVHNVHPFAQEFINEVG VVTLIESLLSFSPSEMRKKTIVTLNPPSGDERQRKIELHVKHMCKETMSFPLNSPGQSGSLKILGQLTTDFVHHYIVANYFSELFHLLSSGNCKTRNLVLKLLNMSENPTAARDMINMKALAAKLIFNQKEAKANLVSGVAIFINIKHEHIRKGSIVVVDHLSYNTLMAIFREVK
7988	38356	A	8043	1	453	MEKLDELKIKIDNINGALICARHFSKCSSNAQSHLCPYLQAFPGGPG/VRGLPGWPGRTGSRELGHGWRGCG/EGLVSGCQ/TMLSGA/PAGSPQ/PTGGTRAHAVRGRP*VPARSQGSRLPARPQGED*GAAP/DFDPGAAGVPGVPALQEAQI
7989	38357	A	8044	3	690	LSLSPSSWDYRRAPPRPANFVFLVETGTMTLTIVLIS*PHHPPASASQNAQIV/GVSHSPRPGIACILTRLDH/HQGTQSRVPALGSS*PIPHARPRGHTLKALPYRLYTQTARGFGQPRVRIPLLSLGLSKPSELRGQVGHAFASAFASISLVCFTLLVEGKLKPPGASVRCLQSNRDLGFRATFTPSHRGHGALGLNYISQRATGTPNLWLPFRFRVVL LQAACG
7990	38358	A	8045	106	299	
7991	38359	A	8046	306	445	
7992	38360	C	8047	570	926	

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7993	38361	A	8048	47	988	ASRPGSRVSLMFGAAGRQPDORS SSSPGTSWPFVPEMEELVHDL VSALERELQSKPRGGFAEPGDP FSEVY/PCPLKRPARKRRGRKR RFV*CASPVGGLVTA*SEGSDS SFRRTKSKKRKLKIRQGPQIQD EGVVLESEETNQTNKDKMECE EQKVSDLMSESDSSLSSTDA GLFTNDEGRQGDDEQSDWFYE KESGGACGITGVVPWWEKEDP TELDKNVPDPVFESILTGSPFLM SHPSRRGFPTKTQSAFMECLQRI LKNLEGLQLQWYFFLAQWVTR EWFIFRILITMTIGLALGLGQS MTSISF
7994	38362	A	8049	3	476	LTRPV D* RFGTHLGRGV RAR P ANRRRQRARRGA AISPPGCSV AGFLRGR LG/PEPGDNGQHLGE PWLGCGLFA*RA*CSRSTRCT* RRRAPGDRELPRAPATWAPPIK LVPRVFSSKVGQGVSLVEAM CLQGDSILNQSNKHNSVASSNT ITVIG
7995	38363	A	8050	2	143	
7996	38364	A	8051	1	161	
7997	38365	A	8052	3	1189	ESPLLGHSSSDAARRRSVSSFP VPQDNVDAHPGSGKEVRVPAT ALCVFDAHDGEVNAVQFSPGS RLLATGGMDRRVKLWEVFG EK CEFKGSLSGSNAGITSIEFDSAG SYLLAASNDFASRIWTVDDYRL RHTLTGHS GKVL SAKFLDNA RIVSGSHDR TLKWLRSKVC I KTVFAGSSCNDIVCTEQCVMSG HFDKKIRFWDIRSESIVREMELL GKITALDLNPERTELLSCSRDDL LKVIDLRTNAIKQTF SAGPKC GSDWTRVVFSPDGSYVAAGSC *RALLYIWDVLTGKVEKVL SK A\HSSHQCGWPWSPSWARTF VSVDKGCKAVLWGT VLTGLSG LGGPQC PPH EAHGLLPWSW QVNVLGYSMDLPELKKANVGH

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7998	38366	A	8053	116	921	LKSNRCW*GCEEKGLTIHCW WEC/KFNPLLKAI*RFLLKLV LPLDPAIPSLGLSIGTGKKVW QRLPNCPTISLFSFFHKNNRHTGT YRRRFLDSLAVRCPNCPATFGS KSDVCNFWVMPSTGKKCALPS HPLFPNGLNADVVCLSDSENLS QKILLILEVSDSVILGKLSHKNI QHDCEEPLTLLRNTQQFRFLCI ACHGCTSQYSTFLVKASWTRS QGLIQRQPSAGSGYPEKLFSEG AGDEGVDLLPLLAKPASPDQL
7999	38367	A	8054	35	422	SCSEVTEASWGSVPFLRDAQLG VGLHSPTYRHPHRETLTCCPAG TLQAWPFCGRIRVRVPVSWLGE PGRGLIPGSGSAASSECLPGLHG RAPLGTSCRPRPLP/WNQPPPR LAQPGHRDPDADAATERPGLQ RPSRTACERFPMGVSVRRRVEA HSQLGVPELRD
8000	38368	A	8055	3	277	GPPRPPA*RGHGGRPENT/PAPP RWPPPP/PRSPAIPPPRRACADV THPPVPTPGKRTPPPIGGAPAA AAPRRPAPSCFSAPTPGCSLTG
8001	38369	A	8056	3	179	PPHPQGP PPPGRPPGC*RPI/QG RQVFSMKPGRTPERTAWS/PPY PGCLGSRPRRPSAPA*SGAHCV VAPYPGCLGSRPRRPSAPA
8002	38370	A	8057	3246	4682	ENTLSFASFFFFEMLSLCPGW SAAAPCQLTAASTYVVKRFSC LRLPSSWDYRRAPQHANSFCI FSRDRL/TMLVRLVSNS*PQVI RLPQPPKVLGL*ACCGFCGSS GMAPGCGRVVSHAGAPGGGTR PP
8003	38371	A	8058	3	718	LTRLVLSPADPD/RATHLIAA/R AGTEKVLQ/AQE/CGHFHVNP DWL.WSCLERWDKIEQLFPLR DDHTKAQRENSPTLPDREGIPP TALSHMPILPKAQSPVEVRIYD SNTGKLIRTGARGPPAPSSSLPI RQEPSSF/RVDDILGEGSDSDS EKRRPEEQEEEPQPRKPGTRRA RTLGA PASSERSAAG/SRG/PRG HKRKLNEEDAASSESSRESGNEY EGSSSEADEMAKALEAELNDL
8004	38372	A	8059	273	468	NVGKTAANGD*G*RGEAAPAG RSRARVPEDAASSESSRESSNED EGSSSEADEMAKALEAELNDL M

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8005	38373	A	8060	1	2886	MEVPAAGRVPAGAPTA AAVE VRCPGPAPLRLLEWRVAAGAA VRIGSVLA VFEEAASQASAGAS QSRVASGGCVRPARPERRLRSE RAGVVRELCAQPGQVVAPGAV LVRLEGSHPVVMKGLCAECG QDLTQLQSKNGKQQVPLSTAT VSMVHSVPELMVSSEAEQLG REDQORLHHRNRKLVLMVDLDQ TLIHTEQHCCQMSNKGFHFQ LGRGEPMLHTRLRPHCKDFLEK IAKLYELHVFTFGSRLYAHT
8006	38374	A	8061	2	680	
8007	38375	A	8062	658	1657	PGILSLRNALLTGVDCKVVVPV PPGHTHPQLRLFHFHPKTCSGW GEWGDHGVVWAGPAPA/YHL HRDVPQALWTNDHALAWP*AM TSERTLWPGHELSARPGRSWRI SCPTGLPQGGDDRTRGHWVTA TCCSADGLRLCRYGD/GVRGGL PTVAWP*LTGCSLRYGSGQQC CYTADGTQLLTADSSGGSTPDR GHDWGAFFRTPPRVPSMSHW LYDVL SFYYCCLWAAPDPGKD RAGLGCTPT*PSTLTASA FGD HFVTFDGTNFTFN GRGEYVGM G*NQGGRLPSGSRSAPTTAGT ETRTGTLTAVAVQEGNSDVVE VRLANRTGPER
8008	38376	A	8063	873	1791	RCAGCPHSSSFERRGQ*AAVGP CCHGGTYRKASSV*RVSV*HPP HDRGSRK/QSLSGR*STGLS*MP SGVASSASV*FVNVSLSASN*L AQSTARFP PGSVRGLGQGRAG GG*APGHGADHPTGRQHS*GSP APVTWLWWPPRHQAALAPAP STTPYDNSPLHCRPSGPSQSSHP HSALPGT/VPGSSPLEIVPGSSL YVS*SLIRALAAPISSSSVGKNC RCTERLAIKPAESCRTRSSSAG QSVFSRFTSL*AFTG*AR*PSAS AADLLVKASILLAQLLILESAS STRMYSFRDCTSSFSA

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8009	38377	A	8064	2	935	YSPARGSGRGLSRPPGAGRRA GQGPQVVGAPKPGGA EYVVRWA AGGMKGAGGSSGSGSGSRE AG*PGVPRGRRGWRTPAEPPG WGPGRRAQACGA*G/EGRAAAQ VGGAPAAAGGVAREEAPS*P GDAAGSGTPGAASVQVSAPP AQPINLSAGARAGVARRCVC RGAES*GPGDPGPGSRR*PPAA QSGPPPCPSALFLHPSGFLCRRP QPSRAQGGVEVGALRAVPRLSG GAGNLAAALPCQLPGSGGLTPGC /QASQGLGVGLVRAGPAWSPL DGPLDQKVFSPTSLWNQRCFS LAAAGPVIIIR
8010	38378	A	8065	3	367	
8011	38379	A	8066	2	1246	TPAWSREILAEELCTPPDPGA VVECPDESFQICENATFQRY QKGADAPVALVHHMAPASVL VDSRYQQWMERFGPDTHLVL NENCASVHNLRSKIQTLNLI HPDIFP/AAHQFPL*EGGPHQC AHGSG*MPQVPAPFQE/WSAR GMPLLLAILRNS*LRRCSFPTSS RALQEYRRSAQDGPAPAEKRS QYPEHFLGTGSAIPMKIR/NVSA TLVK/QSPDTSLLLDCGEGTFGQ LCRHYGDQVDRVLGTAAVVF SHLHADHHTGLPSILLQRE ASLGKPLHPLVVA PNQLKAW LQQYHNQCQEVLLHHISMIPAKL PSGRWLRSPLQWKD*FSSLLR TWIWEFQTCLVRHCKHAFGC ALVHTSG/LKVVS GDTMPCEA LVRMGKDATRKADELISFQG
8012	38380	A	8067	121	880	GAAASQLPAPQPPVGGPAPH QYDSCQMPSGRG*DLQSCSGKI DQFA/AWTTCDLEEFQTCLVRH CKHAFGCALVHTSGWKVVYSG DTMPCEALLVRMGKDATLLIHE ATLÆDGFRRKREA/LEKTHSTTS QGHSAWGMRRMNAEFHY/VLN HFQARRY/SKVPLFSPNFSEKVG VAFDHMKVCFGDFPTMPKLI LPP LKA LFA GDIEEMÆEERREKREL R AGAGRPSCSRGAGRRPLEDGE P QQKRAHTEEPQAKKVRAQ

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8013	38381	A	8068	1	607	SPGSWETRLVWVSFYRSCCKHS LCPCLVGEFLVFNSPMQSGSAG EPPRLQF/GAPLPGAAPGNYRRT GRGREGPWPPPLAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRGRPRRAA*TGPSAQ/PP RSLSTLSPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLAKRPKRLAQMH WGH
8014	38382	A	8069	1	290	QFLDAESGSAGEPPR/LAVPAPF PGGAPGNYGRTRGRGREERSWP PPLAPSLFALSDFGSSPGRTSRR PLAVSRRLGPTFPPPLPPAPGR GRPRAAP
8015	38383	A	8070	1	565	SPGSWETRLVWVSFYRSCCKHS LCPCLVGEFLVFNSPMQSGSAG EPPRLQF/GAPLPGAAPGNYRRT GRGREGPWPPPLAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRGRPRRAA*TGPSAQ/PP RSLSTLSPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLA
8016	38384	B	8071	475	913	
8017	38385	A	8072	145	275	
8018	38386	A	8073	1	310	VEELTARTGGGAPPGCQADAK RMPQFPQRTPWGHGFAGAPFP ISKPHGPPAGQL*PG/PSCEQT/E PPSPVNVTVTHLRANSATVSW DVPEGNIVIGYSISQVQV
8019	38387	A	8074	1	483	GSHRVGRWAALCDRAAPRGLT NRETGGGAPPGCQADAKRMPQ FPSQRTPRGHGFAGAPFPISKPH GPPAGQL*PG/PSCEQT/EPPSPV NVTVTHLRANSATVSWDVP NIVIGYSISQQRQNGPGQRVIRE VNTTTRACALWGLAEDSDYTV QVRSIGRL

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8020	38388	A	8075	2	854	RPPAARARRWLKPKSPARRSRR PAHRCRRRRRTCTPQATRPGMR *APAAACGPTGRRS/RLPALKI. ALEYIVPCMNKHGICVDDFLG KETGQQIGDEVRALHDTGKFT DQQLVSQKSDSSKDIRGDKITW IEGKEPGCETIGLLMSSMDDLIR HCNGLKGSYKINGRTKAMVAC YPNGTGYVRHVDNPNNGDGRC VTCIYYLNKDWDKAVSGGILRI FPFGKAQFADIEPKFDRLLFFW SDRRNPHEVQPAYATRYAITV WYFDADERARAKVKY/RNR*K RCEG
8021	38389	B	8076	1	205	
8022	38390	B	8077	1	806	
8023	38391	A	8078	1	2279	MKVGLDQIIEVVPVSHSVTSAGAA AGECGGVHCDSVCAEGRWGPVN CSLPCYCKNGASCSPDDGICEC APGFRGTTTCRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNEAYSQ/SCPSGR FGKNACIGICTCTNNGTCNPIDR SCQCPGWIGSDCSQPHCADKC VHGRCIAPNTQCCEPGWGGTN CSSVKKQSTVCFES*KCEPWEER PCGGLHWDIAG*/P/GKHGGYL NELGAFGLDRSYMGSLSKDLG KNSEYNSSNCSLSSSENPYATIK /GPTCTYPEKLRVWLCGDEIAG TKRFPICRDQ*LNFSQQECL*S* TYSECCPRSIQQ*WASFPQSI*PP KNSHIPCHYDLI.PVRDSSSSLK QEDSGGSSNSSSSSE*/APKDR LGLLV**RS*SM*TNRLAKHPK QPGRKGPKI**HGTWKSSQEK/ HAEEQSGKLAATLCQKDWLIQ REGWPYILSRMFL/CFISTDGRE SESLWRKSNKSKFK*WGRPG KCGL*EGQREEVWGLGNSLYC LAGQL*CLDCECHH/GFQECPP VLGHSWGYKS/CLNRNPLKGLS SRCAGLAVRDSLAPNSQGWKA TFDFPSLECPSTGYGYGCRQICD CLNNSTCDHITGTCYCSPGWKG ARCDQA/GCYHSWKSEQLKPN QYCSPC*FLPDRGHCRHHHSCP SCSLPTGIVHYL*TAQEGKGIKH
8024	38392	B	8079	1	2909	

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8025	38393	A	8080	332	602	NSLSNRWLKGLPGAFIGEIKE MWRCMSSICQKEGWRMTAGS LGHHRSLLHVGG/AGNDVDRT GSLPASVR/QHAYYTASSVEGR VSYKLYT
8026	38394	A	8081	2	422	FNISLGFACPLRIDFFGWFFVF LSWSFTLFAQAGVLWCDLGLS QPPPLGFKKFSCLSLPSSLDYRC LPRLTNF*FLVEMGFHHVGO AGLELLTSGDPPASASQSAGITG MSHRAQSAALSFK*SGISKNRY FIFWA
8027	38395	A	8082	1	951	
8028	38396	A	8083	1	924	
8029	38397	C	8084	271	738	
8030	38398	A	8085	1	575	
8031	38399	A	8086	2	332	
8032	38400	A	8087	1	897	
8033	38401	C	8088	181	804	
8034	38402	A	8089	1	1923	
8035	38403	A	8090	294	2340	EKCRHNCSRVWQSLVSQSVW ATEGQYGRKTNARPVQVKIDS ASFPYQRRYPLRLAEAQGLQKI VKDLKAQGLVKPFNSPCNTPI GVQKPNQGWKLVDLRINEAI VPLYPAPNPYTLSSQIEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQTLTWVLPQ FRNSPHLFGQALAQDLSQFSYL NTLVRLYRDDLLAAHILETLCH QATQKKTGIALGVLTQVQGTSE QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLNQALLFKRPVLRHLTC ATLNPATFLPNNKEKIEHNHQ VIVQTYTIQGDLLVPLTDPDL NLYTNGSSFVEKGLRKAGIHPS RQWTPLPKAGPEMLSKRQVL ESGILKAFVLPYLLVAVLGSIDF NGKPPVAVFSLSQAHFLCAT WLLLYGEVWHSHTAIKTYQ RRRSQDGRIGTAPVYSSQRRR RRRVISAFPSEGIPTDLQLRVLS VRRKTNKQKGHPHQPICTSPS SRPKVDKTTKMGKKQNRKTGN SKTQASAPPPKERRSSSPATEQSW MENDFDELREEGFRSSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSA MED

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8036	38404	A	8091	158	865	NPAARTPFVVIKKGGKRGEGCL AKAGAIHILNIG/GTPVCCPLE EGINLEDWATEGQYGRKNAR PVQVKLKDSASFPHQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGQKPSGQWRLV QDLRIINEVTVPLYLAVPNPYIL LSQIPEEA EWFTDLDLKDAFFCI PVHPDSQFLFAFEDPSNPMSQL TWTVSPQGFRDSPHLFGQALA QDLSRFSYLGTLVLWYVD
8037	38405	A	8092	1	748	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDSWFTITQIRL LENTGIRVFKDNLVEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSQPKAQLCS QQVKYLGLKLSKGTDRDLTFLP VNEEKIE/P*LSTSNCSKLRCRSG TSRGS LG
8038	38406	A	8093	194	1377	NPAAQTPFFVVKGGKRGAGL LHRQYPLRLKAKQGLKKIVKDL KAQGLVTPCSPCNTPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEA EWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDTLVLQ YMDDLLLVTHSETLCHQATQV LLNFLATCGYKVSQKLAQICSQ QVKYLGLKLSKGTALSEERIQ PILAYPHPKTRKQLRGLLGITGF CQIWIPRYSEIARPLHTLIKKTQ KANTHLVVRWTPAEAAAFQVLK KALTQAPVLSLPTGQDFSLYVT EKTGIALGVLTQHYGEERNS*L PTEYLSNIRKPLGDYYWLYRNL KRWQSYTARVIRKERKGGK
8039	38407	A	8094	3	521	

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8040	38408	A	8095	1	3203	DSPLSTKAMLGMLVKDHWSPA AQTPFFVIKEGGKRGAGLHGGQ LILKDKFITQSAADIKEKLQKST LGPERNLKTLLNLATSVFYNRD QEEQAERDKRGKKKATTLVMA LGQADFGSGSTRKAWANRMP NRAYFQCGLQGHFKKDCPSRK PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGLGQ PVTRYFFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAI HLNIGEGTPICRL
8041	38409	A	8096	13	183	VHLHPQGHVPVKHTPTGLGYS SCRHLLGRACY*KGEVGAKA GMQVSDALPRLGGVS
8042	38410	A	8097	1	2427	MSKFSCASLTATESDGTPLMEQ YVPCPVCEATAWAQHTDPEKS EDVQYFDMEDCVLTAIERDFIS CPRHPDLVPPLQELVPELFMTD FPARLFLNSKLEHSEDEGSVL GQGGSGTVIYRARYQGQPVAV KRFHIKKFKNFANVPADTMLR HLRATDAMKNFSEFRQESML HALQHPCIVALLIGSIHPLCFAL LAPLSSNLTVLSENARDSSFIPL GHMLTQKIAYQIASGLAYLHK KNIFCDLKSNDILVWSLDVKE HINIKLSDYGISRSQSFHEGALGV EGTPGYQAPFIRPRIVYDEKVD MFSYGMVLYELLSGQRPALGH HQLQIAKKLSKIRPVLGQPEE VQFRRIQALMMECWDTKPEK RPLALSVVYSQMK/APDFCHLV *TVLWEADSLLLIPGPGVHRGV LGWKRGVQELHGGNTEKGLM EVQRMCCPGMKVSCQLQVQRS LWTATEDQKIYIYTLKGMCLN TPQQALDTPAVVTCFLAVPVIK KNSYLVLAGLADGLVAVFPVV RGTPKDCSYLCSHTANRSKFSI ADEDARQNPYPVKAMEVVNSG SEVWYSNGPGLLVIDCASLEIC RRLEPYMAPSMVTSVCSSEGR GEEVVWCLDDKANSLVMYHS TTYQLCARYFCGVPSPLRDMFP VRPLDTEPPAASHTANPKVPEG DSIADVSIIMYSEELGTQLIHQE
8043	38411	A	8098	1	1641	

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8044	38412	A	8099	1	1075	VLHKFPYRMVLPALPKRMLGA DREFIEARRRALKRFFVNLVARH PLFSEDEVVLKLFSLFSGSDVQN KLKESAQCVCVDEFLNCKLATR AKDFLPADIQAQFAISRELIIRNI YNSFHKLNRRAERIAS/RAIDNA ADLLIFGKELSAIGSDITPLPSW AALNSITWGS/LKQALKGLSV E/FALLADKAAQGGKQ/EENDV /VEKLNLFLLQSYKDLCE/R GHEKGVF/HTKHQALAQSTA* LKRPD*LSATGAEPSPPEVRGS KLKSRIRGARENAQTMELRN YVFSLYCLHQETQLIHVYLPPTS /HILRAVFNVSQIQGHKEMSKVW NDLRPKLSCLFAGPHRTLTTPPC SPPEDGLCPH
8045	38413	A	8100	1	974	MPQVPAP/PLPSITSGHPGEP/PA RPSCSCLFSPQPCNSITPSSLLLR QLAVAAAGCGGHGAPALSST GWQQVCKSPQVRSVPDNPTTA DSTASLWKFGVLRSHINGCY K*KQQPLLVPVHAQRRRAQVAP/ APPAGLSCGQHS/LPQPPRCSDLS LGLHPGR/LPCDRGHCPPLPPVT PTPDKAGPILDPAQSCPCPSIPA PPKQSPPARFPPEMKRKKTLM MPPSEGSLSLASGMEASVFQRL LSRCTCLDQATVIWGFYCMQV QASQGIQPCRGKDELLRLAPLPV KEARRTKPRSPGKHAKAPPSSS ACSPHLCSSPILQALD
8046	38414	A	8101	1	460	SLQAPRRNSRAEHTRTLNSECP RRRRCCIKGCTYT*LDVAPPPP VLDWLVQPKPRVLGNGWLL DGPPEVLQAEACSTTIDGAEP LCPSGYECHILSPG/DVAEGIPN RGQCQVKQRQADGRILRHKLY KEYPEGDSKNVAEPGKGQQRH
8047	38415	A	8102	3	219	NNHRLDRTLPRDYCHAATAYT THELAFGDFRLPTEGHQELCHN SHLIYFRDK*THCTWRSVDSL TGVTHR
8048	38416	A	8103	230	555	NVRPS*ALQAPWGRHHLCVTP MQLRMTLVVSSLGKGTGGLSL AQ/CAPVQEGTHGSGPPVEGWL AATRTCEGCRRENTMKNVGSR KYAFNSLQLKAFPKHYRPEDL RKS

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8049	38417	A	8104	23	304	KGFLYLFNKQTIEQTNNNGSKSFA KRNTTEGHDDLQLQGFQGSQTPTS FLSSSGRCYSWGAIGPQFGALS GfSPFPFSAANRQSSALDFWIT TSISF
8050	38418	A	8105	99	375	VLEFGALSGSLISPLCTIPALVE PPCGPQPSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSPQGVQ LPLGPRRLKMNTPEPTRP
8051	38419	C	8106	5	376	
8052	38420	A	8107	545	990	GLCHVLQPCDPCLPGMTQEAQ PPEVLKTAGKAGGQEPG*.*RIP *GSLCPPCPVAFGAAELPLPSS DPVSRGTGAPPQG*WLGFGYFS SNEGSPQAGG
8053	38421	B	8108	252	801	
8054	38422	A	8109	169	1226	PNGLRPPCPSPASETPGNAPVCD PGSSSQGAQKKLKPGGLPGL FPFFAQPSPEGLCPPCPVAFG AAAEPLPSSDPVVRTGAPPQQ GSW/PI*SPGSRSGTRADPVKGE VAGRERCLPIE*ASPPPHSG* AGQVPVGAAPPRTAG*GV*TGTA PCPKAOPRK*QR*RCSS*VG* ESAEIVCPQGDAG*RGKSP*/ SHRRNVPS/RYSNSHGPYDSNQ PHRKTITFEEDKVDSTLIGSSS HVEVEDAVHIIPENESDDEEEE EKGPVSPRSPRKR/PSATRAAA SRLRGS*TLGGLLGCIFAFFAPP SPTEGACAHQAQSLSGPLRSFRC HLRLCPARGLHQGRDDG
8055	38423	C	8110	58	504	
8056	38424	C	8111	203	1874	
8057	38425	A	8112	32	1026	KLLEQCLHSVSTWETPQYRRPP SPS*RGSRQPCSFSSPRDTPGE NHWLSLPQRD*AGPPVR/PSAG GFMT/PPRGVPTVEVPPDPTC/S PNHTRPFRPPFSKNPCFRFEPL RAPTLVPGPLPPTHGRVPHLE RNLALGLGLKSEGLKRNPCVEP /PAPTPIREFPKITGTPLR/PAADH ALLGMRDQSLSGQSPGPKSPDA DDQLQNRDHTETEQRISGRSS ALAPESQLQQGCAGIHFRGRFC KAPPLASGPA/RPPCLSLPPPWW APVRPKPPR*APPAP/PVPSPIN HPRAEECGRTARDWQAAPLAA LVDRDPLDEASWAPESGGDVEN LYV

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8058	38426	A	8113	3	909	TEGGASHRAHPVGPAPRG/KRH SGATEPANGTWARRRGPRGRDS SNQSSGGGERSQLRHRGWRL SRPLLPPGAASPLAGEDPERNA G/GWRGGAAPMRPKRGPMMNGG GCGPGAGSGAGGEALGRGRGA VSGCRPAPPVPPPPPPPPPGG WLRRTAGSGPEYV/GSRCARGS GQVSAGGGLCARAARGGKLAP RLRALRGRSPWPAPLGRSPAR APARVPAGRCGPGA*RGRCAL GGQGEAGPAGSEGAGRPLGRP GCPGTSRLLPRRPVRKTDVGN RSSFFPRAPGRAPHACQPTQFLII
8059	38427	A	8114	1	454	
8060	38428	A	8115	2	172	MFIYTSAFI*QFTNSINIPITSFC *TASVHLSICIVAFCHPCQCSS SFIQCTTN
8061	38429	A	8116	1	594	LAPVFKLIPMPVS/YGIFLYMG WAALSSIQFTNRVKLLMPAK HQPDLLLLRHVPLTRVHLFTAI QLACLGLLWIHKSTPAAIIFPLM LLGLVGVRKALERVFSQELLG LDELMPEERSIPEKGLEPEHSF SGSDSESELMYQKAPENISV N*LE*ESGSGDPRKQHEVLTQE VRTFLAFLGTSRCSVGLGKD
8062	38430	B	8117	1	3402	
8063	38431	B	8118	1	4614	
8064	38432	A	8119	3	435	DHAKLGTRTSGMRPHSLSLCFF SSSYDILMRITKDRVKNLTCTY TILPTDLQPGCGLPRSFYPPSSKP TSFWLWACKLFPPLPISFNPSPA HSKTAHGHSKGHTAAGM*WS* TGEGITGRCCFVSIKAPLPSSG PVGGPVGG
8065	38433	A	8120	1	525	MALLPTVLCLWAQAQFLVDLG QNSKHHQEHQLAPDVAFKMK GACVCAAGFRGWRCCELCAFG THGKGQQLPCQCRHGASCDPR AGECLCAPGYTGVYCEELCPPG SHGAHCELRCPCQNGGTCHHIT GECACPPGW/IG/TV*GPPSPGSL LGCLPRETSLIISLQLCLYLLL

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8066	38434	A	8121	1	1050	MLIMTFHGLLPCMQMACKWQ LRVLVAGIRCDSTCPGRWGPN CSVSCSCENGSGSPKDGSCCE APGFRGPLCQRTVHILYPRGCGI RDVGESGNRKQKAVEQYREH WTVSPEVQCSASHFSSVRPKSA CPPGFWGPACFHACSCHNGAS CSAEDGACHCTPGWTGLFCTQ RCAPGTFGYGCCQKCECMNNS TCDHVTGTCTCYCSPGFKGIRCDQ GIMLL/CPHCGAAGPICLASAA AEREGRPGSPCLLHTCHEDDQ HRLLPLSGANSIPTYR*SGRPDS PLRTEALILPQCKQKFSQSGQEV CAVSCAAAGTYGPNCSICSCNN GGTCSPVDGSCCTCKEGRILCLQ
8067	38435	A	8122	3	732	IRCDSTCPGRWGPNCSVSCSC ENGGSCSPEDGSCECAPGFRGP LCQRICPPGFYGHCCAQCPCLC VHSSRPCHHIGICECLPGFSGAF CNQGIQAPTGNPSPGWYRS*EM TDPRCSCR/CLSGESTRHTSPVL LGTDASETQVIGFVNLAQFLIIC PRKLHYKAQNSKKSNGSDASS DWKDWGIWDRESCCEELCPPGS HGAHCELRCPQNGGTCHHIT GECACPPGWTVGA/HC*ALCCP
8068	38436	A	8123	77	864	PAVPEL*VFQAKPERKSRYWQL HFPFHSSSPTS WRKSLEPMYRC TCPPLTPYGCTCPPLSPYRRTCP PLTMYRRICPPLTPYRCTCPPLT PYRMFSSPLHKEITSAQRSPEPS SRPHSSKAAALR*QPRIMEKQRI YGPSPTSVQPASPPCLDDPRKK AERPDHRATGKRHLPETSL/YA ELVRRAPENPEDSEAPAPAPAA LSPASEHRTDPIQETKKARKSSD NDGSTPLAQTPTRRSSQWPRLG QFQQQEDDSSGLYSTG

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8069	38437	A	8124	314	1188	KHFLNFCPLPYMILNKYRNQYCT FNDDIQGNKIFTAYGSITCLKI.V HNCIKKIWL.VDSKGLIVKVRIC HF*PE*R*LCHSGWPSNLEAIVQ EIKPTALIGKHFLLSLLPYPLF*P DCFFNERPIIFALSNPSTSKAEC AEQCYKITKVK*NYNRYFNNOI FIHYREATLYPGQGNNNSYVFP VALGVVACGLRQITDNIFLTTA EVL*NPLSLPRV*NTKCAQPRN TIRDVSLKIAEKVKPLLKLIHYF SFLFLNNMQEAFVRSQMYSTD YDQILPD\CYSWPEEVQKIQPQ
8070	38438	A	8125	1	1115	SPAQVMFQCLWKSCKVSLSTA SAMQRHRLVHLGRQAEPEQSD GEEDFYYTELDVGVDTLTDGLS SLTPVVSPTAS/IAACLPPGGAAR AAGAPSPA*SPAAACPAAPAP CPEHRC*PPVLSQ*PCLPRAA*R PPAWSRMPRRLEPAHPPCPPGS ESS*GSPAATRISAGM*YGMEA PGPPGAQPAAGRKP/PAVPLGL SGSFKNIKLPPSPPPPGPGAET ARRNKPGGAGSPAAAGSAFNW VGVPDLTLEPPPPPGPEGSPPT QS/SPLKKPSFLH*SPNPHPLSPF TPKGGPGSHPSRLSARRFIKGV MGPAALGGQSRCTLRGVGEGTP PLALNSTALGPWGCIFYPCFLFK LQVSHVWAATRRREKLKI
8071	38439	A	8126	116	333	KLRDRCLSH*K*NGASPPRPTN YSIMRPSLV/SLVHHSGL*FPQM LRALS*LRVFGVA/VSSP*MVPL NPCIIH
8072	38440	A	8127	5	829	KPSQPQPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVRGRPPAGG ARRRAASLG/PWVRRRLQARPG /LFRPRDFYLRSPRSYGRTP*KSP QSSPRGSARPD/GPA/PPPEPPV KRRARGVLESSRHAAPRRVFHL GREREQSQEGPAWPKRGRPAPS PQRTATWRPAAGGGK*GSAAT S*ARAGPARRGKRRG*EPREN RAGRPA TRGRPGRCCPPA*S PRPSKRSSPLCSPPRSWPTRPS KSSYGASLARTTTLQWKFSVNL IRKQIRDAQ

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8073	38441	A	8128	5	844	KPSQPQPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVGRPPAGG ARRRAASLG/PWVRRRLQARPG RFAPGTFTCGAPRSYGRP*KSP QSSPRGSARPDGPAAASARATR EAQSARGLGELAAAGSQAGLP LGKGARTEPGGSS/CSQGPAPW KRGRPAPSPQRTATWRPAAGG GK*GSAATS*ARAGPARRGKRR G*EPRENRRAGRPATRGRPPGR RCCPPA*SPRPSKRSSPLCSPPPS WPPTRPSKSSYGASLARITTLQ WKFSMNLIRKQIRDAQ
8074	38442	A	8129	795	914	RGIRLASEMYPLTCFWR*LYR RGLARIALVNCRRNAL
8075	38443	A	8130	4073	5350	YSLKSGSVTPLALFFLLKIDLA MQALFWFHVNFKVVPNSVKK AIGSLMGMTLNL*ITLGSMIAFT ILILPTHEHGMFFHLVSVSISLS NGL*FSLKRSFTSLVSWIPRYFIL FEAIVNGSSLMIVVSVCLLLVY KNACDFTLILYPKTLKLLISL RRFWA/GQWGLFDIQSCHVQTG TI*LPLFLIEYPLFALLPNCPOQN FQHYVE*QW*ERTSLSPVFKG NTSSFCPFSMILAVGLS*IALIIL RYVPSIPNLLRVFSMKGC*ILSK AFSASIE/YNHVVFVFGSVYMQ FLLVPLVEFGCESIWSWTFFGW *AIDYCHNFRSCYWSIQRFNFFL V*SIGRVYVLRNLSSSRFSSLFA *RCL*YSLMVVCISVGLVVISPL SFFIASI*FLSLFFFTSLASSLSILL IFSKNQLLDSLIF

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8076	38444	A	8131	1	1715	MDGISGGKRALRERHSKSKAL GRCPFWTNITPPALPGITNDTTI QQGISGLIDSLNARDISVKIFEDF AQSWYWILVALGVALLVLLFI LLLRVLVAGPLVLVLGLVGLV AYGIYYCWEEYRVLRDKGASIS QLGFTTNLSAYQSVQETWLA LIVLAVLEAILLVLIFLRQIRI AIALKEASKAVGQMMSTMFY PLVTFVLLLCIAYWAMTALYL ATSGQPQYYLVASNISSPGCEK VPINI\SCNP\TAHLVNSSCPGLM CVFQGYSSKGLIQRSVFNLQIY GVGLFWTLNWVLALGQCVL AGAFASFYWAFHKPDIPFTPLI SAFIRTLRYHTGSLAFGALILTL VQIARVILEYIDHKLRGVQNPV ARCIMC*FKCCLWCLEKFIKFL NRNAYIMIAIYGKNFCVSAKN AFMLLMRNIVRVVLDKVTDL LLFFGKLLVVGVGVLSTFFFS GRIPGLGKDFKSPHNLYYWLP MRNPITPTGHVFQTSILGAYVIA SGFFSVFGHVCGRSFLCFLGK DLGVSNNGFPGRPY\Y/MVPRA FLKILG/KKNE\APDNKKRKK
8077	38445	A	8132	1	208	GTRASSAPCPSSSAPAHSEAC CCRMSLWGSCGGSGDGSSACG SGWNLSMAGTSCSPAMCSPSR APS*RSASRPRTWRATTSAA WAPRRCWCGWA*SAT*PSSTTT ISSSPHCGWPCPASCASAAAWL SSTWATASVAGSCWGPIM*SSA PAHSFEACCCRMSLWGSCGGS GDGSSACGSGWNLSMAGTSCS SPAMCSPSRAPS

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8078	38446	A	8133	28	1956	SRAARERGRSDSGGRSDPGCPA VPACVPRSRPMTAPAGPRGSE TERFLTNPNGYGTQAGPSAPPT PPEE/VRPSPSS/TNTFS*VPATSF EPRAASPAS*CCKWSRSWWSR CSSSCLGSVISWL*HSGKRTSP SDTSSCWATRTERMTSPQPTRG SSCTRPSSMLWT/SAGGRAGAG GQAGAVPGVA/WTCHWAGLLS ASGTTTEATWTRPTTHLTIRW WLLTASRWIPPSGPLRPPATIS SWKAAPVTRTSRSNSTSTACSL EGGPGVSTWQGTALALGAGRDP KTPLTLTRASCLGWSMSPSTG *RPLTSRASSIMRSRTAIPAS*S RLTTKHTVGGSPSAWRPRPTSR SVSTPVSSSTGGQLPGSCLTW WSYSPACTSSSPLTPSRLPAA EQSLWGSCGGSGDGSSACGSG WNLSMAGTSCFVTSVDLHHLG HHS*RSASRPRTWRSRRAAAS SWAPRRWCOWA*SAT*PSSTT TISAHSPWCLSACSRSSMGTTCL *RSPPCRRSRAAAA WCGSSPS STFTPSSSLFILHGAQPLHRAHH RAPTYTIKHSRRRRRKRASCR PYIAQCPGPHLRQVPPRERAR PIAILLLRKGPLGGAFAAGELI RPDCRWTVGPGLQRPPPTPLIYL
8079	38447	A	8134	1	2994	MQRPCLCVEPMRLCFDSFLLLV NQEEEEGVVPCLEENGRAAA DPGPQDQDCLLPTLTPSLSGDE APDRTOSSGDPRERCGYLSVTC EEGDNRFAAFCLCGSWRLNHG HADWCDQRRSQISNRLPASLGII VGTGRSRHLLAALRGVKEDRQ TKGCVQTPASLPWLPGLSSET RAQKTCVLLIDYATFLKLAND DDDGCLDCLQPGVRTA WASSQ HGIRAPRKSVQGSASSPSLRTW ALTCTQNWFCVLLVK
8080	38448	A	8135	215	418	

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8081	38449	A	8136	767	1458	WREHLTKFNVWGKQHLESLSN QQKNMRCPVRSQTRPPTDVKP VSRSGRRDRRAAGGEGGADR QGPGTARARAPGSPQRGG*GR NLRIQAGPPGKHGRGIPPPQTRG RSRGAPPGTPEGPRHPPRPA PGPATGAPKRPQPQTQRQGHIA RDSRPSSDPVPLRETGAPPPWD A\SQGQAARPRATQTPSSAPVA TRQSGRRADSRRRGVTRRTER CAQPSLAVSRVPTR
8082	38450	A	8137	3	424	
8083	38451	A	8138	1	813	MVQKELEEEGRKSTPQSWGRE NMEKALNSSLKASLGGSGVMI CASVKALLTVVIKVLGRLLAES LFLLLQTQTAL*QTL/RHTNRNI SHQYQDEIHLDGSDLPMSPRR KYEPVPFGRKTYKISIRKAN KKCEEARQEKEAMVMKYVRG EKESLDLRKEKETLEKKLRDAN KELEKNTNKKIKLSQEKGR LHQ LYETKEGETTRLIREIDKLKEDI NSHVIKVKWAQNKLLKAEMDS HKSFKNPLVRCNFAATFGYVK KLIPEIKTGSSH
8084	38452	A	8139	3	808	NVRVEPTDSSFMEIEFAQKGA FDAYVAVGGGSTMDCKA/AN LYASSPHSDFLDYVSAPIGKKG PVSVPLKPLIAVPTTSGTGSETT GVAIFDYEHLKVKIGITSRAIKP TLGLIDPLHTLHMPARVVANS FDVLCHALESYTTLPYHLRSPC PSNPITRAPYQGRNPISDIWGY TRWGFVG*VS*RRAVQEIPMDL *KARSHIMHLASAFAGIGFNA GVHLCHGMSYPISGLVKMYKA KDYNVHDHPLVPHGLSVVLTSP AVFTFT

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8085	38453	A	8140	2	1154	IDPLHTLHMPARVVANSFGFDVL CHALESYTTLPYHIRSPCPSNP TRPAYQGSNPISDIWAHALRIV AKYLKRAVNSTDK*RRRMSLR APSWEWPSRSGPARCLPRRFY IT*GS*QRYLLWPLETVDEKY VSLQFSFRQGVV*ITCLIFLPT *HFFHHHIF*GSSLFCRNCQC* CVIVRYLYHSQGWQKSR*S*RO GLIWHLGKCFLLGIGFGKCWVF ICGHGNV/SYPISGFRWKDVIKG KGIYNVGIHPTGWPPWAFSVVP HVPQRCFTFHGPRCFPERTPWR WQEILGADTRTAQ/RSQDAGLV LADTLRKFLFRSG/IVDDGLAA VGYSKADIPALVKGTLPP/QER VTSFAPRQSEEDLAALFEASN ETVLNVHLN
8086	38454	A	8141	2	990	WENWISIC*RMKL/DPYFSPYTK IKSKWIKDINVKPTMKLLQEN IRETLQDIGLGEDFSQAQATKA KVDKLDHVFKFNCTAKETIN KVKRKPKEWEKILIFADYPSDK GLITRILFIDHSWVFLGEGNLAG SSDNSGGKAWKHLLPLLASRCS GTHSNLRAKLRLSQGTVAITWP VLKREGEKSCGPSESPDLGAPQ ARDVTPCLGICSSWLLQASGHH HIPWCQLWKLFFVYLVQLQPH REVALVPAPGAHPTTASVPVC AQWLDPMVIHSHTLCCSEPDSP LAGMGFRPVAQAKHNPARPSG WNESRPEQNLDKGATSHRGF WLAR
8087	38455	A	8142	1	196	GQYPWPLETNPRFLRE*TLPKS LQKSL*DSPVPE*SLCGTCQQA RSLSEEVDESSISQVCCPT
8088	38456	A	8143	3	413	ITLGKDCIMHGYML/KLGNPFL TQWQRRYFTLFPKNI*WRRRGE SRQNLLTMEQILSVEETQIKDK KCILFRIKGGKQFVLQCESDPEF VQWKKELNETFKEAQRLLRRA PKFLNKRPSGTVELPKPSLCHR NSNGL

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8089	38457	A	8144	705	1983	EIKVDSLLKSF _{LDL} MNGKQNL ENLNALKDFAMMLNLSYATEH LGLEHMHNRFVYRD _{LK} VRTI DRILHSRYCVNGPLEDKVTEK DFPGNPEIKPS _{GK} WLGCP _S *KS PTLSQRGLMTLPCQTLGSG*LSF PE/VLDLP*WTNAHFADWFSLG CMLFKLLRG*VEMHPSSAVLM AAGAWMKTTVVRGFKTVFLSV W*LSCFIPSKRDVSKRLGCHGG G*AIVPAFRYLQKSKIVLN _{FQ} YPPPLIPRGEVNAADAFDIGSF DEEDTKGKIVHM/CHLFLYFYF WM/VMISVGKQEVTTVYEA NADTDKIEARKRAKNKQLGHE EGKIAHVSQNISNAVN _{FQ} NFLY LTQWQRRYFYLF _{PN} RLWRGE GESRVSLRQPHRACFPVRTMAY GYWLLRAPKFLNKPRSGTVE LPKPSLCHRN _S NGL
8090	38458	B	8145	156	281	
8091	38459	A	8146	2	181	VWCCSR _{TA} TLTRNCARRRCS RGSRTWKRSGRSSRRRAH/SQ YDLERLRAAQQLEREQE
8092	38460	A	8147	3	670	ETGLKNEGRV _{LVR} HS _{AW} CP _{LL} WGREGSRSS _{SS} WPELQGSPLC ASQGVVLQQDSYIEDQKLVLSE RALTRSLSRPSS _{IE} QEKQRSLE KQRQDLANLQKQQAQYLEEK RREREWE _{DR} ERELR/DGRPSWP SARRRCSRGSRTWKRSGRSSR RRAH/SQYDLERLRAAQQLER EQEQLRREAERLSQRQTERDL CQVMGLPAESNLMMLIKTPCV LSKVRK
8093	38461	B	8148	47	699	
8094	38462	A	8149	1	242	MNRGGFAVKILALLDALSTVCS QRVQAKKQQH _{LQ} NKEHFK LLKQKEKLKQEDL/RKKLF*IQ GIRCPQATPHHGQCSL

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8095	38463	A	8150	3	929	ASSCVVRAVPPG/SGVWGFRCG LCGPDCESGLISGSRMFAAGPQ G/PPGAGTAVTLAAAGEEGLES STAQHSGSLCSEEPV/PPRHA WQKGSYSRNWLPAPRPRPALA MSSDTRGQAQLSPSWQLEKKG LSSSTAQRGCRALQGRAASARR VQRKANPTAGTWLRLAPGLP LLCPQTPGGRHSCPPG/K/PGK EGLEQFYSSARLQGFAGKSRQV PDVTRKANPTAGTWLRL/HR GPRGGEACAMAVRGPRSHEQR CPWSAGADSVS*GHCEGTIDGR VASGACLVDSRGSAGQNLP DPEHWHVFCDFP
8096	38464	A	8151	2	1749	WVQGASLCVRAKRAPLPLAR* VQGAELTHPWGPAHP*TRNQ KPALGSSGPHSPHIGNPQTPTQA GQP*PHTARHGVPQEHGRGQR GPHLHKTTETPQEATP*EVGSIAT EQAWLPHLCL*RPFFHQLGLFP RGPCMEGAQQRVGESSAAGT QVCMGPKTAGDWDGPWLVCW FH*GEEAARILRPGLG/GLSGHP LWPQGGQMTVGYGGASEAC GAGELLMRRAPPQSPGKARGL PA/HYWHQGTGPRKAEI
8097	38465	A	8152	1	583	MAAVVAATALKGRGARNARV LRGKERDPGEGRTAEDPFSFTS SPTIAGGILAGATA/NKASHNR TRALQN/HTASPEGKEEP*/DPLS PELENTFPRKEGQRTPMESCGN LPWAIIGFPLWFLPLSSFTQAG KWDK/VTVLKAD*RLRAEHCG FSNTGRV*RRRRFRAFLPEVAPF PLMFGSGVSGGADLRVSCDPP
8098	38466	A	8153	141	341	GTRGSPSKKGERVRRDAQQT TW*TRSPASGCFQICEGNKQDE ACDVRGLQHCERHSLAGPREY
8099	38467	A	8154	1	521	MKNRSRNKGNVEWQAEGIRSK RSVGKQRPSPKAKIPSGDKNGVS LTHNEVINNDNPLESNDEKEGQ EATCSRPIQV/EFQQ**LFRPE* WRRASGNLQIPKKRVS*A*GTR GSPSKKGERVRRDAQQTATW* TRSPASGCFQICEGNKQDEACD VRGLQHCERHSLAGPREYMP

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8100	38468	A	8155	1	619	PEAELHNHGIQINSCSVRLVDIK KEKPPSNSKVECCQAQARTHNN QASDIIHVISSEDESGSTDVDEPLE VFISAPRSEPVINRATPCELCX* KEG/QEAI/C/SRPRDVPRALGFR KFSPPFEESFRKGLLGQDDPDP SIEKKPPAEASSGALRSKHGEK APMTSRSTSTWRIPSRKR/RFS DSDLSNGKELQETCSSSLRRG SGKE
8101	38469	A	8156	362	1043	PTTPPSAGSSWTTASPPS*GKA WLGTRPPSPWRRMSASMRT/S EEDGRLQPQLPL*AHPSESSGQ DRGNQVSVGREADCGQD/SPVS TMTRSHPGRPCAEGC**PCCSSR P*PCPCGSGSLVTSPLSLPAPSF WLPLRPSISPPGLPPLQSSLSFPP PPPPVPQPPAPPALQWGLHLPG VPQPGVPAGRRVVRSLAKHLPR LPDHSV*GAPGRRSLREHLPOH RPGDQ
8102	38470	B	8157	52	633	
8103	38471	A	8158	15	3054	AGPDGLAAPASCQGARGQTRV PGAFSWLAPGSHHASEGLAPG VPPAGGVSAQELTAPPQEGWG LGAPPAAPRPESDEKRAAGSDAV RSFSRGARDSLGQRRLGGTRGA GPAGKGAQRTMGPSAGFSFPP RPHQEPSRSCWQHLLWHCP WPQPSRLPRLTPAQLLQGGPGVL AAPPG*HVPGLAQSPWPLPS GPRSP*DPLHQGALVPLPQGG PHTAPHCLPSVLSPAI/QQPLPT AST/SRSPASTMAP
8104	38472	B	8159	748	3111	
8105	38473	A	8160	1	463	GGGGGRGQRGRSPRPRYLCPGP GPTG/GPGACAAGGVTVGPS NGRPLLPQRHPPVGVDFSRRC RFRLPKHKERSPDARFKEGPGG AA/GPGARGQ*DSARTPDSALK LVRPPLPIPTGRPSCASGGP*PA GKRGHLSAPPRPGRSSPGPSQP

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8106	38474	A	8161	1	2733	MALRRAGAGRTGCFIAIDTML DMAENEGVVDIFNCVRE/LRAQ /RVNLV/QTEEQYVFVHDAILEA CLC/GNTAIPV/CKLQNLFQNTK CTAMSNYTLTQGLLQHWLS*T T*FIWLAGTMRLLCLSLCVDAAS APWVLKTLNIVT/PRVRPEDCSI ARPNHDKNRSMDVLPLDRCLP FLISVDGESSNYINAALMDSHK QPAAFVVTQHPLPNTVADFWR LVFDYNCSSVVMNEMDTAQR GQS FVGPLEFGGAQL
8107	38475	A	8162	1	307	
8108	38476	A	8163	3	969	GLFCSRKTPPSK*KHNVIASDK AAEKSVVHEHSHDHTQLHA YIGVSLVLGFVFMLLVDQIGNS HVHSTDDPEAARSSNSKITTTL GLVVHAAVFYVSLFPNIADGV ALGAAASTSQTSVQLIVFAIM LHKAPAAFGLVSFLMHAGLER NRIRKHLVFLAAPVMSMVT YLGLSKSSKEALSEVNATGVA MLFSAGTFLYVATVHVLPEERL KLVTVLGAGLLCGTALAVIVPE GVHALYEDILEVVPSPFYCHLY VVEYLMFSSHFCSPDPWQDQL LTLRVCSSTSASLGEGLGVSSI RKGMELSVQAQHHVEVAKA
8109	38477	A	8164	164	240	
8110	38478	A	8165	2	417	QQIRKLIKVLIIHKPVIVHSQV GCQKSTFS/RTKGRHMG TG*R KSTANFQMPEKVTWMRRMRIL HWLFGRYHESKKTDHHMYHSL YLKVQGNMFTNKQILMEHNHK LKADKAHKKFLADQAEARSSK TNKASKLREER
8111	38479	A	8166	1	86	RTRGCLSHNNHH*HLHRHHLH HHYPYSY*HHHCLNYH/APYLF HWLYH/APHHLNQHAHYLHLY YHHHYNHHHHLHHHHRSHCH HHHHHLTIHLLCQHHHHHFHT KHLLLAHPQALQTHHNNHDM/ HHHYPYSY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
8112	38480	A	8167	50	1156	LLLQFSRATFILFPQPPANTFTSA FSQTRARRGGSGRGGGQESAEE TSEFGDRHAPEAAAAATRGSA APEPKHASSCGTRGQCACARRE VEAQVRAKGDVTAERARRGGR WLTRSGMEHLERCEWLLRGTL VRAAVRRYLPWALVASMI.AGS LLKELSPLPESYLSNKRNVLVN YFVKVAWAFTFCLLPFIALTN YH/HDRQGWLGPAAD*/CTLLV GTAIWYICTSIFSNIHYTGSCY QSPALEGVRKEHQSKQQCHQE GGFVHGFDISGHSFLLTFCALH DCKKRCLCLQ*R*KTDRLSHCLH TAITTLVVALGILTFIWLMLFC TAVYFHNLSQKVFGTLFGLLS WYGTYGFWYPKAFSPRTSSPEL
8113	38481	A	8168	2	926	
8114	38482	A	8169	2	1053	TRERFSVANRVGTSETVPKAEA GPESAAGGQEEEGEDEEELSG TKVSAPYYFSFWGTLEYHNAMV AGTEEARDGSAGVRVLYLYPT HKSLKPRPVSLGKCRFKENC FSHGQVVSLDELRFQDQDPLSS LQAGSACLAKHQGWPLERQHA SPMWDNGYLSQV*LAAA\RE AVVGGGRHPAPTAKRPQESD SDS\EVVRTFAMPEWGWQMLW TLGPAALPLLGWVHTRGIGSR LLTKMGYEFKGLGRHAEGRV EPIHAVVLPKGLSDQCVELTQ KQTRVKGAGTNKPPRCRGRGA RPPGRPAARNVDFLNEKLQGGQ APGALEAGAAPARRSKDMYH CQCECQAGP
8115	38483	C	8170	166	419	

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8116	38484	A	8171	55	1157	ALDEPHGAGASEERAGDVFGPP RRVPGPSLWPLEAWPTSSQKV MPQVRCRLHLHQVWGQRGGPPR IKRWAWAARGHTGLGPTPHGP SWTHSNFLKEKIF*KMFAKQV GPEAKQSLPNGFPGVATAWSP VRSSVCPLFIKARPC*QLQDSC WDPGGTETADPGHTGLELRFFE PPKPTLPLALSEAPVPQREEKTQ GRGHYPAPQCLPGDPCSPHHPA PQPHQPHPAR/HN*PPPPRPSSH PTTVPPTRPQPWQPGCCAQPPR PCLH*RGGN*VY*GMQLHQKS VSWPHSQWPQKREGNGSSHEI HPSCPPSGFHGPSPEGRMPTQA GALHSWVPGLSLSHSGSPHPPP RWTATVQAARPRVPLTNL
8117	38485	A	8172	1	362	LFDNTVYCPRTERRLLKNDTKH QRHAQSACQLSTTLVCSQHRK VSDFIQHKHSAPLPQKSKRKQ NQQSFMKLTLNKLIGIDEMYRA IYDKPTANIILNGQKLEAFPLKT GTRQGFSLSPLL
8118	38486	A	8173	1	655	MIISTDAEKAFDKIQPFMLKTL DKQGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPF SQLLFNLMLEVLTRAVREEKEI KGIKYLGIQLTRDVKDLFKRN* KPLLNEIKEDTKKWKNI PCSWI GRNTNVKMAILPKFR*WTR*RQ FSTVHKD*KLSETVSHSYLKIKF WKLKRPFLLHSEPLKERQQDSV SLMNWVCMSSKTGQY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
8119	38487	A	8174	2	1936	DKPTANIILNGQKLQAFPLKGT TRQGCPLSPLLFNIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLIS NVS/KV*GYKINVQKSQAFLYT TNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL N/IEKEDTNKWKNIPCS WIGRIN IVKMAIL/PKVIYRFNAIPIKLPM TFFTELEK/VTLKFIWNQKRARI AKSILRQKNKAGGITLPDFKLY YKATVTKTA/WYWYQNRDIDQ WNRTEPSEIMPHIYTL/V/DKPE KNKHGGKASLAFIKW/CWENW LA/ICRKLKLDPFLTPYT KINSR WIKDLNVRPKTIKLEENLGITI EDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAACKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRCWRGCGEIGT LLHCWWDCKL/VQPLWKS VWR FLRDLELEIPFPAIPLLGIYPND YKSCCYKDTCTRMFIAALFTIA KTWNQPKCPTMIDWIKKMW/HI YTMEYYAAIKNDEFMSFVGTW MKLETIILSKLSQEQT/KHRIFS LIGGN
8120	38488	A	8175	2	1105	LPTKKSPGPDGITAIFYQRYKE ELVPVLLKLFQSIKEGILPNSF YEASIIIPKGRDITTKENFRPI SLMNIDAKIP**KY*QN*IPA AH QKSLSHHD/KVGFHPPGMQDW FNIHKSIMLIQHINRAKDKNHM IISIDA EKAFDKIQPPFMLKTLN KLIGGTYFKIIRAIYDKPTANII LNGQKLEAIPFEMLKVMYRAF RQNKQIKGIILEKEEVKLSLFA DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNTT QTESQIMSELPFTIASKRRKYL GIQLTRDVKDLFKKNYKPLLKE IKQDTNKWKNIPCS*VGRINIVK MAILPK*DVLASPSPTMTVTC RKQVQVL
8121	38489	B	8176	120	2036	
8122	38490	A	8177	3	316	

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8123	38491	A	8178	1	1447	MSIRVTQKSYKVSTSGPWFSS CSYLSGSPSAHSSLSFSRAGSSSF QGGGLGRGYGGASGMVEITAVM VNQSLSPINLEVDLNIQAMHT *EKEQIKTLNKFASFIDKVQFLE QQNKMLENKWSLLQQQKMAQ SNLDNMFESYINNLRWQLETLG RKKLKLEAELGNMQGLVEDFK NKYEDEINKYTEMENEFVLIKK DVDEAYMNKVELEYRLEGPTD EINFLRKLVEQEIRELQSQILD SVVLSMDNSHSLDMSIIAEVK VQYEEIANRSWAEARMYQN* YEELQMLAGEHGDDLSTKTEI STINQNISWLQAEIEGLKGQRA/ SLESTITDVEQRGELVIKDANA KLSQLEAALQRAKQDMALQLH EYQELMNFKLAQDIVITTYRKL LESEGSWLESGMQSMSIHMKT TSGYAGSLSSAYGGLTSPSLSYS LGSSFGSGAGSSFSHTSSTRAA VVKKIEAQNGKLVSXSSDVLPK
8124	38492	A	8179	272	1813	KCGLRSRSFSAPSRIAWFGPP ASTPASTMSIRVTQKSYKVSTS GPRAFSSRSYTSGPSRISSSSFS RVGSSNFRGGLGGGYGGASGM GGITAVTVNQSLLSPLVLEVD NIQAVRTQKEQIKTLNNKFAS FIDKVRFLEQQNKMLETKWSLL QQQKTARSNMNDNMFESYINN RRQLETLGQEKLEAELGNM QGLVEDFKNKYEDEINKRTEM ENEFVLIKKDVDEAYMNKVEL ESRLEGLTDEINFLRQLYEEIEIR ELQSQISDTSVVLSMDNSRSLD MDSIIAEVKAQYEDIANRSRAE AESMYQIKYEELQSLAGKHGD DLRRTKTEISEMNRNISRQAEI EGLKGQRALEAAIADAERQGE LAIKDANAKLSELEAALQRAK QDMARQLREYQELMNVKLAL DIEIATYRKLLGEESRLESQM NMSIHTKTGGYAGGLSSAYG GLTSPGLSYSLGSSFGSGAGSS SFSRTSSRAVVVKIETRDGK LVSESSDVLPK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
8125	38493	A	8180	1	3519	MIHKELPALAACGLVADFDPVG EEETADFGPLVLDSDSDSDVDR DIEEAIQEYLKVGSSKDQGSASP VMSRADSEFQSIKRAEIEQFLNE KRQHETQKCDGSEVKKPDTHE NSAKSLSKSHQEPATKVVHRQ GLMGVQKEFAFCRPPRLAKTN VQPRSLRSKVTITTTQEKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSVQQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPQQRVQLQEER
8126	38494	A	8181	208	445	AACVWREHHRHAECCGCPGVH LPPLLHP*KSXWPGRC/RLRGN AAHPPWGGQATPALCCGLQ QPESSQ*GLSSLGSSR
8127	38495	A	8182	1	1607	MDMFRSGIRRDGGLGDGIVRA RRRRQGALAGSSQPIQAAVPR GPAGPAPRDRSPWPCQSSGEA *PYWKLEGAGLE/RKRGTEIRA VGEQLESWRSWRKDVAGCSSP TPIPEFGAAAPTKS/GPAGPSSTQ QPSRSIWAAPKRLAG*DTAHH NHP/SAAP*PAPODRARPK*PPR ADPQRSVTPPRSPKGS*GSPFFP KQ/PRIPKSGAASEASNPLLAITS QVVGGSESETRVEGLMKESV REGNAAFSRFLRKSIV/ACKPPAS EKDRGSRAAEGDEHASSNLQEP IPHLP*TALGERPEARQQIRFRP PGEPCSHPRSVNELGTGEPHTF QLGCLQRHPGAVDQAGPRGPG AGSRARETGKTGTNSEAAVRQ EPKQRILSKIHTSSTPGHRL/EPT AFRTRSARSPELASHGHQAGKVV AGPRVVRARGA/PPTGRPGLAAR PTEAERASRAPCP/PQTDARLFI TARPRGKSGCRLPAHSPDPSPSR LPGPRSRSLSPA VRVVAAGEK EASGAETAFPAWGTMAFWSL QPRALQAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,406,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8128	38496	A	8183	3	683	ERGITAGPPGVHPPTARSAGAA LPVWDSACVEGVPPAPAMDP *EHQLRISGLGCQDTLMLIESGP QVSLVLSKGCTEAKDQEPVTE HRMGPGLSLISYTFVCRQEDFC NNLVNSLPLWAPQPPADPGSLR CPVCLSMEGCLEGTTEICPKG TTHCYDGLRLRGGGIFSNLRV QGCMPPQVCNLLNGTQEIGPV GMTENCNRKDFLTCHRGTTIM THGNLAACI
8129	38497	B	8184	230	252	
8130	38498	A	8185	29	316	GRVSRCLPFKLVTPVLCFLWH RSY*EYRNF*MNQISKTLQKQR PTRFTG**QPWPRWW/PAPPRPS QGRLAGREWSTQAHPRDSQGP RLCGEGRGA
8131	38499	A	8186	1	57	SRPVQAGPKATGTPQPPPS*PEP VERPLSMASGTHAQGSPSPSW PQLTGAVAQDPSPLPPRDT APAPSMPTADGVQRCARQSGN TGPRVAT*PVAPTSFPAGPDSGE MG/ESCRRRPGT*PTPFQSLFR RRPSASRIYGLLGPCVISL/HKK QKSLPPLAPPGTITVDILFTWAS SLFSLNATEGHTVVRHV*CSRRN YQKANAPRTPTASPNTRSHSLG NAKTPPQTVPHRDHPTQEHTG DTSSCVAVLSANTRERAAVEC GVTVLNLD*LK*TARSSMSA STGVAGSVQGKR/LRTSALSSG G*GPKATGTPQPPPS
8132	38500	A	8187	1	3564	
8133	38501	A	8188	154	256	
8134	38502	B	8189	1	1206	
8135	38503	B	8190	1	1311	

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8136	38504	A	8191	2	2491	EAGWEEGPSQNGLVLQGEKL PPDFMPKLVKNLLGEMPLWVC QSCRKSMEEDEQTGREHAVA SLSHTSCKSQSCGDDSHSSSSSS SSSSSSSSSSCPGNFGDWDPSF LAEHKRLGLWNSPHSIGAMP SLGSPPTIPGEAFVSEHHQHSD LTAPNPSPTGHHPPQA/LSNP/AL TPAPLAP/APHPHLLPTTAAFP AQASECPVAAA TAPHTPGPCQS SHLPSTSMPLLKMPPPSGCSHP CSGHCGGHCSGFLPPSSQPLP STHRDPGCKGHKFAHSGLACQ LPQPCANEGLGEEEDSSSERSS CTSSSTHQRDGFCDCCYCEFF GHNAPPAAPTSRNYTEIREKL SRLTRRKEELPMKGGTLGGIPG EPAVDHRDDELLEFINSTEPK VPNSARAAKRARHKLKKKEKE KAQLAAEALKQANRVSGSREP RPARERLLEWPDRELDVNSFL SSRLQEIKNTVKDSIRASFVCE LSMDSNGFSKEGAAEPEPQSLA PSKLSGSSEQPDINLDLSPLTL GSPQNHITLQAPGEPAPPWAEM RGPHPPWTEVRGSPVFVPENG LVRR/HEHRAQPIPGDLGQDQT AGHPSSEEASSKEVPSCQELP EPVSSGGKPKQKGRQGSQAKK SEASPAPRP/TSQPRGSCQCGPG RWP/TSSQAGS*SLPK*AAVLKL ERGAGGAGQDQVGLAVPKLRR
8137	38505	A	8192	277	434	
8138	38506	A	8193	4	168	
8139	38507	A	8194	26	219	PRLQCIGQPRLTLPPGFK*FLCP SLPSSWDHRTPT*LANF*KNY F**IWGFMTLMGMSGTCNP
8140	38508	A	8195	1	498	
8141	38509	C	8196	105	251	

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8142	38510	A	8197	1	1620	MWGVGKIDTPKDVDTLIPGTC GCVTILHGERHFVDVIAKPTRS VQGNPKLGSKKMEVSIMKTQE SIKLTVKATTQRRNRNESNGPT TEFHQSTMTNTHSDTWMVVLD PMKPGPFVEVMAQQTLEKINF LRVHDLVFGDVVWLCSGQSNM QMTVLQTLSCGVVTVIFIMTLA GAHGTLSSGIFSIYQSDSLKCK SGRKAPVGPVRVLRGTYSQS NSTGNPDLFVQDHTWQFCCKH SGSYVASMETVDETAFLSTHT SFRTDWELKCFITVRRQLGRQY ERTCYLSFRPVANTVEYICGFRF ASYINNDMLVQKEPAGAVIWG FGTPGATVTVTLRQGETIMKK VTSVKGLISLLVCLSQFEIVPED DPQNAIVSSADACHAELLRTIS TTMGKLMPLNLLPAGADFFGFS HPAIHNLIQSCPGARKCINLPAS RPVGLSIGPLSPLDSYQWVKFD VCKPGDGLPEGLPENDAAMS FEAFQRQIFDEQNDPLL*SSL* PWLVIHIVPL/WSSGIFS/TISK*L FEV*VGSESSGSPCAEDRLHM VSRKFHRKSRPVCSSGSLAVLH *ALRILCCFHGNSG*NCFHSLHP H*/HSALTGNSSASSQ*DASLGG SMREHATCLLDPLLT*STVLV FALLHTSIMIWCCRRSLLGQ*Y GASVHLEPQ*P*PCAKVRKPS*R K*PV/CKGLISLLVCLSQFEIVPE
8143	38511	A	8198	1	900	
8144	38512	A	8199	915	986	IIIDTRPGFHDESAIYPVGYCSTRJ YASMKCPDQKCLYTQCIKIDGG VQPQFEIVPEDDP/RNAIVSFFW QMLVMQNISQDYKALLWGKL MPNLLPAGADFFGFSPHAIHNLJ QSCPGARKCINQYQWVKFDVQC TLEMGQLPEGLPENDAA/RALK PFQRQIL**RIDKRNLLKIKQL KVFPGKTITTRTFHDEIPLVSSLP SELLPSFIYPKILV
8145	38513	A	8200	3	414	
8146	38514	A	8201	1	2445	
8147	38515	A	8202	1	248	ENGNLGPQAEVKGATGECNIS ERKSPGVKISLRELDGSLVH KIAEGFSESKRSEDENENKIE FRK/KGGF*GGGFLRRK
8148	38516	C	8203	70	324	
8149	38517	A	8204	1	675	

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8150	38518	A	8205	692	808	
8151	38519	A	8206	1	1954	PGTGEETVRLGFPVDPKRVLIIV AGHHNWIAAYAHFAVWYRI KESS*WQVFTSPYLDWTIERV ALNAKVVGGPHGDKDKMVA ASESSIIILWSVQDGGSGSEIGVF SLGVVPDALFFIGNQLVATSH GKVGWVNAVTHQWQVQDVV PITSYDTAGSFLLLGCNNGSIYY IDMQKFPLRMKDNDLLVTELY HDPNSDAITALSVYLPKTSVS GNWIEIAYGTSSGPVR/VIVQHP ETVGGSPQLFQFTTVHRSPVTKI MLSEKHLVSVCADNNHVRTWT VTRFRGMISTQPG/STPLASF LSLEETESHGSGSYSGNDIGPFGE RDDQQVFIQKVVPITNKL FVRL SSTGKRICEIQAVDCTIISSTVTR ECEGSSRMGSRPRYLFTGHTN GSIQMWGSGPLLDWMVNKSE DKDVS GPTVEELLKLLDQCDL STSRCATPNISPATSVVQHS ESNSSLQLQHHDTHESATYGS MRPYRESPLARARRTSFHSY RDFQTINLNRNVERAPENG GPIQAEVKGATGECNISKSP GVEIKSLRELDGSLVHKIAEGF SESKKRSEDENENKIEFRKKG GFEGGGFLGRKKVPYLASSPST SDGGTDSPGTASPSPTKTTPSP RHKKSDSSGQEYSL
8152	38520	A	8207	2	383	
8153	38521	A	8208	13	332	SKGFIVLLKCLQILKTPSLGPGN QGLNAGKESRGGGLSVKA*RA RPDSWRPGPPLSISITLRLKEG RRHHRALPLCCITLLASSPNCI AP/TSVP*IPRLHPFWL
8154	38522	A	8209	1	1839	
8155	38523	A	8210	1	364	
8156	38524	A	8211	3	3723	MIPAGGRAPGPPYSPVPAESEL VNGNHTPQTATRGPSACASHSS LVSSIEKDLQEIMDSLVLLEPGA AGKKPAATSPSPMANGGRYL LSPTTSPGAMSVGSSYENTSPAF SPLSSPASSGSCASHSPSGQEPG PSVVPPLVPARSSSYHLALQPPQS RPSGARSESPLSRKGHGERPPS PGLRGLLTDSPTT/VLAEAR ATVETPRLGGLPVVAISLSEYP ASGALSQPTSIPGSPKFPVPVA PRNKI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
8157	38525	C	8212	398	415	
8158	38526	A	8213	3	45	
8159	38527	A	8214	1	929	IAAAPELLERSGSPGGGGGAEE EAGGGPGGSPDGDARPGPSREL AVVARPRAAFTPGPSAAAMAR PLVPSSQKALLELKGLQEEPV EGFRVTLVDEGDLYNWEVAIF GPPNTYYEGGYFKARLKFPIDY PYSPPAFRLTKMWHPNYETG YVCISILHPPV/DTDPQSGELPSE RWNPITQNVRDHSS*V*SSLLE RRPNTFLRPANVGRLPWMLQG SWEREQGGRIELHRTSFRKQV LGTKVDAERDGVKVPPTLPEY CVKDQGRRAPDEGSDFYDDY YE\DA\VE\EEADSCFGDEDDDS
8160	38528	A	8215	80	430	IAQGFYPPGWPCSGPGGNTSSP RPPPTGGKGK/PGGPQK/PLAPRI PAVFTRGDSG*RSCPATTPLSA GSPSLPHRIPEKPPHRIPEKHLH RACAHAPDPGSGGLRIFLTAHV HGKL
8161	38529	A	8216	3	645	FSVSHLLDLEEAGDMVAAQAD ENVGEAGRSLLESPLTSGTAT PQQDNDQLNSEEKKRKRQRN RTTFNSSQLQA\LERVFERTH*T PSSLFFLSFLMPSCLLTILQVWF QNRRAKFRRNERAMLANKNAS LLKSYSGDVTAVEQPTDLQLCE TNACYSPCSLPCPYSAMATYSA TCA\NNSPAQGINMANSIANLR LKAKEYSLQRNQVPTVN
8162	38530	A	8217	3	907	RVDDFVAVQLGRPIGSCFGGRA QLQEGVQKQAMAVGNINELP ENILLELFTHVPAQQLLNCR VCSLWRDLIDLVTWLKRCCLR EGFITEDWDQPVANWKIFYFLR SLHRNLLHNPCAEEGFWSLD VNGGDWVKVEDLSRDQRKEFP NDQVKKYFVTSYYTCLKSQV DLKAEGYWEELMDTTRPDIEV KDWFAARPCGSKYQLCGHLS DAAQGPHGTFQPDATIQKQSD AKWREVSHTFSNYPGVRYIWF QHGGVDTHYWAGWYGPRVTN SSITIGPLP*HPLSPHLLNPDW
8163	38531	B	8218	117	398	

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8164	38532	A	8219	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGFPPVQNCLS LARSDSREQGLVLMESRNRRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSFTSQFSPISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSSTK GLSPSGNMEKNKVVKREAEAN SINLSVVEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
8165	38533	A	8220	1	1188	MPLDEDPSKLCRHNLCLECN IFQDKTSLATHFQQAADMSSGQ KTCTICQMLLPNQ/CQRHIIQHKS P*TCPECRAICR/SHCEVFYKCP CPMTFKSAPSTHSHTYTQHPSIK IGESKIIYKCSMCNTVFTLQTLL YRHFDQHIEQKRDVYISHVRK EHGKQMKKQPCCQRDKPFSSS HSLCWHNRKHKVIRKVVYTCSH CSDSRGTFTKQLMLEKHVQLT HGKIDPDLKE/TDRRHQ*GGR NKRPPQGPQSQVEVERTGSGV QASQGAITQPKLEINVFKVHKC AVCGFTTENLLQFHEHIPQHKS DGSFYQCREHLFVAHKLKEPOP VSKQNGAGEDNQENKPSHED ESPNGAMSDRKCKVCAKTFET EAALKTHMQTHGMFAFKSRM SSDEK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8166	38534	A	8221	842	2687	KGECLPSALSLNGNGRESLES! ESLSLEGFTTRGAGLRTCSPPCL SLPAPPWAPVLPPEPRGAPPPAP RRPVPSSTTQGLRSAGARRGTGR QLHLRPRC/ADPLGEASWAPES GSAPAILKVRIKTIKMSSGEIKR TVTRVLPEVDLDSGKKSSSEQTA SVMASVTLLSSPASAAILS/SSP QGASPVHGHQCSFTC/SSSPLN RAPA/GAIIKAANAQQQTVVVP APSRANAKLVPKTVHLANINLL P/HGSATN/ISRQ*SMQQ/RSQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPTNAG ITLPTRGYKCEGDSFAVEKS LTQHYDRQSMRIEADTRGQK TCTICQMLLPNQCSYASHQRIH QHKSLEYTCPEGGAICRSVHFQT HVTKNCLHYMRRVGFRCVHCN VVYSDVAALQSHIQGSHCEVFY KCPICPMASNQNKEDTKSMNG KEKLEKKSPPVKKSVECHKVA SPGWTCWECDRLFQIRDVYISH VRKEQKGQMKKHPCRHLCQH NRIKHKGIRKVVYACSHCPDSRR TFTKRLMLEKHVQLMHSKDP DLKE/TDRCHQ*GGNRNKRHH QVPQSQAPLHCTQVKGTASV QAKWSWGR
8167	38535	C	8222	1	438	
8168	38536	B	8223	98	463	
8169	38537	A	8224	1	2679	
8170	38538	A	8225	1	1209	AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKSLEYTCPEGAI CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGSHECVFYKCPICPMASNQNK EDTKSMNGKEKLEKKSPPVK KSVETKKVASPGWTCWECDRL FIQRDVYISHVRKEQKGQMKK QPCCQKRDKPFSSSHSLCWHNRI KHKVIKVVYTCSHCDSRGFTT KQLMLEKHVQLTHGIKDPDLK E/TDRRHQ*GGNRNKRPPQGPQ SQVEVERTGSGVQASQ/GAITQ PKLEINVFKVHKCAVCGFTTEN LLQFHEHIPQHSKSDGSFYQCRE HLFVAHKLKEPQPVSKQNGAG EDNQENKPSHEDESPNGAMS DRCKVCAKTFETEAAALKTHM QTHGMAFIKSRMSSDEK

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8171	38539	A	8226	58	391	FAKNDGFLHPCPEPL/PWSQRTQSAAWA*GCNYLQPTGAADLLAYFEFLGPEGKGTG*QGGLDRDATGAPPSPPTARQ/RVGKALGTAAALIPSFIP*SKKMARETAAWSEW
8172	38540	A	8227	993	2235	NGGPHLWRLPTAHRACGERHGGAVACGGAAVEALVGPAPT VGLRRGCPHSAPGGYACPVSSSTYSGLGQRQCVFPHYSPRAVPN LVPALGAPK*MGPSAGL*GD MLPAASVKRAPTAAGPWMLYP YSPARLDSAA/LQALSTKKVAS DSSKEQVANSRESSLSKEVND SPRAADKSPESQNLIDGTTKTS LKQLDSPRNISSENSIKGTPASP AGSTPPIPKVRITTKTSSGEIKR TVTRVLPEVDLDSGKKPSEQTV SVMASVTSLSSPASAATLSSPA RVPLQSAVVT/KQFPLQSPPLNR SQSSLWLLSSQCLL*RQQDPK SLI*SSLTTPR*KPRSYLLPLSRV PAAPSLKLANAIQQQTVMMMPA SSLANAKLVPK\MLHANLNLPL QVAPATSELCPVSIKTPQI
8173	38541	A	8228	1	3370	MIINTIITTTTTIITIMSSSPIT ITNIITIIQHIIHHHNDQRPSLGK CRGLYIRVKVPGERATANSRC PINAQIESCWNGVMALWLGPNSTCSRLPELTDSEDCQIYGDTERKRRHSRKTCTWEYQVETKDT FLEELLFEPALRTGIQSKQGGPL LQLAANNYNLEPKQHFGSWFG TMKQLGETESIFSAYEVCLTV YEIFGLPGIAPSKTKSFNLSCLT AIAALSTKKVASDSSKEQVANSRESS
8174	38542	B	8229	1	438	
8175	38543	A	8230	38	597	VPCGPHCRLPSAWRTSPRLWN DTTSRKWKSGVAKSSCYNL*PS AGMRKRKF*LRAPSTLSGSALL *NRLMRSRFCATSSCAS**CEQ RTLSFEGSLWRSTITSRPPPSA ARISSASAPTRRRCASESAACRR STGRAGPGPGGGKQQMKAGR\ RGTAQPSSPHPLGIPTHPDTRG ASRQTGHL
8176	38544	C	8231	1	1062	

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8177	38545	A	8232	3	595	WSSAQPRASRAASRSSRLHSS RRLLCLRCRAPRRPQLVASAKGR ASSARSRRGRSRRR*RGRARS GGGMSPLAQRRLK*ASSSSGRG AAWSRASRGAARGSGPLTGRR SAPLHSSSTVPCSPRYARPGPPR ATA/RGPTRATCLPSHRSTITSRP PPS/LPVA VQPALPPGAAAPSP PRAGGALAALGPGLTVGAGR
8178	38546	A	8233	2961	3005	SRLQQTQADAFACAKGCWP GGM/DELEAETSSSLFLLAMQV WMCGRMEDIPCSRVGHIYRK YVPYKVPAGVSLAR/SKNLKR AEVWMDEYAEYIYQRRPEYRH LSAGDVAVQKKLRSSLNCKSF KWFMTKIAWDLPKFYPPVEPP AAAWGEIRNVGTGLCADTKHG ALGSPLRLEGCVRGEEAWN NMQVFTTWRDIRPGDPQHT KKFCFDAISHTSPVTLYDCHSM KGNQLWKYRKDKTYHPVSGS CMDCESDHRIFMNTCNPSSLT QQWLFHTNSTVLEKFNRN*A ALLFDESQFDSSNCQHSCYPR
8179	38547	A	8234	203	314	VPASSPALGSTLEFQLCEPINSG FCLNQID*GFGYL*ARFMSWPY WSLLSPFFLIPLH
8180	38548	B	8235	1	1008	

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8181	38549	A	8236	2	1495	CLVVTSTDSIRFQIIPWAGTEMK QE/IKLKDGSMEEHLKKPLEDY MALFPFSVRIIRTKKREGLIRTR MLGASVATGDDVITFLDSHCEN VNWLPPLLDRINRNRKTIVCPM IDVIDHDDFRYETQAGDAMRG AFDWEMYKRIPIPELQKADP SDPFECQLVRDITLGDADSQQH DVSHLARCQADFLFPWSPVMA GGLFAVDRKWF/WELGGWAFS HGDPPQPPWKESLFFPSSCTSPQ VESHWAPGMPPIPEQYCNWSP AVTCPVTAGRVCLGWGW* *WGTDLLGARWKSPP* NQDVKNPHDLIEQFQRKEHFC TESAWLGCPOGNSWLLQSORS HRERWNHGIFMTVISAVSCGLH GVVCGGRMEDIPCSRNLKRVA/ EVWMDEYAEIYQRRPET/GHL SAGDVAVQKKLRSSLNCKSFK WFMTKIAWDLKFPYPPVEPPA AAWGEQKDMPLSQYTSKGAGI KSYLGSCTHHWGHRGRQKQG NILIAHQ
8182	38550	A	8237	1126	1603	TIMKITGRAGDAIMGADICH/N KDRKVRRKEPKSQDIYLRLLVK LYRFLARRTNSTFNQVVLKRLF MSRTNRPLSLSQMIQ/MKLP GRENKTA VVVGTTDDVRVQE VPKLKVCALRVTSRARSLILRA GGKILTFDQLALDSPKG* LSPRKGR
8183	38551	A	8238	504	737	QLCWAGGKILTFDQLAVDSRK GCITVLLSGPLKGRKVYGHFGK APGTPHSHTKPYVHSGRKF RARG* RAS* GYKN
8184	38552	A	8239	1	360	MLGFALLPAPPGGLV/GSG* DDQIGRTGPALAPSCLSRPSPAT LNSAGSEIHDRPSGAPPTCLR GSAQASTSACSPGANGPEPKPG LGTLRQQLHIMATNRLDEAG WVACYPTDVR

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8185	38553	A	8240	3	666	MSFRQLFQDLKRYVQDADVR WEYCVRAKRQGTDTSLGRLFQ QGPVGPRHRAHSATSPDHRFP VADLTGGQVL*GCGPPAAPWG AG*YPGAPLHAGLGTLPAAAG AHGHQHPAG*GGAGSPATRLM SVEGCSQRPWTEAPDRPLEHEA VCSVRPRPRCF.LGGVGRAGAFL EEEWQHQSVCVPCQPPWGLGT CSSMSGKLSRPPASSLLSRGKA WGQEEES
8186	38554	A	8241	2	443	RTSLEFFFFF*DGSTFLVAQA\ GVQWRHLG*LQP/RPPGFK*FS YLSLLSSWDYRHALSHLANFV VYVLCFVETKSRSRVTKAGVQ WCDLGLSLQAPPPGTFPFCFSL SSWDYRHLPPHLVNF.CIVSRDG VSLCWSGWSRTPDYK
8187	38555	A	8242	1	354	VSLQPVSQEGVSQRTLGQSSRS SGSG/CPGELNSPIFGVPHRW AA*EESRAAGVPWPSSQISGMC SKFRI*NW*DVSWAGWSEDLRS *VDLSHGAKSRRTGD*SPKGGP PIRV TAP
8188	38556	A	8243	2	241	WSTGLLRSSGS/NQSSAGKPRR SQSESPG/PSRSSSGCQESGT CH*G*RRRG*GVLAPAPGKRDL PPRVKDQVRHPCVV
8189	38557	A	8244	5	282	AKKESVREPWARVPALGVAA R*VEQSDFCGPAQMGLGLGG IPGCG/PFLGLVVRFLALVASSC PFPRKAGLAAGGEGPRQASLRG LTPLKRG
8190	38558	A	8245	1	302	LSREGVGQKALGQSSRGSGSVC /LGELNSPISSGVQRWDTA*EE SWAAGIPWPGGQIDFWHL*QA PCPRKSREGVETRREGVGVLAP SPEKRDLP.LRVKD
8191	38559	A	8246	1	200	LSPKGVSQRALGQSSRGSGSG/C PGELNSPISSGVPHRWDTA*EES WAAGIPWPGGQISGTCCKLHS
8192	38560	A	8247	23	187	
8193	38561	C	8248	1	1764	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, Y=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
8194	38562	A	8249	115	872	LRRGRTYPPP*ELPKARHP*WS TGLLRSSGSISLQPVSQEGVSRQ AFGQSSRGSGSG/SPGELNSLISS GVPHRWDMA*EESWAAGIPWH GGQISGTCS/RAPGGGGSGGMP GCCGSGVWKFLCASRKAGKGS GHRDTRSGCGHKGLGRRDMRL GCGNKSGSHRDIRGWGTCPPF RKAGLAAKGEGPQASLRGLT PDLKLVRCPWAGWSEDLRS*V DLSHGAKNRRITGD*SPKGGPPI LGRPLRACSAAVHF
8195	38563	A	8250	85	529	SGSISLQPLSREGVSQRALGQSS RSGSGG/CPGELNSPISQSGVPHR WDTA*EESWAAGIPWPGGQISQ TCS/RAPVGGSGSGGTGRCGSG VWKFLCAGDVAGVCLTVEAR NCNFFLLLYTLKARLIKSCPCPR KAGLAAKGEGPQASLQ
8196	38564	A	8251	1	552	MEARETPGWKEGNVERVASVL IKKGITGLPSTVRVTGSSASVMV YGASEAIGQHQSAAKPRRSQS ESLGPEFQGLWEWLPGPRAVK RLRVIFDEKEPKRYLIWDKEKG ALTLTMPLAPATFLRVNCWAG GGGLVTERNCKP*WSTGLPRRS GSISLQPLSREGVSQRALGQSSR GSGSGCQGLGL*SVLIKKGTGL PSTVRVTGSSASVMVYGASEAI GQHQSAAKPRRSQSESLGPEF QGLWEWLPGPRAVKRLRVIFD EKEPKRYLIWDKEKGALTLTM PLAPATFLRVNCWAGGGGLTV ERNCKPDQKMKGIEIKRRERLK CGSKIERKKLRDSEGGWRRVE
8197	38565	A	8252	535	710	KCFPACHYHHNNHHHHHHYHHH HQHHHHHHHHHHHHHRTIITITIF TIITITIIIIIIITITITIVIFMRVR VKRPPNRLCVSNMAVYFTWQV KKKSSSLAFSSVVTSDLKSKRRR LSGKSLETSSASLMVYGASEAT GQRQSSAAKPRRSQSESLGPEF QGLREW*YDGGDDDDNDGVD DGGDDSGGGGGCGSGGKQESI SIFD

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8198	38566	A	8253	54	563	AEKESVREPRARVPGARGVAA RPSA/RPR*GRLLCSPTYPKH* NCAWHQQAGCWLGTGPAAPA SPPACAAFSWGYGGLPAPIQTA FQAGW/GAPGQGRSKTTRPGV QSVSNPGEPAPEPRAAASSGLSS GAFPAATDPGICSWAEGVLM GKGHHIRPSISARIPCFHV
8199	38567	B	8254	232	987	
8200	38568	C	8255	1	1812	
8201	38569	A	8256	1	1035	
8202	38570	A	8257	2	664	SLIKLIPPPRPFGRNRHLVIRQN ERTQRGKRRGTRYMFSPRF*/R KHGVVPLATYLCEIYKQRCDP VDIQGEWGTCSKKGMP/HHKC Y/HGKTGRSLTIVTPACLPLFN TTQFRRKILAK/RINVRIEHI*AL LRARD*LP*NRVKENDQEKERS PKRKGTVGST*SRQ/APPR/EA HFLPEPNEGEGALSCWEPFYWI SLGLLGVKKKNKD/LWATKK
8203	38571	A	8258	1	747	MSESLKPLPEVDAGAILLVQP AELYSKASRLDDCYQKDSYTH RCQEKRTCHTTGGHSGKHQSL SGASVSPTCsAKTRDKINCDFDS PKSEVITLSNDDSIIVLSDCQEG KPKPCSGPFATFKMQYDRTCE WTALKISNGGKLILISTNVSFIR LIGAFKG VVIHTFGSYANSEAV TLEASFTADSQFVIMIGSEDGKI HVVNEESG/KK*LGWMVNTQA QLPVCNSTPSSMTFASACSNMA FWLPTIDD
8204	38572	B	8259	50	260	
8205	38573	A	8260	1	541	EVWGPGLASEGAVGITHGPFPK AKRNPgKVRSKRDPPIQFQNL RRS*WRSIPRKPGRQTGSRRSL WT/ALHPGAGTAKHPPPA/CA GRET*CKSKSPAGRKWSFHRSS SRRASE*DAQFAVPAGVTSRE PFGSRRGTGPTGTGTPTRTAR SRTWSSSWVRLSGRTGAVGYS RSPSCSS
8206	38574	C	8261	177	236	
8207	38575	A	8262	1	417	

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8208	38576	A	8263	2	475	GIHTRLNSELLKEEESNKRLEAE IEYQSRSLTAAISKHSESVKTER NVKLALAE*TDVSVQVKMSSDI SEVEDKNEFLTQLSKKQIKFN TLKDKFRKKRDTLRKKSLALET L/QNDLSQTQQQIKEMKEMYEN AEAKVNNSTGKWSCVEERICQ LQHEN
8209	38577	A	8264	3	518	IFRAPFRICLGILLSPNTEQAQY KKQLEQ/FKQGYNTASLNKKEL TLKDVECKFYKMKATAYEEVTT ELEEYKEAFAAALKANSSMLK KLTKSNKKIAMIS/TQLFMEKEQ VKYFLSTLRARRGRESPCDENL TSIGL/NRKYIPQMPVRIPTS/SPQ TSNNCQNYLTVSHMTVSL
8210	38578	A	8265	1053	3733	NGRSCCERSSTKKECTDIESSEF VNRKSLTSGLEEEQQRRESEK KQPQDFHNEEVKDLMDENCI LKTDAIPQIECTMKNDNLEKE NKYLKDIKIAKGTNAALENCIK LNEEMITKTAFRYQOEIENDLKA ENTRLNSELKKEKSKKLEAE IESYQSRSLAAAIKHSENVKTER NLKLALERTQDVFEQPAGLEEA ELVLSRLSCGEATEGAARRALA AEEAGRWRRGVG/DSWLAPES RLHVLKTCGSCW/WENLELGRH H*LCLWA VKNFQKRFLPGQKK SPFQLMSQREFQHTL*ITQKQN RVMNNFIKKYLRLMSSV*CMP LT/KHSIDKEVRSTASRLPCLGS EERICPAALSGKYKKLLEMTIN VLSVFGNEFDCHGDLKTDQL KMNILIKKLKHKFDDLTAEKEA VSSKCVDLAKDNQVLQQELLS MKKVQQQCEKLEKDKKMLEE EILNLKTHMEDNMVELSKLQE YKSELDERAMTAVEKLEEIHLQ LNKGNTASLNKKELTLKDVEC KFSSKMKTTYEEVTTKLEEYKE AFAVALKANNMSKKILTKSN KKIAMISTKLLMEKEWVKYFLS TLPTRRGQESPCVENLTSIVLNS KYIPKMTGRIPTSNP*TLNNWQ NYLTEEDMVSGDLISGTWSME EWSLGASSLGTWSAAVGGYLA RWPLCDLSVTVAESPSPLCCGA
8211	38579	A	8266	2	209	

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8212	38580	A	8267	1	1431	MTQKAAASVEHLAIRCHWSQR PAVTGVDVLQVYSGSGGTAIIFCE TQRSVTEIAMNPHIKQNAQCLH GDIAQSQRREFTLKDFREGSFKV LVATNVAACGLDPEVDLVIHG SPPQDVE/SYIHRSGRTG/FVTM TLESLEEIQDVSCAWKELNRKL SSNAVSIQTRMCLLKGNVRVCF DVPTTKSERLQAEWHDSDWIFS VPAKLPEIEEYYDRNTSSNSRQ RSGWSSGSGRSGRSGSRNYF AVDTASAIAIALMTFGTMYPMS VYSGKVLLQTTPPHVIGQLDKL IREVSTLDGVLEVRNEHFWTLG FGSLAGSVHVRIRRDANEQMV LAHVTNRLYTLVSTLTVQIFKD DWIRPALLSGPVAANVLNFS DH HVIPMLLLKGTDDLNPVTSTPA KPSPPPEFSFNTPGKNVNPVIL LNTQTRPYGFLNHGHTPYSS MLNQGLGVPGIGATQGLRTGF TNIPSRYGTNNRIGQRP
8213	38581	B	8268	128	1497	
8214	38582	A	8269	1	618	
8215	38583	A	8270	1	334	LFHSIFGYLPFARQTLLPGSILVF TYTQPPKIQFANGTKGLPDPLM TPK*QK\APLMPLLVSLGLSAST IALGTRIAGISTSVTTFCSLSNDF SASFSPYLHRCFLPWSSL
8216	38584	A	8271	1	2919	
8217	38585	A	8272	1	4192	MRIPVDASTSRRFTPPSTALSPG KMSEALPLGAPDAGAAAGKL RSGDRSMVEVLADHPGELVRT DSPNFLCSVLPTHWRCNKTLP AFKVVALGDVDPDGLTVTVMAG NDENYSAELRNATAAMKNQV ARFNDLRFVGRSGRGKSFTLT TVFTNPPQVATYHRAIKITVDG PREPRNNECVYGNYPEIPLEEM PDADGVASTPSLNIEPCSPATS SEAFTPKEGSPYKAPIYIPDDIPI PAEFELRESNMPGA
8218	38586	B	8273	385	3930	
8219	38587	A	8274	830	906	

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8220	38588	A	8275	483	971	ATMPGHHFYLCETGSNSVSQAG VQ*HDFGSLQPPPGFKQFSCLS LLSSWDYRHMPPRANF/SVFL VEMGFYHVGGAGLGLLTSGBP PASASQSVGITGMSHHAGPTM KLLNPQSEVIFSPRNHSTLLTP LSRHLPHPISISTWCIHYAPLHT VSISAEAP
8221	38589	A	8276	1	2088	
8222	38590	A	8277	1	1822	MMTKDGLVFLGRQSGPILYVQ GLSRFRSFSVASGDSKRTRHRE KLPLLEAGERDHNCYGSPQILA FQAICKIAKPGKEQSCSKLVGH TFDPLLEIARKPEERQKLPDPCV KWGGVGNFPVKRVGDRIFFVS QGGKFSQAPEGPEVTSQSQGLE SKTLEVYPVFYCTVAELANHN VQPSHSTLPPQAEEPHSVATTT GPWGVLPGCCQCSLKAQGLFS QLVMNAACTGIHTSGQWAPLW PSTVPEMPSSKSGLESPTRTCF VLYPAVAKLLPRGTLAYSGKG CQNSSANHWDTQIHSPCHAA AAREYGGKSGISDSRLSPTLFSA SFSNMNKLKDFKVFYGCFCF EATAGANVLKIIRESKYKNTD DIDILSRQATPVIAQLAHEHSGH VAGMEVVFSGFNTDFHLPRTQ WLQPLSHASLLAAETNTESKND TTPQGDQPATWRNLSGYGAF PACNASAKTIHGLTEVLYTVLV DGNHNLLTKLSLEEENCLQLK CENLQKLEQMAAIE*KSLRRK RATQEECLMHSNLKFKESAE YTALARQ/LEAALEEGRQKVAE EIEKMSSRESALQIKILDLETEL RKKNEEQNLVFNKEQ
8223	38591	A	8278	1	5103	MDESSVHSSVGDHVDVRVST QVAERTRCNKMWRIETKSPSG DNEGTVIEKTRLGSGQGFCL QLSEGLQNLQAQRKIKIFREME DPSSRPLCSSLDIALCASVKPSA GFPQRPVKVPLCVLGSAGGTG DAERSLQSSDPLKKQQLARSL RGLCERIVLGGSGCGARGLRG AGGGTALSVPGASRGFEGMFG LDQFEPQVNSRNAGQGERNFN ETGLSMNTHFKAPAFHTGGPPG PVPDAMSALGEPPIILGM
8224	38592	A	8279	1	783	
8225	38593	A	8280	888	4915	

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8226	38594	A	8281	94	757	APTGCLACNLLLCGLGVTSPL *ASAPKCVTVHN*PLCKALPRR *SSAWELS*MRKLRLRGVNFRL TDGLCFICISTRATPPSARARCV STSLKPASLQLAVALYHHGSRSQ GCHLPAGREVCTSSQSRGVRETS PWGCEKGSPIAEGFPAVISLNP PSSSTAHDLPANKASASQPGSH LQCLSVHCTDDVGDAKARASV PTWRSLHSDISNRFGTVAALT
8227	38595	A	8282	2	374	
8228	38596	A	8283	260	500	
8229	38597	A	8284	98	828	RWASVFPHPFPYILPALLEKKT AERRGGAFSRNKQTAGPCGGT LQEEGSARTVGDSYGEASAGG FSCNKEEGNQRYREG*VTEML GVGYHRALLQLRGLDPS/PALS VT*SRTSGPRPSRLNKITYCIPP RQDCYNNLAACLLQMEPVNVE RVREYSQKVLERQPDNAKALY RG/SGVAFFHLQDYDQARHYLL GCRE*AALKMPNVRYPPLRTR VRTQQPTHRKEKQLLPWACL V NKEERCSS
8230	38598	A	8285	396	602	GNCGPEKERTCLRSPSWTPMPS PKQAVPVSSWPPGPHHQ/RCVP SRSSNFSKSSKSNSCDGNSSSS SS
8231	38599	A	8286	3	156	SVVSLSPHR*AIQILSGVAAGW GLSDGFPSSPPSPSGARDTGSPG SSLGL
8232	38600	A	8287	32	515	ARGSWGPGAGARPPGTARRAA RCATGCGSRSSSHAPVSPRRA APSSVHPGGCHGPALPPSPRR VTQAADARRAAPPLRAASAA P SRRWSQAPT/K/RRLGYPPPRP PAHPGPR/PPLRRMVSRSSEDP PRRLT*TGSETPKSTWRELSRR RSLQSKAATR
8233	38601	A	8288	30	460	RRCPAQRGEIWQSGH/RALLSC SGLHFPQTSWLPVYTVRVKLPT QALAMVDAPPPTKLECPRLISV CCYAGSENFKPVDLSLSSIGGS GGVGTGRNLLVCELRRPWDKR SIWAGVSRFLRLSPSRFLA*LG LSSYLTRTKT

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8234	38602	A	8289	2	1094	RMSRISDDSRATASQLDEFQEC L SKFTRYNSVRPLATLSYASDLY NGSSIVSISIEFDRDCDYFAIAGV TKKIKVVEYDVIQDAVDIHYP ENEMTCNSKISCISWSSYHK NLLASSDYEGTVILWDGFTGQR SKVYQEHEKRCWSVDFNLM DP KLLASGSDDAKVKLWSTNLDN SVASIEAKANVCCVKFSPSSRY HLAFGICSDHICVHYADLRNTK QPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQKLWNVVGKPIY CLRSFKGHFNEKNFVGLASSG DYIACGSENNLSLYYYKALSKT LLTFKFDTVKSVLKDREEDD TNEFVSACVWRALTQMGESIN VLIAA*QFRVPIKVLVLV
8235	38603	A	8290	1	667	MRIKATSEDTGTVIAQAEYGSVD IGEEVLKKGFAEKRLASRTDI CEEKKLDPGQLVLRNLKSPIPL WGHRSNQSTFSRPGHLSSEKM TLDLKDENDAGNLITFPKESLA VGDFNLGNSVLSLEKIKQDQKLI EENEKLTETKDALLESYKALEL KVEQIAQELQQEKAADVLTN HLEYTLKTYIDTRMKNLAAM EILKEMRHVDISVRFKGLSDAI QVLG/SKGALLQLL*MD*R*Y GQNTVWLRRILKLSEYVSEGN LIAQRNEMQKLYMSVEDFILE VDESSLNKRKLTLQDLSVSLEA VYQAKEGANSDEILKKFYDW KCDKREEFTSVRSETDASLHLL *HGSKEP*RIKVMQTRR*FQIHI VKYCKRFIQRKGSIPQYKLSTR TVLS/SKKQIEYLLKIPSDVHL LSIK/TDIEKLSSTQMEIG*KE* FGKSQMLMALKLRK*KKK*LK KGFAEKRLASRTDICEKKLD PGQLVLRNLKSPIPLWGHRSNQ STFSRPGHLSSEKMTDLKDEND DAGNLITFPKESLAVGDFNLGS NVSLEKIKQDQKLIENEKLT EKDALLESYKALELKVEQIAQE LQQEKAADVLTN HLEYTLKT YIDTRMKNLAAMEILKEMRH VDSVRFKGLSDAIQVLG
8236	38604	A	8291	1	325	
8237	38605	A	8292	1	593	
8238	38606	A	8293	1	2013	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8239	38607	A	8294	2	1427	LLARGAGRTNPAPPLMSCGPW GKFLKCCVEYKSGPYKVQ*EEI TIHSRAEAESTYQIKYEELQTLA GKHGDDLRCAT/T/EISEMNQNI SRLQAETEGKKGQASLEAAIA DAEQWGELAIKDANTKLESELE AAMQRAKQDMA/RQLGEYQK LALDIEIATYRKLLGEESRLES GMQNVSIHKKTTSGYAGAPARI VSLLQNELLSLEVGVKLGHPPTG KGEELGAPYSECSFGLCRRTVM LTQAPSSVVRNSNRNHTVNSG GSCLSASTVAIPAINSSAAMSA CSTISAQKRTCCTACEPARKYK DTASHQEPACVQACQLETADP KGGGVLLALPQPPSPGMLCWPY CRAHATDYFLANFFSEFPCHFL HRAGAAQTATGDMEHGQS RELKRRKAPREESETSEEKSPNK WGPVSKQKKQLLVILTTIIRPT RGNAYTGLSTRKWPRSEENA LMQPNKKDEKGLTLTKQLGL
8240	38608	A	8295	301	462	
8241	38609	A	8296	2	825	YPPSPPGRSAAHVSCTLYRTTP* WPDQRSAPPTAAWAAS*SPSAR RRPSAESMVPREPL*YRPSAATS AATPAISPARALGAGAPCPLFR RRSGPFGRSTAIRPPSSAGKAVL FPPHGRPVWPVGRRLARYATAS GWGAHI*ASSGASE/PAVVSVLP AGSGASPFHSASWDPPAHPAAA ASAAAIVIPAL*RSGDRPPVLSFQ PLFWFLIRGDNVSFVWLLRGLP CPSQAVTTRHRSLQKEKLKRNR KSCVNFMQSQVSVSKYNSLVK HHHFCIRPL
8242	38610	A	8297	3	251	
8243	38611	A	8298	208	307	
8244	38612	C	8299	18	197	
8245	38613	A	8300	1	1866	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8246	38614	A	8301	2	2558	FEVLWSDSSITSVTKSSSEVTEFI SKLCLQYPEENLEKLIPLAGPD AFYVERNHVLDLSGLRYLASLP SHVLKNDHVRRFLSTSSPPQQL QSPSPGNPSLSKVGTVMGVSGR PVCGVAGIPSSQSGAQHHGQHP AGSAAPLPHCSHAGSAGSALA YRTQMDTSPAILMPSLQTPQT QEONGILDWLRKRLRLHKYYPV FKQLSMEKFLSLTEEDLNKFES LTMGAKKKLKTQLEKEKESE RRCLNPSAPPLVTSSGVARVPPT SHVGPVQSGRGSAAELRVEV EQPHHQLPREGSSSEYSSSSSP MGVQAREESSDSAENDRRVEI HLESSDKEKPVMLLNHFTSSSA RPTAQVLPVQNEASSNPSSGHHP LPPQMLSAASHITPIRMLNSVH KPERGSADMKLLSSSVHLLSL EERNKGSGPRSSMKVDSFGSA MMDVLPASAPHQPVQVLSGLS ESSMSPTVSFGPRTKVVHAST LDRVLKTAQQPALVVESTAA TGTPSTVLHAARPIKLLSSSV PADSAISGQTS CPNNVQISVPPA IINPRTALYTANTKVAFSAMSS MPMGPLQGGFCANSNTASPSR HPSTSFANMATMPSCPAPSSSP ALSSVPESFYSSSGGGSTGNI PASNPNIHHHHHHHQPPAPPQP APPPPGCIVCTSCGCSGCSGSSG LTVSYANYFQHPFGSPSVTFPF
8247	38615	A	8302	2	266	YCGPL*SVWVARNPPGFAFVEF EDPRDAAGV*ELDGRTLCP/ PSWGHPR*DDYCRRGLPPRRRP PRRRNLSCSRSLYSPWTLSL
8248	38616	A	8303	37	535	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMRDSCPL\CKV YVGNLGNNGNKTELERAFGY GPLRSVWVARNPPGFAFVEFED PRDAADA VREL DGRTLIGC/RV REELSNGEKKK/SRNRGPPPS/W GRPPSENDNRKEESFPFR/RRSP R/RRSFS/RSRSRLF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8249	38617	A	8304	2	668	EIAERRITQPAP ¹ GPSRPSQGP GELGGPGTGRALCPADNGGLC CGCPLAVP/GPLAVPR/ALKPQR TSLSHPTSVTNGRGVSQGPGR RHPGLPTQASTKPPQSRDDAA LGGAGRGPGSMAAARTPRGG GH*GVDGPGRPRDASRLGRL RPRSADPVP*P/PVAIGRDLPS PDDNGQR*GAWKVSE/CPERR RVERLAAIGRLVFILPDFAVGRE
8250	38618	C	8305	101	183	
8251	38619	A	8307	329	399	RERET*SSINTTFIPGSVLQPDAS PSKTGTLT ¹ SIPVTIPENTSQSQVI GTEGGKNASTATSRSYSSIIIP GVIALIVITLSVFLVGLYRMC WKAHPGTPENGNDQPQSDKES VKI.FTGKTISHESGEHSA*GK
8252	38620	A	8308	192	537	KFPSTPENGNDQ* ¹ PQSDKESV KLLTVKTISHESVILNQNMDEI TEIEFRIWMAMKITENQKIETHS EESEEFNKTIQGMKYEIALRKN KTDLTELKNSPQEFHNTLEVL TAE
8253	38621	A	8309	1	789	
8254	38622	A	8310	1	423	EDIWFDDVDPADIEAAIGPEAA KIARKQLGQSEGSVLSLVKEQ AFAGEELEVVQKEVAEMLKG RILVGHALHNDLKVLFLDHPKK KIRDTQKYKPFKSQVKSGRPSL RLLEKILGLQVQQAIEHCSIQD AQAAAMRLYVM
8255	38623	A	8311	1	1077	MGKAKVPASKRAPSSPAKPG PVKTLTRKKNKKKRWFWSKA REVSKKPSGPGAVVRPPKAP DFSQNWKALQEMGSKKKPKII QQNKKETSPOVKGEMPAGKD QEASRGSVPSGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKA/GQPQPH PPR/DIWFDDVDPADIEAAIGPE AAKIARKHLTRALALDCMVG VGPKGEESMAARVSVNQYVK CVYDKYVKPTEPVTDYRTAVS GIRPENLKQGEELVVQKEVAE MLKGRLVGHALHNDLKVLFL DHPKKKIRDTQKYKPFKSQVKI QDAQAAMRLYVMVKKEWES MARDRRLLTAPDHCSDDA
8256	38624	A	8312	3	640	

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8257	38625	A	8313	1	1274	MGKAKVPASKRAPSSPVAKPG PVKTLTRKKNNKKRFRWKS REVSKKPASGPGAVVRPPKAP DFSQNWKALQEMGSKKKPKII QQNKKETSPQVKGEEMPAGKD QEASRGSVSPGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKA\GQPPH PPR/IDIWFDDVDPADIEAIGPE AAKIARKQLGQSEGSVSLSLVK E\QAFGLTRALALDCEMVGV GPKGEESMAARVSIVNQYKGC VYDKYVKPTEPVTDYRTAVSGI RPENLKQGEELVVQKEVAEM LKGRILVGHALHNDLKVLFLD HPKKKIRDQYKYPFKSQVKS RPSRLRLSEKILGLVQQAHC SIQDAQAAN*GCYVMVKEGVG RAWPETGAPCLTASRPLQ*RRL SSPALLAACPPRLQRC
8258	38626	A	8314	2	414	
8259	38627	A	8315	1	621	
8260	38628	A	8316	1	885	MGEKPGPILLFSSAKPKNPQEGE HKDEGDHPNNSFSPCSAHDHRR LQKHFAKIRDSTSGGKMKVN GAPREDARPVNKGTYLVSTGG QTVAFITGSDWDQDSESLGC QEDSTALHPTSTSPGSETVPPS LLPEATKRLLSLDFESFGQTQR NLSCPLCPAGVWQEKTLCEWR DAGGNRQAGVPQAPCMKSN ALIVILGTVTLDAVGIGLVMPV LPG/SPALLQRQAEEPSGRRTQG /RRVTPTTASAPVAPMTAGAC RSTSPKFETGAPVGAR*RSMGR PGRMPGL*IKAPTWCPOVGRLL PSLLAPGKTKTQSPA/SGCQEDS TALHPTSTSPGSETVPPSLLPE ATKRLLSLDFESFGQTQRNLSC PLCPAGVWQEKTLCEWRDAGG NRQAGVPQAPCMKSNALIVIL GTVTLDAVGIGLVMPVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPVLGALSDRFGRRPVLL ASLLGATIDYAIMATPVLWY
8261	38629	A	8317	1	396	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8262	38630	A	8318	186	2123	CPAHCWQEAMLSAWRLVMSP GGPCTQHPAPACHPSVLTTTPRK AGEPRP*WPPCPAWGLADSSK PHRWPKPPASCRPLVRRPWGP QRTLTPTLTSHWRASIR*SWNW TPSSCFPQGLGAPRLSWPRAPC Q*ERRRNLKPWT*STSR*PPDQ GATMAPSTAPAPLSRPSAPFA VVASSFPETSPERHEAAVRASS LGTRAGGTSALCPQRVSP/HRP PNSPSISIPCMGSKASSPHGLGSP LVASPRLEKRLGGLAPQRGSRI SVLSASPVSDVSVMFGRTPHSP PLAKEHIAVAAPHSPSTPWWTY PLC*STAAQN/RGSSPPQRTPGH QNSVQPGAASPSNPCPATRSNS QTLSDAPFTTCPEGPARDMQPT MKFVMDTSKYWFKPNITREQG CPGGAVSIISDRIVPAIELLRKE EPGAFVIRDSSSYRGSGFLALK VQEVPAQAQRPGEDSNDLIRH FLIESSAKGVHLKGADDEEYPFG SLSAFVCQHSIMALALPCKLTIP QRGCHTLYLSSVSVELTGTALA VQKAISTTFFERDILPTPTVVHFK VTEQGITLTDVQRKVFFRRHYP LTLTRFCGMDPEQRKWQKYCK PSWIFGFVAKSQTEPQENVCHL FAEYDMVQPASQVIGLVLTALL QDAERM
8263	38631	A	8319	15	909	LHVSHPGHADARGGLLQPCAA PPLWLCRIQCPRWFQTPSQVF YHAATEHGKGDVYPGQCLWE GCEPFQRQRFSFITHLQAANC/ EAQ/RSTPRAQKAIVNHPSAAL MALRRGSRNLVFRDFTDEKEG PITKHRLTAALILKNIGYSEC GRSWPRASRYQQGHQDLFILRS DLPSQVFIRDKLMERRNRRTGR TEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSVPVPIHIFR HSYAMHMLYAGIPLKVLSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8264	38632	A	8320	189	4419	KPGLFP*RVY*EYVFRLSQSLGE FHQF*FKRGQY/ATSSPPSPW ANIIRKATRC*CRWRFRFIMPV MASMSA/GMLNELQQYCDWE QGGAAVVAQHVAAPPGIVEIDS EKFACQWLNHAEVFNPDSCVS RAEMYSEYLTCSKLARGGILT STGFYKCLRTVPNHTVKRVED SSNGQAHIHVVGKRRAIPLPI QMYYYQQPVSTSVVRVDSVPD VSPAPSPAGIPHGSQTIGNHFQR TPVANQSSNLTA
8265	38633	A	8321	27	674	GPQNTMPMPSPSVRVQGPQNSS QPSPFSGSSQPGDPMRKPNQNF MCLWQSCCKWFQTPSQVFYHA ATEHGGKDVYPGQCLWEGCEP FQRQRFSFITHLQDKHCSKDAL LAGLKQDEPGQAGSQSKSTKQ PTVGGTSTPRAQKAIVNHPSA ALMALRRGSRNLVFRDFTDEK EGPIITKHTPTNSCP*Y*KISGKY SECGSADWLKETMENNLSA
8266	38634	A	8322	16	341	PPGRGSAHPAARQLQTPGSAAP LS*HQGPASRGTPGPGPIKARAP SKSRARGLRAAQRARLSARAR AGCA/PP*ARGAARKLGAPGTF QETLPPGTRDRKCCSGDAVVH
8267	38635	A	8323	1	400	MAEGMAMLRWTRLGTWPDDS FDEMDSTLAVQQYTQQNIR/AQ DCSNTDKNLEPPEGQDADCHG F*APRWHCASASYVASSEFAGDD RR1*IPLDPWVKKFCECWCSGPT PFRE/CPRELN*HLKDGCSCRYL RARN
8268	38636	A	8324	3	179	ISWPSPLLQGTAAALCANGAGP AGTPPGRGPVSARFGRGGAAC VCSPPSPPLAPLSR*RFVVMW WQEA*RRGPRLPLLSLPAAG SGRAAAAAELPGGRAGAR/P L/LLTPAQVQGESARG/AGAEG GRGTPG/GCPLPAGRSLCQPIG PRSPPTAALCANGAGPAGTTP GRGPVSARFGRGGAACVCSPPS PSPLAPLSR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8269	38637	A	8325	1	1744	DFQERLSMKDQLIAQSLLLEKQQ IYLEMAEMGGLEDLPQPRGLFR GGDPSETLQGELILKSAMSEIEG IQSLICRRRLGSAANGQAEDGGSST GPPRAETFAGYDCTNSPTKIV EAPGTES/DPRLPTVLESELVQRI QTLSQLLNLQAVIAHQDSY/V ETQRAAIQEREKQFRL/QSTRGN LLEQERQRNF/EKQREERAAL EKLQSQL/RHEQQRWERERQW QH/Q/ELERAGARLQEREGEAR/ QLRERLEQERAELERQ/RQAYQ HDLERLREAQRAAQPPS/HPPSF NGEGLEGPRVSM/PSGVGPEY AERPEVAR/RDSAPTENRLAKS DVPI/QLSATNQFQRQAAVQQ/ QIPTKIAASTKGGKD/KGGKSR GSQRWESS/A*AGPPLRLGLEG ATGQALAAAGSQEIRDTCAILW RGNQKAQLASWLRPPHTGPVW SPGPKLR*STLHLLTSTLKTGV WGPALERARARRQRSLATWD QHSRTGTASFDLKQQLLNK/L MGKDESTSRNRRSLSPCTCGRH SPAPPPDPGFP/APSPPPADSPSE GFSLK/AGGTALLPGPPAPSPLP/ ATPLSAKEDASKEDVIFSKRAV TQANH
8270	38638	A	8326	147	536	WAQEGSGRNTHQYQKILDVML KGLFKVCAGRGQLMAGPVFDL GTDG*TGVLQKDG/WSALRPV LRTTRSSLAAPSLLF/YFDFHNS NWNLLIRWGISFCNQGTGVFNQ GPHSPILSLVRTGVEVAREPSVG
8271	38639	A	8327	59	339	
8272	38640	A	8328	43	510	LLLWGLRELTIMVEDEGEQM SIWVLDKDLGAPHLVLVGSML TARSRCWTPWRSSSHATAATSE GEGWGVGVLIADRPGWASDEG DGEAGGGGLLTSAEFGELAAV GEAGSAHPMFSPRPRYSTWCLT HIGQGGLELTL*STRSASQSAG VTGMSH
8273	38641	A	8329	98	493	FFYFLFIYFFETESRSVTLAGVQ WYDLCSLQLPRLKRFCSLSLP SSWDYRHPPHPANFCSFLVVT GFHHLGQAGLELLTS*/SIPSSAS QSAGITGVSHHARPGPLSLANN PRSQTRTSATVCPEQLGLD

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8274	38642	A	8330	3	328	HSAARRPSSRRSSPRPETSANS VNAGWNQDPHTHIVIRFMSMAT AGSTRYR*GLHAAPSPPHPRRP RSPPGAE*A/RREARSLKR*SPPC HPTKKATMCRCIIVPLIJK
8275	38643	A	8331	24	593	FEQQWGWAAAAAPPGKAHTR *TGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRPPR *GPSRR*VRSARPSRA*RAPPGS HRPGCGAAAPAPAAASAPARAP WAGADSSAPRTAD*SLPTRVC CSLSALHTGESGDLGPGTQIEG KQNYSVTVWFLAR
8276	38644	A	8332	24	832	FEQQWGWAAAA/CSSRQSTYSL RTGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRP/TS MRAFSPLSAIRSPKSGRDAHHQ ASHRP CGAAAPAPAAASAPAR APWAGADSKRASSYSRLEVLIK VIPEAAA WTSAGSFRT*/PENLPI PVNEIMLLSNCPGRMGSVPLKR RLILGVRVLGERGPGIAWCTCG PPTSMCTGALDLVSWAGRGMP WASQRR/PQGRDRVRDKPGTCFL PSAVPVLPCV
8277	38645	C	8333	153	269	
8278	38646	A	8334	615	1275	QKRKTFNTTKCYNKEKGSWPR WPTGSS*CAQLSWRGMEGTSK YRTE/ILKHGQEIPISEPTPPGP/S SLTCRA TWLSRAAPQPHMKPR EP*ILSIYVAPSPSTIEKPSIGERF AIFITLLMRNGDLGEASCDVAK ALRQPWVGKAQVEKNQLSQT KC PAMWHFESQNPALLIVRECLEG WKAYPQSTKEERLLHPEEGAG FTSSSQEKYVRVRGQRLWPTPF FSLQIMDRKERHLIPPVVIKKR GVGQDGRLEAVSVHSHSGEEW KGQVNTPESTTSRSGDPI MNP LHQGLKSDMQSYMESQSSPS ATHEAQALDTQASWKKQQQ LRKSRAISSPADGVQHGHGA RHCHDVLKRDRQTSWPCKMSS LAEEVVAADTWLLDNGT MQA TGRAAQVREQGKGMDLGQYIS CYLMTLSRAIKQKENKKVCFQ RLGKPRVKTASVQKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8279	38647	A	8335	423	998	PPSAVPHDHSSPART*PQSLSVI TAELEPVRAPSLIAFFHGSAC MCPFRWRYSRFSLKQQRILAH PVNTFGIDRRHTIKFCLSAKQRP YPTITIRWQLSDNMVYTEKH ISVTTAAAIHPVIGSFPIG/PIRA RALSTFLPVHIQRL*GVHFPSF SCRAGAGVL*SASWRQQVQRQ EQPVLRRRQQ
8280	38648	A	8336	2	218	HPSPSPGLKHRSSLSGV*PNPLL LPSGFSLLPAGHSHGDGPSAS QMH*FQNQTHPVP*PDPASLPA VQSHQ
8281	38649	A	8337	76	129	
8282	38650	C	8338	1	410	
8283	38651	A	8339	651	741	
8284	38652	A	8340	1	612	
8285	38653	C	8341	1	729	
8286	38654	B	8342	1	313	
8287	38655	A	8343	705	990	TRSSCWGKEASLGDGNRGVVA ALHHFTGAAARQHSGSPLERGP HPQL*SPRS*VEGHWLEI/LQA* S*VLPQKQPHQPARCWQLLSH WLPRLALLC
8288	38656	B	8344	1	588	
8289	38657	A	8345	220	678	MNAIPVASPCMVCSLIVHVLGS RPM*PW*RPPTRFQWSEVQE/V MELTTMRPQPPPPPPPP*QQ QQQQQQQQQQE*L*LAATPR APGTLAQGSLTPSQIFSA*RLKT DAAGSP/GSPQTITDAELRVTLT VEGKSVFVAVLPQSFTDSPH
8290	38658	C	8346	1	411	
8291	38659	C	8347	1	534	
8292	38660	B	8348	1	774	
8293	38661	B	8349	1	705	
8294	38662	A	8350	1	297	MPGHQKAPLRPAVSKK/ESMLE KGKIK*LLKPEGILPISEPPSNRIF ACWGKPAWTACCNLRARR*R AISCCPSHW*KEKPPWRPIRKPP LPARWPIH
8295	38663	A	8351	616	988	DPQLQAGSGHIPGRNVCGERI CWRGTPD/SDPSTPTY*PPLEKE VAQGRDLIHASGLWS*IPLEA LQGPQGCQFQVCCIPVIPTVE MKQGRQQLASDFQDQDLEFY EILSWKGILIIIP

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8296	38664	A	8352	1	1668	MELVPEEATAV SARAYTGRWP LDAAARTILVTPAGVGHNTIVL CGQASLDAYIKSICLKEGRKE GKKKGRRKRRDKYGGKEKK RKKGRKKGRKKKEKKKKEREK ERRKEEKEGGKKRKEKERKKE KERKKLSIGKGVVYCLSSNTQK KQVSQTKIRVISTILFILAGCIVF VTIPAVIFKYIEGWTALESIYFV VVTLLTVGFGDFVAAHPSDHL CWVIVTCKGKYLDPSPQEKAT DFSGVAQKRNEPQKPLIWC/W ELRSYPTALMMQERVV*KEKP KAAAPNRRGLGTEKLEF*R*EV AAAVEPHAVLSMIGDWLRVLS KKTKEE/VCRPPLFKSPSNLRL LGVAAHVGEIKAHA AEWKAN VTAEFRETRRRRLSVEIHDKLQR AATIRSMERRRLGLDQRAHSLD MLSPEKRSVFAALDTGRFKASS QESINNRPNLRLKGPEQLNKH GGASEDNINKFGSTSRLLTKR KNKDLKKTLPEVDVQKIYKTRFN YSLDEEKKEEETKMCNSDNSS TAMLTDCIQQAELENGMIPTD TKDREPENNLSLEDNRN
8297	38665	A	8353	1	418	
8298	38666	A	8354	251	394	GAQVPTLLVGVLTVTISTVQNL AISLLGKAK*GEGILSVSGRMY RVL
8299	38667	A	8355	107	250	EEGHLLDPRMVDPMAACTM QLEKLQTLNASL*KQLGGGLYL AKPQG
8300	38668	A	8356	331	893	SITENCENKNPIPHVENKDIGTK YNSLKLPEHIRAEVMPQSKLD* VNP/LPSTCKERFVMSHRLART VGSSICNL*MSP/CFGIW*QLAE ANPAKCFP/GCWTNSCTSSML CSKYVTPNGTVV*ITREGPISDD SILRFLLSMETKRMQGLLVSTA QPKGHQSSYQLHKRGPEHIERS SSQPPVAAFGIH
8301	38669	A	8357	2	416	SGFRYGSDIVPFSKVDEEQMKY KSEGKCFSVLGFCKSSQVQRRF FMGNQVLK'PFMEDLRQYMFSS LKNSKKYAPTEAQLNAADALI DSMSLAKKDEKDTLEDLFPPT KIPNPRFQRLFQCLLHRAHPL PLPSIQQ
8302	38670	A	8358	1	2130	
8303	38671	A	8359	1	1152	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
8304	38672	A	8360	1	320	FKGTAAPWPLSFARAAAGRQA GTDTRPSLRVRFPREARSQKQ RGRSVRLSAKSPPAKVETKPSG GSRTA*IFRQRSKQGKMGAKG KQAKWLLILRALICFSLSER
8305	38673	B	8361	1	1231	
8306	38674	A	8362	1	2276	GGRPKRLRTGNMVRSGNKA VLCMDVGFMTMSNPISGIESP FEQAKKVITMFVQRQVFAENK DEIALVLFGTDTGTDNPLSGDQ YQNI TVHRLHMLPDLLEDIES KIQPGSQQADFLDALIVSMDV IQHETIGKKFEKRHIEFTDLSS RFSKSQLDIIHSLKKCDISLQ FFLPFSLGKEDGSGDRGDGP FRLGGHGPSFPLKGITEQQE GKLEIVKMVMISLEGEDGLD EIVSFSESLRKLVCVFKKIER HSHWPCRLTIGSNLSIRIA AYKSILQERVKKTWTVVDAK TLKKEDIQKETVYCLNDDDE TEVLKEDIQGFYRYSIDIVPFS KVDEEQMKYKSEGKCFSLV GFCCKSSQVQRRFFMGNQV LKVFAARDDEAAAVALS SLIHALDLDLDMVAIVRY AYDKRANPQGVGVAFP HIKHNYECLVYVQLPF MEDLRQYMFSSSLKNS KYPATRE/AQLNVDAL IDMSLSLAKKDEEGQT PLKDLFPPTTKIPNPSI FRGLFQCLLAQELLHPR IEAFYPPISGRHIWE YAGILPAEGGQRKSSG FPLS*N*RTLFFL*FEA KEGFKWTAQGI FQGPWKVGPTAKK LKTGARGEP TFVSSSLAE GVSIVGSVN PAENFRVLV KQKASFEEA SNQLI NHIEQFLD TNETPYFM KSIDCIR AFREEAIK FSEQRN NFLKAL QEKVEIK QLNHFW EIVVQD GIT

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8307	38675	A	8363	624	1992	GRKVVVVLPPLGNQSTPGGIC LSAQLPL*RD**SASARCSSPGS *TSPPSYFLDPDRGPGRALQRFS RSPSSPGGNPAISAAAPSRKLL GPPGVAATAAAAGAKPELRH RLPPSSATTASVRACHFLAS AAATPAFSPPPPPPASPSQRT KEVQRAGKAAESCPAAPELLGF GGSRDSAGELGGLSSDACV/PD SSEPGVRRPARRRTLALHALTHA STHRTLPGSCARVAVPVALCK GGFT*PIFSPQYVTNTYPGEEGA RLGVLGREQTVSAILLGGSRSK APTITTVASASPPVTAAGRITP HASIRIPRMLSKSPPPQAL*K GVMAQAQCPPARRGQAGLEGT VGFKSPTRPHQLTAASSPCNGL IRIRQGQGGGKRRWRGSSGDP GAWYCFRGRRRGSPCPLRTAT LIPGLGGHGGSGDAASPLLGT RDGGPEAHLGKE
8308	38676	A	8364	123	248	
8309	38677	A	8365	1	540	MLEALGALNKPESSRLPIPELHL ASTAAANLGEHPNQRLKFAS QETPEESANAVPHYHKL CNRVS HVWGNRRQGHIRNTMDNRP/ GKTTFV*IIVSLPALLALTHSW DSQVRPAVL/QP/YSHTGTGP*W RSSSPCAASST*KSPYP*CH*QR LSQSPSA/FRPTLRRLSRSTRCRS WRRK

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8310	38678	A	8366	31	1429	RETRSCWAHYHAESSKHQKAK LKDSRKARRSIELIGPGSSQKGG DICSLIHLSSKLGILCYSKTGNM GGWEGGMQLRVSSSENSMGKSS RERAAADLPQGSWCWHELPGRLI NTRISLKRPHVWNLSSVLCQVV KKVKSMQMFHMPITSAMQGD RLGICVTQFDPKLLERGLVCAP ESLHTVHAALISVEKIPYFRGPL QTKAKFHITVGHETVMGRLMF FSPAPDNFDQEPILDSFNFSQY LFQEQLSKDLTPAVTDNDEA DKKAGQATEGHCPRQQWALV EFEKPV/YLPSAVPGDWLQARC GHS/PNTCLRAFHGQSCSTG*RT GTTPATASCPG*RCTS*STSMGLV ERAMDDYSVIGRSLFKKETNIQ LFVGLKVHLSTGELGIIDSAFGQ SGKFKIHIPGGLSPESKKDPDTP PSKTGPGWVPVGGQPGRRRSPSG ANPHKMGWLTRPFKRYVFDTH KRMVQSP
8311	38679	A	8367	3	119	RSPREGGHRGPSSGGGRCRRR PGWAGNEAM*PDRRARVVGIE VPAEEGGAAVAQDGLGMKR CSLLRDL
8312	38680	A	8368	3	389	SFATHTAGPQPPAA/PAPKRMA ARASWGRNPPRAPVRTSAAAA RAAGTRRPAPARVACPLPAGPG SPRRPPRAARTRRARRRPGPGR AAQQSAGRRWTPPAPAPSGASF AAPAAGSASPSSHRRAPGGGS TQSSLLSPSSALHSSPPSRPWA ARHERSSWS*/PRSALEPTSTEP/ GPGPRRAPVLGTRSCGRGAGQL E*EA*GAA*APPPLGWTP*LLCV HVTLGNAVSHVSCGAAPPHG GVGVGYRARSREGGHRVPA/ RTREVPSPRMGWNEAM*PFK* VSSRWPLRLPSRGMAAPRGA AAGGARRVEGWEGASLLSGSA PGSARWPRAAPASQVVGARC AAGAPCLPRVWRRGAVGAE NAPSELAASTPAG/GGRGAGSG SSDLAARGGAVAAFPFG*GHSR QQHGAEKDGGQGFGLSQPPPR SCAHQRRRGACSGNAAPSSAR RMSASSRSRQPEKATQSRNSA RSSAARPRSRSTAVSRAQVDTA SSCAFWRVFCSSCRFFCESAEP TVSTRWW

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8313	38681	A	8369	3	1130	LDFQHINYKAMRKLKQVQE QCPNITRIYSIGKSYQGLKLYV MEMSDKPGEHE/LGYWHGEW GEVGTGQGRHEPAASPHVSPG EPEVRYVAGMHGNEALGRELL LLLMQFLCHEFLRGNPRVTRL SEMRIHLLPSMNPDPGEIAYHR GSELVGWAEGRWNNQSIDLNH NFADLNTPLWEAQDDGKVPHI VPNHLLPLPTYYTLPNATVSILR AAVEVLWGADPCLCLLPLLTCP IQVAPETRAVIKWMKRIPVLS ANLHGELVVSYPFDMTRTPW AARELTPTDDAVFRWLSTVY AGSNLAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDF SYLHTNCFEVTVELFCDMFPH ENELPHEWENTDA
8314	38682	A	8370	1	2229	MWGLLLALAAFAVGPALGA PRNSVLGLAQPGTTKVPGSTPA LHSSPAQPPAETANGTSEQHVR IRVIKKKKVIMKKRKLTLTRP TPLVTAGPLVPTPAGTLDPAE KQETGCPPLGLESRLVSDSRL ASSSQSFGLPGRGRNLNQSGLE DGDLYDGAWCAEEQDADPWF QVDAGHPTRFSGVITQGRNSV WRYDWVTSYKVFQSNDSRTW WGSRNHSSGMDA VFPA NSDPE TPVLNLLPEPQVARFIRLLPQT WLQGGAPCLRAEILACPVS DPN DLFEAPASGSSDPLDFQHHNY KAMRKLKQVQE QCPNITRIY/ RIGKSYQGLKVYVVEMSDKPG EHHELGEPEVRYVAGMHGNEAL GRELLLLLMQFLCHEFLR/GNP RVTRLLEMERIFLLPSMNPDPGY EIALH'RSS*LVGLSEGRWNNQS IDLNNFADLNTPLWEAQDDG KVPHIVPNHLLPLPTYYTL PNA TVAPETRAVIKWMKRIPVLSA NLHGELVVSYPFDMTRTPWA ARELTPTDDAVFRWLSTVYA GSNLA MQDTSRRPCHSQDFS/L NGNIINGADWHTVPG'SMNDFS YLHTNCFEVTVELSCDKFPPEE* ICPKEWEWNNKDALLTYLEQVR MGIAGVVRDKDTLGIADAVIA VDGINHDVTTALGPGIWRLA* PPGDYIMVDLPSSEGYHSVTRN

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8315	38683	A	8372	409	517	HFRSAGVCW*PPPLSVHGPR*H FRSAGVCWSSTDPVCLGITSR GCRTAKIAAFSL
8316	38684	A	8373	957	1230	
8317	38685	A	8374	1	2658	MVEEVLDDNILKSVFRLGSILPI TFSFPDSQGPLLQVCRSLLEIH SRPCLPGYHQWRLQNSKDCCL FLPLEASSQRGTCQMPAGALFY KVSVDPFWEVSSQETWGSIGIH LRRQSVPYQSSSAVLGDLFFSS EPACKNKSAAEAVPTAAPSPRDA LSREESREAVWPQLSHAPM GSAQLELPGGFVYTVRRKLPTQ ASVMLDAPPATKLEHPRSSSDC CVGSKNFKPVDLSLLGSMGVG SVELDHLAPWLQPPFQESERFC LSGVVPSPLSEEINHALPKATV MASLGAVARKDNADSLHVPPP TPLFASRPVTALKYWQAPREDL QPFTRTLHWGKGNDQTFWGL VDTSELTLTPNDPKHHYGPPIK VGAYGGQVINGVFAHIQLRVN PMGHWTRPLVIFPVPERKISIDI LSSWQNHIGSLIGRKTGDSWR MTVGVRKLNQVVTPIAAAVPD VVMLEQINPSECECLKMSHQI TMRPELPIMNVWLSDPSSHEL G YAQQHFIIKWKWYICDRAPAGS ESTTSPFITQWVHEQSGYGDRD GGYTWAQQHRLPLTKNDLAM AT/AECPISQQ/QRPTLS*HGV/I PRGDQPATWWRVDYIAPLP SW KGQRRFFTRIDTYSYKFIYP PAP NASAKNTICGLMECLIHCHGIP HSIASDEGTHFIAKEVQQWAHA YRIHSYHVPHPHPEGWGKVLQ
8318	38686	B	8375	1	3258	
8319	38687	A	8376	3	196	DWESCQNQC*PQQPRLHGTHW DPC*DME/CPSVCPCQSPCPLR DQWTIPCPDPLSPQIMAAAGR/W
8320	38688	A	8377	248	423	
8321	38689	A	8378	407	683	LSSYCVHAGCYPREAAARMISF SPSQIRWKPFGESWRPPARRGT CTPGAHPRPSPRAAGPAHRP/ PPP/PSSELPRAPQRPGRNRRPG NSGPV

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8322	38690	A	8379	11	888	TGKLHTSVICNSTELTSDWSRR LFLKGGKPLLSAGAGVNVMPST APFPAPCKGSLRGNPSRPTH* RSPQLERDTGGASFRVDEGEER GASSGGSIRDTEGGSGAVPFGE SWRPPARRGTCTPGAHPRPSPS PRAAGPAHRP/PPP/PSSELPRAP Q/GPEAPTLGQPHGRGLFPPLFK LSKLYWPLGETRSRPRPRPYCQ SPGPGVTERGRWSAPRAPGAP RSPRWRRQSGPGALPRPRVNPC IQHGSEASYAPAL*WALRIPQG GNTSSADEPADFTPNQQAQDM PCLHSCSG
8323	38691	A	8380	1	3135	
8324	38692	A	8381	44	2279	RQTVGDAQPHHPPQPPRPSFP PPPALPCTAPAPQLPPSPSCREEF PSSPMGQTPGTWSSGGPWTSP PHSSSRRLASPLAPLSVIPSTSQ MARSSSQSTTRFSPTPTHSSQ ASQAGTLWPWWLRSGTMLTSP LVGGPHFIRNTRSMVNTAC*S SRPSLGLERSQTTGATRPGGP*R SRGSMPTPLPSGPGSATPTKPS SPRTGAGPMPCFSTRAVGCST WPSAQATRCWSASLVEMAISK TAH*CPSCQGRGIALIDS*IPTQA SKGCSSTGYTGKKGPTTVSSAC SG*RASLGGPAGAGTRSPALVP GSRDDGTYSNPSA*VAGASA VGSCAASPLGEEACAAATGPGE SFSEGWHEQ/TSLA VGP GTGAT ELVLPLEG/HSPTSVCTSRGGP TWAVATYRPPSPPGCSGPTSP PWMVSVTPSMGWGTSCWSGP KTGTTPSCFRAAPPRLAQRPPT SSPLRLST/ASSLGPVTQWLL EPHDAIRVLLDNQVTVFQPDHE DGGGQETFNATGVLLSRNGS/G SRPASTAGPPSR*SRSPSTSTPPP ASRPSTRTARRGSGSGITIQRT TSQCPMAPPPQGALRRCFSTL E*PGRSTGQASLARGMTSCLPT SPLFSTHNCKKTAAGLNI*SPTV TEIAHASMTWPACTQASDFTR GKSVKTTSRTPPSISTRPPSMV VV*LKPTRGRPR*FSTPAMLRM

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8325	38693	A	8382	1	2900	MVWGFTCS TTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQTDILTQMMTSTLTFSSPSV HNVMETVTQETAPPDEMITSFP SSVTNTLMMTSK TITMTTSTD TLGNTEETSTAGTESSTPVTSAY SITAGQEGQSRRTS WRTSIQDTS ASSQNHWTRSTQT TRESQSTSL THRTTSTPSFSPSVHNVTGTVSQ KTSPPGETATSSLC SVTNTSMM TSEKIVTITSTGSLGNPGETSS VPVTGSLMP
8326	38694	A	8383	3	468	SSPPLGHP RPISQSCPRPAVSCSR GPSALLCRPLLGPEADP/P*GSS WP/EGPLWGP RPYP SVSVGNHG WSGAGVADE/PAA PSRPAGARR APSGGRPAAARCSRRRASRSSR PGPPAGRAGR*ACPAARSAVA AAPRP PGAP*CGSASSATAPAA APP
8327	38695	A	8384	3	1319	DSSRLCSRRSSRGHTVGLWGQS PGLGTGKRGGGG*EDPPPGTPR GQQDP SHSAKQ/PPAGLPAGVK WGFS\SSPPSPPP\PAKRELQGR PKFGRCSEGRAGDPGPS/GCPR AKQTHSLGTAVPVVVIYYPVH ALSPAANRTL N*NIISSQPLGTPP MVPGE*HGPRGHA*PRHPLK DPPQG/PAQR*RGCRSEVQRRP GTLP*GSPP/GNSHNGLPAMP *PPTAR/PQFPNPQDPRPLGQSSS EPLPRCPKTLCKTRHPDLRGRG KQPRGWAQVPPGEVFGGNGA QLEA*EGARMSASP*P*SLESD TTASPPSQGLFTAQKGLWGFPQR RLGALWLGRRSEKTSWRRRLQ SQVYWSCREEVEKCSRQGARL GQRRGWENVLGKSGSASECLS CPFCASLAMP SGCPWELSKVA QCFPLKTGHGPQEGSNNLKV TQQS

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8328	38696	A	8385	1	771	HSLHSLTHSLSPVPVQSPA WLR PLCLSA PAT*ATA/CRVCLPGSC DSCSDSWQVDDCPESCCEPPCC APSCCAPAPCLTLVCTPVSCVSS PCCQAACEFSPCQSGCTSSCTPS CCQSSCQFACCTSSPCQACC VPVCKPVCCVPVCKKPVCKKP ICCVPVCSGASSCCQSSRQPA CCTTSCRPSSSVLLCRPVCRS TCCVPIPSCCAPASTCQPSCCRP ASCVSLLCRPTCSRLSSACCGLS SGQKSSC
8329	38697	A	8386	1	453	AQSLGRARPWRGASSGRVPDS/ RLE*TPTVCLA/PEHGIVAATAS LGTFFLTQWEGHNGCYQRS LFP PQSMPTPPCPASETP/PVFRYRPP PSPGSSPR SITHAPVPLGSVSNP PHPEVWNLCTWKRLATSLQ KFTFGPKLGTINVDSDLS
8330	38698	A	8387	39	630	IGTWRFGGSDRQEGQSRQNC EANDWPVSTALA/KPRGATGK NKSPGNDPAAAIATAGAAATA GPGSPCSLQ/NRPHLLPFIS*APP EG*TPSTQDRPWYSAGAA*ASV KCRGTGAVQKQLL*NRRRFP GS PAPAQTADPGRGGGRGTGS/GV PSTGSSDWQERPWP CGGMEPP RLRCLLRCSGSIHSPTALQSLRN HQ
8331	38699	B	8388	1	2673	
8332	38700	A	8389	10	281	TTSDPYHPAPEIGLG*SPN/GGP MQGDLPGASGKEVSFL*GNVN EDIHNSGCVWQPSCDHLARQP KNKAVTMETKKRQKDTGSSLF SSSCS
8333	38701	A	8390	3	416	EYGGQCQCHKRPRGPF GFHSPG PRGGSYISDLSGQESPEAGGGFP PRISAL.RPKSNCSFLRPRGRGS* YPAAGRPRAPGGPALQLSPR/PH PAAPP CRAAPQPKPPRRDVEPA P/PKLPHP/P/GGPAPRRQQDLP GRLQP

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8334	38702	A	8391	98	1286	TMPPTFLAHLDPQAYVFCFCCV EGKERNLSRSKHTSPHSSTPAH LLSKPPRSSEVVYHSQVLPGETP RPTSQLHLELVLPVFARLPGRH GIEREQSSPY/RRGHHRGYTEE D*VNS**DGVEPYGKVAAG PQRRGYCCPWRQRHGRHR/ RRPPIALQRRQ/PARTPSARPIA LQRRQ/QARTPSRPIALQRRQ RHGRHRPRP/RHRSAEKTTART PSPRPPIALQRRQRHGRHRGH/ HRSAEKTTARTPSRPIALQRR QRHGRHRPRPIALQRRQRHGR HRPRPIALQRRQRHGRHRPWP PIALQRRQRHGRHRPWPITLQ RT*RHCRHRHGHPL/PLQRT*Q HGCHRPWPPIALQRT*/PAWTP AMATHRSTKITA WTPSRPPI ALQRT
8335	38703	B	8392	128	457	
8336	38704	A	8393	348	1355	GNEGKAGTSSCWDPKPAAPAV ASSLAS*GASNSTPSAAGSTVA SASWLVEWSPGVTVVGVTEG SSKLGPMLLSTSTPDEAWSPSS CLLLVAPGVWLLPEAGFLLGIH SQGAAPPSPSSCFSTSSFLSS SSSSSSSLPMATPCDLGFSKCG SRLSPPAKALLEDALTPRGA* AWMRDRASIGADPVWLCPSLP SSFLCFLKAVCTSSA/PPCYTT GFLSPTQKTKPSKQGLGVCSSQ VSRHPALGQLLDIAEDKSPPH SGSTICSLWLSSSRAPCDRCTSR PSSKVQGYLCQQDSRSRTRAG WKTPTVVGRHVPVKIEKESIRP ANFG
8337	38705	C	8394	154	219	

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8338	38706	A	8395	3	1054	LYLKVCYI*KELFEFSNLYKHPS GEEVWERILRV*DNGGRN\KLI YQAEFIDLGPVSRDSAFNVAQ GVKKGSNRLFPWLAEIWTRWP TVSELEMPDLPWFNVVEEIKRL REIGMVWISHFRCTHPSWKGP EDIPLTNALQNRVRAAPASLK SLVIALFCMSDATAAGTAVTQL QNLNTMGIIIGSRGVDRDQVVAL NHQRQVGVANRQGTPT/QRGT KKRTR*PGQAKRPGPKERGTRS HAYAHTSVTTPKNNRHDTRPS QRTPQQRDAQHQTETPTTTP NTSRPPSHVSFFRSKKRRRRPQ HIEERNKRTRTEEEARERNRAN KDDTKRQPPKKTRENRRLWS
8339	38707	A	8396	140	398	
8340	38708	B	8397	15	192	
8341	38709	A	8398	1	1167	AGTARRAPESSRRRAVAAGHPE TMGKLVALVLLGVGLSLVGEM FLAFREVRNASREVEPV\EPENC HLIEEESGSEDIDILPSGLAFISS GLKYPGMPNFAPEDEPGKIFLMD LNEQNPRQALEISGGFDKELF NPHGISIFIDKDNVTYLYVVNH PHMEVHCGRIF*ILREQRSSGY YLUKTIKTWNFFKSVNDIVVLGP EQFYATRDHYFTNSLLSFFEMI L\DLRWTYVLFYR/PREVK/VVA KGFCSA\NGITVLSQTQKYVY VADVAA\KNIHIMEKHNDWDL TQLKVIQLGTLVDNLTVDPAT GDI\LAGCHPNPMKLLNYPED PP\GSEVLRQ\NVLSSEPRVSTG YANNGSVLQGTI.WASVYHGK ILIGTVFHKTLCYEL

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8342	38710	A	8399	89	1685	KGPLLLSLPCRAGAMAETSAT GACGEAMAAEAGSSGPAGLTL GRSFSNYPFEPQAFGASSPS(WA RLDGAFGSNERAEGCKVPQEG RLLKLLAGLTRPADVRPPLGRG LVGGQEEASQEAGLPAGAGPS PTFPALGIGMDSCVPLRHGGLS LVQTTDFFYPLVEDPYMMGRIA CANVLSLYAMGITECDNMLM LLSVSQSMSEEREKVTPLMVK GFRDAAEEGGTAVTVGQTVVN PWDLLIGGVATCSIANQFEFI(M PDSAVVGDVLVLTKPFRNPGL LFNAHQWLG*FLERWD*S*RW WFSREEVELAYQEA\MFNMA TLNQNCRRV*MHTFNAHAATD ITGFGVLGHSQNLAKQQRNEV SFVIHNLPIIAKMAAVSKRASGT VWGGFGGTS\A\ETSGGITGFCPL R\EQGGLAFCS\EIQILPKYGRGS PKAWIIVGIVEKGNRTAPDPLTS PRVIEVLPRGATAA\VLAP\SS NALLLSLAREIERTEVVWTLEP LSTITDGSQELIVKKFPKKAACI VVPAAALSR

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8343	38711	A	8400	30	2391	ARGRPLLAARSSRPCGRLPFK RAGPAPAAPHRGDQEARWFSG AAPSRLLPPAPRFSGPAAIFLSAQ GPPSGAMQPTLLLSLLGAVGLA AVNSMPVDNRNHNEGMVTRCI IEVLSNALSKSSAPPITPECROV LKTSRKDVKDKETTENTKFE VRLLRDPADASEAHESSSRGEA GAPGEEDIQGPTKADTEKWAE GGGHSRERADEPQWSLYPSDS QVSEEVKTRHSEKSQLREDEEEE EGENYQKGERGEDSSEEKILEE PGETQNAFLNERKQASAIKKEE LVARSETHAAGHSQEKTHSRE KSS/QFSAA*EAGSQENRPQESK GQPRSQEKSEEGDEDATSEVDK RRTRPRHHHGRSRPDRSSQGG SFPSVEEKGHPQEESEESNVSM ASLGEKRDHSTHYRASEEEDPD YGEEIKGYPGVQAPEDLEWER YRGRGSEYRAPRPQSEESWDE EDKRNYPSELDDKMAHGYGEE SEEERGLEPGKGRHHRGRGGE RAYFMSDTREKRFLGEGHHR VQENQMDKARRHPQGAWKEL DRNYLNYGEEGAPGKWQQQG VLQDTK/ENRVEARFQDKQYSS HHTAEKRKRLGELFNPPYDPL QWKSSHLERRDNMIDNLEGE EENELTLNEKNFFPEYNYDWW EKKPFSEEDVNWGYEKRNLARV PKLDLKRQYDRVAQLDQLLHY

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8344	38712	A	8401	73	1922	ILPVPHP/CRQVLKTSKCPTRQA DLGHCSDDPCSYSLHITFPADASE AHSSSRGEAGAPGEEDIQGPT KADTEKWAEGGGHSRERADEP QWSLYPSDSQVSEEVKTRHSEK SQREDEEEEEENYQKGERGE DSSEKHLEEPGETQNAFLNER KQASAIKKEELVARSETHAAGH SQEKTHSREKSSQESGEETGSQ ENHPQESKGGPRSQEESSEEGEE DATSEV/DKRRTRPRHHHP/RSR PDRSSQGGSLPSEKGLPQESEE ESNVSMASLGEKRDHHSSTHYR ASEEEPEYGEGRKRGYPGVQA PEDLEWERYRGRGSEERYRAPRP QSEESWDEEDKKNYPSLELDK MAHGYPEESEEERGLEPGKR HHRGRGGEPRAYFMS/DTREK RFFGEGHHRVQ/ENQMDKARR HPQGA/WKELDRNFLNYGEG APGKWQQQDGLQDT/KENREE A*VFKINHFS/SHHTAEKRRLGL ELFNPPYDPLQWKSSHFERRDN MNDNLFEGEEENELTLNEKNFF PEYNVDWWEKKPFSEVDVNWG YEKRNLAR/VPKMDLKRQYDR VAQLDQLLHYRKKS/A/EFPDFY DSEEPVSTHQEAENEKDRADQT
8345	38713	A	8402	1	381	
8346	38714	A	8403	1	444	MKLIVGIGGMTNGGKTLTNSL LRALPNCVHQDDFFKVPALA RGVLESMDMEAMLDTVQAWLS SPQKFARAHGVSQPEASDTHI LLEGLFLLYSYKPLVDLYSRRY FLTVPYEECKW/KEKYPQLHSP *SPRPLRWPRVAHVPEV
8347	38715	A	8404	3	421	
8348	38716	A	8405	3	4065	SAPPDVTTYTSEHSIQVERPQGS TGSRTAPKYGNAELMETGDGV PVSSRVSAKIQQLVNTLKRPKR PPLREFFVDDFEELLEVVQQDP NQPKPEGAQMLAMRGEQLGV VTNWPPSLEAALQRWGTISPKA PCLTTMDTNGKPLYILTYGKL WTRSMKVAYSILHKLGTQEP MVRPGDRVALVFPNNDPAAFM AAFYGCLLAEVVPVPIEVPLTR KDAGSQQIGFLLGSCGVTVALT SDACHKGLPKSPTGEIPQ

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8349	38717	A	8406	10	580	KQCALLTFICSLPMSFGFAPAIT VTVVN/PRHPLIRDMRLRIKEDE DDKTVLDLAVVLFETATLRSG YLLPDTKAYGDRIERMLRLSLN IDPDAKVEEEPEEEPEETAEDTT EDTEQDEDEEMDVGTDEEET AKMS*ALLTFICSLPMSFGFAPA ITVTVVNHVFLCSKTGSQVFRS ENWKVWAESSRGDHDCLDL CSVLCWGRTATGAFSCPAQLIF AVSSSSSVPTSSSSSCSVSSV SSAVSSGSSGSSSTFASGSMFK LRRSILSILSPYALVSGKRYPD SVAVSNKTTARSKTVLSSSSLI RRSMLSISGCRD
8350	38718	A	8407	1	1967	MTMAAAVVARAGARAATA AALRGCGTAARGRPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGTKKYTTSLNARHY YTHFTEENEDEINSSSSYASQKK TFEINPRHPLIRDMRLRIKEDED DKTVLDLAVVLFETATLRSGYL LPDTKAYGDRIERMLRLSLNID PDAKVEEEPEEEPEETAEDTTE DTEPDEDEEMDVGTDEEETG KESDDPMAYIHFTAEGEVTFKS ILFVPTSA PRGLFDEYGSKKSDY IKLYVRRVFITDDFHDMMPKYL NFVKGVVIRKKLVKTLDMIK KIADDKYNDTFWKEFGPTTKLA GVIEDHSNRTRLAKLLRIQSSH HPTDITSLDQYVEK\MKEQDK IYFMAGSS\KAEESPVERLLA KKGYEVYILTEPVD\EYCIQALP VEFD\GKRFQNVVQGECKFHE S*ENLRK**CKSVEQRISALCLN WMKDKALKDKI*K/ALWVSSA ALTESPVLLLVAQPV RDW/SWP TLGE/RSMKAQAYQTGGHLL QIYYAESERKHFEINPQTPRLIR DMLRRIKEDEDDKTVLDLAIV VLV*NRQLGSGYLFQTTLKAY GDW/RLERMLRLSLNI*PLMPK VEEPR/EEPEETAEDTT\EDTE VQDEDEEMDVGTDEKGRTSKG
8351	38719	A	8408	181	462	GMAASDSSKGTGRGKQVVAG AVGDSAKESQGGPPGAPPRRA AGL/WRHHCSF*AD*TTNAPG GKNRPFGKGAGGEQGTAGDFT QMPRTQNTL

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8352	38720	A	8409	3	228	STGVVPSQQNLPLEKASVLFNT GALYTIQIGTRCDRQTQAGLESA IDAFQRAADMSPPGLTRRSLGP TRWHQGTTH
8353	38721	A	8410	129	311	RCFQDCSHSTPGTGPRRSGCL LSSAAPW*KPPAAPRTPHRSRSH NRGPRRQQHARHQDDP
8354	38722	B	8411	1	789	
8355	38723	A	8412	1	933	TVVLKDFILEHYSEDGYLYEDE IADLMDLRQARRTPSRDEAGVE LLMTYFIQLGFVESRFPPTRQ MGLLFTWYDSLTTGVVPSQQNL LLEKASVLFNTGALYTIQIGTRC DRQTQAGLESAIDAFQRAA/VGP TRGGRASTYEMTPAAS/PEIPGA SLQREE/QWTGAWTHQQIYPQP GTPP*SPPQAQPSRFLFAMDFA ATTSAIGSARPSTNQS*GYFHTG RSWQPVAA**ECHILRGNAENVL HDLSSH***RQN**NOENLQEA LPELGHQQEQTEVSQHLVPPIG RGCTASGGEEAALPFQPSQLRQ FLVL
8356	38724	A	8413	1	389	
8357	38725	A	8414	1	506	
8358	38726	B	8415	125	700	
8359	38727	B	8416	19	338	
8360	38728	A	8417	1	3335	MAALWNTCGAWKNMLIPECH SQLLRVAANPKVREQVRLELSF VNSDLQMLKEELEGLNISVGVY QNTDEDGYLYEDEITDLMDLR QACRTPSRDEARVELLMTYFIQ LGFVENRLFPTWQMGLFTW YDSLTTGVVPSQQNLLEKASVL FNTGVLYTIQIGTRRRYRHTQAGL QSAIDAFQRAAGVNLVLTETFT HNPSYDMIPAMLSVLVKMMLA QTQESVFEKISLPGIWNFFMLV KVAQEAAGVGEVYQQLH
8361	38729	B	8418	1	1689	
8362	38730	A	8419	2	722	CPGSGSERGQRQPCGRSRGRTE PGFSPC*KSAAPRPAVSLKASAP RPSSSS/GPAGISSPGRESRSCGT QNILGPFLVSG*PL*GR*QCFP AAAEPPAVPL*AEDISA/GPPAV *AP/SGLAHLASG/PGPLPPLGG AGLV*QSI**GGHQGADEGP*G EMDAKEAGPAQNCDDLHVCPG ARGAEGAPGEGCIS*QPHAPDA L*AASELPKDELLRQCSGG*RC SPAGSAAPRAGSSAVLEPQ

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8363	38731	C	8420	144	439	
8364	38732	B	8421	1	4747	
8365	38733	A	8422	1019	1880	YCCLPRGGNAGCQTRQDPSCRPGPGSQGLSLPPGR/PGAAVECGARSRGWQQDGGPPSPGKAQVPAEPAPPQTVPGPPEDFCLGPRNEVPDGG/GARQSHHPGPPRSPGPEGGSPQAAARLVDRVSRPQNQLPNPGP* ^Q DQPPRPAIPTATPSGCNGPGFPAPRPRLSSEEEAPSRAGPEEEAPTYTPRLRRGRPARGPVCR/PPAGPPAV* ^{PE} FRRFALPRASVSGFQSS/PVAAGGAPDPGPGRLLYTDAHGDLPLTNTTACTGPWPAGPRHCASGAEA
8366	38734	A	8423	240	763	VLVARRPQRPGHEPAVLQQ/PAGP/PVPRKPNPSPSPAGLRPPGRAGPLTSPRCPLPAFTGHRTP/VVGVPVRPKAAGPRRRTYQGRGMGPRPRRRPVVPVGGERSHSHPSGPPLRSPGEWGLTSSSCPARGLEGVSA/TQNQLPNPGP* ^Q DQPPRTCHPHGYTQRI/PSGPPRLRSPGPEWGLTSSSCPARGLEGVSAPISSRIQGRRTSLPEAPIATATPNGYIGSGFPAG
8367	38735	A	8424	2	609	PYSISIVSTGPSADSVYTKVRLLGETLSVQCSYKGYKNRVEGKVWCKIRKKKCEPGFARVWVKGPYLLQDDAQAVVNITMVALKLQDSGRYWCNRNTSGILYPLMGFQLDVSPAPQTERNIPFTHLDNILKSGTVTTGQAPTSQDPADFTTGVMVFTPLITLPRP* ^{PP} PDLPQRQATASLLPAPPARDPGPWGPRQ
8368	38736	A	8425	1	252	

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8369	38737	A	8426	3	1581	ALHCAIRHEDKWPTAVRANGH LLLNSEKMSKSTGNFLTITQAI DKFSADGMRLAIADAGDTVED ANFVEAMADAGILRLYTWVE WVKEMVANWDSLRSGPASTFN DRVFASELNAGIKTDQNYEKM MFKEALKTGFFEFQAACKDKYR ELAVGRDAQKLVRFIEVQTLT LAPFCPLCEAHLGHSWGKPG LQLWNCFPWACGRVPV*WKFL IHSSQYLMEVTHDLRLRLKNY MMPAKGKKTQKPLQKPSHCT IYV\AKE\YPPWATLPPCLFLT KHFEGLTGKTGLDNK\AIASE LGSMPCLKKYMKKVMPFVAMI KENLEKMGRPLDLQLEFDEKA VLMENIVYLTNSLELHIEVKF ASEAEDKIREDCCPGKPLNVFRI EPGVSRLFLVN/RQPIPMAHFL NPKLEIRQGD\TVIPIRRLMKM NRGI*RPFPKVKPGWRI**SHCW GPRRSSCPWEKEYTREDPPFPE ACLFS/DV\DLMSKKIHLTENGIR VDIGDTINLSGSLNSCTLEIYPG FLGILL
8370	38738	A	8427	1	1052	MIKNIGPQYLTPSFLGEQEGDEE EEGHIVDAEAEEDGADADAK RKEKQEEVDYSEEEEEERE ENDDDMQEERNPHRRGARKT QEQQDEEVGL/GH*GGPVPSRPP DAAPETHPOPGAPGA\EAVER VQAVREIHPFIDDYQYD\TEESL WGQVTVKLPLMKINFDMSLV VSLAHGA VIYATKGITRCLL\NE TTNNKNEKELVLNTEGINLPEL FKYAEVLDLRLRLYSNDIHAIAN TYGIEAALRVIEKEIKDVFAVY GIAVDPRHLVLADYCMCFEGV YKPLNRFGIRSNSSPLQQMTFE TSFQFLKQATMLGSHDELRS ACLVVVGKVVRRGGTGFLKQKP
8371	38739	C	8428	154	219	
8372	38740	A	8429	1	1584	
8373	38741	A	8430	200	277	

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8374	38742	A	8431	3	877	LYLKVCYI*KELFFESNLYKQPS GEEVWERILRV*DNNGRNKKL YQAEFIDLGPVSRDSAFNVAAQ GVKKGSNRLFPWLAEIWIKKW PTVREVEIPDLPLFNVEEQIKL REIGMG*WISHFRPTILHSWEGP EDIPLTRPSQNIIVRAAPASLKS PVIALLYMSDLMVRTAVTQLQ NLNTMGHGSQGGRRDRVAPLNH QRQSGHGYHNGQQRESGNQNS LTGVELWHWLNHNHVSRSSEVD RKPTTFLLNLKYKQKTSRSGRK TSLNYKNRESRPLNQFPDLQSF
8375	38743	A	8432	1	282	
8376	38744	A	8433	1	281	SVHTGHHHHYHRRHHHHHHHQ HQLHQHQHQGGGHHHHHHHH HHH/HYFQ*ATWEMLLWVGHS HL*RQP*KQHEHRDDVVSQAGS VPCASRGFHIR
8377	38745	A	8434	64	302	
8378	38746	C	8435	133	262	
8379	38747	A	8436	1	1962	MFSIPTGQLRAAASGARRHRGR GSIGGPFHAIQGPVETDITTAQH ETVAPPDLAHPSPASRGPRPY/G RHLALDEPFLHISGALF*DSLAV *EPPESRLDARPGARNSNSRCPI TA/RPPTDMDGTPSAQGAQSSA/ FAQLPPPHNSTRRAPAGDMPPS MPGATELLACSVPAQ*TSELRG GGFASSLSGSPCKFGSPASSDA WPRLQPRWPVTFPEAQPLEVPG GTEHGCSWPPELSNSAAQTFFF PPLHPTAPSCPLGLPGSPPGPTSS TGDIPT*QDSGTSKLYCPLQQ GGAEAAHCV/PA/PEQPETNSKR KGETPTPN/DKEGETPTPNEKKE KHQQQTKRRNTNTKRKEGETP TPNEKKEKHQHTKRRRNTNT KRKEGETEPAQGGTNPGRVQQ SPAAL*CFSY*SECQAQCPSDS AGARFTAGSAPDKGL/PPGPSS WAPSS*HLILATTVHLLVTRPC* PPSCTGPSGLVVGGRPSAHH HSDLLF*SSAGKPDSPWPCWTMS AMGILRPRGRASGAPGATPFP GEFQEAHAPPVQPSTAQSLPAP CLPLGASGGPRQHPPDVSRGG DRGLQQSVLSDAAP*PGVRGNP PRGARWGARAAPGAPGAPHS PCPQMPGRDPLVYPSPGTEAQ MSCLTPQFLQILLCDFE

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8380	38748	A	8437	438	699	LLEGKLTNRKDIHTKTPSVCHH HRGPKVDKTTKMGKKQSRKAE NYKNQASAPPPKDRSS\YQQRN KAGHRMTLMS*EKKASENQTS PS
8381	38749	A	8438	1	1334	MDGRLYSVTIQPSVSNLQLLL SGPKSAVLVVITLMCSETNLSF NEFSSEFKTTSPKMSIRKPQEK SADGKQFLQNDKRNPKLGNTQ TLRLNDVSGLLSRTKRNIVPPG WYSVYVTNNYVFKKSPKAKK VSESTTKNDPVKNIHIESHNID LNKIAMNSNLQVVVKRLDITIS IAKSSWNNQPLSEGYKASKKLI EIDGKDQHADRNMTLTLNRMT CKEQLSKSVVASGNIINSHCM PTVDLNNKRLENLKKSSILDMG RLISSVENVPKYEGETSSSVSN YSSPIKLMFLSEVKSEGVKYTL TSVGTSHSNVVLPSKPTTHHV TEETETNEDISNANSENYHSS HYDTDTFQRELNKFSAKETA GSSTMFIGDINSKPKQEEPKNDS SSATDPSE/NKKTR*TKKNRSPS CETD*ATNWKTTKA*N*SNKH
8382	38750	A	8439	115	523	QFFFSLSQALKLDQAIHISMDAF HSVSELFASQSRRLDPAAMDLL VLSQGHQTNILDIVHIIHKEALT KVTENRQHVAAEGKTE/SAEADD VRIT/VNRNSFTTSLIEHHFHPi* RDMKSQMQLFLQQEILFFQKSS RN
8383	38751	A	8440	1	461	
8384	38752	A	8441	3	319	
8385	38753	A	8442	112	480	IFSSLNVAYPWPEKKVVDGSKC PIQQQLERKIKNFVLYLK/RLQL TKCEFKN*RLNFIRVKNKEKY VCT/SYHTKLLFNHLMALILIV FKYQSFFSLHSCNQPHAKVLE PALELQDEDMVH
8386	38754	A	8443	1	528	

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8387	38755	A	8444	2	811	GIHTRLNSELLKEEESNKRLEAE IEYQSRLTAAISKHSESVKTER NVKLALE*TDVSVQVKMSSDI SEVEDKNÉFLTEQLSKKQIKFN TLKDKFRKKRDTLRKKSLALET VHNNLSQTQQQIKEMKEMYEN AEAKENNSTGKWSCVEERICQL QHENPCIEQLDDVHQECLPS RKEKFKSEPPAFLSGNQVKSSS CSLQTLFPPDDLILYLENPKDST KKLLELNLNKFRTGYKIKLQKS VAFLNDKNEQSKEENQECNPIY
8388	38756	B	8445	1	1581	
8389	38757	A	8446	617	2972	EQNKPYQWLQRKNSKRERSE KKQPQVKEGNNNTNKKSEIQLSE NICDSTSSAAAGRLTQQRKIGK TYPQQFPKKLKEEHDRCTLKQE NEEKTNNVNMPLYKKNREELERK EKQYKKEVEAKLEPTLQSL MKSKTARNTPNRDFHNHEEMK GLMDENCILKADAILRQEICTM KNDNLEKENKYLKDIKIVKETN AALEKYIKLNEEMITETAFRYQ QELNDLKAENTRLNAELLKEK ESKKRLEADIESYQSRLAAAIK HSESVKTERNLKLALERTRDVS VQVEMSSAISKVKAENEFLTEQ LSETQIKFNTLKD KFRKTRDSL RKKSLALETVQNDLTQTQQQT QEMKEMYQNAEAKVNNSTGK WNCVEERICHLQREN PWLVQQ \LDDVHQKEDHKEK*\LISQGRG IESGKKDLVLEEKSKLITNECD HLKESLFQYEREKTEGVPKKEN EELRKL FELISSLYNVNRIRKK NDELEEEATGYKKLEMTINM LNVFGNEFDCHGDLKTDQLK MDILIKKLKQKFDLTAKEAL SSKCVNLAKDNQVLQOEFLSM KKVQQQCEKLEEDKKMLKEEI LNLKTHMENN RVLSKLQYK LELDEKAMQAVEKLEEIHLQEQ AQYEKQLEQ/FKQGYNTASLNLK KELTLKDVECKFYKMKATAYEE VTTELEEYKEAFAAALKANSS

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8390	38758	A	8447	1	2794	AVYLSRGCVCCIRCISSLLKEPH EEGVMSCFRSVATQKNDIRPDF QLGKMDSKIKELEPQLTILYQN PKTLKFQGKKS VKFALSPSMAL RK*PFKMFSI*SIFIALQFLHGY KPILFEPNQTWPGHVAVWQD TSIVAI/SANITQKVHPVI/W/SSIP PYGVALSSLTTGTAAPLCTQL GV*IPLDCAQATFISHDKMVISL KGYLFLSSCLGNSLLKYTEKL QEPPASAIACEAADKEPPSQKK RVDTS
8391	38759	A	8448	184	427	WAIAIQRHVVDQEWQIADPC NM**VENAETLPPGPFNLISLES SARRRATSRDDNRRFRPHRSRR SRRSRSDNALHLASE
8392	38760	A	8449	1	903	MAQKFMAPNRARTLRDICTDR EAYPVQESMSGTRGQRKEDM GGAALSTGEGGARDVKAPLPE ATLCSQMGPTRPSGLCDLAG STLAGRWMHQSDFDGGMEAS KLPQGEGVRIQPMSETRRRRAT SRDDNRRFRPHRSRRSRSD FSLHLASEREASRLKDRPPLRA REDYDQFMRQSFQESMGHGS RRDLYGQCPRTVSDALQNAF GDRWGPYFAEYDWCSTCSSSS ESDNEGYPFLGEPPIQPARLYV TSDIDCCTNTAPTASPNLPH*VA EDSCTAGKDQRAKTCIISLY
8393	38761	B	8450	1	322	

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8394	38762	A	8451	1	2460	MEEKSKRRGVLSLLILALKFG DEPLGSPNSCKYKLTTLKELG WREVFSSQLCLCTSVASQMLS QYFEYTPHPGDICHPETCALQ KVFLTSSGQSSSTSSSQQFVLQ INAIQTILEKTPTHISTPTPTLA NPTAVGLEEDREQDVGTSRRG GAWDTRIKRELEKMSKCGGQ INGGDIAFASRAGHGVWCWHP CFVCTVCNELLVDLIYFYQDGK IYCGRRHAECLKPRCAACDEIIF ADECTEAEGRHWMMKHFCCFE CETVLGGQRYIMKEGRPYCCH CFESLYAEYCDTCAQHIGEAIF GSQ/HWSFC/RCGHLCFGEWG* PQLLWMLC*LELTGKPRDAIMS SLHSWHLRKGVRRRRRKEDK SPEVLP*KSSSGTLSH*R*RPH* SLFLGSRVSLPSGECRGPYPYS HSLRLYSQALPTGRGPSSSQFP FCQFYCCYKSLLCDCLSKSPA LEKAMRGIDQGMQTYDQGHV HATETCFCAHCKKSLGRPFL PKQGQIFCSRACSAAGEDPNQSD SSDSAFQNAKESRRSAKIGK NKGKTEEPMLNQHSQQLQVSSN RLSADVDPLSLQMDMLSLSSQT PSLNRDPIWRSREPPYHYGNKM EQNQTSPLQLLSQCNIRTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGAGSFIKECREDY YPGLRSLQESYSMDSSSQSFSET
8395	38763	A	8452	2	942	NKNPKNHYPESYVSLKNDFTK LTSRRHRGVEQALVQLCHVFV CEHGHVIVTLSSGFIVYRTRAN YSSSAQGVGIAAALDAVLIRA HQRTQGCHELSALLAFEKGSE KKEEEGGQVSRSSSLKVQAQE LSATEDKGHISPFWEAVYHYA SGECRGPYPYSLSLRLYSQQA LPTGRGPSSSQFFCQFYCCYK KSLLCDCLSKSPALEKAMRGID QGQMTYDQGHVHATETCFCC AHCKKSLGRPFLPKQGQIFCS RACSAAGEDPNQSDSSDSAFQNA RAKESRRSAKIGKNKGKTEEP C*TSTASCK

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8396	38764	A	8453	1	937	VHQYVYSCLPFEKVPYVNSPGEK LRKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSSQRKRENIG RGNVRPFPVTMTGAICEQCGG QINGGDIASFASRAGHVCWII PPCFVCTVCNELLVDLIYFYQD GKIYCGRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECETVLGGQRYIMKEGRPYC CHCFESLYAEYCDTCAQHIGID QGQMTYDQGWHAHATETCFCC AHCKSLGRPLPKQGOIFCS RACSAGEDPNGSDSSDAFQNA RAKESRRSAKIGNKNGKTEEP
8397	38765	B	8454	214	551	
8398	38766	A	8455	1	1140	
8399	38767	A	8456	1	2525	MLNIQSVPGIGQGHYSRYLHNS PMHSGDFISNIHMRKPKFREIIF ADECTEAEGRHWHMKHFCFE CETVLGGQRYIMKEGRPYCCH CFESLYAEYCDTCAQHIGEAIF GSQ/HWSPFC/CGHLFCGEWG* PQLLWMLC*LELTGPRDAIMS SLHSHWHLRKGVRRRRRKEDK SPEVLP*KSSSGTSLH*R*RPH* SLFLGSRVSL/PSGECRGPYPYS HSLRLYSQALPTGRGPSSQFP FCQFYCCYKSLLCDCLKSPA LEKAMRGIDQGQMTYDQGHW HATETCFCCAHCCKSLGRPL PKQGOIFCSRACSA GEDPNGSD SSDSAFQNAKESRRSAKIGK NKGKTEPMLNQHSQQLQVSSN RLSADVDPLSLQMDMLSLSSQT PSLNRDPPIWRSREEPYHYGNKM EQNQTSPLQLLSQCNIRTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGHAGSFIKECREDY YPGRLRSQESYSDMSSQSSET RGSIQVPKYEIEEEEGGLSTQ QCRTRHPISLKYTEDMTPTQ TPRGSMEALSANATENQDDCS FVNRLKGSNNRPGRRQELMVT WNFIQERNSGMDQCDGGG KILDPVYILTVELTGFAKGWKM FSVKDQSVNVLGFAGCLSDG GAKRQEHLRSFMPDLKSDSG MNVSEKLSNMGTLSNMQFRS

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8400	38768	A	8457	7	302	PLPSSPEQPAGRKGTGLPCALT EIYFRVTIYFYVEIEKLLIIIVAK QEGLSGN\HKP\VERKYMTYLS AQD\HELIQVVQNGHLQMCCK SETGNEASPVs
8401	38769	A	8458	1	241	MTYLSAQDHELIQVVQNGHLQ MCKGSETGNEASP/G*GRGVNP WP/RHARSRMALTRSSASCCR CSGASSICTGSLSTGG
8402	38770	A	8459	31	454	QRSAWRSQIWSASRSV*SVFVR RASSRCLNTGSGPGHPDR*DC RT/ARRCGWTRRRMASPSAAC GRSRCCSACVI/LNIVELKEVVV GNHLESIFLVMGYCEQDLASLL ENMPTPFSEAQVKCIVLQVLRG LQYLHRNFIHR
8403	38771	A	8460	1	914	SYHHLRHHHHHLPHHCF/HHN NHYYHHYHHYYHHHHCHHYH YHHLHHHHHHHHHHDHCYVH NNNNCHHHHHHHHHHHH*Y HHYHPHHHHHHHHHHHHYHH HHHHHHHRHHYYHHHHHQHH HYHHLHHHHYHHYYHNHYHR HHRYSCNNNHYYHHHHPPHY HHHHC*HHHYLYHHHHHNNH HHHYHHHHYHHYYHYH/HHH HHHHHHYHHYCHDHNHYHYH HHHHYH/AHFFHHYHHYHYHY HHHHRHHHHLHHHYCHRP HHYHLSCESTHTLFPQNAISSFD CKYLDGQDDEDFVVYKCLTLY
8404	38772	A	8461	102	420	DTGPGEGAAGCGGGVGEV AAPAAPGHS*VG/GNQPYLSPV CSRGSPTGRAAARGLSGCWP WWSPRSGSAPSQCSSASWSAW SAGAPRFAPSAPGHPEGRRCPA
8405	38773	B	8462	121	215	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
8406	38774	A	8463	44	1584	AVLDRGPRVGSSTSPGGMSTC LSSPLFATAAELGGGLCSAGR GPRRKVYLSVDEKKLRCCQPKS GRSVAERAAGHSAEGWRPVH VGPGLLGLAL*GP*AWGFQGR KGGI*KGAYTAKCMMGSDKAQ ASGIATGGGHSAGEAVG/PQ/ QGTVLSFEGGGGLSFRMPGSL IGPSVPCCKGHPGRCPPHHA EGTDTVATVAAT/GPPLAPSHG TSWQSGSLQ*DTGPGEAA/AA AVVGVGEGAEAPAGHS*VG VISHICPFVAGSGPTGRAAA RGLSGCWPPWSPRSGSAPSQC SSASWSA WSAGAPRSAPSAPH PEGRRCPA*GWN PQGSKSSLKS SELWTPIPYVPAVP*HTCGYA AGPAPVQTPCRGGWNGAQVGL DPIGGHGDGTPHGS/APRLPGRV GGAP*AAVAAISTDPPATASLG PAPGGPACCPSL*ACPASSASP APARSSWPPAPASCGSAAPWW HQTGHGSLWWPEHSCRLSHRS PSGPAPCWPFPRASPDRGTA
8407	38775	A	8464	1	541	MKSLEEKIGCLLKFLGDLDDQT CKEDLHILFSNHGEIKWIDFIR AKEGILFKEKAKETLGKAKDA NNGNLQLRSKEVTWEVLEGE EKEALKKITEDQQESLNKWK KGCRRFGKRRKGSAAQPGSGK GKVQFQDKKTKFASDDAHDEN GSTGPIKRGREETDKE*PASKQ PKTENA

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8408	38776	A	8465	1	1326	PAALGGGVVAVAVCEPVARLL WAGTLKIAVMAENGDNKEMA ALEAKICHQIEYYFGDFNLPRD KFLKEQIKLDEGWVPLEIMKF NRLNRLTTDFNVIVEALSKSKA ELMEISEDKTKIRRSSPKLPEV TDEYKNDVKNRSVYIKGFPTD ATLDDIKEWLEDKGQVLNIQM RRTLHKAFKGSIFVVFDSIESAK KFVETPGQKYKETDLILFKDD YFAKKNEERKQNKVEAKLRAK QEQAQKQKLEEDAEMKSLEEKI GCLLKFGDLDDQTCREDLHIL FSNHGEIKWIDFVRGAKEGILF KEKAKEALGAKDANNGNLQ LVRNKEVITWVLEGEVEKEAL KKIIEDQQESLNKWKSGRRF KGKGKGNKSCPSGSGKGKVQ FQGGKTKFASDDEHDEHDENG ATGPVVRAREETDKEEPASKQ QKTENGAGDQ
8409	38777	A	8466	2	331	CSTSLMIREMQVKTMMRYHLTP ARMAIIKKSRPGVCGPQFTASY CSSWNRGLSRAMAQSLTPRPLS TLQ/PLLA VDRGS/PVLGASHRL PAQC/CMTDSSSTLGSAAAGSW QQ
8410	38778	A	8467	1	209	MNSHFLKEDIQMANKHMEKCS VPLLMIREMQIKPTVRYHLTSAR MPIIKKSKNSRCWHGCGEGHT LLHC
8411	38779	A	8468	2	370	CSTSLIIREMQIETMMRYHLIPA RMAIIKK/SRCWQCGGEQETLL HSWKQPQ/LWRSSSGTARERQF LHPLLLKARIEITPPESLAVLKIP MEGTWMELEAVILSKLTQKQK TKH*MLSLTSGS
8412	38780	A	8469	2	194	CSTSLMIREMQIKTTVRYRLTS ARMAIIKKSKNSRCWHGCGEH RTLHCCLNWKERNVSYVSA
8413	38781	A	8470	341	496	

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8414	38782	A	8471	46	711	SLIHLELJFCIGLDVRLGKDFMT NNLKGNAIKTKINFWDLIKLN FCKAKRNSQ/RANR*QTEWEKT FIICTSDKGLTSRIYNKLLQISKK KTNNPIIKWAKDMNRQFSKEDI QMANKHMKKSTSLMIREMQI KTTVRYHLTSARMAIIKSKSINS RCWHGCGEHGTLHHCWK/SKS LYEKDCTRMFIAAQLAIKWTW NQPKGPSINAWIKDWCQSKTN HNK
8415	38783	B	8472	36	1199	
8416	38784	A	8473	3	184	FFFFLRRSL/DSVAQAGVQWR DLSSLQAPPPGFTPFSCLSLLSS WDYRRLPPRANFLYF**RRGF TMLARMVVIS*PRDPLASASQS AGIQKNSFFLETRVSAFVAQA GVQWCDLGSPPPPPGFK*FSC LSSLSSWDYRRLPPRANFLYF
8417	38785	A	8474	3	295	AAAFFVFFETEFRSVAQAGVQ WRDLDSLQAPPPGFTPFSCLSLP CSWDYRRVPPCANFCIFSRDG VSPC*PGWRSRDLVIHPSRPPK VLGLQAMS
8418	38786	A	8475	1501	1879	IRNTHAKIIECLLPFLTEL*CNF FFFFLRRSL/DSVAQAGVQWR LGSQAPPPGFTPFSCLSLLSSW GYRRLPPCANFFVFLVIERGFT VLARMVLMMS*PRDPPASASQA GITGVSHHARPTLK
8419	38787	A	8476	1550	2469	FFPPFFLRRSSPLPRLQCSCGMI LAYCNLRLGSSNSVASASGVA GITGTCHHTQ*IFVFLVETGFHH VGQAGLEFLTSGDLPTSASQA/ RDYRRDDHTRPEKCF/C*KTHIL WHSPSWSS/EERGSQFFSQDS*K SSRYPKLLGMWVIAINIYGTR T*K*EKFKTREYIGTHSHRGNH GVNTYHVASEKLH*YTYRMK KAKNFFFFLRRRELASVAQAG VQWRDLG/SLSQSPPGFTPFSC/P ASLRSDYR/RVLPPLANFFL YFFS/MRRGFTVFSR/MVIS*PR DQ/PASASQAGITGVSHRAR/L KIIFLFFFSETESRSVAQAGVQ WHDLGSRHRPPPGFTPFSCLSFP SSWDYRGPPRPPANFCVFSRD GVSPC*PGWRSRDLVIRPASAS QKCDWYRREPRPA
8420	38788	A	8477	1	2268	

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8421	38789	A	8478	1	2312	MAGPPSGPGRPEVCGAGRTRV AKARFRRRRAFASLGWSSGRE VVTFGDVAVHFSREEWQCLDP GQRALYREVMLENHSSVAGIG EDAPWGPFPCHSQHPPSQASIR GPCVYTVADVPVTGIAVIPPA VCF SRLKDCDTRTEDKEFLHKE DIHEDLESQAISENYAGDVSQ VPELGDLCDVSDRWGVPEG RRLPQSLSQEGDFTPAAMGLLR GPLGEKDLDCNGFDSRFLSPN LMACQEIPTTEERPHPYDMGGQS FQHSVDLTGHEGVPTAESPLJC NECGKTFQGNPTLFSVKQSHST GEA/SFMCDDCGKTF SQNSVLK NRHRSHMSEKAYQCSECGKAF RGHSDFSRHQSHSSERP YMCN ECGKA FSQNSSLKKHKV/HMS EKP YECNECGKA FRA/SSNLIQH QRIHSGEK/PYVCSECGKA FRRS SNLIKHHRTHTGEKPFECG*CG KAFSQSAHLRKHQVRVHTGEKP YECNDCGKPF SRVSNLIKHHRV HTGEKP* KSSACGKA FSQSSSLI QHRRJHTG\ EKP HVCNVCGK\AF SY* LQCESTRFIHTGRGRPYRC SVCGKA FSHSSALIQH QGVHTG DKPYACHECGKTFGRSSNLILH QRVHTGEKPYECTECGKTF SQS STLIQHQR IHNAGAEAP/YKCNQC GKA FNQSSKFSIHPQKVHIGEK\ PSPC VECGKGFSQSSSHFFQHRY
8422	38790	C	8479	194	458	
8423	38791	C	8480	214	378	
8424	38792	A	8481	107	345	GPLTCRYWEIHSQEPGPPRSLE MVLFSFSQN*SPVWSKEKNL*P *RDMR*/YAKPPGRCK*K*IQQ MTQMRGRNIQEKASP

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8425	38793	A	8482	1	1454	MHEEEGESGDSRVYMSTQCTH VTLNKFLGFVSESVSGLNIQES MKEVLRGQSLKHNPIREAGLET LQSGRQLERRGRLSGMARPLSL AAAGAPDLLFTALCSLLIEAQP LRPFDLQTTLTAAECHYTGKKF SLNEGKPVLRKNSQNTNWEFG TIITWGRGYACVSPGDQSPVWV PTERLKL RVNSDKESHREKTSK SETAFIPAQDLAYNRFYLIILLT LSVSPVSPQTDLPAT*NYSYWA YVPFPPLIRPLTWMDAPAEIYT NDSVYMPGATDDHCPTRPREE GTAFNVMTMGYKYPPCLGHAH VDGCIHLQAQIWAAYLPERLAT REQGHLISLSLSPLRQMKGGVI GDTPNFQYKPVGKPCPKNFEGP SKILIWEDCVNSHVVLKND YGLVIGWAPKGYFK/NNCSSGG RECLEATYFISHWEDKDHHTL HRRVSSFFPL*WEDKGITPPRPH MIFPILSEHSELWKLAIAMSGL
8426	38794	A	8483	49	1393	AEPAPTHLPPPPSTAPQPERNSC CISQQSFSVP*/SPDSDRPRGRH /SPPPP/SPCPPPPCLPPPKSTTAM PTRCQCPCPPPIPTVAAFPLPPSHF LRTLPA PRPPTQPPPLSH/TTHPP EQRTLGPKFRLFSTPSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPQTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRACL PQCRDKELLITK RK YRKKKDFAA GLEDVTEFG REENPRHTFIYSLPLGLQKHQV LTVDIGFGGTAIMTGIA RVPLA GAAGGPGVGRAAGRGVPAGVP IPQAPAGLAGPVRGVGGSQGV MTPQGRGTVA AAAVAATASIM APPPGMRPPMPPIGLPPARGTP IGMPPPGMRPPPPGIRDCGSLT PLGDCVCLKGSLARVLCRAIVQI YSICVLLTTSEQQLSIRIHPQNA V

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8427	38795	A	8484	49	752	AEPAPTHLPPPPSTAPQPERNSC CISQQSFVSP*/S/SPDSDRPRGRH /SPPPP/SPCPPCLPPPKSTTAM PTRCQCPPPPIPTVAAFPLPPSHF LRTLPAFRPPTQPPPLSH/TTHPP EORTLGPKEFLFSTSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPQTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRRACLPPQCRDKELLITK KKYRKKKD
8428	38796	B	8485	511	1349	
8429	38797	A	8486	3	431	ADAVGGPGGPGMAGCDGLPG GFGSDIRPRLWLWLGPRLWSS* RGTNIIILASVPKLLLM/DCYA LARDRTATLG/TFDAISK TASN WIPDLWKETVTFKFPYQFTDHL L/VKTHTRVSKQKTQVPAVATT AARQTMEGQAPVEYI
8430	38798	A	8487	1	470	
8431	38799	A	8488	3	314	
8432	38800	A	8489	1	458	
8433	38801	A	8490	1	855	PTRPLVLRVGATARALPRPSRS CSPSAVVPSAPSSCPPQPRVTPK PEPEPEQVIKNTYTELKVPPEDED CIISMEKLSTASGYSDVTDKAI GSLAVGHLLTKCSHAFHLLCLLA MYCNGNKDGSQCPSCKTIYG EKTGTQPGQKMFVLRFQMSLP GHEDCGTILIVYSIPP/GIQGP.EH PNPGKAVSLPEGFPAQCYLPEQ RPGPAKSLRAP**RWA WK/RRLI FTVGHVPAPTGETDTVVWNEI\ HHKTEMDRNITGHGYPDPNYL QNVLAELAAQGVTEDCLEQQ
8434	38802	A	8491	1	3797	MEYYAAIENDEFMSFVGTWML LEIIILSKLSQEQKTKHRMFLSID FGFSNLFTPGQLLKTWCGSPPY AAPELFEGKEYDGPKVDIWSLG VVLYVLVCGALPFDGSTLQNL RARVLSGKFRIPFMTGLVPEL DKRLKAGCLSAIECEHLIRHML VLDPNKRLSMEQICKHKWML GDADPNFDRLIAECQQLKEERQ VDPLNEDVLLAMEDMGLDKEQ TLQSLRSDAYDHYSAIYSLLCD RHKRHKTLRLGALP

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8435	38803	A	8492	1	2563	MGDFNTPLSTVDRSMRQKV DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDNIG SKALLSKCKGTEIITNSLSDHSA IKLELRKKLTQNHSTTEKLN LLNDYVWHNEMKAEJMFSET NENKDTTYQNLWDTFKAVCRG KFIALNAHKKRQERSKIDTLTS QLKELEKNQEEVESLNRPTG AEIVAINSLPTKKSPGPDGFTA KFYWRYKEELVPFLCLKFQSIE KEGILPNSCYEASIIIPKGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNICKSINVQHINRTKD KNHMIISDAEKAFDKIQPFML KTLNKLALQNLKLISN/SQQSLR IQNQCTKITSILIHQ*QTNREP NH E*TPIHNCFKENKIPRNP TYKGC EGPLQGELQTTAQGNKRGYKQ MEEHSMMLMGRKNQYLENGHT AQGNL*/IQMPSPSSY**LSSQN WKLL*SSYGTKKIGPHSQVNP KPKEQSWRHHTT*LQTILQGY S NQNSMVLAPKQR*RPMEQNRA LRNNAAYLQLSDL*QT*QKQA MGNGFPI**MVLGKLASHMEK AETGSLPYTYLKN*FKMD*RLT H*S*NHKNPRRKPRQYHSHVIRH GQGLHV*NTKSNNGKSN*RM GSN*TKELLHSERNYHQEQAT HKMGENFRNLLI*QRANIQLQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
8436	38804	A	8493	1	1839	MPRALAFQAPVNIQAEQAGTA MNISVPQVQLINPENQIVEASSN LWELSAETTFFAISLLPFLISNS MPDGTNLNLSDEGEEPSPEALV RYLSMRRTVGVADPRTEVME DLQKLLPGFPGVNPQAPFLQVA PNVNFMHNLPMQNLQPTGQL EYKMSGLPLSPRLPLISWSVLPT LFLAEQSLLOPPTLQLLNGMGP LGRASDGGANIQLHAQQLLK/ RPRGPSPLVTMTPAVPAVTPVD EESSDGEPDQEAQVQRYLANRSK RHTLAMTNPTAEIPDLQRQLG QQPFRSRVWPPHLPVDQHRSTY KDSNTLHLPTERFSPVRRFSDG AASIQAFKAHLEKMGNNSSIKQ LQCECEQLQKMYGGQIDERTL EKTQQQHMLYQQEQHHQLLQQ QIQQPAQSQQVTIQVQEPVDML SNMPGTAAGSSGRGISISPSAGQ MQMQHRTNLMTLSYGHRPLS KQLSADSAEAHRLKWETREKQ LEDSSVSSNTGGDVTNEGKST ESADFGFSNLFPPGQLLKTWCG SPPYAAPELFEGKEYDGPVKVDI WSLGVVLYVLVCGALPFDGST LQNLARVLGKFRIPFFMSTG YFHLGSHCNVVLNAKDKVGF
8437	38805	B	8494	1	3879	
8438	38806	A	8495	1	4065	MGKKQSRKTGNSKKQSASPPP KKRSSSPATEQSWTENDFDEL EEGFRRSNYSELREEIQTKGKE VENYEKSLEECITRITNTENCLK ELMEPKTKARELRKECRSLRSR CYQLVERVSAMEDEVNEMKDT HRLKVKGWRKIYQGNKGQKK AGVAILVSDKTDKPTKIKRDK EGHYMMVKGSIQQEELTILNIY APNTGAPRFIKVLSDLQRDL SHTLIMGDFNTPLSLDRSTRQ KVNNNTQELNSALHQA
8439	38807	A	8496	1490	1813	TGNLQNGRKLFPHTLTKG*YP ESMMNSNKFTRKKQTTPSKSG RRT*TDTSQKKTQMPPKNT*KN AHHHWPSEKSKSL*DTISHQ LEWQSLKSQETTGAAGEDVDK

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8440	38808	A	8497	1614	3085	AGEKNKADKQLQQSLRIQNQC TKITSILIHQQQTNRPNHSTPI HNCFKENKIPRNPTYKGCEGPL QGELQTTAQGNKRGYQMEE HSMLMGRKNQYHENGHTAQG NLQI/QMPSPSSYQ*LSSQNWKK LLSSSYGTTKIGLIHQVNPCKPK EQSWRHAT*LQTLQGSYNQN SMVLVPKQRYRSMEQNRALRN NAAYLQLSDL*QT*EKQAMGK GFPI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RFKR*T* NHKNPRRKPRHYHSGHRHQGG L/LCPKHQKQW/HTKAKIDKWD LIKL/IELLHSCRNYHQSEQATY KMGENFRNLLI*QRANIQLQ* TQTNLQEKNKQPHQKVGEHGE QTLKRRRLCSQETHEKMLIIT GHQRNANQNHNIPSHTS*NGN /QLKSQETTGADEDVEK*EHFY TVGGTVN*FNHCGSQCGDSSGI *N*KYHLTQPSHYWVYQTQTIN HAAIKTHAVCLLRHYSQ

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8441	38809	A	8498	2	2013	LNQEEVESLNRPTGAIEIVAIINS LPTKKSPGPDGFTAKFYWRYK EELVPFLLKLFQSFKEGILPNSC YEASIIIPKPRDITTKENFRPI SLMNIDAKILNKILANRIQQHIK KLIHHDQVGFIQMGQWFNICK SINVIQHINKTKDKNHMIISIDAE KAFDKIQPFMLKTLNKLQAN LLKLISN/SQQSLRIQNQCTKITS ILIHQ*QTNREPHE*TPIHNCFK ENKIPRNPTYKGCEGPLQGELQ TTAQGNKRGYKQMEEHSMMLM GRKNQYLENGHTAQGNL*/IQM PSPSSY**LSSQNWKLL*SSYG TKK/GPHSQVNPKEQSWRHH TT*LQTLQGYSNQNSMVLAPK QR*RPMEQNRALRNNAAYLQL SDL*QT*QKQAMGNQFPPI**MV LGKLASHMEKAETGSLPYTLY KN*FKMD*RLTH*S*NHKNPRR KPRQYHSVHRHGGQLHV*NTK SNGNKSQN*RMGSN*TKELLHS ERNYHQSEQATHKMGENFRNL LI*QRANIQLQ*QTQNLQEKN KQPHQKMGKGHEQTLLKRRHL CSQKTHEKMLIITGHQRNANQN HNEIPSHTSQNGD/QLKSQETT AGEDVEK*EHFYTVGGTVN*FN HCGSQCGDSSGI*N*KYHLTQP SHYVVYVYQRTINHAATKTHAH VCLLRHYSQ
8442	38810	B	8499	1	2860	

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8443	38811	A	8500	3	2202	EGRNKDVI* ^N QREQRHNIPESL GHIQSSV* ^{REI} *NTKCPQEKAGK IQN* ^{HPN} ITIKRTRKARANTFKS * ^{QK} ARNN* ^{NQ} SRIEGNRDTKNP SKN** ^{IQT} TIREYYKHLHANNLE NLEEMDKFLDTYTL ^{PRLN} QEEV ESLNRPTGSEIVAIINSLPTKKS PGPDGFTAKFYQRYKEELRIKY LGQILTRDVKDL ^{FKENY} KPLLK EIKEDTNKWNIPCSWVGRINI VKMAILPKVIYRFNGIPIKLPTF FTELEKTTLKFIWNQKRARVAK SILSQKNKAGGIMLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEIMPHIYNYI ^{IFDK} PEKN KQWGKDSL ^{FNKWC} WENWLA CRKLKMDPFLTPYTKINSRWIK DLNVRPKTIK ^{LEENL} GNITQDI GMGKDFMSKTPKAMATKAKID KWDLIKLSFCTAKETTIGVNR QPTKWEKIFATYSSDKGLIFRIY NELKQIYKKKTNNPIKKWAKD MNRQFSKEDIYAAKRHMKKCS TSLAIREMQIKTTMR ^{YHL} TPVR TAIIKSGNNRCWRGCGEIGTL LHCCWDCKLVQPLWKS ^{VWRF} LRDLELEIPDPAIPL ^{LG} YPKDY KSCCYKDTCTRMFTAALLTIK TWNQPKCPTMIDWIKMWHIY TMESYAAIKNDEFMSFVGTWM KLEIIILSKLSQGQKTKQRFSLI DGN

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8444	38812	A	8501	437	2163	KQKCNISHLWNAVKVERIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWNIPCSWVEESIP*K WPYCP*FTDSMPSPSSYQ*LSS QNWKLL*SSYGTKKEPASPSQ S*AKRTKLEASHYLTNSYSTRL Q*PPGKRGPPEVQGHNADENN HTFDRQGNRRHEHSIDQLAVT DVHSTTAETFLSTRGGFSKID HMLGCKTNLKNYKEIEIQSIFS NHNEIKQEINSRRKTRKSTNLW ELSSALLMNGSEKKTQVNLN WKLMAKMQHITLMECSERK NKIPRNPTYKREGPLQGLQT TAQGNKRGYKQMEHPMLMG GRINTVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLRFIWNQK RARIASLSQKNKAGGLTLPD FKLFYKATVTKTAWYWYQNR DIDQWNRTEPSEIMPHIYNYVIF DKPEKNKQWGKDSLNFKNWCW ENWLAIACRKLKLDPLTPYTKI NSRWIKDLTVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTGKET TIRVNRQPTKWKKIFATYSSDK GLISRIYNELKQIYKKKTNNPIK KWVKDMNRHFSKEDIYAACK HMKKCSPLAVREMQIKTTMR YHLTPVRMAIHKSGNRCWR GCGEIGTLLHCWWDCKLVQPL WKSVMQFLRDLLEIPDPAIPL
8445	38813	A	8502	1	2001	MPHIQVMLMQEMDSHSLGKLC PYGFAEYSPSSCFHGFVLSVC GSSRDKATQVRDALVRQVIVN GGIVLDQFAVHDVALADLIDL LVDSLAMMLCGVPTTGDPFVA FALGHPDDFDHLILPKHLVDRY LLEPLLPVQLLSHSAVHLD LHQFCSDFSQYGIQLTRDVKDLF KENYKPLLKEIKEDTNKWNIP CSWVGRINIMKAMRPR*FID SMPSPSSYQ*LSSQNWKLL*SS YGTKKEPVSPSQALA
8446	38814	B	8503	152	3166	

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8447	38815	A	8504	15	2745	HPTVNIRQINETESQQGYPGIEL SSAPSGPNRHLQNSP/PPNQQNI HFFQHHTTPIPKLTT*LSLDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEH TNYLSDHSAIKLELRINKLTQSH STTWKLNLLNDYVWHNEM KSEIKMFFETNENKDTTYQNL WDAFKA VCRGKFIALNAHKRK QERSKIDLTLSQLKELEKQEQT HSKASRRQEITK
8448	38816	A	8505	2853	3925	AVGPSVRTPRPYLCVRKDVHD VVPILRPSATSLFMPRAAGQGG QKAGGTEKSSGP*KDDV*RLQP PNGFRHII*VQ*TCRKGCPLSK RNTFQFQN*R*NLLYPALPNIPH SSVEEGVGS*ARSEDLEGAQLP *LLARLFTCRSNTYRGLKFTEA* GGE*QSI CYSTRRANYPKY/HM HPIQEDPDS*SKS*VTYKET*TP TQ**WETLT/PPLSTLDRSTRQK VNKDTQELNSALHQADLID/TT ELSTPNQKNLHFFQHHTTPIPKL TTYLEVKL/PQQM*KNRNYNKL SLRPQCNQTRTQD*ETHSKLLN YMETEQPAPE*LLGT*RNESRN KDV L*NQREQRHNPESLGHQIS SV
8449	38817	A	8506	2	376	IPYLP*STYMETGMIVVVGQIY GYHHYMQDRIDDNGWCAYR SLQTICSWFKHQGYTERSIPTHR EIQQALVDAGDKPATFVGSRQ WIGSIEVQLVLNQLIGITSKILFV SNTRKNKKVGNIVS
8450	38818	A	8507	1	1008	
8451	38819	A	8508	218	343	
8452	38820	B	8509	306	1434	
8453	38821	A	8510	3	659	

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8454	38822	A	8511	3	1990	EPHRIASPRFQAFDSGDTDRTL *FLSDIEEELTRGDPEQRHVPL RRKSEWKWAADRAIDSRWN WLQAHVSDLEYRIRQQTDIYK QIRANKGLIGLGEVPPPEHTTD LFLPLSSEVKTDHGTDKLIESVS QPLENHGAPIGHISESLSTKSC GALRPVNGVINTLQPVADHIP GDCSDAEEQLHKKQRLNLVSSS SDGTCVAARTRPVLSCKKRLV RPNSIVPLSKKVHRNSTIRPGCD VNPSICALCGSGSINTMPPEIHYE APLLERLSQLDSCVHPVLAFPD DVPTSLHFQSMKLSQWQNKPF DKIKPPKKLSLKHRAPMPGSLP DSARKDRHKLVSFLLTAKLSH HQTRPDTRHQHLLDVGAVPM VERVTAPKAERLLNPPPPVHDP NHKSMRLRDHSSERSEVLKHH TDMSSSYLAATHPPHPSPLVR QLTSSDSPAPASSSQVTASTS QQPVRRRRGESSFDINNIVIPMS VAATTRVEKLQYKEILTPSWRE VDLQSLKGSPEEENEPAAPDV SSSHSLSEYSHGQSPRSPISPELH SAPLTPVARDTPRHASEDTRC STPELGLDEQSVQPWERTFPL AHSQPAECEDQLDAQERAARC TRRTSGSKTGRETEAAPTSPPIV PLKSRHLVAAAATAQRPTH
8455	38823	A	8512	119	739	ADDRDHLHIQTWCAKAPVFLQ PGSSWLSTKGKKM/PETPASDE PPLRQPAVRFELQHAAPPDQLQ LGSFGHS*GPSSDTGQPAAGRW PRRQP*AAVQDLGPQTRGSASP ESQTVLPAAPSPAGSARPHGSM SASAPSPASQMSKPPCAAAC LRGSGAGGGTVGPCLEPGGSAP PRARLPRCAAGSARPGAAAGPP PGAGTTTAVP
8456	38824	A	8513	1	343	MRMCLRIPTLMTKCTNWHVT GHLCRPT/MREPTPEP/WTGDDT TA*METRWPAEQPALAERLFR AAPRGAFAGIAAPSPAAPPQPG SLGILPEPTPAQAWAARNQLRG RIKERGS

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8457	38825	A	8514	3	405	KKFNPAGERVCTILVDPSIPSTA YPSYGVPHS*GPSLSLPHL/SSSS RPSSISCPLNGPWKGCs*PPCRA QCAQPQQT*ESCHS/SSNCIPP AWEGETPSKKNKINGNPWSKIR DKTSGGEVEVWGLVAVAPVM
8458	38826	A	8515	100	1397	PPASTYLMLERLKAPWSAALQ RKYFDLGIWTAPISPMALTMLN GLLIKDSSPPMLLHQVNKTAQL DTFNYSQSCFMQSVFDHFPEILFI HRTYNPRGKV/CIYLPGGWTSQ AAGGSSCPSSLCHPC/ARRDT/ CRPVPDVPSIQEV*SSMGESLYH PGGSSFPSTAYPS/SWSSPQLRSF SQPSTFVSSSRPSSISCPLNGPW KGCS*PPCRAQCAQPQQT*ES CIHS*ATASLQSPCSFTHTGCS TTASGWLTAAGEAELRAATTSR ASRSPPTSSASSLVPPHLRNKV WLLCSVTCRSLQTRQTSTRAC VPRTIMLPQTPSKAPNWSSW* NPTSTSPMPSAQQQPNCWA ASLLWSRNPHTSLALAQKR*TY RSWKIPIRCSPLPAAAAATLTR PSTCPAATS*PCSVPAARCSSPT CCRLSGRQAVLPV
8459	38827	A	8516	1	326	CLTQMYFLIS/FANVDTFLLAIM ALD/RLLAICSAALRYCSITPGIYS HFYCDAYLLMKIACSIHVNQH VFLGAVVFL/APCALILVSYIRI AAAILRIPSPTRRRKACISIC
8460	38828	A	8517	2	669	TISYPQCLTQMYFLISFANVDTF LLPIMALDHYVAICSAIQ*CSII P/ELCQGLPVLA*AGSSLISPVHT VIMSRlafCSSAQISHFYRDAY LLMKIACSHT*INQHVFLGAVV LFLAPCALILVSYIRIAAILRIPS PTRRRKACISICSHLSLVTIFYG TVLGICI*PPDSFSAQDAIATIMY TVVTSMLNPFYSLMNKEVQEA VRRLFSRGSHSSWCW

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8461	38829	A	8518	1	3594	MVAAAAATEARLRRRTAATAA LAGRSGGPHCVNGGRCNPGTG QCVCPAGWVGECQQCHCGGRFR LTGSSGFVTDGPGNYKYKTKC TWLIEGQPNRIMRLRFNHFATE CSWDHLYVYDGD SIYAPLVAA FSLGIVPERDGNETVPEVVAT GYALLHFFSDAAYNLTFGNITY SFDMPNCSGRGECISNSSD TVECESENWKGACDIPHCTD NCGFPHRGICNSSDVRGCSFCS DWQPGGCSVPVPANQSFV
8462	38830	A	8519	1	471	ALCAPQPGKCFCTTKGSSG/DE CQLCEV/ENRYQANPLRGTCYN TLLIDYQFTLSQEDDRYYTAI NFVATPDEQNRDLDMFINASK NFNLNITWAASFSAGTQAGEE MPVVSKTNIKEYKDSFSNEKFD FRNHPIITFFVYVSNFTWPIKIQ VQTEQ
8463	38831	A	8520	1	4289	
8464	38832	A	8521	1	3488	MDYGVLTRLTGSSGFVTDGPG NYKYKTKCTWLIEGQPNRIMR LRFNHFA TECSWDHLYVYDGD SIYAPLVAA FSLGIVPERDGNET VPEVVATSGYALLHFFSDAAY NLTFGNITYSFDMPNCSGRG ECKISNSSDTVECESENWKG ACDIPHCTDNCGFPHRGICNSSD VRGCSFCSDWQPGGCSVPVPA NQSFWTREYSNFKALPRASH KAVVNGNIMWVVGGMFNHS DYNMVLAYDLASREWLP
8465	38833	A	8522	4794	5740	YICNWKMKDSSFSLVQSPRS PGSCGLSGWGWGCPRVASAGS ACSCNSAVPARRTQACRRELI GGRSTIFTDVQGGWAGPGTVN EGNSACPPTLRVTVAAWLSLLF VLCRCVAASVPSLVRLRWGPQ CSGPWGA WAPPWAARVSQPG AGPGRGAE AQLPAASIQWPC HQAPHLLLVLALVTSQGPSRCR GFCLAGPCQGGPGGLJLIFCHW NVPLQFSSLFFF*DGVSLLLPR LECSGSISGHCLNRLPGSSDRPA LGS*VAGDYRCLPACSANFFVF LVEKGFHHVGRAGLKLL/MVIH LPRPPRVLRLQA

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8466	38834	A	8523	594	2868	CWTSRNRPRIPGSCHPMELPRPF RGKAKVQNHQLVHHNKALIN RGSLSFWLDDGAIQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSLWNEDPFVCEYQ GQSSDLPPQPVNAGGSGGGGS GGGSEGGSGEGGSGEGGSEG GGSEGGSGGGSGSGDFDYEK MANANKGAMTENADENALQS DAKGKLDVSATDYGAIDGFIG DVSGLANGNGATGDFAGSNSQ MAQVGDGDNPLMNNFRQYLP SLPQSVCECRPYVLSAGSEIGAA CASRSGYDNKGVRDIGYTDCK RSEDLPLRHQLGGKKA/QFTL QGFTLPEGAPAGNSGSLAVHK TAQSSYRHHALLILTPMSGTRF PPIPGPVNNIRVFPFAPSSECRC YWSWVPGSPVHCQSDGSPVPI SYAPLASQYSSSFLFFNRQPYA PYDYLVSVMTPSRTLREQIRIYA PSAPRLPPPEVYCSNSTIVYVRN NPSGPTPGFAGGTLLEGRSGGP FRFYAKRAKGDVLPFSLNLPL QTLIRFMVDIACGMEYLSRNFI HRDLAARKCMYEFWRTRGWE TAAAYVGGGTTFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFDTDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTLGLQ/MGLDPND
8467	38835	A	8524	302	409	
8468	38836	A	8525	199	359	ARRQQSVSVKSYRWEEEDQHCG ELQGSE*VSDGLFKPP*S*HGW VEEERQKEQN
8469	38837	A	8526	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLSILVLIRIVMMVMSMLP QLALSGWGRFVLP
8470	38838	A	8527	118	445	AAGGEPGDAPWVPGVWEPPES VCRGPPPSSTFPHVPLSTFGASG PENSRDCLSWLSPQH*AA*VASG NNGPQAAQGSLSGIPDAATLSG I*RASILHVSVEIISSPGFR

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8471	38839	A	8528	1	770	MRVLGIETSCDEGTGAIYDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCWKIPAPNFR CALLGSAAYAVNHGTGLSKKP TTLGSDHSHKTPAQLAKRAGEA RRNGWQGA LFPWESARSGEEE TP/VICRH*HSHRAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVL D
8472	38840	A	8529	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRRPFRGKAKVQNH QLVHLQSSHQFWLPHFLAG* WGD SGLGGGS/EGGGSEGGGSE GGGSEGGGSGGGSGSGDFDYE KMANANKGAMTENADENALQ SDAKGKLD SVA TDYGA AIDGFI GDVSGLANGNGATGDFAGSNS QMAQVGDGDNSPLMNNFRQY LP SLPQSV ECRPYVFGAVRHDV RRIRVTGVT RVPPEEVDTSVH SRGAHRIRSGFAPKRSVRVTTD TCIKRNSTCGVKLSLWDGGGF
8473	38841	B	8530	1	811	
8474	38842	A	8531	1	1044	
8475	38843	A	8532	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRPVPPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCR TSGSVYITLKKCKQREGS RAMLP GPFPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQGQSSDLPPVFNAGGGSG GGSGGGSEGGGSEGGGSEGGG SEG D GSEGGGSGGGSGSGDFD YEKMANANKGAMTENADENA LQSDAKGKLD SVA TDYGA AID GFGIDVSGLANGNGATGDFAG SNSQMAQVGDGDNSPLMNNFR QYLP SLPQSV ECRPYVFGAGKP YEFSDCDKIKILRGVFAFLLYV ATFMLPVIANIAIPQKRPFMQQT RCEVQCRE D IEVQKLKSYDKLL ASINKKPGVNGWQKRRTVNA GEAHDQQALDYALYHLRIMTP AHDERS SIAAKGLTGE GYKGH VFWDTEVFLLPFLHFS DPTVAR SLLR YRWHNLPGRARRKR DGN GWAGGAPISVGKARAAKK
8476	38844	A	8533	609	855	

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8477	38845	A	8534	369	1278	GHTACFWYSQGRHPGPELSPFL *GPG*NAGHVISMPAARPMPC LGTGGLDVLHHLRDLPPAAL PGSAWPGEGALPLPGQVSGRG RSAACLQPGAWPGRGAAPVRR RPRAAAGSVREAELESPLHA AHRDC*LARKLNSGGYIPQAEY GKHAGLPLPGARALSCGCRAR APVPAALPHLLDHQDPGPAGR IYGTGAGTQTLDGSAPTSRAL GSTQMPEARPLAGWGVAGV WSRG*SR*TRGSAS/SPRPRRCA LLALPGAASVGLDRLARNPRGSR PPKAPSGRGGPLPPHRSTPRR
8478	38846	A	8535	3	2494	YQRQSSPEDPAETASPTYALIA ACQSEIQLQTRQQPCDMPAGPL DCDPVKGSSSRKRMFLMNAPPV VALQPKWEASVPPGSFRPECF SEADKGVESMSPTMHKELPAL AACGLVADFPVGEETADFG PLVLDSDSDSVDRDIEEAIQEQ L/KGGGSRCKRELAHSS/APTAL CSPKLVPGGG/GGPGSQVGSS KDQGSASPVMSRADSFQESIR AEIEQFLNEKRQHETQKCDGVS EKKPDTHENSASLSKSHQEP TKVVHRQGLMGVQKEFAFCRP PRLAKTNVQPRSLRSKVTTTTT QEKEGSTKPA TP/TRPSEAVQN KSGIKRSASTARRGKRVTSVQ APEASDSSDDGIEEAIQLYVQV KTRKEADGDPQRVQLQEERA PAPPAHSTSSATKSALPETHRKT PSKKKPVPTKTTPGPGDLAD IISPKIPKETKAPPTSPASRSKF VEWSSCQADTSAELNVLDFK TILP/APMEGSDGSLASPLFYSP NVPSRSDGSSSVSDSDSIEQEI WTFLLAKVQSRSLARGAAGQ APERVEKQAPAGAEELPKSKRD SCEGSRKKPPSVFGSRAERTKP RPSCSSVSDSDSIELEIRKFLVE KAKESGVPGQAQPLWKPTLA GEEGLRSPAKQEGLTSAIVAGIS AALGPEHTWVPGATTPTPSVA PVLVPAVPTHWKKLAPACGGP

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8479	38847	A	8536	1	2463	MHKELPALAACGLVADFDPVG EETADFGPLVLDSDSDSVDR DIEEAIQEYL/KGGGSRCKRELA HSS/APTALCSPKLVP GSGG/GG PGSQVGSKKDQGSASPVMSRA DSFEQSIRAEIEQFLNEKRQHET QKCDGSVEKKPDTHENSAKSL KSHQEPATKVVHRQGLMDVQ KEFAFCRPPRLAKTNVQPRSLR SKVTTTTTQKEGSKPA TP/TR PSEAVQNKSGIKRNASARRGK RVTSIAQAPESDSSDDGIEEA IQLYQVQKTHKEADGPPQRV QLQEERAPAPAHSTSSATKSA LPETHRKTPSKKKPVPTKTDDP GPGDLADHSPKIPKETKAPPP TSPASRSKFVWSSCQADTSAE LTA VLDIFKTL/P/AMEGSDGS LSASPLFYSPNVPSRSDGDSSSV DSDDSIEQEIWTF LALKVQSRSL LARGESCPQAAQGPLSPPGLSS QTGSPKAPLSKTLDDL/GCKRK HRGG/SKAQPARPRDGRAPLG WDL SIQGTASEAPGGEGAARVP GDTRTSQGQKTD EARHLDDK KSSDKSSSLDSKDLDTAID LLRESQGPAPSPGSLSDNSSSV DSDSIEIRKFLVEKAKESGVP GQAQPC LWKPTLAGEEGLRSP AKQEGLTSAIVAGISAALGPEH TWVPGATTPTPSVAPVLVPAV PTHWKKLAPACGGPGQSLDID
8480	38848	B	8537	1	3345	

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8481	38849	A	8538	1	1339	MTKKSPGPDSTFGHWCVSIPS GYERSRLKVTLP EEGRGALPFL VSVAISSGSCSDNNAAVPTVLE GATTVISAAA VLRDPHDGAREII LEAMTISA VAI AAEISWTSQCG LCLHPGMFMPYRHGDGIRDLLP LVL SATICA EFFKGDSKKPSKK RVKRKPYSTTKVTS GSFNENI RRYAVHTNQCRPHGSRVKKK RYPQEDDFHHTVFSNLRLDKL QPTLEAEESLVHKDRGDGERP VNARVVQVAPLRLESSYSGIT CQENNLDAKKA/TP/CRTPYMT SLTRTPHTTSLTRILSTA/SANEA ADKGANEDAAQGANEDAAH GMPARMPPRASPTRSPPRASPT RTPPRASPTRTPPRASPRTPPT GSPRRTPPRASPTRTPSTASPTR TPPMASPTRTLTALLTRMPCT ASLMRTPYTSLMRVPYMTSL MTPYKAR
8482	38850	A	8539	1	3090	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDDSDVDR DIEEAIQEYLVKGSSKDQGSASP VMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSEKKPDTHE NSAKSLSKSHQEPATKV VHRQ GLMGVQKEFAFCRPPRLAKTN VQPRSLRSKVTTTTTQKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8483	38851	A	8540	1	2919	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDDSDVDR DIEEAIQEYLVKGSSKDQGSASP VMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSEKKPDTHE NSAKSLSKSHQEPATKV VHRQ GLMGVQKEFAFCRPPRLAKTN VQPRSLRSKVTTTTTQKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8484	38852	B	8541	1	1122	
8485	38853	A	8542	1	1074	
8486	38854	B	8543	1	1017	

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8487	38855	A	8544	1	1436	MNLPRAERLRSTPQRSLRDSGD EDGKIDVLGEEDEDEVEDEEE EASQQFLEQSLQPGQVQARWG GVALPREHIEGGGGPSDPSEFG TEFRAPPRSAASSEDARQPAKP PYSYIALITMAILQSPHKRLTSL GICAFISGRFPYRRKFPWQWQ SIRHNLSLNDCFVKIPREPRGPG KGNVWSLDPASQDMFDNGSFL RRRKRFQRHQLTPGAHLPHFPF LPAAHAAALHNPRGPLLGAAPAP PQVPVGAYPNTAPGRRPYALLH PHPPRYLLLSAPAYAGAPKKAE GADLATPA/ALPVLQPSLATVK PVGQFCNSSSGIRRRTGNGCAP TKGAVLGGHLSAASAAAASVSG GGRGLWADIARALWAERDLTS FFSIAHAQFPGRVRRALLEPGSR QPHSPTGVQKRPLLAPAGLGQ SKSSETTENRG/CPMSCQLLAGL RSNSPLSVVRKRLRADLPSFIAN KRPGRAATAAEPRRDFL
8488	38856	A	8545	1	1287	MNLPRAERPRSTPQRSLRDSGD EDGKIDVLGEEDEDEVEDEEE EASQKFEQSLQPGQVQARWG GVALPREHIEGGGGPSDPSEFG TKFRAPPRSAASSEDARQPAKP PYSYIALITMAILQNPCHKRLTSL GICAFISGRFPYRRKFPWQWQ SIRHNLSLNE*FVKIPREPGHPG KGNVWSLDPASQDMFDNGSFL RRRKRFKRHQLTPGAHLPHFPF LPAAHAAALHNPRGPLLGAAPAL PQVPVGAYPNTAPGRRPYALLH PHPPRYLLLSAPAYAGAPKKAE GADLATPGTLPVLQPSLGPQPW E/RGQGGGVATGR/GCISFSIESI MQGVRGAGTGAAQSLSPTVAW SYCPLLQRPSSLRTILQQQQQH QEEDCANGCAPTKGAVLGGHL SAASALLRYQPVAKGLWADIA AAPLGEGTSPVFL

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8489	38857	A	8546	202	823	AQNPTAFGVKHTSSGGEETFPN IRGIKSPPOLSSSIRL.SKNILST TGKTVHQTRDDQPRDFFKKR NRVNESHQKSSNMNAGPSWVK VQHSKNSSGKRQSKSQVPHASS QPRSSLTAVTQPTEEKLIESISPE ARRKRNP.LGFRCCGASRNK.LFL DFQSMKIIKENADEDSASDLS/D SGKNSSHSSPHTSRSSQSS*RN RVNESHQKSSNMNAGPSWVKV QHSKNSSGKRQSKSQVPHASSQ PRSSLTAVTQPTEEKLIESISPEA RRKRNP.LGFRCCGASRNK.LFLD FQSMKIIKENADEDSASDLS.DSE RIPIPSP.LTPPDLN.LRAEEIGSSL L
8490	38858	C	8547	219	1013	
8491	38859	C	8548	252	452	
8492	38860	A	8549	25	443	
8493	38861	A	8550	20	1371	RLRGPALGAGGGSVTLRL/PRS EQAARKEAGLNTMIPLEKPGSG GSVPRRHLRLPGGSSGS*AGRA RTPPPQARGLLTEIRAVVRTEP FQERLQPVPRAGSWAGGKFSSG EK.MYKEKILGKNLLQSS*EKRR K\SQDCRM.EIHEIAVLELAQDN PWVINLHEVYETASEMILVLEY AAGGEIFDQCVDREAEAFKEK DVQRLMRQILEGVHFLHTRDV VHLDLKPQNILLTSESPLGDIKI VDFGLSRILKNSEELREIMGTPE YVAPEILSYDPISMATDMWSIG VLTYYVNL.TGISPFLGNDKQETF LNISQMNLSYSEEFVLSA VDFIRTL.LVKKPEDRATAEECL KHPWL.TQSSIQEPSFRMEKALE EANA.LQEGHVSVPINSDTDKSE TEESIVTEELIVVTSYTLGQCRQ SEKEKMEQKAISKRFKFEPELL
8494	38862	A	8551	1	1275	
8495	38863	A	8552	1	4173	

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8496	38864	A	8553	2	5115	PDQFHNMDLRGGPHDGVITPRS TSDTDLVTSDSRSLTMVSSYY SIGHSQDLVIHWDIKEEV DAGD WIGMYLIDEVLSENFLDYKNRG VNGSHRGQIIWKIDASSYFVEPE TKICFKYYHGVSGALRATTPSV TVKNSAAPFKSIGADETVQGG GSRRLISFSL.SDFQAMGLKKGM FFNPDPYLKISIQPGKHSIFPALP HHGQERRSKIIGNTVNPWQAE QFSFVSLPTDVLIEVVKDKFAKS RPIIKRFLG
8497	38865	A	8554	202	260	ARVHIQPVSLKQRFPLELRHH QDSEAHAPPPGAAASRGGI*V AWPAPRAGVVSLGCRSSWTA AMELSAEYLREKLQRDLAEH VLPSPGGVGQVRGETAASETQ AGERVPSRRAPAHPL
8498	38866	A	8555	72	578	GSKGSVAGARAWVVSLLGCRS RWTAAAMELQRRIPPREAAGP WRRSMWRWRTRPSTVAPVASE SWWCRPSSRGNRCFQRHSLDPS MTIHCDMVITYGLDQLENCQT CGTNYIISVLLNLT LIVEQINTKL PSSFVEKLFIPSSKLLFLRYHKE KEVVAVAHAVYQAML
8499	38867	A	8556	299	939	LPSPGGVGQVRGETAASETQVL YRAMRRVTAANQAFFSEAEVT AAKERGIVLPLRC/DPS/QTIHCD MGITYGLDQLENCQTCGTNYII SVL/NLLTLIVEQINTKLPSFVE KLVIPSSKLLFWRYHKEKEVVA VA/HAVLSRPMQLGRNIPCFG RTAY*V*YWGRKWTCGPLNNL PGTVCNFPEACSEIKHAEAFKNH VFVNDNAKFVVKFDLN

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8500	38868	A	8557	1407	2783	SSAASHSSSPGAASRARATAGS RRRSSPIQSCHPASACGQSGQS ETHRLAMRNRTPPS*GFSSK/H MRRSSSLASS*RG*KSVAVIL*IS ASGILPTDVILSPTPGSSETCHR PHPGH*EPDCLQKLPAALG*S *QFQLSHNSPRSA*AQYA/ESSG NSFFSSKVG*D*RFITTTVA/PGGP GRRTLPGKPSPEHPHRLPELPPP RSPAQVCDQTLVAPHDHNTAG/ TPGDQVCLTLVTSRSLSVLSK GCFFLHIIISTLSVQAGVRHLSLV S*AAEPTSYL*VGPKLMAVS*K LKIRTRKPRADDSPGTSRYSSA HTRTRKPRADDSPGTSRYSAH TRMWKPRADDSRH/SRYSTGCR SPGQMTLHAPADTALHTPG/PR KPRADDSPGTSRYSTAHTRTRK PRADDSPGTSRYSTAHTRTQKP RADDSGTSTSYSTPLASRRHRI AASASWALVVLICLTL
8501	38869	A	8558	92	1817	PLRNTGLCRGKGHPGLESSGR RRRDGRASERRQTQREGKTL CSSHSPWWLKANASAPAVWSQ AHTRTQKPRADDSPGTSRYSTA HTRTRKPRADDSPGT/PD TALQTP GRRSPGQMTPGTSRYSTGRGSP GQMTPGTSRYSTERRSPGQMTL QTPADTAQDAEAQGR*LQAPA DTALHTPGRRSPGQMTLQAPA DTALHTPGHRSRGKMTLQAPA DTALHTPGRGSPGQMTLQAPA DTALHTPERSEPGQMT/PRRPA DTALHTPGRGSPAQMTLQAPA DTALHTPGRRSPGKMTPGTSRY SAHTRTRKPRADDSPGTSRYST AHTRTQKPRADDSPGTSRYSTA HTRMRKPRADDSRH/SRYSTGC RSPGQMTLQAPADTALHTPG/P RKPRADDSPGTSRYSTAHTRTR KPRADDSPGTSRYSTAHTRIRK PRADDSPGTSRYSTAHTRTQKP RADDSRHQIQHRMQKPRADD SPGTRRYSIAHTRTRKPRADDS PGTSRYSTAHTRTRKPRADDS TSRYSTAHTRTQKPRADDS TSRYSTRAGCCPPGLASSAWAGL RLKTRKGWTW

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8502	38870	A	8559	13	299	EKGQDILQNLFWQLRHGPMSS APSASNTGWGSSS*SIIPSSTVSS WSTAMKLSLSEELAMTFHST ENIVVLGVWQWLTVPVVPALWD SEAGRSP
8503	38871	A	8560	337	1879	VHVGAAARRGFGVYPVLSLTVS GTQNCGPCLQTVVSTYQRV*PI SVIMVS*RLSRKETFSGRAVPILI LEPQSLASRTVHAIMM/HNQS MYVFGGCTQSSCNAAFNDLWR LDLNSKEWIRPLASGSYPSPKA GATLVVYKDLLVLFGGWTRPS PYPLHQPERFFDEIHTYSPSKN WWNCIVTTHGPPPMAGHSSCVI DDKMIVFGGSLGSRQMSNDVW VLDLEQAWSKPNISGPSHPHR GGQSQLFKDAWLLHMHSGPW AWQPLKVENEEHGAPELWCHP ACRVGQC VVFSQAPSGRAPLS PSLNSRPSISATPPALVPETREY RSQSPVRSMD EAPCVNGRWGT LRPRAQRQTPSGSREGSLSPAR GDGSPILNGGSLSPGTA AVGGS SLDSPVQAISPTPSAPEGYDLK IGLSLAPRRGSLPDQKDLRLGSI DLNWDLKPASSSNPMDGMDN RTVGGSMRHPPEQTNGVHTPP HVASALAGAVSPGALRRSLEAI KAMSSKGPSASGRH
8504	38872	A	8561	25	313	

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8505	38873	A	8562	1	1409	MIERVLGKQWALSRAEGLRRH QCLEFLIHLVFQLMKVVNEMCP NITRIYNIGKSHQGLKLYAVEIS DHPGEHEVGEPEFHYYAGAHGN EVLGRELLLLLVQFVCQEYLAR NARIVHLVEETRIHVLPSLNDG YEKAYEGGSELGGWSLGRWTH DGIDINNNFPLDNTLLWEAEDR QNVPRKVPNHYYAIPWFLEN ATVAAETRAVIAMWMEKIPFVLG GNLQGGELVVAYPYDLVRSPW KTQEHPTPTDDHVFRLAYS ASTHRLMTDARRRVCHTEDFQ KEEGTVNGASWHTVAGSLNDF SYLHTNCFELSIYVGCDKYPHE SQLPEEWENNRESLIVFMEQVH RGIKGLVRDSHGKIPNAHSVE GINHDIRTA/TDGDYWRLLNP/G EYVVTAKAGRFHCIPRTCMV GYDMGAHK/CLNFTLSKTN/LA RIRRDHWRSGKAAPSALPSPG G*KLGR/KRRQRG
8506	38874	A	8563	3	749	KTDHILGHKTCCLKTRFKIEIISGI LSDHSGIKLQINNKGNGFNHTS TWKLNNMLLNDQ*VNEEIKKEI *NHPETNDNGNATYQNL*DTG KEVLRGKL/IPISTYIK*VEKLQI NNLTMHLKELEKPEQTKRKITR RKEIIRAEINEIEAKKTIPKFN ETNSWFLENIHKTNEHLARLRK KDPNKIRFEKEDIITDTVEIQRRI RSYYAKKWENLEETDKFLDTY NLPRLNNEEVQNLRSRPTTTVPI
8507	38875	A	8564	1	842	

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8508	38876	A	8565	1	1203	VPELFNGCRQLIEEVEVAT*PR RFRDSPGGSVQGLWTSRLRAAE MLFPVHLVPRPM*ILERFVPHA LDYLLGSRLFKPEPLPKQVNP RSLDHLQRIAREHFNYLTQCH CYHVAEFELPKTMNNSAENHT ANSSMAYPSLVAMASQRQAKI QRYKQKKEHRLSAMKSAVE SGQADDERVRGYLLHLQRW VDISLEEIESIDQEIKLRRDSSR EASTSNSSRQERPPVKPFHSFH GTWLHSQSTFGAGYSKGWPTY RTVSIDWYEQHRKLWSTYPDQ GIAKAAPEEFKRAAQQQEDQ KKRRKRMRTKQLPQSPGVGM TGS DTHP*GPMGTDRTWADLP TTPQDISGVHITPLPRKTMQSSP PPVSWLQLCTTEGDKAKSCFAF SKVSSDLSVYLYP
8509	38877	A	8566	1	995	GTKELLT*LGGSPLLLT*TKPL GVDPL/LKGGVTQGFNEKAVFA ALRPSYGGPAGKPAFAGAMSL AGAQQSLWSVEGGNKLVCGL LKLTKANVIHATVTSVTLHSTE GKALYQVA YENEVGNSSDFYD IVVIATPLHLDNSSSNLTAFGFH PPIDDVQGSFOPTVSVLHGYL NSSYFRFRP*AFPLSNILTTDF PSFFCTLDNICPVNISASFRRKQP QDAAVWRVQSTKPLFRTQLKT LFRSYYSVQTAGVGRANPLYG FRPHGFPFALHDQLFYLNAL WAASSVEVMVAANKVAFW LYNRWYQDLKDIDQKDLMIH
8510	38878	A	8567	1	372	

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8511	38879	A	8568	1	1699	MHAKSIKTQALADMEKIKVTV RDKNWVARIIPQMTSGKHVGV TTTSSAKLSQGGKDSVAVKRV RSGLMIGFRFMVIPPYSFGPQVL MEIPKADADKLLCPSCAAVVLG QKKHETQTLSELKELPVQDNVV PKEDPGTWEWRTVKEGILEEV MCWLQSRVEGDWAKEERKIFH EGELAEAKAGRGGLASCTCCPL TPGKMAGPWTFTLLCGLLAAT LIQATLSPTAVLILGPKVKEKL TQELKDHNATSLQQLPLLIAM REKPAGGIPVLGSLVNTVLKIH WLKVITANILQVQKPSANDQE LLVKIPLDMVAGFNTPLVKTIV EFHMTTEAQATIRMDTASGPT RLVLSDCATSHGSLRIQLLHKL SFLVNALAKQVMNLLVPSLPNL VKNQLCPVIEASFNGMYADLL QLVKVPISLSIDRLF/*PSVSC QG*HHSALPGGQVVGLTGKGD QVVHNSAASLTMPITLDNIPFSL IVSQDVVKAAVAALVSPSEFM VLLDSVLPESAHLKSSIGLINE KAADKLGSTQIVKILTQDTPEFF YRPRPCQGGPTDRAGSVSLQ
8512	38880	A	8569	1	1060	MGLPAQGVGGNTLAKLLASDD IAKGGKRNKSEASVVRNAADA PKVLQDLSARLMGDFELRNCN SPCTLLIGIVVLINAAETLVFLS DHMEDQGSQNLNVAVLSYFQQ QDPEGQKEETAGIDLMDMASDI LQPKGDDVARISWYLRDIITRY QETFNVIERCPKPVIAAVHGGCI GGGGAAAPMPRPLASSLSSVM GQTVSQEAAPPQSGQWFWWS FSIPGLYLLGVDLVTACDIRYC AQDAFFQVKEVDVGLAADVGT LQRLPKVIGNQSLVNELAFAR KMMADEISSKSPVALQ/S/KVN LLYSRDHSVAESLNYVASWNM SMLQTQDLVKSVAATTENKEL KTVTFSKL
8513	38881	B	8570	331	1200	
8514	38882	A	8571	3	379	TSLTFHSPÉVPSS*PPSCTR*AGA ARGPRPPGAAGRPR*SC*GPGT RRWQS*GGTSPGLPVPGGRSGA ASCGLPDCEL*PLKRSQAQGRNQ CPV*SSPRWSRSRSEPCAARG WPPSACRHGNNR

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8515	38883	A	8572	384	1718	SLQLPRGLLPESCAADPGA*PPS CTR*AGAARGPRPPGAAGRPR* SC*GPPGT/PALAKPPSCPVVTS AAPTQARPMIKPQGAAWSTQK LPIPTASPTQKSPIPTASSTQK LPIPTAAWSTQKLPPTAAWST QKLPPTAAWSTQKLPPTAAW STQKLPPTAAWSTQKLPMTAA SSTQKSPIPTAAWSTQKLPPTAA WST*KLPIPTAAWSTQKLPPTA ASSTQKYTIATAASYHAKATDA WST*KLPIPTAAWST*KLPIPTA AWSTQKLPPTAAWSTQKSPIPT AAWSTQKLPMTAAWSTQKLP PTAAWSTQKLPPTAAWSTQKLP PMPTAAWSTQKLPMTAAWSTI TTMGATTHGPSTDTQNVVFLH PRCPEQASSQKSGAGAD*GLSN PKVSSAEAPSCAKDEPEVEKGR GPAPWTSQRWRAVGRPRG
8516	38884	A	8573	302	543	KLHLGWGKTPG*HWGLY*NLP RLNGPNSLMPSLRRVRRNKAR QVTSIAGCALQMEQWMHGMT RHPTRISTPITAAREVRI
8517	38885	C	8574	253	396	
8518	38886	A	8575	1107	1751	LQDLSQYFGGSQLIK*IG*TTSI ITNSNL*TTLEM/SVKGIAEQLG TNCQMAWENRIALDMILAERG GVCIMIKTECCAFIPNNTAPNGS ITKALQGLTALSNEALSSGVN DPFTGWLEKWFQKWKGITASIL TSLTAVMGVILVGCVPICIG LVQRHRGPPLVVIETKPLGLER LAGLPVGHALKLGSQIATPQN GENADRRREAFPAAS
8519	38887	A	8576	1	1365	
8520	38888	A	8577	3	263	QLILKDKFITQSAADIKEKLQKS TLGPERNLKTLNLAT/CCFL** RSGGAGGTGQTR*EGGHFHS GPRASGLWRLWNAESLGKSNA
8521	38889	A	8578	365	470	
8522	38890	A	8579	1	1278	
8523	38891	A	8580	23	257	
8524	38892	A	8581	1	1812	

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8525	38893	A	8582	265	699	LLGSTVLFHDPQLLIELYHSSHG PKVPFLGIREAKNSRSENTRLAT ILGAGLLPSWKVFTTILGAL*A RTPR*HFGNH/VTDIQS/RIEAVK LQMEPKMQSKTKIYRRPLDRPA SPRSDVNDIKGTPREEISAAK/PL LRPNSAGSS
8526	38894	A	8583	2	181	
8527	38895	A	8584	1	69	
8528	38896	A	8585	1	674	MDLNYLTLEQMDLTDIYRTHFPT TTEYTFYSTGHGTFSKTDDVIG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLLNECWVKNKMKMEIKKLF ELNDNNDDTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKNKNHMIISIDA EKA FDKIQH PFMIKTLISKISIRGTYLNLIKDI/S *QTHSQHNAEWGKIESIHSENW NRG
8529	38897	B	8586	1	415	
8530	38898	A	8587	1	516	
8531	38899	B	8588	110	382	
8532	38900	A	8589	140	253	QNKACQHPPKITRVHQWQIQT KKKSSYLLKKEFRRLVIKLIREA PEEGKAQCKEVQKLIQVQGEI IDEIDTINKQPKLQETMDTLTK MQNAQESLSNRIEQEEHKSLS ENIFGSIMEENFPLARDLDSQI QEAQRTPGKFITKRSSPRHIVIR LSKVTKERJLRVVRQKRKIVL KS*PGNMTKQGLSTSPKNHTSS PTMDPNQEEILDLEKRIQEVSY
8533	38901	A	8590	89	194	
8534	38902	A	8591	2	633	

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8535	38903	A	8592	298	2648	GSSKILLFNQNEDDKINFELFFF FVASALVLVQKAFSRSSWSSMA LADKRLENLQIYKVLQCVRNK DKKQIEKLTKLGYPELINYTEPI NGLSALHLASVSNDIDMVSFLL DLGAHPDVQDRMGCTPTMRA AELGHELSMEILAKAKADMTIV DNEGKVLGETGGLTSSPLAHIA VALHIPRDTQGVLFYCIPTKR HYRCALIALEHGADVNNSTYE GKPIFLRACEDAHVDKDVCLTF LEKGANPNAINSILKLLFAYNG DVGLISINGNTPLHYAAMGGGFA DCCKYIAQRGCDLKWKNLCHK TPRAVAKEGGFKAAASKEIRRC RENRR**TSQARSQKSQIPLWAL RLHDWSVEREAFLEAFVLD RGDGSISKNDFMVLEE*SRIM QAQNSWLPFAHLHEKTRGGGV NIN*ILLKEPDILNKSFLVGSYGP KKKEKGMGKKGKKGFVLP ICVPEIYAFRRQDGGPPYIMIE TYKNVTDSSRFNRDHPPEHIQ DDSVWYIDDSEKVFSPNINIITKA GDLASLKKAFESGIPVDMKDN YYKTPLMTACASGNIDVVKFLL EKGYASPSGQDQDVELLVESGA LIDAASJNNSTPLNRAIESCRLD TVKYLLDIGAKFQLENRKGHSA MDVAKAYADYRIIDLIKEKLDN LPKPAENQKLKGKTPILKTEG PEIKKEEELSSIYGVPTTSEK
8536	38904	A	8593	3	838	MGRGWTQAVGPRWSGGSSCTL YSVGADGRGQGHQSRGCRPPG PPSASSAPCLAWGAAGRARE GLRQNAERSPLTAPAGRP*PC GAGPCR*SR*RLVGLRPW ASPGTGAAACGRCCCP*P/P*P NPWHFTVSKAFSYMPSTTA/RL VRGPRLLVGPVPVAPYIPP/PGS PASRRGSRGRSRPSRPRPSV LSCHGVSL*TGPSLPGWLLQIW QRSQMS/P/PPKGPP*GREGPP PP/GPALLPAAAPGGQGHRAPA AGSCGRRRAARRMEWVRNSPP
8537	38905	B	8594	1	2700	

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8538	38906	A	8595	1	1240	FPPYATNEIGKVTGLNRRELGH GALAEKALYPVIPRDFPFRTIRVT SEVLESNGMRRIGQPPASSRPV RRVRAPLPPPLLEVRAPLPASRP SGEVLCTVTFDSLESGIKSDQVI TAINGIKDKNFMLHYEFPPYAT NEIGKVTGLNRRELGHGALAE KALYPVIPRDFPFRTIRVTSEVLE SNGMRRIGQPPASSRPVRRVRA PLPPPLLEVRAPLPASRPSGEVL CTVTFDSLESGIKSDQVITAINGI KDKNFMLHYEFPPYATNEIGKV TGLNRRELGHGALAEKALYPVI PRDFPFRTIRVTSEVLESNGSSSM ASACGGSLALMDSGVPISAV AGRTN*DWSPKPDPEKGEIRKII VC*QIFLGIEDYNGDMDFKIAG TNKGITALQADIKLPGIPIKIVM EAIQQASVAKKEILQIMNKTISK PRASRKENGVPVETVQVPLSKR AKFVGPGGYNLKKLQAETGVT ISQVDEETVFCNLHQHPVLMLE GKRLSFTEICKDDQEQAIRNLG AVILPAHNWVKSEILVGMGKII
8539	38907	A	8596	152	305	DNQNGKLIKCS*PCNFVHRAPY AVEITVLRFCNWTQVQAQRE RTFLILIK
8540	38908	C	8597	414	611	
8541	38909	B	8598	1	403	

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8542	38910	A	8599	1	1702	MDSDEGYNVEFDEDEECSEEDS GAEEDDEDDEDDDTLDLG EVELVEPLGVGGGERDGLLCG ETGGGGGSALGPGGGGGGGGG GGGGGPGHEQEEDYRYEVLTS EMILQHMVEICREVNEVIQNPA TITRILLSHFNWDKEKLMERYF DGNLEKLFACHVINPSKKSRT RQMINTRSSAQDMPQCICYLNY PNSYFTGLECGHKFCMQCWE YLTTKIMEEGMGQTISCPAHGC DILVDDNTVMRLITDSKVLLKY QHLITNSFVECNRLKWCAPD CHHVVKVQYPDAKPVRCKCGR QFCFCNGENWHDVPVQCKWLK KWIKKCDDSETSNIWIAANTK ECPKCHVTIEKGGCNHMCVR NQNCKAEFCWVCLGPWEPHG\ SAWDTPVP*NEDDAKAARDAQ ERSRAALQSYLFYCNRMYMH MQSLRFHEHRLYAQVTQTMEE MQQHNMSWIEVQFLKKAADV LCQCRATLMYTYVFAFYLLKK NKPSFHIFENPNKARFDENATE GLSGYLGTRKFPKDS/LQDIKQ KVP RPSTRYCESRRKGFVTSMC HEGYEKDLWEYIED
8543	38911	C	8600	118	219	
8544	38912	C	8601	16	408	
8545	38913	B	8602	1	996	
8546	38914	B	8603	1	1302	

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8547	38915	A	8604	983	2127	DNWKSIRGSCWQDPRELLTFM APCIGVVVMQTTTR*K*NTLAGH PSAGVCWCVTSAACIGAWD ATSPLSSTFATAPGLPRCCSQAS PAPRAEPLHGQPGAPPHALKRP PGLPWP*PQEARQYRHNQAY YSIQGDGAEDDDERIVRFHTRV INHHKKRKNSPRIVQSNDLTEAA YSLSRDQKRMLYLFVDQIRKSD GTLQEHDGICEIHVAKYAEIFGL TSAEASKDIRQALKSFAGKEVV FYRPEEDAGDEKGYESFPWFIK RAHSPSRGLYSVHINPYLIPFFIG LQNRFTQRLSETKEITNPYAM RLYESLCQYRKPDGSGIVSLKID WJIERVQLPQSYQRMDFRRRF LQHIFVLRERPETVLIDLIQRTK DAVRELDNLQYRKMKKLLFQE AHNGPAVEAQEEEEEGWNLD RAYDYVKERRTVTKPNPFSMR QLEEQGILLARPKRTAYIYGS VYRRCGYADHKVEIKHPGWAS ISRGVLVCDECCSVHRS.LGRHIS IVKHLRHSAPWPTLLQSGFPGP SRRAAPRAARGPTPRTEEA AAMALTFLLVLLTLATLCTRLH RNFRRGESIYWGPTADSQDTVA GSPDHGLLAFAYHRLVRFLLW VLCPGWAFFLVNSRGGVFNPI LHPCPRHGQARFAGVGAEDY TFLYHPCAHWPWLKQLALLAY ACMANPSLTPDFSLTQDRVDIE
8548	38916	A	8605	1	224	RKQEWLSKQKENIQHFQAE ANLLRRQRQYLEECRRFKRR MLLGRHNLEQDLVREELNKRQ TQKDL EHAMLLRQHESMQELE FRHLNTIQKMRCELIRLQHQTE LTNQLEYNKRRELRKHKVM EVRRQPKGLKSKELPNKSSSQ GYLQNSQTRQYKALRNHLLT TPKSEHKAVLKRLKEEQTRKLA ILAEQYDHSINEMLSQTAVSLFF LGQNKFSAPFLPPP*AVSEQLCA HSLV

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8549	38917	A	8606	1051	1875	SDQLTAHLNLCVEVAELQFLHR FMLSFPIHHLRLFTAPAQDASL VPLKGDILGVKLSGDDGRGKP AQHLFLSGLSSQQLPVLPSQ CQSLCVHHFPAVVVNLHDIIGAC VSCLPDLGP*QSCGSLAARSC GQSPGVWCLPSGSGRSSLCRC H*GRSWTPGAPS**TPISSPRSP GPCAASPGARGCPPAASPPAGS PGTEAAPAPGPGYSQPPGAL SSRCDSPCPLRRAPGAHGHTP RCPSVVARCRGVPRRGSSCSMS TSLTRSCSKL
8550	38918	A	8607	714	2148	MPAVAKSKPINRSKRRMCPQV LRSASPIQEGEKISANENSLAVR STPAEDDSPGDSQVKSEVQQPV HPKPLSPDSRASSI.SESSPPKAM KKFQAPARETCVECKTVYPM ERLLANQQVFHISCFRCSYCNN KLSLGTYYASLHGRIYCKPHFNQ LFKSKGNYDEGFGHRPHKDLI GQAKMKTEEILER/QPQLANAR ETPHSPGVEDAPIAKVGVLAAS MEAKASSQKEKEDKPAETKKL RIA WPPPTLGGSGSALEEGIKM SKPKWPPEDEISKPEVPEDVDL DLKKLRRSSSLKERSRPFTVAA SFQSTSVKSPKTVSPILIRKGWS MSEQSEESVGGRAERKQVEN AKASKKNGNVGKTTWQNKES KGETGKR/R*GKVHSLMENEN VFVINGARLPEDDNQLPPKQQ SSTKNPSLLEFGPSFVDNHLKK EFTTQNKQSQDVLEWEGEVVK ELSVEEQIKRNNYYDEDEDEE
8551	38919	A	8608	I	4479	MCFSPPKLYKHEIHLKDLTCL KPSIESPLRQNRSSIEEEQKQE ENGDSQLILEKIQLQOWSISLNM TDEHGNLNLVCDIKKPMDEVY KIHLNQTDPPDIDINAMVALDF EYPMQTQENYENLWKLIAYYSE VPMKLHRELMLSKHPRVSQYQ RQDADEEALYYTGVRQAQILAE EWIMQPSIDIQLNRQSTAKKV LLSYYNQYSQTIATKDRQARG RSWVMIEPSRAVQKDQIVLEG GRCQLSCNVKASEP

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8552	38920	A	8609	1	9009	MDEFAPGKHLATSGDLFGDHN YGRRTYHTLEVKCAEEHPAVS DPFQRQSLRALSPLEDLPPSSG LRSGLTLELLMIHGNIPSPD GALRDLSSLQVFKFSYNKLRVI TGQTLQGLSNLMRLHIDHNKIE FIHPQAFNGLTSLRLHLLEGNLL HQLHPSTFTSTFTFLDYFRLSTIR HLYLAENMVRTLPASMLRNMP LLENLYLQGNPWTCDCMRWF LEWDAKSRGHSCRGCAIISLSH EIQLAKGFCEMLLL
8553	38921	A	8610	1	4971	MKASGILKCKDKAYEGGQLC AMCFSPKKLYKHEIHKLDLTC LKPSIESPLRQNRSRSEIEEQKQ EENGDSQLILEKIQLPQWSISLN MTDEHGNLVNLVCDIKKPMDV YKIHNLQTDPPDIDINAMVALD FEYPMTQENYENLWKLIAYYS EVPMLHRELMLSKHPRVSYQ YRQDADEEALYYTGVRQAILA EPEWIMQPSIDIQLNRPQSTAKK VLLSYYNQYSQTATKDTQRAR GRSWVMIEPSRAVQK
8554	38922	A	8611	1	1283	LSFTTCSTFTSNYRSLGPAQAPS YG/SRPVSSVASVYAGTGNSSGS RISVSCSTFRGSMESGGLAAG MT/GGLAGMGGIQNEETMQSL ND/*LASYPDRVRHLETKNRKL ESKIWEHLEKKGPQVRDWSHY FKTIRNQRAQSLAITVDNACIVL QINNTHLAADDFRVKYETELA MCQSVESNIHGLCKVNDNTNV TRLQLETEIKALKEELLFMKKN HEEEVKGLQAQIASSGLTMEVD PKSQHLAKIMAAIRAQYDELA WKNGEELDKYLSQQIEESTTVV TTQSAKAGAAEMTLTELRCITV QSLINLNSMRNLKASLENSVR EVKACYTLQMEQLNGILLHLGS ELAQTQAKGQCAQAYEALLN IKVKLEAFIATYCHLLEDGKDF NLGDALDSSNSMQTIPKTTTHQ RVDGKVVSETNDTKVLRH

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8555	38923	A	8612	2	1365	RPQSLSPVLSLSPDSMSFTTRST FSTNYRSLGSVQAPSYGARPV SAASVYAGAGGSGSRISVSRST SFRGGMGSGGLATGIAGGLAG MGGIQNEKETMQSLNDGVASY LDRVRSLETENRRLESKIREHLE KKGPPQVRDWSHYFKIIEDLRAQ IFANTVDNARIVLQIDNARLAA DDFRVKYETELAMRQSVENDI HGLRKVIDDTNITRLQLETEIEA LKEELLFMKKNHHEEVKGLQA QIASSGLTVEVDAPKSQLAKV IMADIRAQY*RAGLGKNREEEL DKYWISQQIEVSTTVVTTQSAE V/GAAIETTLTELRRTVQSL LDSMRNLKASLENSLREVEA/R RTPLQMEQLQRGSLHLESELA QTRAEQQRQA/QEYEALEHQ GSSLEAEIATYRRLLEDGEDFN L/GDALDSSNSMQTIQKTTTTRI VDGKVVSJETNDTKVLRH
8556	38924	A	8613	170	399	
8557	38925	A	8614	141	287	LPSRRAGLGTCSPPCLSLPPASR APVRPEPLR*APPPAPRRVPVST TQG
8558	38926	A	8615	356	574	
8559	38927	A	8616	552	770	
8560	38928	A	8617	158	368	
8561	38929	A	8618	1136	1410	
8562	38930	B	8619	1	631	
8563	38931	B	8620	321	2234	
8564	38932	A	8621	170	444	
8565	38933	A	8622	325	722	LIELRHLVFFVLLFRDLQHIMA CNMRDAVRFFVCFVFFREGL SRSSGA/DDRFLAGP*LLSRGAG LGTCSPPCLSLPTPWAP/AAAP ASLT/TPPPAPRRVPVSTTQGLRS ASARHGTGRQLHLQPRCGIH
8566	38934	C	8623	1	1449	
8567	38935	A	8624	326	626	LPSHGAGLGTCSPPCLSLPPPLW AP/AAAEPPRQAPPPAPWCPVPS TTQGLRNASTRRRTGRQLHMI WPPASLKSPPATLPCHECAPIT LTFSCSSNMQT
8568	38936	A	8625	2009	2227	
8569	38937	B	8626	182	1513	
8570	38938	A	8627	497	761	NHTSCLPLGPGTTAAEELPSLVA GFGTCSPPCLSLPPTPWAPVRPE PPR*APPPAPQRVPVSTTQGLRN ASTRHRTGRQLHLQPRCGIH

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8571	38939	A	8628	218	855	GAGLGTCSPPCLSLPPTQRA PV RPEPPRRAPPPAPRRPVSTTQ G LRSASTRHRTGRQLHLQPQCG V H*VKPAGLLSLALETRTNPA A/ DKHLWQSIIISLQLKSDLLKE ML GSQTGNNGNVQDVLRYLVKSE T QKAIKVSLDCVRKRYRSSL SL QLKLCDCWGQALFSSALTLDP KEVVVRDLEELSNIYKTTLEGS G IFDSVARVREESEAEGL
8572	38940	A	8629	350	615	
8573	38941	A	8630	186	566	RLLSPAACRSGMTMIFPSIHPS QC RMIGLGWKK*SSVHNATPWAP VPPEPPGRAPPPAPGRPVPLT TQ GLRSASARRRTGRQLHLQPQCG IHVVVKPAGLLSHEGPRLRSS SQ SDQEPTNSGHS GMCL
8574	38942	A	8631	656	874	
8575	38943	A	8632	415	634	LPSRGAGLGNCSPCLSLPPTPW APVQHKPPRRAPPTPRHPVPS TTQGLRNASAWRRSGRHLHLQ PQCGIH
8576	38944	A	8633	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDOEAVI DGRRKPEESRTTSHICRCRS

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8577	38945	A	8634	1	1743	MGQVWALVHSTLETFTTDEEE GEYNEVTEQVCLPAKAGSAAV DLCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSYNGEIQVTS TSVPWKAKPGDHIAQLLIVPKK FARFEGTASSGKTKFLPRFRISF LMAAIVKPPEPIPLKWLTDKPI WTEQWPLSKEKLEALEDLITQQ LKKGHIAPIFSPWNSPVFIKKK SAEQDCEWFVFTILAVNNLQLK PAKRFIHWKVLPGQPNQQPIWIP SRYLKPYHKPDAKEEIPESGSG FPVAAMSRLLRRTPTVTSNTH RTQPPTWGQIEKLPMMAEENLR KAGQPVTISNWILPRITKFKPIE GAENVFTDGSSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIQRCPTCQVMLSAAE QHLQKSAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKIPGESR/ETPGCSHVKTDAE EDANCHEQHPSNTATHLGTQD EAVTDGGRKPEESGTTSHNE*F NDSGDHHCLQOQGL
8578	38946	A	8635	820	1344	PDGTTDRADGRDLRSVSWETL RGCPAVRKDSIGWIRLSRTLKK NVHLCLPLRQGGLFVCPVTSSS PQHISSHRGFWNISKDAPMSWP GSYSCHNVVAVPGQGQ*SRRA RMLRGLLSKAGHHSFCTDQAI LEITKFTFTWD*VTLGQ*FMLS ES*SSCKPNSCCPVQCLVHSGG
8579	38947	A	8636	3	760	

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8580	38948	A	8637	1	1354	MGISCPGSSKMLNSRALPVLKL TQGA LR DCKERANYTNFN IYK AVESQKGFVCVLYNGQSP EY VMIPCTSVSPITGQEVPE DRGMR MVMKNKPNKPSKMQSLKSSKH LTNSVIVIAVGIFFSVTLQARDP QLDDAIEQLRGVCIRAWEKITS GGEQYPSFSAIKQGPKPEYIDFI ARLQESLKKMIADSAAQDIVLQ LLAFDANPDCQAALRP IRGKA HLVDCIKACDDIGDSSNGKAS YFGSKSVFQTSYTSQAQAE LV AVIEVLTA FDMPINVIDSSYM VYSTQLIEN AQLRFHTDEQLMT LFTQLQTA FRSTMHPFYITHIRA RHTPLPGPLTEGNQMA DCLVA TAVSNARHFHNLTHVNASGLK CRYSNTWKA AKAIHQRRPTCQ MVHSSSFTGGVNPQGLEPNSL WQMDVTHVPSFGR LAYVHV C VDTFSHFVWATCQSGES
8581	38949	A	8638	596	1820	
8582	38950	A	8639	275	1495	RLGSSLL EYTLPDQGNIIATFE PPFFKFGKAHSVDYIKACDGIG GPLTEGNQMA DCLVAN AISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIQQCPTCMVHSSSF TGGVNP RGLEPNSLWQMDVTH VPSFGR LAYVHV CVDTFSHFV WATYQSGESSACVSKHPLLQC FVVVGIPAFIKTDNAPGYTSQA LATFFSVWN IKHITGIPYNSQGG AIVERMNL SLKQQLQKQGGN RDYR/TP* MQLNLALLTLNLS LPKGQMFSAAEQHLQKPAAKT KTEQLIWRDLITKSWEIGKIIT WGRGYA YISPGQNQQPIWIPSR HLKPYHEPDA RKRLQEDPEDP PSCSHVKTD AEEDPNCHEQHPS NTAIHLRSDQEA VTDGRRKPEE WSGTRTWWRPWSCRT
8583	38951	A	8640	232	789	ERPWGPEGNSEGSFCPKGLEPR TCLRGPAASAAAGAEGRQDDP GGPWCSPAAGDLGSPGVQSPG GGSPRGAQVAMSGSRRRRAP GVWGALQ*HRR*ARRMHSFPP SL/PLL*NG*SPLFLVSKCLTGSP LRSASPCPPAARSC*KHPDSSPG RGPGARQSPALHPALPSLARRA APGRSFPLTSRK
8584	38952	A	8641	1	149	

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8585	38953	A	8642	1	2541	
8586	38954	A	8643	1	989	MQRGQQATGSSANAWGILQPK WVQTGPDNKRMARNVLYKER LLAESPNHVVAEAVIQRPNPHL QTRDITYEGLCQTLGSQPTLYQI PSLYCSYETNSNAYLLQLPIRKE VIHLEPYIALYHDFVSDSEAQKI RELAEPLWQSRVVASGEKQLQ VEYRISKSAWLKDTVDPKLVT NHRIAALTGLDVRPPYAEYLQV VNYGIGGHYEPHFDHATSPSSP LYRMKSGNRVATFMIYLSVVE AGGATAFIYANLSVPVVRVQ/ WPGTS*AFDNQCQNAALFWW NLHRSRGEGSDTLHAGCPVLV GDKWVANKWIHEYGQEFRRPC
8587	38955	A	8644	2	505	AWLKDTVDPKLVTNLNHRIAAL TGLDVRPPYAEYLQVNVYIG GHYEPHFDHATSPSSPLYRMKS GNRVATFMIYLSVVEAGGATAF IYANLSVPVVRVQ/WPGTS*A FDNQCQNAALFWWNLHRSRG GSDTLHAGCPVLVGDKWVA NKWIHEYGQEFRRPCSSPED
8588	38956	A	8645	298	401	KKSLLVRRSWRMKELKKKIGQ Y*KKLGRLLGKAI
8589	38957	A	8646	1	417	FRAAPAPESGGESVFGETHRAL QGAMEKLQR/RLWKEKVDLKE RVEKLELQFIHLSGQTDITGRK YISQGVASETQHWKEDIVRL AQDQEEMKVNQLQELR/EQVLQ LVGDHKEGHGK/FLTIAQNPAD EPTLGAPIAQELGC
8590	38958	A	8647	2	430	AAVKPLGSAETAVPARLGCRR FSRRCRRRRGRGSLLSFSAK VAFFNSAGANAQEEQRVCQP LAHPVASSQKKPEVAAPAPESG GESVFGETHRALQGAMEKLQR/ RLWKEKVDLKERVEKLELQFIH LSGQTDTHNKISY
8591	38959	A	8648	1	2769	
8592	38960	A	8649	1	314	FVNLFEPVVRVVEFGATCRAVA EPEQQR*SPSARPRPCCPLASV AAAAAAGGAAAYCL SPRRR*GAVSARPAGEPREPHE WDRNRSDFKRRRRGRDG
8593	38961	B	8650	46	307	
8594	38962	C	8651	1	4584	
8595	38963	B	8652	438	532	
8596	38964	B	8653	832	927	

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8597	38965	A	8654	320	1136	RIMETIANI.SSQSPVSLPLRVGL AEYLEMEED/DL.DSEQAAPRPM PNIPGDLSEREP/QVAFNSAGA SAQEEQRVCCQPLAHPVASSQK KPEVAAPAPESGGESVFGETHR ALQGAMEKLQVTTLWKEKVD LKERVEKLELQFIHL.SGQTDITV SERI.GHRWGELPGHPRGSI*A MSSCRKVHQPGGSVRDAAALGE EDIVRLAQDQEEMKYNLQELR/ EQVLQLVGDHKEGHGK/FLTIA QNPADPTLGAPVAQELGCAD EQGGFYPRSPDC
8598	38966	B	8655	97	235	
8599	38967	A	8656	1	2104	
8600	38968	A	8657	3	1107	FMTTDERKLFNHLKSPHLKYW VPFIWFGNLTAKARNEGRIRDS VDLQSLMTEMNRYRSWCSLLF GYDWVGIPLVYTQVVTAVYT FFFACLIGRQFLDPTKGYAGHD LDLYIPIFTLLQFFFYAGWLKVA EQLINPFGEDDDDFETNWCIDR NLQVSLA.VDEMHMMLPKMK KDIYWDSDAARPPYTAAADY CIPSFGLSTVQMGLSGSDFPDEE WL.WDYEKHGHHRSMIRRVKRF LSAHEHPSSPRRSYRRQTSDDS MFLPRDDL/HSQGP TGALCKK PPQGLTHLE/DNPA SQKEAPRCT SAWESCPSGRPARQALYRA*P HSPV*ELPPSKCHGT*GIDHSSR STSAHIRGLPP*FRYLHLEL
8601	38969	A	8658	3	397	
8602	38970	A	8659	346	474	

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8603	38971	A	8660	1	1344	MHSTWLFCFARLLKLEPFQGL PRLTIRASARTPPAALERVTRD PCAATCLDRGSLKGILGHSPFQ SPPVTSCHCAENPTLKAPPYV GATSALVLSLGGPVPWLSVEL SIRTFASSGLIYYMAHQNQADY AVLQLHGGRLHFMFDLGKGR KVSHALLSDGKWHVTCTDYV KRKGFTVDGRESPMVTVVGD GTMLDVEGLFYLGGLPSSQYQA RKIGNITHSIPACIGDVTVNSKQ LDKDSPVSAFTVNRQYVAQE GTYFDGSGYAALVKEGYKVQS DVNITLERTSSQNGVLLGIST AKVDAIGLELVDGKVLHFVNN GAGRITAAEYEPKATVLCDEGK WHTLQANKSKHRITLIVDQNA GWR*KSHTPQSTPVDNTNPIYV GGVYAGVKQCLRSQTSFRGC LRKLALFRGPPQVQSDFSRFAE LHGVLHSCPGTES
8604	38972	A	8661	3	92	
8605	38973	A	8662	2	158	HTFPTFSSPHLVMMIQPSSSP PPPLPPPPSSPPLPLPPSPPLLL FFL
8606	38974	A	8663	21	471	DGPQDQPPHQSSSSPPPLPPP PFPPPLPLPPSPPLLLFFCDEA LLCCHTGVELFFVIFAYCSG/PE TEPAISPRYASSGLNGFPLPT PPA YA*IPSSGIHFNP SLAIPST TTTLVTRPTTHHSRRPTTTQS STTAPSLHP
8607	38975	A	8664	2	105	
8608	38976	A	8665	3	265	RKDLVANTALSGGTTMYPGIA DRMQKEITALAPSTMKIKIAPP ERKYSVWIGGSILASLTFQOM WISKQEY\DESGPSIVHRKCF
8609	38977	A	8666	3	757	NTPAMYMAIQAVLSLYTSGR TGIAMSDGDGVAHTVPIYEGYT LPHAILHLDLAGWDLTDYFMKI LMECSYRFTTMAEQEIVCDIKE KLCNIALDFEHKMATGASSSSL EKSYEVDPGQVITIGNEWF/*VP EALFQPS/MGMESCGIQTTFNS IMKCDVDICKELYAKMVLSSGT TMYLGIADRMQKEITALGRPST LRFRFIAPP/ERRKYSVWIGG/SI LASLSTFQOMWISKQEYDES GPLHPSTANCF

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8610	38978	A	8667	3	171	CPLCRGNHWK VHCPSGR/MVP* VRSPQDDPTTGQRVP GASASS CHHPH*APGTFNH
8611	38979	A	8668	1	325	SPSRTCYQCGLQGHF*KDC/TSE KPPPRPCLLCQGNHWK VHCPR/ VTKVLWVRSPQDDPATGLRV PDD*EHTIRRAYALGKSAVTSK PPPPYPARSRLNVRRLCSLATN
8612	38980	A	8669	3	377	
8613	38981	A	8670	1	423	
8614	38982	A	8671	1	1659	
8615	38983	A	8672	1	1449	MVNDTRPKVQVEYKGETKIF YPEEVSSMVLTKMKEIAEAYLG KTVTNAAVTVPAYFNNSQHQA TKDAGTIAGLNVLRIINEPSAAD IAYGLDKKVGAEARNVFIDLRG GTFDVSILIIQDGIFEVKSGDTHL GEEDFDNRIVSHFAEFKHKYK KDTIRDVKLDKSIQHDIVSIGG YTHIPKIQKLLQDIFNRKELNKS INLDEAVAYGAAVQAAILSGD KSENVQDLLLLDVNPLSFGIEL AGGVMTV/LPVLIKHSTTIPTKQ TETF*QPIYSDNQPGVEGECAM TKDDNLLDKFELTGIPSAPHGV PQIEVTFDIDANGILNVS AVDKS VGKENTITTTNDKHRLSKEDM NIWSAEKYKAEDKRQDKVSS KNSLESYAFHMKATYKDEKLQ GKINGEDKQKILDKFNEVIKWL DKNQAAKKEFEHQQTLEKV CNLIISKRYQSAGGMPGGMPGG FPGGGAPPSSGASSRPITEVD

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8616	38984	A	8673	18	1388	TRLQLLGFLWLPSSLLEPLHPS NHGPRGPAVGIDLTGTTYSVGV FQHGKVEIIANNDQGNRTTPSY VAFTDTERLIGDAAKNQVAMN PTNTSF*LPNGLIGR/RFD/DAVV IQSDMKHWPFMVVNDAGRPK APS*NTKGETKSLYPEEGVFLW V*PKMK/EICRSLTLGKTVTNA\ VVTVPVSIFYNDSQRQATKDAG TIAGLNVLRLNNEPTAAAIAYG LDKKGLEQKRNRAHLLTWGG GTFDVSILTIEDIGIFEVKSTAG DTHLG/GEEDFDNRMVNFHIAE FKRKHKKDISENKRVRRLRTA CERAKRTLSSSTQASIEDSLYE GIDFYTSTIRARFEELNADLFRG TLDPVEKALRDAKLDKSQIHDI VLVGGSTRIPKIQKLLQDFFNG KELNKSINPDEAVAYGAAVQA AILSGDKSENVQDLLLLDVTP SLGIETAGGVMTVLKRNRTTI
8617	38985	A	8674	2	1559	RYLNLWIGTPTKGMSLKAFVQ PHKSYWLKTLDPDNMEALQIR K*VPNIGTCAVSWLKGPCSDV AVKKFFIFSLGNYWEGN*LI*EH GYKVV*HSNSYLEPISPAQTPK KRTTSYFSTLLCLRRLSCLSLFK RIECYEVNYQLDEELDR*EPAP QSQGLDLSPSFDIL*DHQSRTV YYLMNIHVTPRSIYLCRHGESE LNIRGRIGGDSGLSVRGKQVG WATHQMGWLGCPRWAAGFP ILPSRPYPNAGVTLAAPVPTHDS VLPALPTRAGGQDETEPLKAG PTGLPSAPPLEMGGGAPGKALS WMATPWCLPFCYVEVALTCAA PTVYQAVVWVLPPIHYLKCSPQT AGQMRQCSDLMPERGRDVSE GTRDHYRELREFNLWLIPPCQG LLPTSHMKRTIQTAEALGPVE QWKALNEIDAVRCMG*ISC/VW G*LESGLPLRDQDKYRYRYPK GEVRFAGWPNA*DYSVSSQL NVLLCHQASMRCLLAYFLIKS SGTTLISALGMFDGI
8618	38986	C	8675	16	206	
8619	38987	A	8676	157	413	ALVCS/SSLAIREMQIKTTMYRH LTPVRMAIKKSGNNRCWRGC GEIGTLLHCWLDCKLVLQPLWK SVW*FLRNLELEIPFDPAIPLL
8620	38988	B	8677	877	2126	

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8621	38989	A	8678	1	1731	
8622	38990	A	8679	2	1675	
8623	38991	A	8680	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLIGDGTLYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAAQIRQEKEI KGQLGKEEVKLSLFADDMMILY LENPIVSAQKLLKLSNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIGLG KEEVKLSLFADDMMIVYLENSIV SAQNLKLSISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYREN DIPIKLPMFTFTELEKTTLKFIW NQKRACIAKTLSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSIYNNH LIFYKPDKNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELQIYRKKTNN PIKKWAKNNMRHFSKEDIYAA NRQMKKCSSLVIREMQIKTTM
8624	38992	A	8681	1	1242	

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8625	38993	A	8682	14	1785	FDQVEERVSVIEDQMNMKRE EKFRKRVIRNEQSLQEIWDYV KRLNLHLIGVPESDWENGTKLE NTLQDIQENFPNLARQANIQIQ EIQRMPQRYSSRRTTPRHILNA HKRK*ERYKIDTLTSQLKELEK QEQTYSKASRRREITKIRAELEK IETQKTLQKINESRSCFEKINKID RLRLARLKKKKREKNQTDVIKND KGDITDTPTEIQTIREYYKHLV TNKLENLEEMDKFLDTYTLPR NQEEVESLNRPIGTGSEIAHNSL PTTKSTGPDRTAEFYQRYKEE LVPFLKLFQSIKEGILLNSFYE ASTILIPKAGRDTTKKENFRPISL MNIDAKILNKILANRIQHIKKL IHYNQVSFIPGIQGFNICKSIN VIQHINRTKDKNHTIISDAEKA FDKIQQPFMLKTLNKLGDGT LKIMTAIYDKPTASTILNGQKLE AFPLKTGTGRCGPLSPLLFNIVL EVLARAIQKEIKGILGKEEV KL.SLFADDIMIVYLENPVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRKIYVVGQLTRDVKDLFKEN
8626	38994	A	8683	1	5127	
8627	38995	B	8684	1	1461	
8628	38996	A	8685	2	1879	
8629	38997	A	8686	1	1299	MKLPEEGSGSIICSAIFAVLQL PLVIHRQTGYGEDLQQTPTDLQ LRDLTDHSSSPAMEQSWMEND FDELNRSRLQKANKLENLEETD KFLDITYTLPRLNQEEITESLNRPI TGSEIAIINNVP TKKSPGPDGV TAKFYQRYKEELRTVNKNHMI SIDAEKAFDNIQPPFMLKTLNK LGIDATYLLKIIRAIIDDKPTANIL NGQKLEAFPLKTGTGRCGPLSP LLFNIVLEVLAIRAIQKEIKGI QLGKEEVKL.SLFADDIMIVYLEN PIVSAQNLLKLINNFSGVYKI NVQKSQEFLYNNNRQTENQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYNPLLEIKKDTNK WKNIPCSWIGRINIMKMAILLK VIYRFNAIPKLLMIFFTELEKAT TLKCI* NQKRAHIAKPILSQKNK
8630	38998	B	8687	1	2187	

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8631	38999	A	8688	1	1698	MMGDFNTPLSTLDRSMRQKVN KDIQELNSALHHMDLIDYRTL HPKSTEYTFPSAPQRTYSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRICKLTQNHISITWKLN NWLNDYVWHNEMKAEIKMF FETNEIKDITTYQNLWDTFKATL NQEEVESLNRPIGTSEIQAMINS LGTKK/SPGPDGFTAKFY/PE*H DCISRKPHRLSPKSP*ADKQLQ QSLRIQNCQSKITSILIHQ*QTNR EPNHE*TPIHNCIKDNKIPRSPY KGCEGFLQELQTTAQRNKR HKQMEEHPLMDRKNQYHEN GHTAQGNL*IQCHPHQATNDFL HRIGKKYSKVHMEPKSLHLCQ VNPKPKEQSWRHHTT*LQTLQ GYSNQNSMVLVPKQRYRPMH NRALRNATYLPKSL*ET*QK QEMGKGFPI*QMVGLKLASHM *KAETGSLPYTLYKN*FKMD*R LKCT*TNKHHPRRKPRQYHSGH RHGQGLHV*NTKSGNKSQN* QMGSH*TKELLHSKRNYHQSE QATYRMGENFCNLI*QRANIQ NLQRTQTNLQ/RKKQPHQQVQ
8632	39000	A	8689	1	5073	
8633	39001	A	8690	128	1407	EKKASDDQTTSPSYRRKFKPKA KKLNTLKKI*TN/RIITRNREKC LKELMELKAKARELREECRSLR SQCDQLEERSVMEIEQTIRE YYKHLYENKLQNL EEMDKFLD TYTLRRLNQEEVESLNRPIGTSE IVAIINSLPTKSPGPDGFTAKF YQRYKEELIPFLKLFSIEKEGI LPNSFYEASILIPKQGRDITTK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQ WFNICKSRNVIHINRTKDKNH MIISIDA EKAFDKIQPFMLKTL NKLGIDETLYKIJRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNIVLEVLARAIQKEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLFLISNFSKVS KINVQISQAFLYTNYRQSAKS
8634	39002	B	8691	1	1443	
8635	39003	A	8692	1	1878	
8636	39004	A	8693	1	1479	

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8637	39005	A	8694	I	2091	MVFLEKISVGISRLSKQHPPFIR VALPLDADPTVSRIGSFQWVLG LADFRNEAVDPRDVQMCPEFIP SGGFVVFLTSGVKPQTFTVSITA LKGEPTQMRNRQKTNNGNMTK LGYLTPOKNHTSSPAMSPNQE IPDSPEKEFRRTTEASLTGGTI NPIISWAVNGSSKNLYHILGK GRKIFSSSGIKQKSIA SGERQNF QRNDQTAAFAVHENPLFCSHR CWYPGKQEKCLKELMELKAK ARELREECRLSRCDQLEERV SVMEDEMNEMKREGKFKREKRI KRNEQSLQEIWDYVKRPTLHLI DVPETLNAHKRQKERSKTDLT SQLKELEKQEQTHSKASRRQEI TKIRAELEIETKTLQKINESR SWFFERINKIDRPLARLIKRE KNQIDAINDKGDITS DPTIEQT TIREYYKHLIYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRP TGSEIVAIINSLPTKKSPPGPGST AEFYQRYKEELLISNFSKVSGY KINVQKSQAFLYTNNRQMESQI MSELPFTITSKRIKYLGIQLTRDI KDLFKENYKPLLNEIKEDRNKC KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLRMTFFTELEKTT KFIWNQKRARITKSVLSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITP
8638	39006	A	8695	I	3514	MELKTKARELREECRLSRCD QLEERVSAMEDEMNEMKREG KFKREKRIKNEQSLQEIWDYVK RPNRLIGVPESDVENGTKLEN TLQDIIQENFPNLRQANIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFPSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSIAIKLELRINKLTKSRSTTW KLNNLLNDYW
8639	39007	A	8696	I	2091	

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8640	39008	A	8697	1	2781	MGKKQNRKTKNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSVMEDEMNMEN DGENGTKLENTLQDIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKRKEGHHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRLD
8641	39009	A	8698	1	1584	MSISGTVRMSAKSKGNPSSSCP AEGPPAAASKTKVKEQIKIIVEDL ELVLGDLKDVAKELKEQHWW HPISGDTATSICTVLESEKSKIK VTAFDVWLHLWGKGTDKQKD SSNFCRLKCPCLTALKRAVVLP ARSWRCENGQTASSSGSLTPDP RAANREAPPSSRGRLTPHTASDG ENGTKLENTLQDIQENFPNLAR QANIQIQEIQRTPQRYSSRKATP RHIIVRLTKVEMKEKMLRAARE KEIQTAIREYYKHLYANKLENL EEMDKFLDAYTLPRQNQEEVE SLNRPITGPEIVAIINSLPTKKSP GPDGFATAEFYQRYKEERHINRT KDNHMIISIDAFAKFNKIQQPF MLKTLNKL.GIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QECPLSPLLFNIVLEVLAIRAQ EKEIKIGLKGEEVKLSLFVDY MIVHLENPIISAQNLKLISNFSK VSGYKINVQKSAFLYTNNRQ TESQIMSELPFTIASKRKYLGIQ LTRDVKDLFEEND

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8642	39010	A	8699	1	1722	MAGYPSEMKLPEELSGSNICCS AVFTVLQPLLIPRQTGSGVDL RQPTDQLRLVLTVRRKNNKQ KRTSTPKPHLYVTHKDQSRKKL TQNHSTTWKLNLLNDYVWV NNEMKAEIKMFFETSENKGTIY QNLWDTFKAVCRGKFIALNAH KRKQERSKIDTLTSLKLEKQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAIGN DKGDTADPTEIQSTIREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEDES LNRPITGSEIEAIINS LPAKKSPGPDRTAEFYQRYKE ELHINRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLVLA RAIRQEKEIKGIQLGKQEVKLSL FADDVIVYLENPIVSAQNLLKLI SNFSKVS GYKINVQKSQAFLYS NNRQTESQIMNELSFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKDDTNKWKNI PCSWVGRIN IVKMGI LPKV VYRFNAIPKLP M TFFTELEKVTTLKFIWNQKRARI AMTILS*KNKAGGITLP
8643	39011	A	8700	3	1033	
8644	39012	A	8701	1	1068	ANKLENLEETDKFLDTYTLPR NQEETESLNRPITGSEIEAIINNV PTKKSPPGPDVGTAFKYQRYKEE LRTVKNHMHISIDAEKAFDNIQ QPFMLKTLNKLGDATYLKIIIRA IDDKPTANILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSL ADDMIVYLENPIVSAQNLLKLI NNFSKVS GYKINVQKSQEFFLYN NNRQTESQIMNELSFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKDDTNKWKNI PCSWVGRIN MKMAILLKVIYRFNAIPKLLMI FFTELEKVTTLKCI* NQKRAHIA KPILSQKNKAGSITLR
8645	39013	B	8702	69	1055	
8646	39014	B	8703	1	2301	
8647	39015	A	8704	1	3189	

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8648	39016	A	8705	92	1139	ASAADTQANRVWSPFPANSNR PAAIRVLTVRRKTNKQKGHPH QNPICTPSSSKTEIQTTIREYYQ HLYTNKLENLEEMDKFFDTYT LPRLNQEEVESLNRPIGTSEIAI INNLPT/KKSPGPDGFTAKFYQS VGSSGQGNQAGEGNKGHSIRK RGSQIVPVC R*HDCISRKPHRLS PKSP*ADSQLQQLRIQNQC AKI TSILIHQ*QTNREP NHE*TPIHNG FKQNKIPRNPAYKG CERPLQGE L*TTAQ*NKRGYKQMEHSM L MGRKNQYHENGHTAQGNL*IQ CHPHQATKNFLHRIGKNYFKV HMEPKKGPHCQVNP KPKEQSW RHHTT*LQTLQGYSNQNSI
8649	39017	A	8706	1	2199	
8650	39018	A	8707	1	2238	
8651	39019	A	8708	3	1889	RSMRQKVNKDTQELNSALHQA DLIDIRTLHPKST EYTF SAPH HTYTKIDHILGSKALLRCKRT EITNYLSDHSAIKLELRK NLTQ NRSTTWKLNLLNDY WVHN KMKAEIKMFETNENKDTTYQ NLWDAFKA/EIQTTIKEYYKHL YANKLENLEEMDKFLDTY TLP RLNQEEVESLNRPIGTAEIVAIIN SLPTKKSPPGPDGFTA EFYQRYK EELVPFLKLQFQSIKQGLPNSF YEASTILIPKGRDTEKENFRPI SLMNIDAKILNKILAKRIQQHIK KLIHHDQVGFI PMQGW FNIHK SINVIQHINRAKDKNHIISIDA EKAFDKIQORF MLKTLNKL GID GTYFKIIRAIYDKPTANIILNQ KLEAIPLKAGTRQGCP LPLLFN IVLEV LARVIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVT AQNLLKLISNFSK VSGYKIN VQ KSQAFLYTNNRQTESQIMSELP FTIASKRIKYLGIQLTRDVKDLF KENYKPLLKEIKEDTNKWK NIP CSWVGRINIMKMAILPKVIYRF NAIPIKLPMTFFTELEKTK/FIWN QKSAHITKGILSQKNKAGGITLP DFKLYYKATVTKTAWY WYQN

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8652	39020	A	8709	1	1779	MGDFNTPLSTIDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSNIDHIV GSKALFSKCKRTEIITNCLSDHS AIKLELRKKLTQNHSTTWQLN NLLNDYWVNNEMKAEIKMFF ETNENKDDTDQNLWDTFKA VC RGKFMALNAHKRQERSKMG TLTSQLEKEKQEQTHSKASRR QEITKIRAELEKIEI/QKTLQKIN ESR/TEIQTITREYHKHLYANKL ENLEEMDKFLDTYILPRLNQEE VESLNRPTVGTSEIEAII NSLPTKK SPGPYGFTA EFYQRYKEELHIN RTKDKNHMIIISIDAEKAFDKIQ QPFMLKTLNKLGDGTYLKILR AIYDKPTANIILNGQKLEAFHLK TGTRQGCPLSPLFNIVLEVLR AIRQEKEIKGIQLGKEEVKWSL FADDMIVYLENPVSTQNLFKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKEDTNKWKNI PCSRAGRINI VKMAILPKVIYRFSAPIKLPMT FFTELEKTKFIWNQKRAHIAKS ILSQKHKAGGITLP

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8653	39021	A	8710	1	2093	MEITTNCLSEHSAILQLRIKKL TQNCCTTTWKLNYLLNDYVW NNEMKEEIKMFFETNENKDTT YQNLWDVFKAVCRGKFIALSA HKRKQERSKTDILTSQLKELEK QEQTSHKASRRQEITKIRAELEK IETQKTLQEINDSRSSFSEKLNKI DRPLARLIKKREKTQIDAIAK DKGEINTNPTEIQTIREYYKYL YANKVENLEEMDTFLDITYTLP RLNQEEVESLNRPTGSEIEAIIN SLPTKESPGPDGFTAIFY/HEGN QERERNKGYRIRKRGSHIVPVC R*HDCLFRKPHLLSSKSHEAVK QLQQLRIQNQWAKITSMMPVH Q*QTNREPHE*PIHNCYKEN KIPRNPTYEGCEGPLQGELOTT AQQNKRGQKEMEKHSLMDR KNHYHENGHTAHGNL*IQCHP HQATNDFLHRIGKNYVNFHME PKKSLHCQENPKQREQSWRHH AT*LQTLQGYSNQNSMVLVPK QIHRTMEQNRGLRNNTTHLQPS DL*QI*QKQEMGKQFPI**MVL GKLASYM*KAETGSLPYTLYK N*FKMD*RLKC*T*NHKNPRRK PRQYHSGHRHGQGLHD*NTRS NGNKNQNRQMGSN*TKELLHG KRNYHQSAQTTYRMGENFCNL PI*QRANIQLQRT*TNLQEKNK QPHQKVGKGHEQTLLKRRHLC SQQTHEKMLITGHQRNANQN

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8654	39022	A	8711	3	1805	PLSTLDRSSRQKVNKDIQDVISA LHEAGLIDIVRTLHPKSTEYTF SAPHHTYYKIDHIVGSKALLSK CKRTEITTNCLSDRAIKLELRI KKLTQNYTTTWKLNLLSDY WVNNEMKAEIKMFFETNENKD TMYQNLWDITKAVCRGKFIAV NAYKRKQERSKIHTLTSQLEP EKQEQTSHSKASRRQETIKIRAE KEIDTQKTLQKISVSRWFSERI NKIDRLIARLMKKKREKNQIDA IKNDKGDITIDPTMQTTIREYY KNLYANKLENLEEMDKFLDTY ILPRLNQEEVELPFRPITGSENE AIINSLP/TKKSPGPDEFTAKFYQ RYKEELQGMQEKEREDTQLG KEEVKLLIFAEDMIVYLENPV SAQNLLKLINNFVKVSGYKINV QKSQAFHLTNNRQTESQIMSEC PLTIASKRIKYLGIQLTRDVKDL FKENYKPLLNKIKEDTNKWK IPRSWLGRNNIVKMTILPKVIYR F/NTLNFIVNQERARIAKTILSK KNKAGGITLPDFKLYYKATVT KTARYWKQNIKKGSVWPISLK SEKRGHRTPLWKLCHNDVQG ELLKTIQFLFGSPLGHSSLDPSA
8655	39023	B	8712	1	1743	
8656	39024	B	8713	1	1260	

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8657	39025	A	8714	1	1842	VPP TTCGNYGSTIQDEIWMGTQ NQTISVSEEMMFQAEIISAQK MWNQHHITPSKVDHIVGSKAL FSKCKRTEIITNYLSDHSAIKLK LRIKKLTQNRSTTWKLNLLLN DYWVHNEMKAEIKIFFETNEN KDTTCQNLWDTFKAMCRGKFI TLNAHKRKKQRCIDTLTSQLK ELEKQEQTTHSKASRRQEITKIRA ELKEIEAQKTLQKINESRSWIFE KINKTDRLLARIKKKREMNQI DAIKNDKGDITNPTIEQTIRE YCKIILYANKLENLEEMDKFLN TYTLPRLNQEEIESLNRPTGSEI EAIINSLPTKKSPGPDGFTAEFY QRYKEEMIEKKA FDKSQPFM LKTLNLGIDGTF LKIRRAIYDK PTANII LNGQKLEAFPLKTGRQ GCPLSPLL FNIVLEVLAREIRQG KEIKHIQLGKEEVKFSLFADDDVI AYLENPIVSAQNLLKLISNFSKV SGYKINVQLQAFLYTNNRQTE SQIMSEFPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWIGRINIMKMAIL HKVIDRFSAPFKL/PKD/FFTEL EKTTLKFIWNQKRPRISKTLISK KKNAGGITLR

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8658	39026	A	8715	I	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAEMEDEMNEMK REGKFRKRIKRNEQSLQEIWD YVVKPNLHLMGVPESDGENGS KLENTLQDIQENFPNLRINKI DRPLARLIKKKREKNQIDTIKN DKGDITNTPEIQTTIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPTGAEIVAIINS LPTKKSPPGPDGSAIEFYQRYKE E/PADKQLQQLSIQNQCTK/TSI LIHQQTNRPNHE*TPIHNCFK ENKIPRNPITYKGCEGLLPGLQ TTAQGNKRGYKQTEHSLML GRKNQYRENGHTAQGNF*IQ HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKEQSWR HHTT*LQTLQGYSNQNSMVLV PKQGYRSMQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
8659	39027	A	8716	I	1578	MGDFNTTLSTLERSARQKVNK DIQELNSGLHQADLIDIYKTVKP KSTEYTFFGPHRTYSKIDHIVG SKALLSKRRTEITNCLSDHSA IKLELRICKLTQNRSTTWKLN LFLNDYVWHNMKAIEKMFFE TNENKDTTYQTLWDTFKAVCR GKFIALNAHKRQERSKIDTLT SQLKELEKQEQTHSKVSRRQEI TKIRAELEKIEIETQKTLQKINESKI QTTIREYYKHLYANKLENLEE MDKFLDTYTLPLRNQEEVESLN RPITGSEIEAIINSLPTKKSPPGD GFTAIFYQRYKEE/RPISLMNID/ AKILNKILANGIHDIKKLIHDD QVGFIPGMQGFNIRKSNVVIQ HVNRTDRKNHMIISIDAEKAFD KIQQPFMLKTLNKLIGDGMYLK IIRAMYDKPTANILNGQRLEAF PLKTGTTRQCGPLPLFNIVLEV LARAIGQEKEIKGIQLGKEEVK LSLSADDMIVYLEKPIISAQNLF KLISNFSKVS/GYKINVQKSQAF LYTNNRQTESQIM
8660	39028	B	8717	I	2982	

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8661	39029	A	8718	617	1155	SIAYQKSPGPDGFTAIFYQRH KEELLISNFSK/VSGYKIDVQKS QAFLYTNNRQTESQILSEFPFTI ASKRVGYLGQLTRDVKDIFKE NCKPLLEIKKDTKWKWNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEK/TLRFIWN QKRDHIAKSILSQKNKAGSITLP
8662	39030	A	8719	1	1827	MGKKQSRKTGNFKKQRHLSFS KGIAVLHQQWNKAGQRLTFDE LREGFRPSNYSKLQKEIQTKGK EVENFEKNSDECITRITNTKKCL KELMELKAKARELREECRLRS RCDQLEERVSGMEDEANEMKR EGKFGEKRIKRNEQSLQEIWDY VKRPNLRLIGVPESDGENGTCL KNTLQDIIQENFPNARQANIQI QEIQRTPQRYSSRRATPRHIVR FTKVEGKNIGSQRERAEIQTIT REYYKHLYSNKLLENLEEMDKF LDTYTLPSLNQEEVESLNRITITG SEIVAIINSLPTKSPGPDGFTA FYQRYKEEVVPFLKLFQSIEKE VILPNSFYEARIIIPKGRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIHHDQVGFIPGMAI RQEKERKGIQLGKEEVKLSLFA DDVIVYLENPVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQRESQIMSELPFTIASKRIKW GIQLTRDVKDILKENYKPLLEI KEDINKWKNIPCSWVGRISIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTFK/FLWNQKRARIAKS ILSQKNK/AGGITLPDFKLYYKA

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8663	39031	A	8720	I	1551	MEKFLDITYTLRLNQEELES LN RPITGSEIEAIINSLPTKKSPGPD GFRAKFYQRYNEELVPFLKIF QSIEKEGILPNSFYEASHILPKPG RDTITKKDNFRPISLMNIAVKILN KILANQIQKHIKKFIIHDQVGF PGMQGWFNIRKSNVQIHINRT KDKSHMIIISIDEEKAFDKIHLPF MLKTL SKL.GIDGMYLKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQRCLP.SPLL CNIVLEVLARAIR QEKEIKGIQLGKEEVKLSLFD DMIVYLENPTVSAQNLLKLISN FSKVSGYKINVQKSAFLYTNN RQTESQIMSEL.PFTIASRKIKYL GIQLTRDVKELFKENYKPLLNK IKEDTNKWKNI PSSWMGRANIM KMAILPK/VTWMKLEIIVLSKL P QEQT KHRMFSLTGVFIEGRAL QNKSETSQSRHPGATHSLPEYTI PGSSPSNFYWFTLGLKEEVTSG WKREKKKKRKEGGKEGRKEG RKEGRKEGKKEGRKKGRKEVP
8664	39032	A	8721	I	1983	
8665	39033	A	8722	I	2436	
8666	39034	A	8723	I	3139	
8667	39035	B	8724	I	3558	
8668	39036	B	8725	I	2133	
8669	39037	A	8726	I	3051	MGDFNTALSTLDRSMRQKVNK DIQELNSALHQADLTDIYGLH PKSTECTFFSAPHHTYSKIVHIV GSKALLSKWKREIHTNCLSDH SAIKLELRICKLNQNCSTTWKL NNLLLNYYWTNK/KKREKNQI DA/IKNDKGDIITNPTEIQTIRE YYKHL YANKLENLEEMDKFLD TYTLRLNQEEVESLNRPITGSE IEAIINSLPTKKSPGPDGFTAIFY QRMNYSIFKSTWKIINKNAYS LA HSRELRDGGQ
8670	39038	A	8727	I	2706	
8671	39039	A	8728	I	2573	
8672	39040	B	8729	70	2029	
8673	39041	A	8730	81	385	
8674	39042	A	8731	301	515	SSWQAPAPVLGSSWASKK*MK KKYAAQIEKQKSP*CKSIKSP LRSASYAQLLSFSLSSCLCFSTC HSTLA WYCL*SSWQAPAPVLG SSWASKKRSLLWKEPSRSLPSF SITARS*ACCCCLCSSTEPQLLKA QYLLSHSRTRSFRLQ

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8675	39043	A	8732	2	4207	DTHRLKIKGWRKIYQANGKQK KAGVAILVSDKTEFKPTKIKRD KEGHYIMVKGSIQEEELTILNIY APNTGAPRFTKQVLRDLQRDL DSNTIITGDFNTPLSTLDRSMRQ KVNKDIQELNSALHQADLIDIY RTLHPKSTENTFFSAPHHTYSKI DHIVGSKALLSKCKRKEIITNCL SDHSAIKLELRIKKLPQNCSTIW KLNNLLNDYWVHNEMKAEIK MLFETNENKDTTYQNLWDTLK AVCRGKFIALNA
8676	39044	A	8733	1	2770	MGKKQNRKTONSKTQASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKGE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAEDEMNEMKRE GKFRKRIKRNEQSLQEIWDYV KRPNRLRIGVPESDVENGTKLE NTLQDIIQENFPNLRANVQI QEIQRTPRQYSSRRATPRHIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKL

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8677	39045	A	8734	3	2169	FKPTKIKREKEGHYIMVKGSIQ QEELTILKIYAPNTGAPRFTKQV LSDLQRDLDSHTLIMGDFNTPL STLDTSTRQKVKKDTQELNSAL HQADLIDYRALHPKSTEYTFSS APHITYSKIDHIVGSKALLSKC KRTEIITNYLSDHSAIKLELRKN I.TQNHSTTWKLNLLNDYVW HNEVKAIEKVFFETKENKDDTY QNLWDAFKA VCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKASRRQEITNIRAEKKEI ETQKTLQKINESRTEIQTIREY YKHLYANKLENLEEMDKFLDT YTLPRLNQEEVESLNRPTGSEI VAIINSLPTKKIPGPDGFTAIFY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEAIIIPKPGRDITTKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIPHDQVGFIPMGQGW FNIRKSINVIQHINRAKDKNHMI ISIDAEKAFDKIQPFMLKTLNK LGIDGTYFKHRAIYDKPTANIIL NGQKLEAFPLKTGTTRQGCPLSP LLFNIVLEVLAIRQEKEIKGI QLGKEEVKLSLFADDMIIYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKISQAFLYTNNRQTENQIM SELPFPIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIK\EDTNK WKNIPCSWVGRINIVKMAILPK LIGNCSKISGYKINVQKSQAFLY
8678	39046	A	8735	1	5166	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRSSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSADEDEMNMCKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL

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8679	39047	A	8736	1	4553	MGRKNRKLDSRQHSYTSQSRSHEDPAAVLQALSSSGVVIIYQSLVAVQSPLAAPGCDGSRCEVRGLTVGSRYGSRWLAGCRDNEMVNACQSGWCYQNLTVLRGWKV LLEMTPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAMKR ELRIKNTQNRSTTWKLNLLNDYVWHNEMKAEIKMFFETNE NKDDTTYQNLWDIFKAVCRGKFI ALNAHKRQKERSKTDTLTSQL KELEKQEQTTHSKASRRQEI
8680	39048	A	8737	1	2673	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNTQSRSTPWKLN LLLNDYVWHNEMKAEIKMFF ETNKNKDDTTYQNLWDFAKAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTTHSKASRRQ EITKIRAELEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDITIKNDKGDITDTPTEIQ TTIREYYKHL YANKLENLEEM DTFDLYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEFY/PESYL*QTHSQYHTEW AKTGSIPFENWHKTGMPSLTAP IQHSVGSQGGQNGAQEGGNKGY SIRKRGSIQVPCV*HDCLSRKP HRLSPKSP*ADKQLQSLRIQN QCTKITSILIHQKQTNREPHE* TPIHNCFKENKIPRNPYKGCCEG PLQGEQTTAQRNKRGHKQME EHSMLMGRKNQYRENGHT/SQ GNLQIQCHPHQATNDFLHRIGK NYFKVHMEPKSPHRQVNPKP KEQSWRHHTT*LQTLQGYSNQ NSIMVLVPKQYRSMEQNRL RNNAAYLHYSDL/*QT*EKQA WGKGIP/IYKMA/LGKLA/PM*
8681	39049	B	8738	1	2792	
8682	39050	B	8739	156	391	
8683	39051	B	8740	1	2824	

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8684	39052	A	8741	3	4167	PLSTLDRSTRQKVNKDIQELNS ALHQVDLIDYRTLHPKSTEYTF FSVPHHNYSKIDHIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTQNRSTTWKLNPNLLND YVWHKEMKAEIKMFFETNENK DTTYQNLWDAFKAVCRGKFIA LNAHKRKQERSKIDTLTSQKLE LEKQEQTTHSKATRQEITKTRA ELKKIETQKTLQKINESRSWFFE KTNKIDRLLATLIKKKREKNQI GARKNDEGAITTN
8685	39053	A	8742	1	1107	MKVEIKTFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQKLEKQEQT HSKASRRQIQTITIGEYKHLTY NKLLENLEEMDKFLDTYTLPRLN QEEGESLKRPMAGSEIEAIINSL PTKNSPGPDRFTAIFYQRYKEE L/PDKQLQQLRIQNQWEKITSI PIHQ*QTNREPHE*TPHNCFK ENKIPRNPITYKGCEGLPQGELQ TTAQRNKRGHKQMEEHSMLM DRKNQYCENGHTAQEETAFCF HSRRESSRLGLLVANFRACHQE RFRRRERSVPAGVHAEAHPCWE NRGREERHWEQHPGPETVLLQ AGGHVCDQGLHHGQPQVGQV PRGSRGHSQHFLPSVQDRSWL
8686	39054	A	8743	1971	5654	RSPTAGRNTNYPSTRDYKHLTY A/NKLLENLEEMDKFLDTYTLPK T/ITQEEVESLNRPTIG/SEI/AVI NSLPTKKSPGPDGFTAKFYQRY KEELHINRTKDNHMIISDAEK AFDKIQPPF/MLKTL/NELGID GT/YFFKIIRAIYDKPTANIRLE WGQKLEAFPFEKLAQEQQMPL LLNPLPQSNIVVGKFLA/RAIRQ EKEIKGQVEKQEVKLSL/FADD MIICLENPIVSAQN/LKLIISNVS

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8687	39055	A	8744	1	4901	MTGSNSHITILTLNINGLNSAIK RHRRASWIKSQDPVSCCIQETH LTCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDKPT KIKRDKEGHYIMVKGSIQEEEL TILNIYAPNTGAPRFIKQVLSL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFFLAPH HTYSKIDHIVGSKALLSKCKRT EITNYLSHSAIKLELRINKLTO SRSTTWKLNLL
8688	39056	A	8745	2	1887	SASVVPASGLRPSSTSLTSRQP RFLGLLRSHPALVA VPGDW DLAVCCIVAPSHVCRMVFMMD RTLGLSLPGLLKREEDACWVEA NINGRVLAQCNIDELKKEMNM NFGDWHLFRSTVLEMRNAESH VVPEDPRFLSESSSGPAPHGEPA RRASHNELPHTELSSQTPYTLN FSFEELNTLGLDEGAPRHSNLS WQSQTRRTPSLSSLSQDSSIEI SKLTDKVQAEYRDAYREYIAQ MSQLEGGPGSTTISGRSSPHSTY YMGQSSSGGSIHNSLEQEKGD SEPKPDDGRKSFLMKRGDVIDY SSSGVSTNDASPLDPITEDEKS DQSGSKLLPGKKSSERSL FQA SLK\KGRGLRLSKLP/SEEDEC GAEEEDNTPLLKDDKDRKPEG KVERVPKSPHVSVEPIRTFIKAK EYLSDALLDNKGNSSDSVSD PRES\SPNHVSAQCKACDLPD LKRHNLELEDSDSHSGKRGIPH SLSGLQDPIIARMSICSSEDKKSPS RIASLD*PSSPLEENW/PACQKA YNL\NRTPSTVTLNNSAPANR ANQNFDMEGIRETSQVILRPSS SPNPTTIQENLKSMTHKRSQR SSYTRLKSPELHAA/SSSESTG

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8689	39057	A	8746	1	385	EGNEAQTCSFWNTRQLASS DPSLSVSQRMDPSWRRSSHSWP QPMPPDSGRAPVRPHLAKLEED VWPCPQFHQTAAASGPPFVTFQ PANCFPSVISFHLCHTWSEQD RAYHPVYQMR**GSDVQLLEY EASAAGLRSFSERFPEDGPELE EILTQLATADARFWKGPSEAPS GQ/ALRK/SVWPCPQFHQTAA SGPPFVTFQPANCFPSVISFICT AIRGVSKTGLTILSTR*NGSSE KSLV
8690	39058	A	8747	2	2015	QDFLDSQNLASAYNTRLFKEVD GEGKPYEYVRLASVLGSEPSLD SEVTSKLKSYEFRGSPFQVTRG DYAPILQKVVEQLEKAKAYAA NLSHQGQMLAQYIESFTQGSIE AHKRGRFWIQDKGPVIESYIG FIESYRDPFGSRGEFEGFVAVV NKAMSAKFERLVASAEQLLKE LPWPPTFEKDKFLTDPDTSLDV LTFAGSGIPAGINIPNYDDLRTQ EGFKNVFAGGIVLGCGLTPRK REK/LTFLEEDDKDLYLWKGPS FDVQVGLH/ESLLGHGSGKLFV QDEKGAFNFDQETRDPPQKRG EQIQSWNRTGETWDSKFSTIAS SYBECRAESVGLYLCLHPQVL EIFGFEGADAEDVIYVNLNM VRAGLLALEFYTPFAFNWRQA HMQARFVILRVLLEAGEGLVTI TPTTGSDGRPDARVRLDRSKIR SVGKPALERFLRLQLVKSTG DVTTEGRALYEGY*STVTDAPPEA CFLTLRDTVLLRKESRKLVSQP NTHLEGNE/VSDVQLLEYEASR AGLRSFSERFPEDGPELEEIFIQ LATADARFWKGPQ*GPHSGPS LRKIVVALPPKFHQTAA/SGPS HSVCVFRGWGGGAGAWTLV LPQLEGW*HNPLPICQHVSSLP NCFPSVIL/SFICTAIRGVSKTGL TILSTKMRNGSSEKSLV
8691	39059	A	8748	1	519	
8692	39060	A	8749	786	864	
8693	39061	A	8750	1	468	

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8694	39062	A	8751	128	605	MTWGTVPPLHFQMRCCWVSC QGIMRGWGLCSQTLNCLLSK C*TCSSGGGQIWSRKFRVVRVE *G*GNFKTPQLQPGVPPGLPP PGSCFKCRKSGHWAKECPQPGI PPKPCPICAGPHWKLDCPTRLA ATPRSPGTLAQGSLTDSFPDIDG LAVED
8695	39063	B	8752	1	615	
8696	39064	A	8753	1533	1767	PSPTCPAIYS*KGGWSQRHSQG ACYTCRKSGHWAKECPQPGIPP KPRPICVGPB*KSDCSTHLAAN PRAPTLAQGS
8697	39065	C	8754	84	329	
8698	39066	A	8755	911	1497	SQRKARDQRRKRNRASSIAK HKEPKRPILPSGKNSQEGVATH TKPLAQGGVWLD/NETNEIPN ANFRQQIRKLIKDGILIRHRKPV TVHSRAQGWKSTLARRKGRHL GIESKKIDRHMVHSLYLKLGKN VFKHKRILTEHSHKLKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEEIKTLSQEEKAK
8699	39067	A	8756	34	280	EVIHAAIGEEKGSY/NA**PWVE EQLTRQPLIHHQPASLHVSYY/RC RYHSLYLKVGKGVFNKRIILM EHIHKLKADKARKKLLA
8700	39068	A	8757	1	692	AFLQELCLKSSTGELFPFAAV AAALSMLRLQKRLASSVLCCG KKNIWLDPNETNEITNANSRQQ IRKLIKDGILIRKPVTVHSRLRC RKNT/LAR/*KGRHMGIGRKRV PANA/RMP/KEVTWMRENEGF CRR/ASEDTRES/KKIDRPHVVT ALYL/EVKGNVFKNKRI/MEHI HKLKA/DKARKKL/LAD/QAEA RRSKTKEATKRREERLP/ARPK REII*TLKSEETKK
8701	39069	A	8758	46	131	
8702	39070	A	8759	5	447	PATELPGLPTRPGMLCIWRGAP DWPEGPPSSGELSSIQPTQGLHN CFQPDGARPAAPGPVPQGLGAL PWSCRPPAEPTLFMESLVQWPP GDGIRQ*CEDAAELREPGVQRH QGSPP*VRTLPPLRGPSQVPA/G SSSSASPRSPGSRG

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8703	39071	A	8760	1	201	MPNIYTMEEYAAVKKDEFMSF VGTWMKLETHLSKLSQGGQKTK HRMFSLIGTRMKLETHLSKLLQ GQKNQTPYILTHRISFEDVRNY MPLAVIHSDESPILPLHEQQDAS ENGWIKDTERDADLEIYIVSGIG SFRWVLGLADFKSEAADPCGM KLQTFVAVSVTALKGGASRVVH SSWWVCVLTDFRSEAAYLSVT ALEGGASRVHSSRFVVSLSG VKLQTFVTNATAHKGSADPKS EQHQDLLQRAKKHTFHSMKGE PRRVVAAGWGAIAKADSNLI LLFQTIEKYCPWFPDKGSDVLL DWDVRVGTTLQLMRDGVLLPI SVWTDWALIRVALLPFQSGDTL QLPQVNADVEPLPLPCIGGITG PEGGDPGPGSFHYLVGVYYFLT CRSTWEQRKSPVALR**KLGPG GSPSGPVMPPMHRGKSGSGTS ALTCGS
8704	39072	C	8761	42	179	
8705	39073	A	8762	11	1713	PKTLKMGGGTAGLVGMGFSTT GRTPSAPGRPHPCRGAP/GSPG KAGLFLQRPRLGTGL*GSAPRG PG*MGCPGTGRGNSNRH*RGPP RRPQAS*AAPFQPGPLETWTPG *SQVPGAPSPCNFSYPHREVPP WGPVPPAPHGSCGWALALPR RKRAAVFSSWAPGQAGQLLDA ASVGAAP*QDIPPCRGSAPS SPHPPPGLESGBK\PGAASWAGP QTPFSGRAQQLCQEGPAGAGN TSGRSA*AASAGTCDGPRSGGR VRTYPGLP*CRWTPGSRSSAAS SHHCRMPSPGGHCTRLSMKRV GSAGGRQLQGRAPS*PARGT*Q RPRGGQSLGAAPLESRH*DGEC *AFWRAETVRSSVQRRREFATG LSGPSS*PRWSTCSVP/ASSPGG GDVAGPQEGPRSFHCLPSCL*V RPSHPEGDAAP*GALHK*RMII EEGRPGPCGGWGLV/GSWEPV QGCRRLNLRWGRAWNCLQFPE *PPGGPGLADSGFIQTARLNFQ GWASVSFSIKRPGRAILRPCPTS EFLLPESFVSGNCSSITERAMWP FWAPPSPAPGAENFPCASVPCK

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8706	39074	A	8763	1	409	LTHLTAQNVPNLFARNERVICL FDTEFGPMAQILVGATIVGSIET VWAGTITPPREGIIRWTWPAG ENDGVSALLKGQEMGRFKLGS TVINLFAPGKVNLEQLESLSV TKIGQPLAVSM*SKATQLGNPR
8707	39075	A	8764	1	1528	MTFVNAQAEDSQIFLYKRRVVP VEGYAPWLVSNGASELERIHYE GMDDVILLDFLPKELGDFMNM HILSFAPGANHGYYIEHTFKEHG GATQAFAKENNHKAYKDTYG VSHITRHDMLQIPKQQQYKEYQ DTHIDTPYCEPLPGETRLWGD DVIGLFDAAETDMNDVVAILENH PLLGAGFAHKIEQLEDKDWERE WMDNFHMPMRFERLWICPSWR DVPDENAVNVMLDPGLAFGTG TIQTLSPAMLDSTHTRRMRS TLNLYEITRMSTVSTSEHSMTY TLVQVDMKEAQKPDATASYRTF NEFFVRPLRDEVRPIDTPNVL VMPADGVISQLGKIEEDKILQA KGHNYSLEALLAGNYLMADLF RNGTFVTTYLSPRDYHRVHMP CNGILREMIYVPGDLFSVNHLT AQNVPNLFARNERVICLSDTF GPMAQILVGATNGGSIETPESE GATVDES FVVGPGVGD FELL LC IQERSALSGRCVI*SFNSAKVRFI QQSRRPVKS A
8708	39076	A	8765	2	420	QNFKEIFVRPLRDE/VRPIDNDP NVLMVPADGVISQLGKIEEDKI VSNLFARDERVICLFDTEFWPN AQ/ILVGATIVGSIETVWAGT/IT PPREGIIRWTW/QAIEEDSWQ NLGRVAG*NKLPTEL CN NFDW AQTLSRRNRG

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8709	39077	A	8766	1	1130	MHFAKKEDVSEITGSDGEKPK ARAGCLIGNSERLFSVTFVQF QATLPLSYTIMKHKDTGTSSVP ESIDASLEASQQNPFLKTLTRS CSPSWPCSRNWPILLIPTCPA QAGATPQLPGLGPPGHLPMNQ PASSFPPRPNAASQILTSTFHKP PPGSSLACCCCPGCDWQEDSQ *PTPACPSWPPWPTQLSPSAAGS PNIHSPIQGFHSQLLS*RSPTG TEE P*EANKLPWWTGHRPEPHPLG PGHIPCAAG/MHRPLAPTTR/PL ATLHGERQRHLHPGQRRRVPR APAESTEAPALWLHRPPECPEC SGHGPAALEQAGAMA*CRSCR HLPFCFGEADAGSREGPHQEV PRSKICQPPQAASFRICLHSIF
8710	39078	A	8768	179	1908	KKQNKSRGCVNVNWMRRALK MCIPYRNGHSIFLVMVKVERSK RFALKLSVAEKNQMPRNATVIE NSAGYSYGKMAFS*PRICTQIV GPRIISTTAVIS/SPATHHRAIR GAIIRTAFCGPGCFGAGDTPINNG LSIRHTTRNFPNREGSKPANGQ MSAVALMDARSIAATAANGGY LTSASELDCWDNVPEYAFDVTP YKNRVYQGFVKGATQOPLIYG PNIKDWPELGALTDNIVLKVCS KILDEVTTTDELIPSGETSSYRS NPIGLAEFTLSRRDPGYVSRSK ATAELENQRLAGNVSELTEVFA RIKQIAGQEHIDPLHRVYRHCS RSGNCPSDVFDISKDPVQDHRP QKRVTLIWGYDIHPQIEIIQTGD NFFQFRAIANNFGFLRFYQIRHF GLSGQHGVQIFTADVERGVGL RLQRFPVVKHAIVQRQVEVIAV AHIEVQADIFRSFRAIEANGHK VEQHFDHRPANGVRGTGGAVA ELMHPFAQLFRAGQVETAPCG GLGLIAQLFKVIRLQILRGESKK FSANLTALKLPLPMVYEGDKV LKHLRLPKFNLPLVPQPKKML
8711	39079	B	8769	1	1881	
8712	39080	A	8770	2093	2287	

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8713	39081	A	8771	1	1358	MKINLKLTDNSKVADGQFANI VVFLINWFYIHATTCEIDNGGVI VADGQFQASKAYSADSIVDYN AHYKTSVDQDAWGFVPGGDN PWKKYEPAKAWSASTVYVKG DRVVDGQAYEALFWTQSDNP ALVANQNA TGSNSRPWKPLGK AQSYSNEELNNAQFNPETLYA SDTLIRFNGVNYISQSKVQKVSP SDSNPWRVFVDWGTGERVGT PKKAWPKHVVYAPYVDFTLNNH HRRTDSFRSKATAELENQRLAG NVSELTEVFARIKQIAGQEHDP LQTEIGSMVYAVKPGDGSARE QAASCQRVIGGLANIAEEYATK RYRSNVINWGMPLQMAEVPT FEVGDYIYIP/GIKAALDNP GTT FKGYVIHEDAPVTEITLYMESL TAEEREIIKAGRIRHLLSDAMLA HLIRPTNRIESVGQIRHFRSIRHL LSDAMLAHLIRPTNRIEP
8714	39082	B	8772	21	1623	
8715	39083	B	8773	32	1850	
8716	39084	A	8774	1	1193	MSEVEAAAGATAVPAATVPAT AAGVVAVVVPVPAGEPQKGGG AGGGGGAASGPAAGTPSAPGS RTPGNPATAVSGTPAPPARSQA DKPVLATRLVPGTAKRFNVRS GYGFTNRNDAKEDVFVHWA VKRNNPRKFLRSVRDGETVEFD VVEGEKGQAQTNVTGPRAAGV PMKGSRYAPNRRFR*FIPRPPS VAPPPMVAEIPSA GTGPGSKGE RAEDSGQRPRRWCPFFFYRRR FVRGPRPNQQPIELTGAFACS QGTDRVEPKETAPLEGHQQQG DERVPPPRFRPRYRPRFRPRQ QPTTEGGDGETKPSQGPADGSR PEPQRPRNRPRYFQRRRQQAPGP QQAPGPRQPAPEEAPTEAIKP MIAHDGHAPPNPSPTCCLEPSY QLVDVN

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8717	39085	A	8775	3	933	RHQESLCAPLEILQKKKCPCLE EPLQROPCPCQSSSEVTA**NISF RFASPGGN/SPWASH*APSVRG AAPAGPVGLEAAAGSEPHGP/ PDAGGARVPVGGAGSRPRMVL/ SPRSAPHLGGGRSA/PAMRTGN PCTHTQVVTTSPNLPNIP*GAKS HPI/VERPLS*KGTGPSAQIATE NIYP*QLHGKGLIRD*KIVPHD GAAGQSPLLPVRSCQRGYLP SAK*FFDALKIKFTLKFHLRRFSC TSLRLGLLVSPLLPVRLLAG WAHAWMHGCGGWEPRTQQR ASCQLPDRTKSKMRVKIPAAANS SWLCH
8718	39086	A	8776	3	925	RGSEQIPSSIPGAP*KMLFSPG/ SSEPEHL*TVPASSLGCRRPGGPV ASRSRPPRPPARAALRGPPASSP IRFP*GASPRAPPTS*MRSGAGS KT/TPRPGPSASGDRPRAPCVRG PGCGSEPAASSTPGPAGVPRA R*GPGHGQTSPHGW*PSSMQQ RTRRCSPSSVPGQFPLP/LSCS QVSPWTW*GLPYSLLIPVSSLLP WPEDRVPSFVA/GPLPSFDNTS LPVEGGS*LHPVCLLYVYQENS SKHIPYSCRGSRIFPFSQRQVRM AGQRKLCDHPGGLISKPLAWT RIPEAPVVAAMVEGGGGL
8719	39087	A	8777	144	503	
8720	39088	A	8778	15	427	
8721	39089	A	8779	1	1055	
8722	39090	A	8780	280	1480	FQTRMGISVATIPGTSCSWSMR ASEKEKDTFESTVQVSKLQDLI HRSKMARCRGRFVCPVILFKGK HICRSATLAGWGELYGR/QATT YFFSGGADDAWADVEDVTEED CALRSGDTHLFDKVRGYDIKLL RYLSVKYICDLMVENKKVKFG MNVTSSEKVDKAQRYADFTLL SIPYPGCEFFKEYKDRDYMAEG LIFNWKQDYVDAPLSIPDFLTH SLNIDWSQYQCWDLVQQTQNY LKL.LLSLVNSDGGTDSKSLVAI RTSVGVALAQTSGNALAYGTK KAQEQSQDGLIHTSLKPTILYL TVAYDWFLFGHMLVDRLSKGE EIFFFCFNFLKHITSEFSALKTQ RRKSLPARDGGFTLEDIC*DE RTVAVPPDLVCDCLPGHGEFPR

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8723	39091	A	8781	2	588	HSFFFFNPREKCKTKR*RLSASRF PP*PWSRLPSG/QPAGGASAGSP SAPRGITGRGAGSRPAHG/VQPP RAHPEAPCPACPRSVGGAR/RA PEPSSNLSGEAPASGDRDVPVPPS PLAR*VPLGGREFGWPWANA L.RPGKTP/RSDRV/SRSPWS/PAG FSVPASWPRRSTSGNRGPPSRFS RLSRTSGPLNRLGEFFDVQGPL
8724	39092	A	8782	1	198	
8725	39093	A	8783	1	275	MAGAPAPASLPPCSLISDCCAS NQRDSDMGVGPSEPGAGYNLVP VIEKRSIRVGVTFGRSCCPSPSL TRKGNLTPWASQVRQCLAL QLAH
8726	39094	A	8784	349	478	KLKSFYTEELSSGLYIGISLCP HKYNCLVSSHRCCKN*VTGY
8727	39095	A	8785	1	325	FSEGNLYLVGIMHPLKAMLPL QYQTETFPFGYLM/PCRLQQ SHLLTLRDCCASNQRDSVGVGP SEPGAGYNLVVRRFLSLLEKRSI WVRVTRFSSALNHELKVNNDH
8728	39096	A	8786	113	313	
8729	39097	A	8787	2	1991	
8730	39098	A	8788	512	1178	
8731	39099	A	8789	135	1562	DTLVPTSQGDISRGLEGNLNSC PT*Q**RAPFLWCQ/PKAEWGT WIFNPEAEESLEPRSLISDCCAN NQRDSDMGVGPSEPGAGYNLVP RSFLSPSEKRSVRGVTRLSRCR PSPLSLTQKGNPLTPCASQVRQ CLALLRLRHVYFYFNGWKDYG VASLTTILDMVKVMTFALQEG KVAIHCHAGLGRGTGLIACYLV FATRMATDAQIIFVRAKRPNISQ TRGQLLCEAQSGAFSADVSGS HSPGEPVSPSFANVHKDPNPAH QQVSHCQCKTHGVGSPGSVRQ NSRTPRSPDCGSSPKAQLVE HETQDSKDLSEAAASHALQSEL SAEARRILAAKALANLNEVEK EELKRKVEMWQKELNSRDGA WERICGERDPFILCSLMWSWVE QLKEPVITKEDVMDLVDRAD AAEALFLLEKQHQHTILCVLHC IVNLQTPVDVEEAFLAHAIAKAF TKISIIIVNQNPVETVLL
8732	39100	B	8790	563	2017	
8733	39101	A	8791	108	194	
8734	39102	A	8792	1	164	

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8735	39103	A	8793	1	1068	MEESSRYWGTGRNRRREGKIQ WAQAPALFNIRQGPNEGDNQQ GSYWEALASIMQIHLLVPSGLG MVTAFHCSWYLSTTATFPGLV NPALTEIKSGNYYVHGSFILQV ADYKEFQTLMLITKATFHQKTQ CWACEEGVQQSFHCPCRMQAA ASVERYTELLKEFLFKEHTCDN QEPTSTLHYHSLKTVHIHVYSS RCTLPCQPSQAAQAEIGSPAP ACEDFVFAALAPP/ESG/RCPTL RLLGGLCTPTNARRTRTHSTTA CWARAQWDSLGLPLKLSHR/PR VCGGTRAPGRQCGMGNQRLGT SNSEARDPGGLRVKHR/CEAIQ EPPNRSRRQGAPLHSPPAY*MS SWRP*SFSKRHNLS
8736	39104	C	8794	78	331	
8737	39105	A	8795	129	1734	QWMHRMLDIFKGSQQHPSVPR VSSRPPLGPQGYSLHHFGTQGI HSATPINTQGLQAPAMGTQQPQ PEGKTSAAVVLADGATIVANPIS NPFSAAPAAATTVVQTHSQSAST NAPAQGSSPRPSILRKKPATDG MAVRKTLIPQPHDVASPRVES SMRSTSGSPRPAGAKPKSE/STC LWPLRSLCPWRLYPIKIMISLPL PSLKLPSPPHPRFQL*LQQPVPR HNQPLPFQPFLESPSLHPSPLA HCTTSISHCGWQSFRLGLPSRS* N*SERRSRTNGYHEASF/SVPPL ATNTVPSPLALLANNLSMPTSD LPPGASPRKKPRINNSMWISTEE GDMMETNSTDDEKSTAKSLLV KAEKRKSPKEYIDEEGVRYVP VRPRPITLLRHYRNPWKAAYH HFQRYSDVRVKEEKAMLQEI ANQKGVSCRAQGWKVLCAA QLLQLTNLEHDVYERLTNLQE GIIPKKKAAATDDDLHRINELIQG NMQRCKLVMDQISEARDSMLK VLDHKDRVLKLLNKNGTVKKV SKLKRKEKV
8738	39106	A	8796	1	169	RPTRPKSNKRQCLVFVTPKEE EPVRNILEKFTNISGKVRSLYL HAPLLPLER
8739	39107	B	8797	156	398	

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8740	39108	A	8798	20	723	VWGGELPRIWFMLPTSHQWM LFSVFLGWGSCQWSCSHLLSCL WRAAFSEFPLGPEPGEGIPELC LCFQMEAIELSVDPKSNKRQCL VFVTPKKEEPPVRNILEKFNTISG SK/CTEVQRGVYIPGHIR*R**SI PRGF*FYSK*GRPDSAGGHGPG GVLQGEKGHSACARQGGRFQE GAAFAQRETAGRRVGQRWCG DCFRTPVHRKSLSSPNFGGFGA GSEAVPCHLVLYLVW
8741	39109	A	8799	79	256	LRLLTLFFQNLGGKSSMLWTA HPCPEGACSSCTSLGSHLLSS FPVLGR*PGPSGDH
8742	39110	A	8800	402	996	TFFKFPPDSGAQLASPRGSRIGA AGGAA/SSPEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPO/GRQ SGSPGRGGAESERGL*GLPSCC HLSPGSGAAAVPRSVGSRWPC GA/PTLATPPTASFFSAATPEGP PLAS
8743	39111	A	8801	7	602	TFFKFPPDSGAQLASPRGSRIGA AGGAA/SSPEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPO/GRQ SGSPGRGGAESERGL*GLPSCC HLSPGSGAAAVPRSVGSRWPC GA/PTLATPPTASFFSAATPEGP PLAS
8744	39112	A	8802	262	349	KEGEGGK/DP*PVRMCPKPSG HWKHPGE
8745	39113	A	8803	2271	2863	GGASGVVRSWWARGLAGFRS EAADLRGLPVELRASAPCVRT PQPLGGR/GIGRPGAEGGPCWG GSGRTGAHGGAGAGSSLGQP RKGLPQCSGG/PEGLLKCGQSG SPGRGRAQSERGL*GLPACCHL SH*PQGRQI*PRTCPTPFQSKTS DQGGPSGPAVSGSERQV*LHHQ *PGCRDYLCGFCSWEINPVWG

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8746	39114	A	8804	3	561	NCPSLLVESCFCQECGSSIPFALPS TQVEHALYASER*QRAGSPHSP HSLSVPLPGLPLWRHLRSPS/G PPLH*PP*ASTLTGGPQ*RLGSA GINVSSEPVSSSRPNV*SFFFPQY TVTLVKGWSREPSPKSSVLGS/ MVP*STKSEP*REPI*SLTGKA GERGEKGREKAIGSGR*GVAKC SDHVR
8747	39115	B	8805	298	380	
8748	39116	B	8806	1	1292	
8749	39117	A	8807	1	1224	MKPRTLAVSVTALKVARLEFV PSDVRMCSEFLPSGGLVVSLAS GVKLQTFVSVTARNVDPKN SGAQLASPGSSSTRAASGAAC* SPSPPPCARTPQPLGGR/GTGCP GAGGGTRRGGSGRTGAHGAAE GVGSGLGQPRKGPPPTVQWWAE GLLCKRQSGSPGRGGAESKRGL *GLPASTLSMPPGIECAGKSENS HMNLNCSGGSLPGGTGAHLPL GPDGQPAETLLWGPCGCGPG TGLTSGQTISLGCQGGQPRRE VKPPVPQRVSVLLVAVNPPDS RCRVETDRPWLRCIQSCLCGTL KRDVLHSPSVFNTTRGGTAE WSREDKDALLPEYALHMPFAV GFKLEYKEGVLSNLAAGPEK ELCEAKRNQCPKSGVSHTSRPL KPEWSDFVAEIDESKLPRDS
8750	39118	A	8808	1	1298	ESLRAGSFQEQIPELAPLIILRG FGTWPGWSFQATGFCVGVVRGS PGSGFRGCGAYRAP*SFRTQLW PWQPLQGLDPKPLKDALARPSPL GRRACAEHHLCSADERPDLGFE GLQRWGGCRGSQKPAVHQ WGRGCGEGTGGGHTGSPPPRLTP P/PGGSGFRAQPGERRPAACGQ QRALGPMRPPAC/GPSPT*GCA LNPTSPAPLV*GFIHIVAAFCF VTPVSKSHSFQLGGELRVAGSD VGGRWGERENTQGSTLPPSSPAS SPGSPSPDPATPPGPATPGLIDIL LLLPMVASSRKHDFSGFSGRLP PQGEFFQ*GPTGWQSWVWPLD PSYLGCGCGGCGQGPRTGRRG ASSHCCVPAAP/GLSMDCSRGS GGSPRSPPWALLGDLPSLET VCLVMMFPCPIWMASEFAMEI QLLGPFWQIMLIGLCW

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8751	39119	A	8809	2	662	RIPLLVTRLKINEKVLQVLTNIF LFHDFSVQNFIFGLQLSLEHFY SQPLSVLCCNLPEAKRRINFLSN NQCEINIRRLPSFRRYVEKQASE KQVALLTNERYLKEETQLLEN VLHVYHMNYFLVLRCLHKFTSS LPKYPLGRQIRELYCTCLEKNI WDSEYASVILQLRLMAKDEL MTILEKCFKGFKSYCENHLGST A*RIEEFLGQFQSLDEPRGR
8752	39120	A	8810	326	1215	NPILHGNFIFMLDHSKLVQDQ E*TLN*/HYGPQVVTMCQCSFIE RNKRIPVVQGIIRGRGHVQWG RYVEKQASEKQVALLTSECL KKETQLLENLHVYHMNYFLV LRCVHKFTSSLPKYPLGRQIREL YRTCLEKNIRNSEEYASVLQLL KMLAKDELMTILEKCFEVFKSS CEKHLGSTAKRIQEFQAQFQSF DETKENEALKREEGCPNITPDI CIAAYKLYLECRRLINLVDYSQA FATILTAEEKMDANSTSEEMN EIIYAWCIRTVFLELLGFIKPTK QKTDHVARLT
8753	39121	A	8811	70	613	SLEMKELRRSKKQTKFEVLRE NVVNFIDCLVREYLLPPETQPL HEVVYFSAHAHLREHLNAAPRI ALHTALNNPPYYLKNEALKSE EGCIPNIA/PDICIAYKLHLECSR LINLVDWSEAFVVTAAEKM DANSASSEEMNEIHARDIRAVS ELELLGFIKPTKQKTDHVARLT WGCG
8754	39122	C	8812	598	762	
8755	39123	C	8813	138	296	
8756	39124	A	8814	1	395	

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8757	39125	A	8815	2	1289	DDLALAFKVLHDKQRGPTGF YAPFNSRPL*KPQLAHSIILMET ATERISRLLLPFADQHV EIPSLT AGNIALTVGLKHTATGDTIVSS KSSALQLV EPNGREKRSTDK TMKAERLLLAGSGRFQEPVFFC TIGTPITV*GSQIWEHAFEMSFS VRIPVLKVR LDPDSGGQTVLCG MGELHIEIIHDRIKREYGLETYL GPLQVAYRETI LNSVRATDTLG *EL*GDKRHLVDLLGSGKARPI ETSSVMPVIEFEYAESINEGLLK VSQEAIENGIHSACLQGPLLGSP IQDVGNYLYIP*QIHPWAPSTTY DFCLCLKMPCKKALERKADKQ VLEPLMNLEVTVARDYLSPLV ADLAQRRGNIQEIQTRQDNKV VIGFVPLAEIMGYSTVLR TLTSG SATFALELSTYQAMNPQDQNT
8758	39126	A	8816	545	849	LAHLSLISRHDDEATRTSTSE GLEEGEVE/GETLLIVES/EDQAF S/VDLSDHQSGGISLNSDEGDVS WMEEQLSYFCDKCQKWIPASK ELLNSFDLSIPV

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8759	39127	A	8817	1	2395	MDSSIHLSLISRHDDEATRST SEGLEEGEVEGETLLLIVESDQA SVDLSHDQSGDSLNSDEGDVS WMEEQLSYFCDKCCQKWIPASQ LREQLSYLKGDNFFRFTCSDCS ADGKEQYERLKLTHQVVMVL ALYNLSLKGSGRQGYFRWKED ICAFIEKH*TFLLRNKKKTSTCR STGAGCLSVGSPMYFR*GA*EF GEPRWWKLVHNLPLTMKPERE KTAASTLNIFAASKPTLDPIITVE GLRKRASRNVPESAMELKEKR SRTQEAKDIRRAQKEAAGFLDR STSSTPVKFISGRRPDVILEKG EVIDFSSLSSDRTPLTSPSPSPS LDFAFGTPASHSATPSLLSEAD LIPDVMPQALFHDDDEMEGD GVIDPGMEYVPPAGSVASCPV VGGRKKVRGPEQIKQVEVESEE KPDMDIDSEDTDSNTSLQTRA REKRKPQLEKDTKPKEPRYTPV SIYEKLLKRLAECPGAVAMT PEARLKR/KLIVRQA/KRDRGL PLFDLDQ/VVNAALLVDGIYG AKEGGISRLPAGQATYRTTCQD FRILDYQTS/LPSRKGR/HQ/T TKFLYRLVGSEDMADVDSIVSP YTSRLKPYIRSDPHWTEPDAP LDYCYVRPNHIPTNSMCQEFF WPGIDLSECLQYPDFS/VVVLV KKVIIAFGMV/DVKYNEAYI SFLVHPNWRRAGIATFMIYHL
8760	39128	A	8818	3	364	GDSVPTAEGGDQVCVILSSVPQ TVWEPMFNKRACG/P*SP*SLSA TSIYPRELKAGTKDTCPPVFR AVLFTTATQCPSTDAWMNKM WYSRTMECYSALKRKEIPPHAT ARHPMCLQFCRW
8761	39129	A	8819	292	508	ARPGDQATSGGQGTTFQHPLFC FELGGSQNPALQ*PFAAACPVG AD*TKFTAFCCRLK*KRTCCCL SLGSRCL
8762	39130	C	8820	253	369	
8763	39131	A	8821	295	393	IYFGCLLGEPVVAAEAGIWDN DCVKKQLLHSW
8764	39132	B	8822	91	479	

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8765	39133	A	8823	I	544	ARHPDMKKRRVEDASILPCNVSL EYEKTEVNSGGFSKSAEEREKL VKAERKFIEDRVKKIILKRRKV CGDSDKGFVVINQKGGIDPFSLD ALSKEGIVALRRARRRNMERLT LACGGVALNSFDDLSPDCLGH AGLVYEYTSAPCPKQSGLCILSS TLGEEKFTFIEKCNNPRSIVTLII KGPKNHTLTQIKDAVRDGLRA VKNAIDDGCVVPGWCRCRKGW AMAEALIP*APVLKGRAQLGS PKHLLDAFAHYFPKVLCFRNSG FLTQGNIKLKFKAEHSRIQVQL VGVDLNTGEP/MVASRSKAVW GHT*LW*KKTSLPSTPTW*IA\ TNILLGLNEIMRAGMSFS*KGF VVINQKGGIDPFSLDALSKEGIVA LRRAKRRNMERLTACGGVAL NSFDDLSPDCLGHAGLVYEYTS PACPKQSGLCILSSTLGEEKFTFI EKCNNPRSCHIIDQRTK
8766	39134	C	8824	636	1025	
8767	39135	A	8825	33	1505	KCISASVKVDFSDLLLSNNTS*S AFTPTRTQKSSSKLLRKESHYS GMMSIQEKSSESSKVTKKSD DKNSETEIQDSQKNLAKKSGPK ETIKSQAKSSSESKINQPELETR MSTRSSKAASNDKATKINSKNT VTVRGYSQESTKKKLSQKKLV HENPKANEQLNRRSQRLQQLT EVSRRSLRSREIQGGVQAVKQS LPPTKKEQCSSTQSKSNKTSQK HVKKRVLEVKSDSKED/GKSSN **SNKFS/SKGKNAR*NIR/SACA CSSQCTQGSEKCPQKTTRRDET KPVVPVTEVKKRSMATSVVPK KNEMKKSVHTQVNT/KHNTPK KSTAISA*TK**AGASRKEQTR *YSPA\REEIAGEIESDNVEVKK ESSQMESVKEEKPSKLEETSV ERQILHQKGTNQDVQCNRRFPS RKTKPVKICLNGINSSAKKNSN WTKIKLSKFNSVQHNLDSQVS PKLGLFTNQFTTSFRNASSSDS KYIFRDKAT
8768	39136	A	8826	I	394	AISRALGRYVLPCLIQDGFVA HTAHAILTSLED/SL*MFQPKTC WCL\AN*HDTLSVNMETPHPSF QEELSGLLLLKMLRSPIEASKD KDKVKSNVRAVRLGNLLHFLQP SHIE*PTFAQINEEAIQALIS

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8769	39137	A	8827	52	730	KSACDALSSILPEAFRNLPNDR QMLCITVLLGLNDSKNRLVKA ATSRVALGVVYLFPCLRQDVIFV ADAANAMVMSLEDKSLNVRA KAAWSLGNLTDTLIVNMETPD PSFQGRVLWSPALENGYDQAL EASKDKDKVKRHA/VRA/LGNL LHFLQPSHI/GKTPHLQKFJ*GSL SRALNELLF*QKLA MKVRWNA CYAMGNVFNKPALPLGTAPWT SQAYNALTSVVT
8770	39138	B	8828	47	1576	
8771	39139	A	8829	2	2753	
8772	39140	A	8830	1	273	
8773	39141	B	8831	104	206	
8774	39142	A	8832	1	987	
8775	39143	A	8833	111	2187	DERRVGAADMFGRSRSWVGG GHGKTSRNIHSLDHLKYL YHVL TKNNTTVTEQNRNLLVETIRSITE ILIWGDQNDSSVDFDFLEKNMF VFFLNILRQKSGRYVCVQLLQT LNILFENISHETSLYYLLSNYYV NSIIVHKFDPSDEEIMAYYISFL KTL SLKLNHNTVHFFYNEHTN DFALYTEAIKFFNHPESMVRJA VRTITLNVYKVDNQAMLHYIR DKTAVPYFSLVWVFIGSHVIEL DDCVQTDDEHRNRGKLSDLVA EHL DHLHYLNDILINCEFLNDV LTDHLNLRLFLPLYVYSLENQD KVFLIIHHAPLVNSLAEVILNGD LSEMYAKTEQDIQRSSVLP TLSS LWQGSLSLNLQSLGHLKCSS HLCGAQAAADS VTGEIPAIRSL EWLISAGSKARTFFFLKMLIGF WEKVDCEYQRRQVLSTRLQEA LPSNRLTDVA AVHSSCMLGFGS TAPRGSWIGDPA AVHLPLPGEI AEHLGSKGTTT VTKHQPAKPS IRCFIKPTETLERSLEMNKHGK RRVQKRPNYKNGVEEEDKEG PTEDAQEDA EKAKGTEGSGKI KTSGESEEIFMVIMERSKLSELA ASTSVQEQNTDEEKSAATCS ESTQWSRPFLDMVYHALDSPD DDYHALFVLCLLYAMSHNK/G KSPEKEEGLSGTQSHPGKAGTF GKEGAEEERKRAQV

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8776	39144	A	8834	1	3050	RNLLVETIRSITEILIWGDQNDSSVDFDFLEKNMFVFFLNILRQKSGRYVCVQLQLTILNILENISHETSLYYLLSNVYNVSHVHKDFDSEIIMAYYISFLKTLKLNNHTVHFFYNEHTNDFALYTEAIKFFNHPESMVRIAVRTITLNVYKVS LDNQAMLHYIRDKTAVPYFSNLVWFGSHVIELDDCVQTDDEHRNRGKLSDLVAEHL DHLHYLN DILINCEFLNDVLT D HLLNRLF LPLYVYSLEN
8777	39145	A	8835	111	270	
8778	39146	A	8836	240	406	
8779	39147	C	8837	86	286	
8780	39148	A	8839	172	243	DPS*EARSMLLLFLPPDHSGLP H
8781	39149	A	8840	280	526	GRNAVVSQ*AHCRSQTGPQK*S SL/LVFPSWYTRHMPHILAN* KKFLLHRDGLDMLPRLVWNS WPQVILPQPPKALGLLL
8782	39150	A	8841	3	1785	VLDARNAGAGGLAGPAGVLRGRASRCDPGAAVAGAGQGGAARVPGRAAAAPSPGPPGGA*CVPTDAGAGPGSAGARQPLPFAAGALS HSGHC*RGLRGPGLASPAQAK AAWSGLLSPAAAGRDGGRGH NPRDPPLREHGPPIPGFHGDR G*ELYQCHLGGEGG/GPDKPGSPCASCGLDGHWYRALLETFRP QRCAQVLHVVDYGRKELVSCSS LRYLLPEYFRMPVVTYPCALYG LWDGGRGWSRSQVGLKTLIL GKAVNAKIEFYCSFEHVYYVSL YGEDGINLRNVFGVQSCCLAD RVLQSQATEEEEEPESTSQSPAE EVDEEISLPALRSIRLKMNAFYD AQWKENGYYRAIVTKLDDKSV DVFLVDRGENSENVDIINMLL RFLTNQEQGEETISKVIAQAGY AKYQEFETKENILVNAHSPGHV SNHFTTESNKIPFAKTGEQEK AKRENKTTSVSKALSDTTVVTN GSTELVVQEKVKRASVYFPLM QNCLIEIKPGSSSKGELEVGSTVE VRSYVENPGYFWCQLTRNIQ GLKTLMSDIQYCKNTAAPHQ RNTLACLAKRTVNRQWSRALIS

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8783	39151	A	8842	2090	2901	THLLVPGMQPLTWQMPFSPFLS ISPTRSNLPSAATPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLA FVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGIPHSIA SDQARIHRSRNQEEVEVEVAPLT ITPSDPLAKFLISVPVTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPPGHFGLLLTLSQEAENG VTVLAGVIDLDYQDEISLLHN GGKKEYARNTGDPGLRLLVLP CPVIKINGKLQPNPGGTTNGS DPSGMKV
8784	39152	A	8843	1	585	
8785	39153	A	8844	1	1697	MDKYFMIKTPKAMATNTIDK WDLIKLKNFCTAKETMIRVNR QPIECKMFAIYPSDKVILLFKM APKRNAEGLSTVSTCKKAAMC LIEKGCELVGPGVQTHPVVTS PVSECIIGIDILSGWQNPHTSLT GRVKAIMVAKDKLPLEPLPG KIVNQKQHCIPGWIEISA TIKD LKDAVIGIPLTPFNPSPIWPQK TNGSWRMTVDYHKLNQVVTPI AAA VPDVVSWEQINTSPGTCL HWWPHGEFPLVDREERTRW FTDGAQYAGTTQKWTPAALQ PLSRSTLKESECFIHGHGIPHSIA SDQGTHFMAKKVRQWAHAHEI HWSYHVPHYPEAAGLIEKWNG ILKPQLQCQLGDNLTQGWDKV LQKALYALNQHSVYGTISPIAR IHRSRNNQEEVEVEVTLIITPTD PLAKFLLPVPSTLHSLDLEVLVP EGGMLPPGHTAMIPLNWKRLR PPGHFGLLLPLSQAKKGVIVL AGVIDLDYQNEISLLHNGGKE EYALNIGDPLGHLVLVPCPVIN VNGKLQPNPGRITNGEDPSG MKVCVTPPGTTITTKKP
8786	39154	C	8845	1	720	
8787	39155	A	8846	57	261	WNF/CDPGGPMMKLIFISFKLKT ISSTFLSPTCLVL*RRPSRSASSL TVLCTTTTRSSSPLLALV*TWTP
8788	39156	B	8847	1	1158	
8789	39157	B	8848	1	2523	
8790	39158	A	8849	3	375	
8791	39159	A	8850	3	169	DFQPFRVTVHWGKNDQTFR GLLDTGSELTLIPGDPKHHYGP PVKVGAYGAQQL
8792	39160	A	8851	3	376	

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8793	39161	B	8852	1	592	
8794	39162	A	8853	1	319	
8795	39163	A	8854	1	1071	
8796	39164	C	8855	1	862	
8797	39165	A	8856	1	1488	MGRARRLTVPVIALWETADGS RALTVETVTQLQHLNVTGII FRGGRGQVAAVNCQKRDIQPF TRVTVHWGKRNDQTFQALVDT GLELTLPQDPKHHCDPPVKVG AYGHQVINGVLAQIQTIVGPVG PWTHPVVIFTVPKCIIDILRW QNSHTGSLTGRMKAIMVGRK WKPLELPLPRKTVNQKPYHTPV GTAEISATMKDLKDAGVVIPTT TLFNSPIWSVQKTGGSWRMV DYCMLNQVVSAAVEIVLDVVS LLEQINTS/P/WP*SGSCTAAFFHH QMEVVHT*SGSSRS*RHNCTN GLMGSL*SVDRGREYDGLVH RRFFTC*HHPKLDSCSTTVPF* DIPEQL*REIFPPVSWRGWR LCMGSAWTFTTHQG*PGYGHG *VPNLPAAETNTEPSIWHSSG* SASYLVAG*LYGTSSIMERAEEV CPHWNRHLF*IWVVCLSTLCF C*DYHPWTLEMPYPSPYSTKL CCCPRHILLYG*RSAAV
8798	39166	A	8857	1	1056	MSSVLLRLIYQLTKQTASFEGG PEQKALQQIQAAVQAALPLGPY DPANPMVLEVSADRDVTWLSL WQVPIGESQQRSLGFWSKVLFPY SADNYFPFERQLLACYWALLET DRLTVGHQVTLQPELPMNWV LSDPSSHKVGHVHQHSIIKWK WYIRDQTRAGPEGTTTPVITQ/ WDAHEQSGLSGRDGKGRFV LTGVDITYSGYWFAYPAHNAA KTSIVGFTECLIHCHGIPHSIAD QGTFLTAKEVWQWAHAHGIH WSYHIPPHPHPIAAGLIEWNWGLL KSQQLQCQLGDNTLQGWGKDL QKAMYSLNQRLLIYSTVSPISRIH GSRNQREVEVEVAPLITLSDPL AKFFFFLP
8799	39167	B	8858	603	1785	

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8800	39168	A	8859	3	467	RIHVRPEITLTA/ANTARPY*IDP HDTLLSHSNFGSSDCPSSSKMR QALELVRERAPELMIDGEMHG DAALVEAIRNDRMPDSSLKGS NILVMPNMEAAARISYNLLRVSS SEGVTGVPVLMGVAKPVHVL PIASVRRIVNMVALAVVEAQ TQPL
8801	39169	A	8860	1	1878	
8802	39170	A	8861	3	684	MPNYLRFVRGLIDSSDLPLNV REILQDSTVTTRYLRNALTKRVL QLLEKLAKDDAEKYQTFWQQF GLVLKEGPAEDFANQEAIAKLL RFASHTDSSAQTVSLEDYVSR MKEGQEKIYYITADSYAAAKSS PHLELLRKKGIEVLLSDRIDE WMMNYLTFDGGPPFQSVSKVD ESLENLADEVDESADAEKALT PFIDRVKALLGERVKDVR LTHAGSGLVGENV
8803	39171	A	8862	2	393	LEFGKKLGNAADYFIANKIDQ PKIAVINCEAFVVCVQRKRGFE EVLKSRVPGAQIVANQEGTVLD KAISVGEKLIISTPDNLAIMGES GGATLGAVKAVRNQNRPEKL LFSVRI*QPKLLRSWKTRC
8804	39172	A	8863	414	805	TPSRVEGNQEPYPSLVYIP/SQAP WNM*TRDHKHGLNLYVQRFVI MTDAEQFMPNYLRFVGGIDSS DLPLNVSREILQDSTVTRNLNR ALTKRVLQMLEKLAKDDAEKY QTFWHQFGRGIIIFTSQFN
8805	39173	A	8864	3	684	MPNYLRFVRGLIDSSDLPLNV REILQDSTVTTRYLRNALTKRVL QLLEKLAKDDAEKYQTFWQQF GLVLKEGPAEDFANQEAIAKLL RFASHTDSSAQTVSLEDYVSR MKEGQEKIYYITADSYAAAKSS PHLELLRKKGIEVLLSDRIDE WMMNYLTFDGGPPFQSVSKVD ESLENLADEVDESADAEKALT PFIDRVKALLGERVKDVR LTHAGSGLVGENV

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8806	39174	A	8865	1	624	AKLLRFASHTHTDSSAQTVSLED YVSRMKEGQEKIYYITADSYAA AKSISPHLELLRKKGIEVLLLS RIDEWMMNYLTFDGGKPFQPG AKVDESLEKLADDEVDESAKEA EKALTPFIDRVKALLGERVKDV RLTHRLTDTPAIVSTDAD*M/TP RMAKCFGGAGQKVPEVKYIFE LNPDHVLVKRA\ADTEEEAKF CVWGKNCVLPF
8807	39175	A	8866	471	659	
8808	39176	A	8867	638	834	SSNTMMHFQIHMKESTEQQT MTARR*Q*SEVDE*REDTTLAA RGRTEA*SARYQLT*QSVPSPH
8809	39177	B	8868	1	1383	
8810	39178	A	8869	4452	4896	SQHSEVFVCHMLSQPRAPGAG RYL/LQRKA/SEALEVEV/VDTW QADAVRDTRTLVGESFLVSL ALALALSDLVSHKTRIDSLFLD EGFGTLDSETLDTALDALDALN ASGKTIGVISHVEAMKERIPVQI KVKKINGLGYSKLESTFAVK
8811	39179	A	8870	31	185	GHRRRPFKRGRKSR*RGGSQRR VNEDARRSAWMRKKQRRLISK ISDR\ARK
8812	39180	A	8871	1744	2670	

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8813	39181	A	8872	1	1680	MGFWVENGEIQYPVSEITIAVSS LVFSSASFAADLEDNMETLNDN LKVVEKADNAAQVKDALTKM RAAALDAQKATPPKLEKSPDS PEMKDFRHGFILVGGIDDALK LANEDVFTRTLGDADLYQFQNI RHVLRMQRIAAGEGNTLAFDT SVIQIVNDLVFHCFGKWLGTGY PPCAFIATGAFMNTPGDKQGA TSAGAVDDVDRISNEITIGIPML TGYILLHVKGVRKSSADHRR RPLASLATPPHKSWTCTLLFFR LPNVVCYANRQQLTPILETLQP SDELPHEETVVLNWRQVHE QCLALHSQQQTLQQQDVLAAQ SLQKAQAQFDALQASVFDDQ QAFLAALMDEQTLTQLEQLKQ NLENQRRQAQTLVTQTAECLA QHQQHRPDDGLALTVEQIQ QELAQTHQKLENTTSQGEIRQ QLKQDADNRQQQTLMQQIAQ MTQQVEDWGYLNSLIGSGEGD KFRKFAQGLTLDNLVHLANQQ LTRLHGRYLLQRKASEALEVD VVDTWQADAVRD/TRLTSGGE/ SFLRLRLR*VTRRHQLWLHLRLH
8814	39182	A	8873	3	823	
8815	39183	A	8874	287	426	YSGLSAVNPVNDAYGVRFQLP SVNRIPVS***VKLAPPAHQIKRI SGKCRFIPLC*YAPPGFSSASTM RATGILSTASQPPGKLCMEEST AERRVGLPLAKW
8816	39184	C	8875	1	2058	
8817	39185	A	8876	1	1989	
8818	39186	B	8877	1	3132	
8819	39187	A	8878	194	789	LTKLPSLFTFTRLSSDNDLRRGG DKRGGANGARIAL*PQTRTGD VTRRQPIRVCTVIEMFELLE/PIA DGRFNRYARLDVST/TESLLIDK AQQLTLTAP/EMTALVGGMRV LGANFD/GSKNGVFTDRGVLS N/DFFVNLLDMRYEWKATD/ES KELFEGRDRETGEVK/FTASRA DLVFGSNSVLVFRILGGFFCEYS LTIRILH
8820	39188	A	8879	1120	1395	

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8821	39189	A	8880	1	629	THRPPKSGPPCAKTRTTHVTA KPLFPQTNPQKTVRRMQGELY LVDESQGEFVSALNYRRRKTR NNATAYPIRLFYLSVRPRAGSK SSRTIWILLAD/AKITPYERRQL VARIEA/LSTEIPAQVRPLYQLW RDGQALQLQLAEERQR/YTGG ADTKQDGATTTKDKQQR*TKG TRSQPSTREVQQSQTKHSTSR PPNHAQPSNSALVTRQ
8822	39190	A	8881	3	307	
8823	39191	C	8882	161	337	
8824	39192	C	8883	34	168	
8825	39193	C	8884	172	456	
8826	39194	A	8885	174	516	VSGVRCWIHSSAFPVPFGFFLP VAFFDRPPARLYRMHTWSHME SQEPARLPSHYAD*GQGSQKR\
						DSCSSGWAGLLFISQFVLWSA EIEGSLNHITLGFRLSHGTTSD GMTF
8827	39195	A	8886	1	2964	
8828	39196	A	8887	1	2724	
8829	39197	A	8888	3708	7098	
8830	39198	A	8889	115	339	
8831	39199	A	8890	445	634	VINTFSLHMTGST*HQGNWR HLTLHPRNSKHLEQPTPGVLQ LRPTASLRQLLSNAGCSG
8832	39200	A	8891	1663	2234	GEGLRRGLFPGAEEAQGRAETA GCLRRGRGALALALPGSPGLSP WVEDAGGHRVLHGRAVLRCA RAPVPQPAGLAKVEPYSGVSS LTAFPQAPILLSGGQSRAGERT TM*G*PEMEKL*SCIGEGHQPC HR/KSRPAAPCPPPSAMLFLT SSATLLSSSKGASGGWEPSSAA PLGGSGQPFREMVSH
8833	39201	A	8892	202	542	
8834	39202	A	8893	564	1179	QHRLTYRTALWIHYPDPKPL MSFRPGHQRLSVTSLVCHGLL MVGTSGLVVALPVPRLSSPSL PPVELL*HSVCVSVCRGISCL*W RLWDQISDWISRTLQPPRPSPC CPVVASPGPGKGPQCNGDPKW KSCEAAVSKGTSPATGKSRPAA PCPPPSAMLFLTFRYSATLLSS SKAASGAREPSAAPLGGSGQPF REMVSH
8835	39203	C	8894	321	539	

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8836	39204	A	8895	630	983	NLETNGKIPFENPWSKVPIRFGRL QNLRRVCLTTGGQIPTGRWVT ATDSRGAGDYRLCLHHLR*PD GARLSAGSADCAANRRDVGDS GRGLPGRLSVQQPRRVRGQP DVQPVSWPGC
8837	39205	A	8896	31	144	MEISFTRVALLAAALFFVGCDQ KPQPAKTHATEVTVLEKTMG TFWRASIPGIDAKRSDELKEIKQ TQLDADDQLLSTYKKDSALMR FNDSQSLSPWPVSEAMADIVTT SLRIGAKTDGAMDITVGPLVNL WGFGEQPPVQIPSPQEQIDAMK AKTGLQHLTVINQSHQYQLQK DLPDLVVDLSTVGEGYAADHL ARLMEQEGISRYLVSVGGALNS RGMNGEGLPWRVAIQKPTDKE NAVQAVVDINGHIGISTSGSSRG D*DGYGQGLSRVIDPQTGRSIE HNLVSVTVIAPTALEADAWD GLMVLGPEKAKTCSPPGLRGT ESLNTLRDRITQINGIDEVRMD DSWFARLAALTGLVGRVSAMI GVLNVAAVFLVIGNSVRLSIFA RRDSINVQKLIGATDGFILRPFL YGGALLGFSGALLSLILSELVL RLSSAAVEAVQVFGTKFDINGL SFDECLLLLSSMVTFWCRNLF TSLELWTHADKQDDNSCLSS ASVYLKAKMMKVMPLMQLLS SGTGFYRDRLENSGGRYESRRS LTRQFREETAIPRECSQRIDFL LFETPSVSASSAGFWLRFGSTA
8838	39206	A	8897	1	1775	
8839	39207	A	8898	10	300	PTSIPRESSSGTWQVASTTVLF SAILAGLGSASAFCLGPQIPQAR PNNASVNSKNSRFGIPRQAE*P EQGGVYHHTAGVLKLLIPPSAR QHPDRC
8840	39208	A	8899	1657	2061	QMPGNPAPFALLVAFKHQFAI AGGIFIKEVTFIAIKTSQLLWFGQ PIFNNETTHQTACFLSVEADDL KFAVLLIEEHLRLDNI.GIQFLRLH RFKILI*QINHHIALCCEERLVQ LVGDDISPEFELELRFSEVH
8841	39209	B	8900	26	1540	
8842	39210	A	8901	1	3396	
8843	39211	A	8902	1	3522	

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8844	39212	A	8903	1	105	SPQPDHRHYRHHRGQLVCIVIIIF YFCAKRWMAAIL* TQHRHRFL TTDDGKFVANGSFS* RGLHH/ ATGLRRFPIC* GPLVCIVIIIF FCAKRWMAAIL
8845	39213	B	8904	1	960	
8846	39214	B	8905	1	2618	
8847	39215	B	8906	1	490	
8848	39216	A	8907	2820	3332	ATEGYRQQRQFHAAAYDESP HRNRKRKWRPTYRCHPAPDHR TACLRSAFYGNAPGCVQTGPV RRSGAASASSPAVFLSGTSPWS FARTIALVRGRS/LKIDTNSPWA YFSALLM/F/DLLSHVHEWCGR YISPPRFAQTGETLPCRRHQGSR YSAYLSASRYPARRKWYFSPR
8849	39217	A	8908	3	716	EVDDTAKHRRRDSFPQ*DP/LM NIRYAPS/HLPATVALTGA VIIT VLYALAGKRLFCWSVCLNPIT DLANWLRRRFDLNQSATIPRII RYVLLVVILVGSALTGTLIWVW INPVSLMGRSLVMGFGSGALLI LALFLDLLVVEHGWCGHICPV GALYGVVLGSKGVITVAATDRQ KCNRCMDCFHVCPEPHVLRAP VLDEQSPVQVTSRDCMTCGR VDVCSSEDFPITRWSSGAKS
8850	39218	A	8909	3	323	
8851	39219	B	8910	94	2205	
8852	39220	A	8911	504	694	FNQLGRDWRITYYRKSDPPR/Q WLRHSPVR* VLKMPMAIRGL LWMLSAQPAICSSRQTKMV
8853	39221	B	8912	1	2031	
8854	39222	A	8913	3	190	FIATPGYTGEAGYEIALPNEKA ADFWRALVEAGVNPCLGLGARD TLRLDGDESYG/QEM/DETVSP* AMKLRCPMKKRPSIGVRWWK RVLTHVAWARVTRCVWTGMN LMARDGETVSP
8855	39223	A	8914	1	621	MWPSVSHLTQMNIPSRFSEPSG AIEVPPDKVHELRLRLAQQGLP KGGAVGFELLDQEKFGISQFSE QVNYQRALEGELSRITETIGPV KGARVHLAMPKPSLFVREQS PSASVTNLLPGRALDEGQISAI VHLVSSAVAGLPPGNVTLVDQ GGHLLTQTSNTEGRDLNDAQLK YASDVEGRIQRRIEAILSPIVGN G/TAQLDFAS
8856	39224	A	8915	1	2274	
8857	39225	A	8916	957	1067	

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8858	39226	A	8917	1	1242	MDGLNTDKGSSVFHTPTDRLVI CCPVDADERMTTPPRLWDHEP SKPLFFTNYPVSAFFVGL/PPGK RPQGGFRAGNL*TSKTTIGRDL NDAQLKYASDVEIGRIHRRIEAF LSPIVSGSNIPAQVRAQLDFASK DQPEEQYRPNGDESHAAALRSR QLNESEQSGSGYPGGVPGALSN QPAPANNAPISTPPANQNNRQQ QASTPSNSGPRSTQRNETSNYE VDRTIRHTKMNVGDVQRKLGII GQGKNEKPLQLERVEEKPNG EGWEKKWQGEVWKKEDGTI YLQKNKLRAPTDSTLWFAKNG RVAKIAKALVEPANNFNPGVD EDDTEKLLLEVPEELTNEKLDL EQKCIHIYDDKRRQTKQTPQDV FLKRVTSPPQEPQPGSGGIPEEG IVIIGEDSSVQVLAPEDLPVEKL
8859	39227	A	8918	256	1510	RRFVGFRGTGVTKEDAIQGRGV DQFFRQSQYRLVGVTVAGMPE LTRLFVQRFTQFRMRMAQRVH RNATREVDILFLLIPQARTFAT YRYKGCGRSVNRYHPFIKVFTRN WREADLSLKRVTLLNDTGYQ EVITYSFVDPKVQQMIHPGVEA LLLPSPISEMSAMRLSLWTGL LATVVYVQNRRQNRVIFESGL RFVPTQTAPLGIRQDLMLAGVI CGNRYEEHWNLAKEVTDFYDL KGDLESVLDLTGKLNEVEFRAE ANPALHPGQSAIYLGKERIGF VGVVHPELERKLDLNGRTLVEF LEWNLADRVVPQAREISRFP NRRDIAVVVAENVPAADILSEC KKVGQVNVVGVNLFDMYRGK GVAEGYKSLAISLILQDTSRTL EEEEIAATVAKCVEALKERSQ
8860	39228	B	8919	47	156	
8861	39229	B	8920	139	993	
8862	39230	A	8921	1	284	MRRKRLIRPTVQAQVCRPDKTR KRRIRQWC/YGCRMRRKRLIRPI KYANRQAETA*GLDALHLCSS HG*KGPT*SSGHGFRGCKPQAL EASMWC
8863	39231	A	8922	1	813	
8864	39232	A	8923	1	1176	

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8865	39233	A	8924	3	618	AGGPPLNPIEMA*KS/WDEIIVK LEKDPQLKQTFLFVYPQFSGE NITDAIAEFKLTITPDSPFDKW LRGDENALTAQQKKGYLQFKD NKCATCHGGIILGGRSFEPLGL KKDFNFGITAADIGRMNVTKE ERDKLRQKVPGLRNVALTAPY FHRGDPVTLTGAVELMLRYQV GKELPQEDVDDIVAFHLNLGV YTPYMRDKQ
8866	39234	A	8925	2	212	QYPGLDLHGAKGLGDLAGKR YRQLLVSCVRHVLRYHPAGPGT RK*RRSGIRWLHRLCGNEPRGK LLVDQ
8867	39235	A	8926	1	640	
8868	39236	A	8927	1	704	MSSFQFEQVIRSPYKEKFAVP RQPLVKSSANGELHLIAPYNQA DAVRGLEAFSHLWLFVFHQT MEGGWRPTVRPPRLGGNARM GVFATRSTFRPNIGMSLVELK EVLCHKDSVILKGLSLDLVDGT PVVDIKPYLPFAESLPDASASYA QSAPAAEMAVSFTAEEVEKQLL TLEKRYPQLTLFIREVLAQDPRP AYRKGEETGKTYAVWLHDFN VRWR/VSP*ACSTFQLEP
8869	39237	A	8928	3	313	AQRGGI*RGSLATAGLRSFGLL HPRTSQQFCLPVRGKPPQTQAS VMVDAPHSTKLKHLRSISDCCT GSKNFKPVDLSLLGSMGVGST LDHLAPWLQAPFGE
8870	39238	A	8929	13	453	
8871	39239	A	8930	380	966	LRHAVLLTEGF/SYKPHAFALG FVEAPRGEDVHWSMLGDNQKL FRWRCRAATYANWPVRLRYML RGNTVSDAPLIIGSLDPCYSCD RVTLVDVRKRQSKTVPYKEIER YGIDRNRSLNRSLYPREVPSTT LQPLRTPRCPGKNLALAVNVST GTNGQKPESCGPGRCRMKGGE YKRTISGGRTIIRVHIARLLRTF

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8872	39240	A	8931	1415	2085	SQVPICQRSTSCRVKRLFSWKMA AYRSALVTWPWRVFRNPAVPR TSPVVFTGGDVFSRVMVRVKE T/FDSLAMLEFALDNMPDTPLL TEGFSYKPHAFALGFVEAPRGE DVHWSMLGDNQKLFWRWCRA ATYANWPVLRVYMLRGNTVSD APLIIGSLDPCYSCTDRVTLMP QCIACGACACAPANALTIQTD DQQNSRTWQLYLGRCIYCPST NNNGPVISFN
8873	39241	A	8932	1	1127	MKKRKTVKRKYVTALVIVIA LMTLWRIRNAPVPTYQTLIVRP GDLQHSVLAPGKLARTSKNFA Q/FIRVRYSAFSLAGEKKR**P RVHGVQNASSGRYRGTCRLG SDSRKKLVEIL/LATPNMEQRT QGIGILDPQIARDLRFDPHYAEY DNIPK/TLFTFTAADVFSRVMVR VKETFDSLAMLEFALDNMPDT PLLTEGFSYKPHAFALGFVEAP RGEDVHWSMLGDNQKLFWRWR CRAATYANWPVLRVYMLRGNT VSDAPLIIGSLDPCYSCTDRVTL VDVRKRQSKTPYKEIERYGID RNRSPNRRCTGEGWTRAWITL PLLKPLTPLMIASFAFNFNFFV LIQLLTNGGPDRLGTTTPAGYT

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8874	39242	A	8933	1	2466	MLRGVNVLADAVKVTLGPKG RNVVLDKSFQAPTITKDGVSVA REIELEDKFENMG AQMVKEVA SKANDAAGDGTATVLAQAII TEGLKAVAAGMNPMDLKRAS RSRKGYGPARIQELNQKGISR EATEKAMRECDIDWCALARDQ ATRKYGELPTVFSEKSRKLI GVKRAFTHQAVNAGFCTQPAV SVIAGDFDRHGFNTRHFTRL DDFSFETTRFCPAQIHTLKHAR P VLCFRTARPLNIEVAVGAVIF AREHTAELKLRQFFQGAPOKA VISIPVVPQVTGVVIEVTDKKNT LIKKGVLFRLLDPTRYQARVDR LMADIVTAEHKQALGAELDE MAANTQQAATRDKFAKEYQ RYARGSQAKVNPFSERDIDVAR QNYLAQEASVKSSAAEQKIQS QLDSLVLGEHSQIASLKAQLAE AKYNLEQTIVRAPSDGYVTQVL IRPGTYAASLPLRPVMVFIRSET SLRTHCPGHADYVKNMITGAA QMDGAILVVAATDGPMPQTRE HILLGRQVGVPYIIVFLNKCDM VDDEELLELVEMEVRLLSQY DFPGDDTPIVRGSALKALEGDA EWEAKILEL/RWLPGLFYSGR ACD*QAVPAADRRR/SSPSPVV VPLLPVV*NAVSSKLVKKLK/R WYPRDSEVLYWR*NVPTAG RRPCW*ERRCSAAWYQT*RN

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8875	39243	A	8934	1475	2904	FWRAAAPIDCWRSAGVKKQH VEVTQLDWTTPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGFTGT MQTAGSSVFNLTYDTPQESDSIG VRHIPMGVPLQTEMHAPGLPLA SSMKRWIRATGFIIFGKEQFED VVPVLGSKVNGVQFNALVAD SLGISQIRCRCAIFLTVVFFVLH KQAFDLISLLQPPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFTT LVQGSLELHQAQWAVDERPH ANRFLPPDEIQSLNGVHYQHH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRJLTRSQRLQ LAWPQQQGRYPLTYHLFLGVI
8876	39244	A	8935	1	920	MARADTVSVPFMGLAAKPC WRDTEPNTGYRGPHVRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDACLSNAILVHNKGGP LADGIVITPSHNPPEDGGIKYNP PNGGPAADTNVTKVVEDRANAL LADGLKGVKRISLDESDGIRSK NDVIDTSDDDM**QCLSRRSN GHPGAKVANLVPKTTFIDGVD QTSFFLGTNGQSNRKAHEYFLN GKLAAVRMDEFKYHVLIQQPY AYTQSGYQGGFTGTVMQTAGS SVFNLYTDPQESDSIGVRHIPM GVPLQTEMHAYMEILKKYPPR
8877	39245	A	8936	471	668	
8878	39246	A	8937	1	1233	
8879	39247	C	8938	1	1548	
8880	39248	A	8939	1	1260	
8881	39249	A	8940	1	1468	
8882	39250	A	8941	261	596	RSESCCGHEPDGPETROP*PQR LWTCAYSPGTESERYFPRSDRK SDA*M*HRLVRTGARSGDAKI WRTFANCLFRKIKKTYRRSQGT FYAPGGERRFLYASRKRNR F

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8883	39251	A	8942	2	1356	CLPGLKLVRLLYRLEERNARRT SAAVDAT* RAGAWLAQCGLTV EQLARIQVDPDMITTRAHLYHC DHRGLPLALISEDGNTAWSAEY DEWGNQLNEENPHHVYQPYRL PGQHQDEESGLYYNRHRYYP LQGRYITQDPMGLKGGWNLYQ YPLNPLQQIDPMGLLQTWDDA RSGALTWYGWGDRLTTIQND RSKIQTIIYQPGSFTPLIRVETATG ELAKTORRLADALQSQSGGED GGSVVFPFVLVQMLDRLESEIL ADRKRAATTWSHNHYANKKE GIKATGYRLAQLGFKCEESSV FRVTRKSHSSFVWLDKAVTPHP TSNVRAGCLMRRWRVLSGLHR CEVLHPHTPHPAYHAGCGVSL QRNIRHFFLNGLRFRQLRFRRTIC CLRLVVVQPHFAGVLQLAFC CRYITVQLASIRNRDRFQRLPL RAGNTIAKYFFQIQHNRGG
8884	39252	B	8943	1	1159	
8885	39253	A	8944	1	1304	MAETQQQFKRMAASGLETRF DEVGNLYGRLNGTEYPQEVVL SGSHIDTVVNGGNDGQFGAL AAWLAIDWLKTQYGAPLRTVE VVAMAEEEGSRFPYVFWGSKN IFGLANPDDVRNICDAKGNS/IC RCDFGLRIYSSERPTNS/VVRIL KPLLNCILNRA/DVLERITAWD KPDCHTLHHHADLSGHFPPEIG PLLFAFGSSAWQNGPSAFSWQK HGSAQTSSIAVLHRTPRHAGCL AQCDFTRAFFQIMLKNYLRKK RWKKKIHFPNASGKSS/RAIFEG YVTITYGDVAKLGGIAPGRAPG GR/VQRQALLAEGAGTAEDGFT *VGEVEDAARDGP* TDAERTG* TYADAGRQDPQSAEDRQRANL HGNADR***RFASGGFHRGYHP RAAAGFCDHRKPACGNARRAG WPDRA* SKSSAYAFRYRYEHR LAGRSG

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8886	39254	A	8945	1	1695	MRSDDPTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRV TLEMKYGRIMLDTAKIIDQDV PTHILSKLFTLRNHPEGVVMK NFEVLQPLQNSLSGLPLWVSE ILQQINQLTHYEPVIGIMKGTGA GKSSLCNALFAGEVSPVSDVAA CTRDPLRFRLQIGEHFMTIVDLP GVGESGVVDTEYAALYREQLP RLDLILWLKADDRALATDEHF YRQVIGEAAYRHKMLFVISQSDK AEPTSGGNILSTEQKQNISRKIC LLHELFPVHPVCAVSVRLHPV VALLQQFRITDDERTHYHYDS QHRLVDYTRTQYEEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPKQVTWYWGWDGRL TTIQNDRSRIQIYQPGSFTPLIR VETATGELAKTORRSLADALQ QSGGEDGGSVFPPVLVQMLD RLESEILADRVSEESRWLASC GLTVEQMOMQMDPTEGTTAW Y/AEYDEWGNLLNEENPHQLQ QLIRLPQQYDEESGLYYNRHR YYDPLQGRYITQDPIGLKGGW NFYQYPLNPISDIDPLGLSMWE
8887	39255	A	8946	605	1395	SMSLLKNIRLSSASKQCAACSG WPAAGIRGVSGGQG*ARVSSS ANTATALSSRLLPQNSVTVPH A*RMNCVLRVTPLSKNRGGKP APSGTEGKGLPEVQPGQLRAH GLPVSENLEQDFYASGPNQK WAGDITYLRTEGWLYLAVVI DLWSRAVIGWSMSPRMTAQLA AGCPKPLWGTPSPGPACGLAP SSAGVLPGRGFPAVWLDSDEPE EYVGSSDFLTQMOSMKKVDLK KNRAATDADGQFSRCCMPEK YAGSHN
8888	39256	A	8947	1	1914	
8889	39257	A	8948	1	4767	
8890	39258	B	8949	1	2294	

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8891	39259	A	8950	115	3551	NPALTRIVPAQONLYTNTLLAA RIKQRLTEQFELMLRQAQIDFA GKAHSLTEAQANTTQVSAERD RLFKNYQRYLKGSQA AVNPF ERDIDDARQNFLAQDALAQIS QLDSL VNGEQSQIVSLKAQLAE AKYNLEQTIVRAPSNQVVTQVI IRPGTYAASLPLRPVMVFPDQK RQIVAQFRQNSLLRLAPGDDAE VVFNALPGKVFSGLAISP AV PGGAYQSTGTLQTLNTAPGSDG VIATIELDEHTDLS
8892	39260	A	8951	845	1213	DKGEIGGWAAQTHRSHEQGA RRVPEDRDARARRKNEEPAAR PRTTNTNRNGSRKGPERK/WADG RGHKA EAGRRKRRKRQ*KEEM RKIRQESGGKKRGLCGRPPG GGNNCMEGERRRGRKR
8893	39261	A	8952	843	1061	NRPPPVCACHRQVVLPPVNVN APAEKWQVPRVTLPGRQSTSW FAAVVYRN*YQYCALTAQRGR RSRQLPHR
8894	39262	A	8953	1	682	MIRIFGCEDKLGADQQPAFVLY LEIDPHQVDVNVHPAKHEVRF HQSRLVHDFIYQGVLSVLQQL ETPLPLDDEPQAPRSIPENRVA AGRNHFAEPAAREPVAPRYTPA PASGSRPAAPWPNAPGYQKQ QGEVYRQLLQTPAPMQKLKAP EPQEPALAAANSQSFGRLTIVH SDCALLERDGNISLLSLPTGIW CSD*H**PMIPRLIPASVRSSSM VESAK
8895	39263	A	8954	1	1887	
8896	39264	A	8955	189	552	LFRGEKGARNEVLATRYRQT VSGDFRHLHCLADQYALGGAY QF*AGLY*LHQAWEMNRGLQL LSDALGEQYAHGNWRLRNN DRFVFQILRSFEHDNSDKPGP GMPPHGWRTQFWGG

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8897	39265	A	8956	263	3549	TGGPSSPSSHWKTPVVIYWDGT ALRCVFVPVLGETGAQRKRISA RKGSILTTSCPGALSEHCPTTP APLPSQRRNHWMENISPFERSVG VSASRCSES*MRPWNSRMRPLG RSQGDSSAL/MSTGVAFGRGF LKGGLPQAPAVAAATPWLCTQ GVAGETTPAVNVKYNVVRVRS EYISMHVHREVTARNVYVTQT RRPMTTFTPLAWETPHYHRRY GVSLSSAVVQVGPFRYCRQT NALSNLPNFKSGADTQ
8898	39266	A	8957	1	1799	MMRDLINHAIRPACE*QLGA DQQPAFVLYLEIDPHQV/DVNV HPAKHEVRFHQSLRVHDFIYQG VLSVLQQQLETPPLDDEPQPA PRSHIPENRVAAGRNFHAEPAAAR EPVAPRYTPAPASGSRPAAPWP NAQPGYQKQQGEVYRQLLQTP APMQKLKAPQPQEPALAANSQ SFGRVLTIVHSDCALLERDGNIS LLSLPVAERWLRQAQLTPGEAP VCAQPLLIPRLKVSAAEKSALE KAQSALAEALGMVNSTRFSLHE HPDAERSPGQSGEQRQPAVD DYAIVDEYGRHYRRAVAGTLL HVSVDSGTTQTVMYTWLSMA LIALPAFIFARVPNDTHQNVAIS RRKTESRNEVLATRYHRQTVS GDFRHLHCLADQYALGAPIPPD GTRRPILVNGAEVGAVIASPVE RLTRNTDINFDKQQRQTSWLIV ALATLLAALATFLLARGLLAPV KRLVDGTHKLAAGDFTTRVTP TSEDELGKLAQDFNQRASTLEK NQTPITSRGHPRIFLARHPAPAP TTLTSLALKIIRSPAFLPDTASEC AMAIIDCYILAASTQAYKAASSL SLSVVLATSARFKTSSTSIWVKS SSTNSCE
8899	39267	A	8958	1348	2190	
8900	39268	B	8959	1	105	
8901	39269	A	8960	1	781	
8902	39270	B	8961	1	1716	
8903	39271	A	8962	754	807	
8904	39272	A	8963	821	875	FFSLFFFISLASGLSIL*W*FVFL WDRW*YPLYHFLHLHFDSSLSFS SLLVLLVVYQFC

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8905	39273	A	8964	1	315	SGSVMPPALFFWLRLDLAMQALFWFHMNFVVFSNSVKKVIGSLMGTALNL*ITLGSMAlFTILILPYP*AWNVLPFVCLFYFLEQWFVLLLEEVLIHPCCKLDS
8906	39274	A	8965	42	403	GLCSVPLVVISVLVAVPKLFW*L*PCSIW*SQVA/SIPPALFFWLRLDLAMWALFWFHANFKEVFSNSVEKVGSLMGMLNL*MTLGNMAVFTILILPTHEHGMFFHLFVSSFISLSSGL
8907	39275	B	8966	179	1225	
8908	39276	A	8967	342	407	
8909	39277	B	8968	143	3122	
8910	39278	A	8969	692	1360	MCGIIEGSLFHCSITLFWYQS HAYLVTVL*YFLKSGGLMPP ALFFWLRLDLGMLALLWFHMNLKVVFSNSLNKVGSLMVMALNL*ITLGSMAlFTILILPIHEHGMFFHSFVSSFISLSSGL*FSLKRTFTSLVSWIPGYFIFFVAIVNGSSLMIWLSVCLLLVYKNACDFCTLLYPETLLKLLICIRRFWAETMGFSRDTIMSSANRDLNTSSFPN
8911	39279	A	8970	2116	2418	FFSLFFFISLASGLSIL*W*FVFLWDQW*YPLYHFLHLHFDSSLFS SLLVLLVVY/PILLIFS KIKNKKP APGFIDFFEGFFVLSLPSVLL*S*LFLAFC*LLNVFALASLVLIVMLGQCF*IFPAFSCGHLVL*ISLYT
8912	39280	A	8971	1	558	LYKNSVKYFHN*PVGNIMSNIPV GALFSGPAFGIGILAAGVILAI MIIPYIAAVMRDVFEGTPVMM KESAYGIGCTTWEVIRIVLP TKNGVIGGIMLGLGRALGETM AVTFIIGNTYQLDSASLYMPGN SITSALANEFAEAESGLHVAAL MELGLILFVITFIVLAASKFMIM RLAKNEGAR
8913	39281	A	8972	1879	3735	
8914	39282	A	8973	16	452	VGQLFWKGYPLAGFPDPCAQS WKVAHVLLRLGLHIKSVSANG KEVTSKFHRKENI.ARG.LHSRPR RGQVRVGGVAQHCEPR*TPPPA CRVRLPGCPVDPASPRGRRTS AGTPEPALRHPTPRGPVAART LPAEPGARPSGLPP

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8915	39283	A	8974	158	531	CSLRRRGPPDP/PGAYCKRRATG AASTRSLSGAVAGSPAHRCESR PLQAMGAGGLPHPEGGRRGGSG GRKRTDGPVCGCGERAPREYP DPSRSWRGPQRKPAPSQHPCLP RLSRGPGRRHPEGPHIQVR
8916	39284	B	8975	22	387	
8917	39285	A	8976	241	389	VASQAPGVRLQVGPAAHSC*G RGHVSWPPWPWGPPCCCLCL LNLGPN
8918	39286	A	8977	1620	1936	TLFFFESESHSVTQDRVQWYDL VNSLQPPPPGLK*FSCSLSPSSWD YRRPPPCPANFFLVELEFHHV GQDGLLELTSGDPPALASQSR ITGMSHCAQQNKHIL
8919	39287	A	8978	3	105	
8920	39288	A	8979	1	1821	MLKNFKKGFNGDYGVTMTPTG KLRLTCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIMPLREQRYTGI DEDGHMAERRVFCQPFSTAD LLNWKNNTPSCTEKQALIDL QTIQTHNPTWADCHQLMLFL NTDERRRVLQAATKWLGEHAP ADYQNPQYEGKEESPAQFYER LCEAYHMYTPFDPSPENQRMI NMALVSQSAEDIRRLKQKQAG FAGMNTSQQLEIANQVFVNRD AVSHTGAHVSVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFWEDPESGVTTQYTTWTW LPQGFKNSTPIFGEALARDLQK FPTRDLGCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSKKKVAQICQQQVRYLGFTI RRGVRLGSEKQVICNLPEPKT
8921	39289	B	8980	209	2272	
8922	39290	B	8981	1	228	
8923	39291	C	8982	375	472	
8924	39292	C	8983	266	408	
8925	39293	A	8984	1	1105	

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8926	39294	A	8985	108	708	LTNQKSRSTRRIHSRILPEVQGG AAADRHCPIDRLGSLQDHHRRS RLLSQWSP*KSTHD*HGFSYQS AEDIRRLKQQQAEEFAGMNTSEL LQIANQAFVNRDAVSRKNIHR DNERQAQRNTDLLAAAIRGVPP KRQKGKGGPKETQPGCQSLQR NQCA YCKEIGHWKNKCPQLKR KPGDSEQEAPDKDEGALLNLA EGLLD
8927	39295	A	8986	125	444	DCLAVKRASVWQPTGYSCPKL L/QGVLT YQRRQAAPPLRRR LASSSRDKPKCAGKHTSSLVRA GDMQGTIVTGTTEVLRLDMEPK FEDDQLRPVLLEHKVPRREMA
8928	39296	C	8987	80	325	
8929	39297	A	8988	566	1857	
8930	39298	A	8989	1	1037	MEEGWIRLPDGRVAAPQLLGA AVVLAVQETHRGQESLEKLL GRYFYISPLSALAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWVVLGLTDFKN EAKELRLYKQEKREKAKRWKE TEKGFNGDYGVMTTPGKWRT YFEIDWSKLEVGWPSSEGNLERS LVSKVWHKVTGKSGHSDQFPY IATWLQLVLDPPQWLRLGQAAA VLVAKGQIPRKDPTPPAEGNQ LLK/SLFDP TSEDPLQEME/PSDP SGALPLPGKDAPH S*AHSPCAS TRQTYP*ATRSRQERR*SLERNP YIGSFKTQNWDTNAPERAVV
8931	39299	B	8990	1	2082	
8932	39300	A	8991	6	367	ENLNIKAPHAVVTMLTTTGPD WISNAILTKDFCLLCENTHISRW GCNTLNATTL LVSSEPVKHNC LEVLD SVYSSRPNL RDHP*TSV DWEL YVDGSGFANPCKVTLKK ETSPAPVTPRS

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8933	39301	A	8992	1	2991	MLKNFKGFGNDYGVMTPTG KLRITLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPSTDDPLQEMAKVIPVVP SPYQGERLPTEFSTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGQMSLRQRYTGI DEDGHMAERRVFCQPFTSAD LLNWKNNPTSCTEKQALIDL QTIQTHNPTWADCHQLL
8934	39302	A	8993	1	444	SSASTPETRAKFT*DNLCASW QRLASANFRVLVDCILSDTFED LRLQCDAVNLAFGRRCEELED ARYKLHHHLHKA VE*GGGA EH VPHRLREKLLEAEQSLRNLEDI HMSLEKDIAAMTNSLFIDRQKC MAHRTRYPTILQLAGYQ
8935	39303	A	8994	1	1576	MVQTDVLLPEPAQPTVSPCELP CKEYDVARNMGPGHRQLVEVW FQNCYARYHQAFADCNQSERE LQGREGQLAAETQALAQPTQ QDSTCRVGERLQDTHSWKSEL QHEVEVLA AETDLLAQKRL ERALDAMEVPFSIATDNMQCS QRHQHANLV RDYV VETELLKAY PPAPSQCLKNCCSSRKPSACNK GACEVMETLTVQEEANPGTEG CRTRALAHKEEA EPIRNIQELLK RAIVQAVSQIQLNREHTEICEM DWLDKVEAYNLDETCGRHHSQ STERP/WTKFTQDNL CRAQRKR LSSANLWVLVDCLRDTS EDL GLQCDAVNLA FGRRCEELEDA RHKLQHHHLHKMLREITDQEHN VVALKEA IKDKKEPLHIAQTRL YLP SHIRPNMQLCREAAQFRAA FPG*ESQWRLPRTSLPAPNWE FWVPFHPSRCILLSPAPAH TTP TPPSW*VRWRSLYKSITALREK LLQAEQSLRNLDIHMSEKDV TAMTNSVFIDRQCKMAHRTCY PTILQLAGYQ
8936	39304	C	8995	99	442	

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8937	39305	A	8996	177	622	TESSASEKTTGEDGTRVVFVSL RSLLSLLPSAPLRHHPPSA*L SCLSCVSD*AVALIPQSAHHFPNIS *PFPLHCF/AHAKPPVWIFHSH/S LWLP*AFLAPMTSFTDQVAVD DFLSIVYLFITFTPLAFCEPST ALATREQVWVESAS
8938	39306	A	8997	1	329	AAARPGRGSETGDWVLLCYPG WSAVV*S*LTA/SELLGSRG*G SLLSLPSSWDYRLSAPCLANSK KPSEK*GLSMLP*LVNSWPQVI LLGPPKALGLQAPGTMGRLP
8939	39307	A	8998	1	814	
8940	39308	A	8999	57	274	TASSSLTLVYGHRLCWLGSPH *PSLWLP
8941	39309	A	9000	1	1236	
8942	39310	A	9001	1	1095	
8943	39311	A	9002	1	2313	
8944	39312	A	9003	166	494	FSQQLCGENHPLHRTENTQAQR AGVPLGVRLSRPGFP*LSTHSC FSCPLV*PPSQGQPGPLSLWTL SAIQAPAELESCRSSCDRDGRSH WPRVSGGLWLSQVPRPR
8945	39313	A	9004	3	974	MGESPAV*GYFVLAGMNSAGL SFGGGAGKYLAEMWVHGYPSE NVWELDLKRFALQSSRTFLR HRVMEVMPLMYDLKVPWF KTVSQLRTSLLYDRDLAQEAR WMEKHGFERPKYFVPPDKDLA ALEQSKTFYKPDWFDVIESEV KCKVEAVCVIDMSSATKFEITS TGDQALEVLQYLFSLNDLDV GHIVHTGMLNEGGGYENDCSI ARLNKRSFFMISPTDQQVHCW AWLKKHMPKDSNLLLEDVTW KYTGTVRALYGDVEHESWLS CVRHAHHPDPCIAHTYLHLRS FSQADGREWRKVLDKHKIFLF ARSLC
8946	39314	A	9005	1	1872	
8947	39315	A	9006	1	2250	
8948	39316	A	9007	1	1257	
8949	39317	A	9008	1	1596	
8950	39318	A	9009	1	1584	
8951	39319	A	9010	1	1461	

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8952	39320	A	9011	110	993	TSTELSTPSQQNIHSSQHHIALV PKLTT*LERIKYLGQLTRDVKD LFKQNYKPLL/NKIKEDTNKWK NIPCSWTGRINIVKMAILPKVIY RSSAIPKLPMTVTFTELEKSTLK FIWNQKRAHIAKTLSQKNKTG GIMLLDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIIPHC NHLIFDKPDKNRKWGKDSLFN KWCRENWLAICRKLKLDPLTP YTKINSRWIKDLNVRSKTIKTIE ENLGNTIQDIVMGKDFMAKTP KTMATEAKIDKWDLIKLRASA QQKKLPSE
8953	39321	A	9012	1	1185	
8954	39322	A	9013	1	185	
8955	39323	A	9014	2	1321	
8956	39324	A	9015	2	1757	
8957	39325	A	9016	1	1008	
8958	39326	A	9017	1	1311	
8959	39327	A	9018	1	1152	
8960	39328	A	9019	1	526	MPSLTTPQHVSQGSSGRAIRQEK EIKGQLGREEVKLSLFADDMIV YLENPIISAQNLKLIISNFSKVS YKINVQKSQAFLYTNNRQTESQ IMSELPFTIA/KRIKYLGIQLTRD VKDLFKENYKPLL/NKIKEDTNK WKNIPCSWVGRINIVKMATLPK MTWIANWLRNSLQAQ
8961	39329	B	9020	1	1626	
8962	39330	A	9021	1	2361	
8963	39331	A	9022	1	1140	
8964	39332	A	9023	1	2112	
8965	39333	B	9024	1	1065	
8966	39334	A	9025	1	1416	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8967	39335	A	9026	1	1690	MPMVEELYGNYGIMADTTERV GQHKDAYQVILDGVKGGTKEK RLAAQAYFILKFFKHFTELADSAIN AHLQTVSGRQQVLKLVAEQAD LEQTFNPSDPECVGRLLQCTQQ AVPFFSKTVHSTRSVTYFCEQV LPNLGILTTAVEGLDIQLEVLKL LVEMSSFCGDMKLETNLGLK FDKLL EYMPLPPEAENGNGNA GDEEPKLQFSYVECLLYSFHQ GQKLPDFLTAKLNAEKLKDFKI RLQYFARGLQVYIRQLHLALQ VKQCFAYMEKENGIDAKILN KILANRIQQHIKLIHHDQVGF PGMQGWFNIRKSNVIQHINRA KDKNHMIIISIDA EKAFDKIQPF MLKTLNKLIGDGYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRAIQ EKEIKGIQLGKEEVKLSLFA DD MIVYLENPIVSAQNLLKLSNFS KVSQYKINVQKSAFLYTNNR QTESQIMGKLPFTIA/S/KRIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNI PCSWVGIRNIV KMAILPKNWKLL
8968	39336	A	9027	1	1575	
8969	39337	A	9028	1	2682	
8970	39338	B	9029	1	2088	
8971	39339	A	9030	1	2406	
8972	39340	A	9031	1049	1500	
8973	39341	A	9032	1	4341	
8974	39342	A	9033	103	366	NHPQLKVAGLKGCCVCMCV CVC/CVCVVRVWVWVCVVCVC VCVCVC/CVCVC/CVCICVCI*V WVCVCVCLCLSLPKCWDYRHE PQRPA
8975	39343	A	9034	232	735	YLSGNGGEGKFCHALPDHRLR VLHQHPHACVETDTVDLGITS ISLADRVVCVCMCVVCVC/CVCV RVWVWVCVVCVCVCVCVC/C VCVC/CVCICVCI*VWVCVVCV CVCVCVCICVCVCVCVCVCV CICVCI*VCVCVYVCVCVCLCT VLGIHSFLTARNAHQPIGH
8976	39344	A	9035	163	795	

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8977	39345	A	9036	34	758	RVPHRHGMKRVVRQRHGMKRV PHRHEMKRVPHRHGMKRVPHR HGRKRVPHRHGRKRVPHRHGR KRVP AQVQDEEGHCQKPGRCV CMCVCVCVCVCVRVWIVCVC VCVCVCVCVCVCVCVCVCIC VCI*VWVCVCVCVCVCVCIC\ CVCVCVCVCVCICVCIC*VCVC VYVCVCVCLCLFYLVLCFCIS/ CIISGGQRWC*RKTMCSLPFAH SHHSFPGHFFLIFQSRSFQVSFHP
8978	39346	B	9037	34	156	
8979	39347	A	9038	3	419	GGENVKAINQQTGAFFVEISRQL/ PPN/GDPNFKLFIIRG/SPE/QIDH AKQLIEEKIEVGWGG/LWGFL TARIPAHLPWLLSFLGLPLCTV GPGPGGPGPAGPMGPFNPGPF NQGGPGAPQ*VSSASWVLRP/E GLLSWQEE*QTPFFFP*KCRAG ALIAHFCEGYHQALSCL/PGR ACAFQHPSVHVQVSRLLSCPQA DAARPPSSCFLSRFPFGAPLSLVV WVSGASPLKNIPTPGGPAA/PPP HHCSSIPFFSPA VPGGPLLTSTH PRAGAIPTPSGS/QPAPHDPSK* WALQPGATRGSPVLSLCLLGF EAGLLSWQEE
8980	39348	A	9039	1	445	ATADPNAAWADDYSHYYQQP PG/PVPCAPAPAAPPAQGEPPQ PPPTGQSDYTEWAWEEYYKKI GQQPQQPGAPPOQDYTKAWE\ EYYKKQAQVA/TGGG/PGAPPG SQPDYSIAAWAEYYRQQAAYY GQTPGPGGPPPTQ/GQQQA

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8981	39349	A	9040	38	1297	TCVSALSVLASDDGTGPEKIAHI MGPPDRCEHAARIINDLLQSLR VGGPGC*RGWQGLQGSARFDR LPGFIHLLLLSCRVVPPQGPVGG PGMPPGRRPKKEGGQGNWGSF WAGKMTFSIPTHKCGLVIGRGG ENVKAINQQRGAFFVEICRQLPP NIGTANFKLFIRGSPQQIDHA KQLNEKMKGPLCPVGGPGPGG PGPAGPMGPFNPGVPPNQGPPG APPHAKPPPHQYPPQGCNGT YPQWQQHAPHDPISAGKAAA AADPNAAW/AAYYSHYYQQP PGFVP/GPAPAPAAPPAQQQQP Q/QPGAPPQQDYTKAWEEY/YK KQAQV/ATG/GGPGAPPQSQPD YS/AAWAEYYRQAAAYYGQ/T PGPGGPQPPPTQQQQQQWVA PETPSPRGVPLMPAAGAVWPE VPGVPTHRQGSIRWVQR
8982	39350	A	9041	1	1777	MPVLPVTATEIRQYLRGHGIFP QDGHSCRLRALSPFAESSQLKGQ TGVTTSFSLFDKTTGHFLCMTS LAEGSWEDFQASVEGRGDGAR EGFLLSKAFEFEDSEEVRIWN RAIPLWELPDQEEVQLADTMFG LTKVTDCTLKRFVRYLRPARS LVFPWFSPGSGRLGLKLEAK CQGDGVSYEETTPRPSAYHNL FGLPLISRDAEVVLTSRELDL ALNQSTGLPTLTLPRTTCLPPA LLPYLEQFRRIVFWLGDRLRSW EAAKLFARKLNPKRCFLVRPGD QQPRPLEALNGGFNLRLRATA LPAWHKSIVSRQLREEVLGEL SNVEQAAGLRWSRFPDLNRLK GHRKGELTVFTGPTGSGKTTFIS EYALDLCQGVNLTWGSFEISN VRLARVMLTQFAEGRLEDQLD KYDHWADRFDLPLVFMTHFG QQNIRTVIGTMNHAVYVYDIC HVIIDNLQFMMGHEQLSTDRIA AQDYIIGVFRKFATDNNCHVTI VIHPRKEDDDKELQTASIFGSA KGGWSAPHSTSSRPSAQPKSD STVAEAAPLASDFATYWIWFLT WGRGRASRDREFGYLAALN

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8983	39351	A	9042	3	679	SPLIVSSARMHAGRDI.PLYFMT FHGQQSIRTVIDTMQHAIVYGAY DICHVIDNLQFMFMGHEQLSTD RIAAQDYIIGVFRKFATDNNCH VTLVIHPRKEDDDKELQASIF GLSQRQAREADNVLDPAAGTGK LGNRGQGGKRYFAGVPKEPF*W EM*GVFPLEFNKNSLTFSPPKN KARLKKIKDDTGPVAKKPSSGK KGATTQNSEICSGQAPTPDQPD TSKRSK
8984	39352	A	9043	90	317	GTLRKRYRAFHCRITIFKALTEV CKNFSAHCEFSWGFFFCFSFFF LASS*G*NCLPSQPQPCWFLQPP CPWQIL
8985	39353	A	9044	2	2136	PRLSVSLSEFITTHIYFLLSETTY NYEWNLSISLYVVDPSRLAC*TV QLFFMLQLSVGLYVFNVDNDIC LHKMGSVTVLFFVTARRVNLPP VAVIKLMSSSSCISFLSLFLNLV ESTDDTEIVSYHWEEINGPFIEE KTYLCFFTLFCVFIFVFAIT*G VQTPYLHLSAMQEGDYTFQLT GLQT*CKEIIHFHTVSVIPENNRP PVAVAGPDKELIFPVESATCLS YSKPHAPSLMLTTSMFYRGPSA VEMENIDKAIATVTGLQVGTY HFRFYSITGVNLQSLCFHFAIFD LENNSPPRARAGGRHVLVLPN NSITLDGSRSKPRNWDPRIDSC PVIRVLSQDVIDGSDHSVALQL TNLVEGVYTFHFLML*SLCKCP SANPVSSLSPPDKSGVELTLQ VGVGQLTEQRKDTLVRQLAVG VSW*SPSDHVAVLSHCLLHSTV IVFYVQSRPPFKVLKAAEVARN LHIS*SRDSLFCMLPSALHTS/S AGCLLKCSGHGHCDPLTKRCI* K*SWSTNSL*LCPLWFSCVSEW SIFYVTVLKS*LSVTLFKI*VELF IVPFRQKRKIRKKTLLNMY*VH LKYYFH*ILILPIAVRGMCDNDYP HD*QLEVNHGVPQMLLCFSLG IKHRSTEHNSSLMVSESVRSFD RDCLQSLNYLLSGLLQKEKNLQ KAGLTSPAPSLWEDKCSGRTEH AQ SARLPLKEDTEKTLMQF
8986	39354	A	9045	47	157	FDKICIFKRQVTKSEVILNLTN* VL*YLEYHIRNIN
8987	39355	A	9046	1	393	
8988	39356	C	9047	274	357	

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8989	39357	A	9048	727	1089	
8990	39358	A	9049	175	608	CGWEYGN* AIDTMDQEYCKVC QAYKAPRSHHCTKCNCTCYMK MDHHCPWINNCCGYQNHASFT LILLAPLGCIIAAFIQVMTMYT QLYSFGMENNFFRKQNFYLLSS WDWKEEGLKDPDFSIQLGWK SFVFFHMDMGEVDGEGTF
8991	39359	B	9050	780	1166	
8992	39360	A	9051	3	681	HIRGPRYSGHHSFAGCPYSDMN LKKEATLHDLRLEQTQANLES DSSHKSLSLCSLNFNGKHEKV NSQPRLVQQAQCKIKGKEDID LDNLFREYSVEQAQVVLHQS SMSTVSAHPFRDLPLGREQHCK LLPGVADIRASQVARWTVDEV AEFVQSLGCEEHAKCFKKEQI DGKAFLLLTQTDIVKVMKILG PALKIYNSILMFRHSQELPEEDI ASGQEVRG
8993	39361	A	9052	30	981	TQDPWPSPVLVWSRASSDPAAG HRAEHI*TYWPWKLEGTDIWL VLYMPLVQPDNFIKKHSLPTY CLFKEDVKFPFRTCLTYCWLN YTEEITYLHTKKVSVGQSAVRE EFAAACTWSIRIGEKLAILLSLY LCRQQALLNMRMSVPIHESGV AQRSPVMDKLAQYSVEQAQV LHQSVMSTVSAHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLIQTQTPHLDISIS KGESPALVVTLMCMMTATEP LVPTKNPYQERGHIGDSFLHYT DQEPQPDQSSVHPTAPIYSV SSGFRVTRGSDI
8994	39362	A	9053	1	864	MVSALPEVGRAQLRLIAYIRSP APPVVGVERAARRPAQAFGLV ALPSTDATVFANQPLARACIGA ARHREPDAPGQSAWVGEECLK DALRSPETPKLGLSLPPCQDTRP GRASNDFSLEMGYSLSAARLK IHGQVFQCCGPGPLRTLHWQ S*TYLNLIALET*GAQNQP*EW QAVD*GAPGLFSLTGVFPRL PQHPKQIICFQNYEYSVEQAQV VLHQSVMSTVSAHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSAPRGPELSAGANS SRGA

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8995	39363	A	9054	1	1737	MKEKPAVEVRLDKWLWAARF YKTRALAREMIEGGKVHYNGQ RSKPSKIVELNATLTLRQGND RTVIVKAI TEQRRPASEAALLYE ETAESVEKREKMALAQMIMPQ IIDQLHRYLFENFAVRGELVTV SETLQQILENHDPQPVKNVLA ELLVATSLLTATLKFDDITVQ LQGDGPMNLAVINEINERAQNP LLCAFRVCNTYGSYECKCPVG YVLREDRRMCKAVFPYCQNES SDVLWQFDSTQIFLKGTPKTT VRRGGEHNLKNPDECEDNPNIC DGGQCAGIPGRNRLCYDGF ASEDMKTCVDIDECSLPNICVF GTCHNLPLGLFRCEIGYELDR SGGNCTEDPDHKSRSRGSQND WGRRRKT/S*KRSAVYR*RQLY IRRQPYAERPSLR*RQRP*IPCIR SQHGNRKRMRRRRJI/STKRRT AAARTSSVKARSFSRALKNA MLS*RTAPSVS*S*IMITH*KK** SR*SLQTR*LMKSSARVFSK*TA NGTWSL/HSRGSKVTIDGINSND IYMLGYVSNLSLTGPYPVDKGTG LGLEMGLDPNDVTLTYSHFRVP EAEAMWVSHAT

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8996	39364	A	9055	1	1743	MTTSTMTHMMTMHFPIIIVCAD SRDDVDVNTDNDVNDHDDSAKR KSHRERPIAAKRTETK/KRRRRA RPKR/RTKARS*SAK*QTAQHT RTTAAIIMRDTQARRV*RP TKH AAEQRQNTTGKQRR*TKRVKA AKKEGE*RRRKMARRTTPTQR R*TRAKRRINRPRHGAKKRA*N /RRLKSAPKRHRVNRDENART TTRHKKRRNRVKAERSGAE RTPYKQRHQQTREKRTCKRRQ TK/RRTKAK*T*RDHENDGTRA YNKTPKKAARKTRNNLRHNA TKGGDNRGQTRRA*TKPRKYR PDENRYNTSSPERTPRKRRGKS E/RDKTAQRAQ*ADRYNSRKT QQRL*KGHTHTER*RQARMHT RHAQNLDTOHSTRLCNA*ST/C HDRRSSSTMCHRYDQLYSRSH ALTMIIIVNKPLRQCIRMLSFHD RHRSLAIDGDSASTGSPAFCV NTYGSYECKCPVGYVLREDRR MCKDCTCEKAFAPAGCEVDKT HTVPQERAYIHRTRLGRARTKK RDLYRRAHNDRRRQKSAAYYE STSVRRRAHKYNSGKSDTQNGS HHRQKLRQYGDAGKSHYLQY NIHFMYPLFNT
8997	39365	A	9056	3	451	FFEMKSHSVAQAGVQCSGVILA HCNLHLESDDSPASAFRVAGII DARPHAWLIFVFLVETGFHHVG QAGLELLS*VIHPPWPPKVLRL QHETPCPAVSLYLNQSPENNLE EDSLAMSNNRRSGPGIWWQNP GFEILALSTFLVESDLK
8998	39366	A	9057	53	343	
8999	39367	A	9058	14	234	CLFIRIFNVICYSKTCKNSICIGV IEIVIDGCMCGGEDGGGGGGSV TAGGAPSPJETGSHGPPQAVYF WRF

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9000	39368	A	9059	3	865	INFSVCVLARFFLGVVVLCVSC CWFRCCVACVICALAFPCSCC VVVLCVPVGRCTLFAV/CCCL/ CVICALFCGFLRLFLCLCV/CPC S/CSARCRC/VCLALGAVVCFPP CSVVASCGCCDWWVWLCGAV VALVGLI.CCVLVCAWSFRGC/C V/CLC/V/CVVVVLVVRCC/VCW CGSCVVDCAAGVVLVCCLLVVL MMSL/CGCRVYSWYGVWCVCS VVCRVIDL/CPCLCLW/CVT*RG CWSVWCM/CTCCG/CVCGLA V/CWCRCVVRLVCLCAV*FIC ACVCFEAVGGFVGGCLGSL
9001	39369	A	9060	1606	1849	QGVASLCREAGLTKISPGAPL WLPCSPGVTAECSGERTVRHN VTDRCVGLGAVTSPGRN*RG HVTHKFCILCTDTRDC
9002	39370	A	9061	2	682	ALEAVFGKYGQIVVHLMKDC ETNKSRGAFITFERPADAKDA ARDMNGKSLDGKAIVKQATK PSFESGRRGPPPPRSGPPRVL RGGRGSGGTREPPSRGGHMD D/SGRDSYRGPPRESLPSCR/D APPTRG/PPPSYGGSSRYDDYSS SRDGYGGSRDYSSSRSDLYSS GRDQVGRQERGLPPSMERGY PPRDSYSSSRGTTPRGGRGGS RSDRGGGRSY
9003	39371	A	9062	90	443	NVYYIQFIVLPYYLTIDPAGNSR SAPPTRGPPPSYGGSSRYDDYSS SRDGYG*SRDSYSSSRSDLYSS DRIVSTLFFVSLNWDGPKFCLF LVSASAPSIRSASSRSTSWCS AA
9004	39372	B	9063	12	1373	
9005	39373	A	9064	2	206	

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9006	39374	A	9065	2	1423	IHFREMAKSWLNFLTFLCGSAI GFLLCSQLFSILLGEKVDTPQNV LHNDPHARHSSDDNGQNHLEGQ MNFNADSSQHKDENTDIAEKIL EEKVRILCWVMTGPQVLEKKA KHVKATWAQRCNKVLFMSSEE NKDFPAVGLKTKEGRDQLYWK TIKAFQYVHEHYL*DADWFLK ADDDTYVILDNLRLWLLSKYDP EEPIYFGRRFKPYVKQGYMSGG AGYVLSKEALKRFVDAFKTDK CTHSSIEDLALGRCMEIMNVE AGDSRDTIGKGNFFHFPV\PE\H IIFNLKGYLPRTFWYWNYNYP PVEGGELRFLFSTVTIRHSAKS LGVAQCSWLLKQVISDDKTK RPDFPDRSRIMKERVQIVLYES GQAPVESSPPLPGYCSALFATCF QVTGKNFSQDPTQAILYTQADK IEGWMRASGERVAEQSQGTA MDGGKKEAEWKRTKAKYRD DVCSKHHPPYPTPVPPSLED
9007	39375	A	9066	1	311	
9008	39376	A	9067	1	493	ITRQHMRKAVPFQVPRKEILKL LKGGVVVGHALHNDFFQALKI*S TLGARPGDTTYVPNFLSEPLH TRARVSLKDLALQLLHKKIQVG QHGHSSVEDATTAMELYRLVE VQWEQEQEARSLWTCPEDREPD SSTDMEQYMEDQYWPDDLAH GSRGGAREAQDRRN
9009	39377	A	9068	45	365	NQAAASRPHCAARTMAGEEQA ACVHEDRTQCRGDKAAPQAAH LCGPPRGSVSTAPRAR*CPV CSSCPGPGAPEDTPEEVDVGAA SAHRSPRLCCSHLTHRWPKH

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9010	39378	A	9069	3	1687	ICVPKSVPSFLWAGRGPHCLLP CGSSSP*SGGLARA*GVFQGRA GVARAPSHLSFHNSPCVWSLST CCRAGSQDGPCHAAGQGP GK QTSSGTGASSSPWTSCL*KSLPK VCS*GLETITIGRGRVKPIKVT D TAQ*CAASVTAPL.LSS*LQDGG STAKVTRCT/TAGGRAVYGTAE GKAFPEAPELTCRS/ALAA LGT WPLPPLQVSCGLRNPSPDLPSV VGSRAV*TKSGSPPAKVWPLA EWFKSGSA/PVTGQEA WLLWA SDSSSELSLCPRKHAAPPHSAEH RQISQGLASSCWGAGGDKVVS ASMVGSAPGQCPCMSALMTGSA SGQCPGHPCWSGTNADS*GRDP HRASRLALPTASYEQ*PQPHW GSWTAHQNGLGIFFRVSWF V*GQTMVSRPRISGLGQPVCLS AASPQAAPLGSHDPTAGR*GL EPGGRQPSSS*YVWEAPPGLW VPPGPFLSH*SWRFGRTKAAPL KEPRPGGRCPGDRPSPRAEAGL PQTRKPAIPAIGR/PKKACSLRR PRVILEQSSQHLAAALSSWMQP ALLETGGKAVFFTPGGL

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9011	39379	A	9070	66	1956	PLLAIPAHSTFPARKPEEPPRPD* LCPHIHCAAV*GEIRTVP/SKTV RGVATRTPRSSASLGIITGLR VSSVRRVQLSIKPGCSRVENSS NSPCSSSQPGTSLPCPTVCRE AGP/AGP*PPG*ALSLPAAGFTT ATEWKQSLSSGG*THSGEDM GRATAAATEKAQEQCMLREKL GTRQKAESGSRGA/VGLQHFCS APRTAWQPRASRA/RAGVRAW PCADPM*PPSHSPSPKPFIPAA/ PGAQTLGAAGVEHVAGSARIPC CRTGLE/PHPHSPRRTLERQARI SGAGRRSSPNAATGARPRPAA SPVSARRAPRRRPA*SSPCSGPW TAVSAPRSPGPRGGRRPSPGR RRPCCSVFSGGASPSARVSSPS GSCSASPAAAPA/PASGAVVA GPVVGSPREHGG*LRPPLPRLG VPGLLAARTSGAEVIHEQAAAQ GTAADTPGAPGLLLAPAAAGA V/TRPGPPGASGCPRPAPRPPT ASRSGRP/VPGGGRGRRGGRGA GGEALQGA/VVGGQVGGSGAL A/ATARGSPAAGVSRWTAPRCR HRRSDASASGTPARFPGAGRKG RTLWQ*SWRSAPPPGLSELL*G LPRPLPESGRSKAPLPSGSTPLPS GRTPLPSGRSPSTRSSPS
9012	39380	A	9071	95	1423	GLENKRAKGTEAHTRACP*GK STEQDITWNTGRNEQQGPRP KGEQTQRKTERKPGRERQVQV LSPPGRWC*DVGPLGGLPSRA KAEAAALTAQKAQGRGSPGS LPKSSPLSAPGKR/TPPRGHLL VPLPSPIYPALLSQHPQGPCCG ASAPPSALLQRAPPPGRTL/Q PPGPRVTCGTTP/MAAKAKSQS NAPRGSLLKKSNSFYNIPLKQV SCLITISKHSRNEVSYYQTSRPR AAATDVPRT/PSLSVGCSWSCT RGHWPSSCCPTAPRGQGL*EHS QGPGSRSKLPWPTGPCGGLTPS CWSLAGSAGERVDLNAQAAASR PHCAARTMAGKTLSGCGCVD VGAASAHRSRRLCTTSPDGP NTERGSRKTGWTPGPGFWPCP RPPTSTNTTPLGLMDSARPGKA PAPFTDFRTPSGLLLPGWAVRA RREEDGCG

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9013	39381	A	9072	42	380	LGAPCTPPRSPRTGRPEYA*ARG*PVGDLRCRGEAVVSTQVLLPRGLQ*NFAVLLQMSCATPPPNCALKGCV*VPLEQSPFFHQAVACREWKRKGGMVCGGNASQ RTEA
9014	39382	B	9073	116	341	
9015	39383	B	9074	52	190	
9016	39384	B	9075	70	310	
9017	39385	A	9076	1349	2456	HCSVPGA EWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG*SPQPPVMSLHEGP PRGPQV/PSPVANPQPKPWLLRSVDLPVPWHLPTVDRITSL/APLSQSDV/PAPSGAL*PSGRACSGV/PPID*APEAALSA AAPRPSLGGGQNASGLPAASLPQDSSQPHKTVPSPARSVPLGAQARAAPPRLWCPHALVSG*EASPEAVSVAAGPPVPGPTPS TSGSTASHSRRC*SPR*TPAPPRRDHGRSAAFEVLAAAASAQPCASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPF CRHPSL*FSW*SSPSGLSLSDTPHSPRRPLGPVCGLRAPCPPQIPACRVPA AHSQRWPGSSSRSCRCQCC
9018	39386	A	9077	462	739	ACEPMVLFCLLALLQDLFLGSYPRVLA AFDIQVFFLGTSDRM*NTG/LEYFMLNSWLWLLNRL*SWGELCHFPLHSPVKRGLNFYLOEFFI
9019	39387	A	9078	1	678	GTRVNMILMKMGFSGIVVHQESVCATYGSGLSSTCIVDVGDQKTSVCCVEDGVSHRNTRLCLAYGGSDVSRCFYWLQRA GFFPYRECLTNKMDWLLQLHL/KRNFLSFRSRTSLGFRMTSFRFRHPDS PALLYQFRLGDEKLQAPMALFYPATFWICWTGK*RPLHTDLRA ILKILTMNITCWPHKAHENSQKLLLTESLHPNLLDLKGIFVASP LIFQKDSIPR

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9020	39388	A	9079	227	1980	GERLRYGV TENGKEKGGEKEK EQRGVKRPVPALVPESLQEQIQ SNFIIHVPGSTTLRIGRATDTLP ASIPHVIARRHKQGGPPLYKDR WLLREGLNKPESNEQRLNGLIM VDQAIWSNKMNGTRRNVPSP EQARSYNKQMRPAILDHCSCN KWTNTSHHPEYLVGEEALYVN PLDCYNHWPIRRQQLNHGPG GGSLTAVLADIEVIWSHAQKY LEIPLKDLKYRWRILVIPDIYNK QHVKELVNMILMKMGSGIVV HQESVCATYSGLSSTCIVDVG DQKTSVCCVEDGVSHRNTRIFS WRSGHLWVQDHEFQIRHPDSP ALLYQFRLEDEKLQAPMALFYP ATFGIVGQKMTTLQHRILRAILR ILTMNITCWPFRANKNSLQKLL LTESLHPNLFERGFELWASPLI FQKDSIPRR*IWGLHREMA*WP ATIPRRPLTALMSRKTAISLFEG KALGLG*SPSSAIDCCSSDDTK KKMYSSILVVGGFDFVIFKASR IFCSTEFSTKCPPSLQADYDKM WM*SQGLKMDMDPRLIAWKG AVLACLDTTQELWIYQREWQR FGVRMLRERAAAFVW
9021	39389	A	9080	1	756	MRRIVALVETGEQPFGAATVGS RFGCLEDLGTDQREHHDHEMA AAHTYFIGDGDLTDEDED WGMAKGHHAINIEGFKLARVE DEMVFQEREPEKVKIRGRTRGY TFIMLAALAAAEADMVQVGE L/C*KVSLKASQLGQMALMLQS VTVQIGMVYGLPACGAQVNLQ DDKGSVMVLMCASKHGHMEIK LLLAQLGCNVHLQDNDGSTML SIALEVGHKGITVLLYAHISFAK AQSPGTPRLGMKPKQSF
9022	39390	B	9081	5	5440	

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9023	39391	A	9082	1	4294	WAVFDGNYYYLPWAHTKPV VTLTSYWEDISHRLDAVNALLA MAERLQTNIEALKSGIQGKIPA NQLAELWLKLIDEVIEDTRYTL PLTEGKANVTVLDTOIRKLRSR SLSQIHEAAVRMRSEATDVKST LAEIEDWLDKLMQLTEEPQNS MPDIIWMIRGEKRLAYARIPAH QVLYSTSGENASGKYCGKTQTI FLKYPQEKNNPGKVPVLELRVNI WLGLSAVEKKFNSFAEGTFTVF AEMYENQALMFGKWG
9024	39392	B	9083	1	339	
9025	39393	A	9084	2	1767	KLYRGKSDENEDPSVVGFEKGS FRIYPLPDDPSVPAPRQFREL DSVPQECTVRIYIVRGLELQPP DNNGLCDPYIKITLGKKVIE/DR DHYIPNTLNPVFGRMVYELSCYL PQEKDLKISVYDYDTFTRDEKV GETIIDLNRFLSRFGSHCGIPEE YCVSGVNTWRDSLRLPTQ/LLQ NVARFKGFPQILSEDGSRIRY GRDYSLDEFANKILHQHLGAP EERLALHILRTQGLVPE/HV/ET RTLHSTFQPNISQGGKT/LQMWG GMFFPKSLGPPGPPFNITPRKA KKYYLRV/IIWNTKDVILDEKSIT GEEMSDIYVKGWIPGNEENKQ KTDVHYRSLDGEFNWRFVF PFDYLP/AEQLCIVAKKEHFWSI DQTEFRIPPR/LIIQ/WDNDKFS/ LDDYLGFPRTLTCRHTIHFLOK SPGGNCRVWT*FPGSKAMNPL KAKTASLFEQSMKGW/PCY AEKDGARVMAGKVMETLEILN EKEADERPAGKGRDEPNMNP LDLPNRPETSFLWFTNP/CKTM K/FIVWRRFKW/IIIG/LLFL/LL LFVGRAP/TL/LLPNYFVQWKIVK PNVLT/KGKG/FISRV/IIQ
9026	39394	A	9085	2	407	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
9027	39395	A	9086	15	759	SARPSHDYSHYYGTIEYLCYKI LGDIIENSRIVLQINNACLAADD F*TKYEREQT/LA/RTDLEMQTE GLKEELA YLKKNHGEINALRG QVGGQISVEVDSALGADATNIL SDMQSQYENRKDAERWFTSCT EELNWEVVGHMEQLQMNRSQ VTDLRCLNQLGLEIELQWQLSM KAALEARFGPQLAQIQAIISSIE AQLGDVRADSERQNEQYQLLM DIKLWLEQELATYLSLLEGGEE HYNLSSTSKIL
9028	39396	A	9087	3	2026	AGPWDRMGAMGSLVGGDLGL VWGCAGEGFAGIPFSCALTCQ EGNQGTAKWVQTSTRIKGGQ VKQARGAQVTPYSPLWHGKLG RAAFTFNAPGRWLLPLLLPPL L*ITTCLLGKRTLQEALSLKLE LRKVCLQEA VRAWP*GYQAGR LGGGEELGPLGRPPTARAYPPP HPNQAHHSLCPAEV/MQMGEV SKRVGRGDRYRGVARRIMALA PDLSTEQRRRRRQVQADALRRL HELEEQLRDVRLRLGLPVLPLP QPLPLSTGSVITTTQVCLGMRL AQLSQGEHPLVRVGEWTLANG RGRAGMGDSYPPNLPPTTSL* PIPIFIHPVSGGSPERRTPWKPPPS DL YGDLKSRNRNSVASPTR*E*A PPPLRRSWEWDSKPGLAEGPAS DRASLFVARTRRSNSSEALLVD RAAGGGAGSPPAPLAPSAGPP VCKSSEVL YERPQPTAFSSRTA GPPDPRAARPSSAAPASRGAP RLPPVCGDFLLDYSLDRGLPRS GGGTGWGELPPAAEVPGLPSR RDGLLTMLPGPPPVYAADNSNP LLRTKDPHTATRTKPCGLPPE AAEGPEVHPNLLWMPPTTRIP SAGERSGHKNLALEGLRDWYI RNSGLAAGPQRRPVLPSVGPPH PPFLHARC YEVGQALYGAPSQ APLPHSRSTAPPVSGRYGGCF
9029	39397	A	9088	1	136	
9030	39398	A	9089	14	310	TFLFIYFFFTETESHVPRLECS GVISAHCNHLHLLGSNNATSAS *VAVITGACHHAWLIFVFLVEA GFCHVG/RRLVNS*PQVIRLPW PPKVLGLQA
9031	39399	A	9090	1	436	
9032	39400	C	9091	75	410	

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9033	39401	A	9092	1	6691	MVNTYREVKEGPVIL EDVLIEV FRTLYSQCKAELDLQTEPPFSK DHAQLSSKLRENKKTAELIKTA NLLFNSFEPYMWWDYVARWFE ECCRRTLHVRLQIGPGDSNDSS ELQLTNFCLLVDLFDIVSLIETY IEIQTEHLPQLLLRMISAL TSHL QTLHLSELTDLSRLCSKILSKVQ PPLL SASTGGVLQFPSSGQNNV KEWEDKKVSSVSHENPTEVFE DGENPPSSRSSESGFTEFIQYQA DRTDDIDRELS
9034	39402	A	9093	293	687	PTAKVYIFSIPLYTHIVCCINTSS LFGFLQKNPEEDNSGRITLQWE PGHLLALTICTVRSMEQLLPFFN VLSQVFNKVTSRCCGHSGSPI LYSNAFPNKDMKLENHKKPCSS KARQKIEEMVEKDFLEGMKT
9035	39403	A	9094	3	4173	IPMVVDFDLDPDQIEILQSSDS GCSQSSAGDNLSEYVDPETVNA QEDSQMPKESSPDDDVQVVF DLICKVVSGLVEVASVTSQLEI EAMPPKCSDDPDDEETIKIEDDSI QQSQNALLSNESSQFLSVSAEG GHECVANGISRNSSPCISGTH TLHDSSVASIETKSRQRSHSSIQ FSFKEKLEKVSSEKETIVKESGK QPGAKPKVKLARKKDDKKKS SNEKLIKTSVFFSDGLDLENW YSCGEGDIS
9036	39404	A	9095	5	1055	FDLERVRNLTYMVTTRREIKRS VCKVQEQIFNLTYKLEQERVS GVPSSCSSLNMLLFNSPSVG PDAPKIEDLKW/PFCISSENKWW LPWVSFG*KRPKISRILLQN*PW K*RQNPAAEARPVW*KGDDGG PRELFGFRKDLCRSTSHISTTEK WCGDARPEWKKRQSFL*SH*R RLKGRIF*TESQAS/PGPQMCP GIWTTQELPPLEWGSQHLGTR KEIVPKCNGSLIKVNYNQTAVK VPTTPASPVKNWGGFRIPKKGE RQQ/PGRGRWGLPPALRLPIFG LRPSS/TKERAKSKLSDNEND GYVPDVEMSDSESEASEKKCIH TSSTISRRTDIIRRSILAS

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9037	39405	A	9096	3	1136	FDIPFPKIGKLIKSNVPELRGHFP LSITLVLRMLLASKGDDPEDA KAKVLSVLKHSLLSFQPRVM DMLKLYFLFSLQFLGGKRAI*IQ EG*SYGVCWDLVFTFGIYPWNL SNLVFVSFLVNGLFHDLCOPT KGSKHFSQDVMKELVLVLAHL FGRRYFPKFDQAHFEFYQSKV FLDDLPEDFSADALDEYNMKIME DFTTFLRIVSKLADMNQEYQLP LSKIKFTGKECEDSQLVSHLMS CKEGRVAISPFCVCLSGNFDDDL LRLETPNHVTLGTIGVNRSQAP VLLSQKFDNRGRKMSLNAYAL DFYKHGSLIGLVQDNRMNEGD AYYLLKDFALTIKSISVSL/HVT YCENEDDNNVLAFAEQLSTTFW
9038	39406	A	9097	2	522	
9039	39407	A	9098	3	1080	FLLPFSHQSKKENSQDLMTLFT SFNSLHSAVESFFQATGNSSTNL ADDGKRRTVTPVILTKIDGVN VDTHHIPVNVTLRRIAHGADAV AARWDFDLNQGQGWKSDGC HILYSDENITTIQCYSLSNYAVL MDLTGSEL YTQAASLLHPVVY TTAILVLCLLAVIVSYIYHSLI RISLKSWHMLVNLCHFIFLTCV VFVGGITQTRNASICQAVGIILH YSTLATVLWVGVTARNIYKQG H*KS*KMPRIPEP/RTFNQDQW LRFYPDLVGGYPPSLVLA*LA AANIKELRQSAKPHY/WLGW HGNPPWEAFYGPASFSTFVNC MYFLSIFIQLKRHPERKYELKEP TGQQRLACQ
9040	39408	A	9099	1	307	
9041	39409	A	9100	2	286	

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9042	39410	A	9101	35	1211	EKDLLWEEKFPDRTTVTELQPT SHVSFSEPDIPSSKSTELPVDWSI KTRLFTSSQPF TWADHLKAQE EAQGLVQHCRATEVTLPKSIQD PKLSSELRCTFQQSLIYWLHPAL SWLPLFPRIAGADRK MAGKTSF WSNDATLQHVLMSDWAVSFIS LYNLLKKNFSPYFYVCTYQFT VLFRAGLAGSDLITALISPTTR GLREAMRNEGIEFSLPLIKESGH KKETASGTSGLGYGEYVVIKIL/S SSTDLTWTHEIDLHRNSL*NRDS NCSNF/LREQAISDEDEEESFSW LEEMGVQDKIKKPDILSIKLRKE KHEVQMDHRPESVVLVKGINT FTLLNFLINSKSLVATSGPQAGL PPTLLSPVAFRGATMQLKARS VNVKTQALSGIQRPI
9043	39411	C	9102	48	464	
9044	39412	A	9103	1	140	MNRLKKEWMLHEIVENNSGM ESQDIKGHFHAADKDLLEMGY LQKRGLIGLTVLHGWGGLTIM AEG*KRSGCLSTLWKITPAWNL KTLKAIFMLLIKTYLKWAIYKR
9045	39413	B	9104	1289	2767	
9046	39414	A	9105	3	1278	INNTNTFRVLPHPSFVYTAKFHP AVREL VVTGCYDSMIRIWKVE MREDSAILVRQFDVHKSFINS CFDTEGHMYSYGDCTGVIVVW NTYVKINDLEHSVHHWTINKEI KETEFKGIPISYLEIHPNGKRLLI HTKDSTLRJMDLRILVARKFVG AANYPGEDS*YFD/VH/GGTFLF AGSEGDGIVYVWNPETGEQVAM YSDLPFKSPIRDISYHPFENMVA FCAFGQNEPILLIYIDFHVAQQ EAEMFKRYNGTFPLPGIHQSQD ALCTCPKLPHQGSFQIDEFVHT ESSSTKMQLVNQRLETVTEVIR SCAAKVNKNLSFTWPPAVSSQ QSKLLQSNMLTAQEILHQFGFT QTGIISIERKPCNHQVDTAPTIV ALYDYTANRSDELTIHRGDIIRV FFKDNEWDWYQGHRERQEG

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9047	39415	A	9106	1	1249	MAVLIFLGLLGGIAIGLPIAWA LLLCGAALMFWLDMDVDVQIMA QTLVNGADSFSLAIPFFVLAGE IMNAGGLSKRIVDLPMKLVGH KPGGLGYVGVLAAMIMASLSG SAVADTAAVAALLVPMMSA NYPVNRAAGLIASGGIIAPIPPSI PFIIFGVSSGLSISKLFMAGIAPG MMMGATLTGKRARFTEDDTR ERDAISVINHQRNAVLIRQVRK LQQLFVIRVLAMRIFYGSLRH KQGNSHWMTNAQLLGDFSIDN YQLYSLGHYPGAVPGNGTVHIG EVYRIDNATLAELDALKTRGGE YARQLIQTPYGSAMWYVYQRP VDGLKLIESGDWRVLRWLRVH SIDVPDPFGLTVTGDRDTRAG KTSPAQAGCKLFLTNPLGIGVL TTAEKKSLLKPEHQGLATEVM CRMNIAGASFANIEGVKAMTD VTGFGLLGHLSEMCQGAGVQA RVDYEAIPKLPVVEEYIKLGAV PGGTERNFASYGHLWLR*LAL AP/LEVVEANGSL*CSGERGCL YGQTTTIQLNFRPAFCPEHAIG QKVAILRLNMQIDIKRVSSRTH GNHFTNFKFTVQHYRSCLT

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9048	39416	A	9107	162	2106	KMSKLLKIAVSDSCPDFCTTQRE CIYNESNRNIDVAAIVLSLNDVT CGKLDEIDATGYGIPVFIATENQ ERVPAEYLPRIISGVFENCESRRE FYGRQLETAASHYETQLRPPFF RALVDYVNVQNSAFDCPGHQG GEFFRRHPAGNQFVEYFGAVPC RLVIPALKKQKRLSDLETAIVV VDRFSGEVRAMVGGSEPFAG YNRAMQARRSIGSLAKPATYLT ALSQPKIYRLNTWIADAPIALR QPNGQESVRVMLVDALTRSM NVPTVNLGMALGLPAVTETWI KLGVPAKDQLHPVPAMLLGALN LTPIEVAQAFQTIASGGNRA'PL SALR*TIAEHGKELYQSFPQAE AVPAQAAAYLTLWTMQVQVQR GTGRKLGAKYPNLHLAGKTGT TNNNVDTFWAGIDGSTVTITW VGRDNNQPTKLYGASGAMSIY QRYLANQPTPLNLVPPEDIAD MGVDYDGNFVCSGGMRILPV WTSDPQSLCQSQSEMQQQPSGN PFDQSSQPQQPQQQPAQQEQ KDSGDGVAGWITDMFGSNEHLS GYELDSYPLSSARRRARFTEDD TRERDAISVINHQRNAVLIRQR VKLQQLFVSNHIACWIRRPQDA NHPGFFANMQMLKIDVVFKLA FRQQFNIRTRRDQIQQSGVT
9049	39417	A	9108	1	66	
9050	39418	C	9109	79	150	
9051	39419	A	9110	2	475	GRGRWGAPRLRGAL*DP*GHF LGQQPRPQLHSPAPDR/PAPTPT DAEGL/PPAAAAAAGATARVP GSRGG*GQAAELHEAGEAQA CRGGTEDEEHG**HLCHGRAS* CPGVSGSTGSPHPSMAPDDT SGLLEFVGVPQLTLFAVWSPAE AAEQQL
9052	39420	A	9111	171	462	PTSMGHLYSFPGN*SHAHYHPI KT*SPLPHSTPISNPSA/PLKGLK PVITRLIQHGLLKPINSPYHSPL PVLKPKDKAYKLVQNLRLINQIV LPIHSM
9053	39421	A	9112	1	573	
9054	39422	C	9113	100	297	
9055	39423	A	9114	1	1401	

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9056	39424	A	9115	24	482	VGSGDLPWEGNPLSSCSLLHEK DPPTTSGPQT/GP/GPRNISPILNR AAPRQAQLGPNSSASAPPYPN PFITSPHTWSALQFRFVTSPPPP AQQLTLKKVAGAKGTVEHFC IDLPASSMQSNYPVHDSGHILT TGPSLFKPTLNIEYSTGHAP
9057	39425	A	9116	1	489	
9058	39426	A	9117	1	642	
9059	39427	A	9118	237	748	ETNPLSSCSLLRKDPPTTSSPQ THQPKKHPPISNPAAAPHQAE LG PNPSSASAPPYNLFITSPHTW SGLPFRSVTSPPPAQQFTLKKV AGAKGTVKITITDIELQVTLTVE ARLRPGEINSHVAHTKPVWWS LHTDTCDIWCRRPGTGGLLQET SPLSPSLCEEIHL
9060	39428	A	9119	63	255	WVSGSVQVKVERGWDEGCKGI VKKACLTYTNRMHCVGRY*A *ESIWVWHHGVNRQNNLVDKA
9061	39429	A	9120	24	389	SDVKANLSTGGPVGCGGDTL/P VAEKPSDAVEAPGV*APSAGG AGPA\PSPGLEPSGAPPP/ALPP RAVLDSGLAPGRPLPLASSNP/P PAGRRLLCTSPGRRGGAAAGSG PRCPESKSIPLRCL
9062	39430	A	9121	704	867	CVKECLDVRHLRPFAYFTTRII* ILQDQGIQSAIF/CVIWNYCRVCI GVKRHSRRK
9063	39431	A	9122	1	7068	
9064	39432	A	9123	2	165	LLKRELNFDFYKISTTKERHLQ QS*PKDS\VPSSLASQTPNAPFL APQRRCLLA
9065	39433	A	9124	1	148	IRHSVNLLRAG/RIFVFEPPPGLK ANTQRTFESGMKHVRIIYMMEF HVF

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9066	39434	A	9125	1	2340	QFGIWLDSSEPEQTVPYLWSEE TPATPIGQAIHRLLIQAFRPRD LLAMAHMFVSTNLGESVMSIM EQPLDLTHIVGTEVKPNTPVLM CSVPGYDASGHVEDLAAEQNT QITSIAIGSAEGFNQADKAINTA VKSGRWVMLKNVHLAPGWLML QLEKKLHSLQPHACFRFLFTME INPKVPVNNLLRAGRIFVFEPAP GIVKANMLRTFSSIPVSRICKSP NERARLYFLLAWFHAIQERLR YAPLGWSKKYEFGESDLRSAC DTVDTWLDDTAKASGRQNISP DKIPWSALKTLMAQSIYGGRR DNEFDQRLNLTFLERLFTTRSF DSEFKLACKVDGHHQIMPDGI RREEFVQWVELLPDTQTPSWL GLPNNARVLLTTQGVDMISK MLKMQMLEDEDDLAYAEOTEK KTRTDSSTDRPAWMRTLHTT ASNWLHLIPQTLSHLKRTVENI KDPLFRFFEREVKMGAKLLQD VRQDLADVVQVCEGKKKQTN YLRTLINELVKGILPRWSWHYT VPAGMTVIQWGVPIARRIKQ LQNISLAAASGGAKELKNHVC LGGLFVPEAYITATQYVAQAN SWSLEELCLEVNVTTSGQATLD ACSFVGTGLKLQGATCENNKL SLSNAISTALSLTQLRWVKQTN TEKKASVVTLPVYLNFTADLI FTVDFIATKEDPRSFYERGGG
9067	39435	A	9126	3	6375	HKVAAPDVVVPTLDTVRHEAL LYTWLAEHKPLVLCGPPSGK TMTLFSALRALPDMEVVGNLFS SATTPELLLKTFDHYCEYRRT NGVVLAPVQLGKWLVLFCDEI NLPDMDKYGTQRVISFIQMV HGGFYRTSDQTVVKLERIQFV GACNPPTDPGRKPLSHRFLRHV PVVYVDYGPASLTQIYGTFR AMRLIPLSLRTYAEPLTAAAMVE FYTMSQERFTQDQPHYIYSPR EMTRWVRGIFEALRPLE

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9068	39436	A	9127	3	617	SWFQPPSGPPWPGA\PPPPPLAR VNPGV\PSLTTSMDVEP* A Q V ELPSHPRVPSAPGPAP* VLEPP RSLTTSVVGPPQGPSWAGGMA VRQALEEAACRDPCIAISSWAG GDRPLWWLDGLLLRRVYPDSC PPCPSRIPIFGASLQGSINPILQ MRKLFPHMDLL*GQDPFSCR RPESWNRDVGWLGALGVFCLVP FSLVGSLN
9069	39437	A	9128	1	702	
9070	39438	A	9129	1	1317	
9071	39439	A	9130	1	2641	MGLKARRAAGAAGGGGDDGGG GGGGAANPAGGDAAGDEE RKVGLAPGDVEQVTLALGAGA DKDGTLLLEGGGRDEGQRRT QGIGLLAKTPLSRPVKRNNAKY RRIQTLIYDALERPRGWALLYH ALVFLIVLGLILAVLTTFKEY ETVSGDWLLETFIIFGAEF ALRIWAAGCCCRKYGWRGRLLK FARKPLCMLDIFVLASVPVVA VGNQGNVLATSLRSLRFLQILR MLRDGPGEGGTWKLGLSAICA HSKELITAWYIGFLTILSSFLV YLVEKDVPEVDAQGEEMKEEF ETYADALWWGLITLATIGYGD KTPKTWEGRLAATFSLIGVSFF ALPAGILGSLALKVQEQHRQK HFEKRRKPAELIQAAWRYYA TNPNRIDLAVTWRFYESVVSFP FFRKEQLEAASSQKLGLLDRVR LSNPRGSNTKGKLFPLNVDAI EESPSKEPKPVGLNNKERFRTA FRMKAYAFWQSSSEDAGTGD MAEDRGYGNDFPIEDMIPTLKA AIRAVRILQFRLYKKKFETLRP YDVKDVEIQSAGHLDMLSRK YLQTRIDMIFTPGPPSTPKHKE VFRKGQHFTFPSQSSRGLNHH *ARPS\TSEI\EDQRH*WGKFVKS LKGVVQGLGRKLDLVDMMH QHMERLQVQVTEYYPTKGTSS PAEAEKKEDNRYSDLKTIICNY
9072	39440	A	9131	353	477	QNEILPQISKSNNI*SRSPH*ITR NLNNSNMAHKMKFAN
9073	39441	C	9132	170	310	

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9074	39442	A	9133	1	859	MSCGRPPDPVDMITLKVDNL TYRTSPDSLRVFEKYGRVGDV YIPREPHTKAPRGFAFVRFHDR RDAQDAEAVMDGAE*EGRAL RIQVARYGRRDLPRSRQG/PTP RGRSRGGGYGRRSRSYGRRSRS PRRR/HRRNRFPCSCSRRRGR YRGSRYSRSPYSRSPYSRYSR SPYSRYSRYSRSGSHYSSSG YNSRYSRYHSSRSHKPGSSTS SRASSTSKSSARRSKSFSVRS RSR/SRSSMTSRPPGVSKRKSK SR/SRSKRPPKSPEEQQMSS
9075	39443	A	9134	161	332	SCLNQLN/YLEMWKLFRKAQE DHTLGRDISYVAEVRPGEAGGR AHTGDSLLTMNPSFL
9076	39444	A	9135	1123	1489	LQTLQGHNSQNSMVLVPPKQR YRSMEQNRLRNNVTYLQLSD L*QA*EKQAMGKGFPI*MLVG KLASHM*KAESGLPYTLYKN* FKMD*RLKH*T*NHKNPRRKPR HYHSGHRHGQGLHV
9077	39445	A	9136	277	367	
9078	39446	B	9137	1	1136	
9079	39447	A	9138	3	1168	
9080	39448	A	9139	1	1460	ERGLETNCSSEELSSPRGGG GGGRLLLPPELPPVPFPLQD LVPLGRLSRGEQQQQQQQPPP PPPPGPLRPLAGPSRKGSKIRL SRLFRTKSCNGSGGGDGTGK RPSGELAASAASLDMGGSAG RELDAGRKPKLRTQSAFSPVS FSPLFTGETVSLVDVDSIRGLI SPHPPTPPPPRRSLSLDDISGT LPTSVLVAPMGSSLSQSFPLPPP PPHAPDAFPRIAPIRAAESLHSQ PPQHLQCPLYRPDSSSFAASLRE LEKCGWYWGPMNWEDAEMK LKKGKPDGSLVRDSSDPYILSL SFRSQGITHHTRMEHYRGTFSL WCHPKFEDRCQSVVEFIKRAIM HSKNGKFLYFLRSRVPPELPPNS CQ/LIYPMRSFSIYESFQHLAKF RIRQLVRIDHIPDLPLPKPLISYI RKFYYYDPQEEVYLSLKEA/QS VSKQKQEVPEPST*RGAPCWSPP RAFGCAAPALKNQIKLP

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9081	39449	A	9140	2	418	KSPSKYLCYTFIISTAALVLLIM LPHESMPVYLGMACTLGFGAIV FTQRAVFFFAPIGEAKIAENKTG AAMALGSFIGYAPAMFCFSLYG YILDNLNPGIIGYKIVFGIMACFA FSGAVVSVMLVKRISQRKKEM LAAEA
9082	39450	A	9141	26	180	KPAHQCVFFCPVVSAAHQGEV LPYKSGVTSIESFVTHICKVIRR* LLSFLA
9083	39451	A	9142	299	921	FGTAALVL*IVLPPEISPSH*GM ACTLGLGAI/VLTQRAV/FFAPIG EAKIAENKTGAAMALGSFIGYA PAMFCFSLYG YILDNLNPGIIGYK IVFGIMACFAFSGAVVSVMLVK RISQRRIRRLRRIRQFHRRNTSS RYGSGFARGGRKATRGISSQEL GQGLSGEEQDGASGGVTAGDI ATGDYFLLTPHLQICTGAKGGL GCVVEGR
9084	39452	A	9143	1	752	MSELPFAIASKRKEYVGIQLPR YTIQKLEENLVFLDRSGHRT KFTNVGRMILLERGRVLLQAAD KLTTDAEALARGWETHLTIVTE ALVPTPAFFPLIDKLAANKANTQ LAIIT*VLAGA WERLEQGRADI VIAPDMHFRSSSEINSRKYLT MNVVYAAPDHPHQEPEPLSEV TRVKYRGIAVADTARERPVLTV QLLDKQPRLT VSTIEDKQALL AGLGVATMPYPMVEKDIAEGR LRVVSPESTS
9085	39453	A	9144	389	760	SWRIDVHPV*YTRLFPFVLVY MQKGT SIRTSSRQLLDKQPRLT V/STIEDKQALLAGLGVA/TMP YPMVEKDIAEGR/LRVVSPESTS EIDHMAWRVTKRTPKN*WTM MPENIGEYTKTHILG

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9086	39454	A	9145	1	941	MTAMERSRILRRVVDILRRND ELAKLETLDTGKAYSETSTVDI VTGADVLEYVYAGLIPALEGSQI PLRETSFVYTRREPLGVVAGIG AWNYPQIALWKSAPALAAAGN AMIFKPSEVITPLTALKLAEIYSE AGLPDGVFNVLPGVGAETGQY LITEHPGIKVSFTGGVAGSKKV MANSAASSLKEVTMELGGKSP LIVFDDADLDAADIAMMANF FSSGQAKR/NGARVLCGGDGVR ARDRPNLRRNLRGKYHS*QR HRRPDAC*YRPL*RCGGRYAD D*VQAGAGSDGL*ATGHGRR EC*PYVTGEAG
9087	39455	A	9146	3	504	DQQQNRQR/LIDCFHPAQWAKE VDVSDKEARCGVRCATRDHLP MVCNVPDYEATLVEYASSAEH KDDAVSAPVFDLFL/GSRGLC SGPLCAEILAT*IS/DEPMPMDA SMLAALIPNRLVWRKLLKGKA VKAGAVHFRRSIYFHPQQANA LDFPSTHIKYCTMLL
9088	39456	A	9147	197	353	YGFRWPD*AHPAIN*ASAAISIF LRWLRLTSITETAPLNAKQAI MPNTIL
9089	39457	C	9148	1	1263	
9090	39458	A	9149	3	726	GAKNAREAIYHIEGDPDHP/EN RLRYPEYRAPGSDKWQRISWEE AFSRIAKLMKADRANFIEKNE QGVTVNRWLSTVNKKKISLRT VGAALVLQVVIGGIMLWLPPG RWVAEKVAFGVHKVMAYSDA GSAFIFGSLVGPKMDTLFDGAG FIFGFRVLPALIFVTALVSILYYI GVMGILIRLGGIFQKALNISKIE SFVAVTTIFLGQNEIPAIVKPFID RLNRNELFTAICSGMASIDG
9091	39459	B	9150	1	1662	
9092	39460	B	9151	1	2658	
9093	39461	C	9152	1	2526	
9094	39462	A	9153	422	585	PYRLKQNIAGA*PIKLNPAAAP VLFSIAFASTIGAKIL/LAVLRSLR PHPSVHA
9095	39463	A	9154	1275	1485	
9096	39464	A	9155	1	439	

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9097	39465	A	9156	1049	2195	NMPKASSCRFSTATTYLRDRSC K*PWAGS*KKNSWR*CRRTTS SHRTRLNATWGSVVKRRTKAR CSMVCSARGSSNARGLELVKE GRAQACVSAGNTGALMGLAK LLLKPLEGQNHMRLLRWEAKL AALVRLQENTAQPVFPAPNNA RPLTLEDDRLSCTVRGYNFAITF SKMSGKPTSWQLVASALATKI AHEVNPQNQVGCMLAGGNFYF YSCKPEDVWAALEKDRENLFIF DVQARGTYPAY SARVFREKGV TINKAPGDDEILKNTVDFVSFSY YASRCASAE MNANSSAANVV KSLRNPLYQVSDWGWGIDPLG LRITMNM MYDRYQKPLFLVEN GLGAKDEFAANGEINDYRISY LREHRCNGRSDCRQAFR
9098	39466	B	9157	482	542	
9099	39467	A	9158	115	1662	TPYPDAITTHDIVDTPYVQGGG VRVLVFSASLVRVSSVLFSLV WGFVSFCRRFVPCRVCVLLCCL FWCFVFGVWLPRRHMSNHAAL GVGEQQCQRGNINGAPETFAS MANTGT*QW/QRISWEEAFSRI AKLMKADRDANFIEKNEQGV VNRWLSTASLAPTEFRGAMTN HWVDIKNANVVMVMGGNAAE AHPVGRWAMEAKNNNDATLI VVDPRFTRTASVADIYAPISGT DITFLSGVLRyliENNKINAEYV KHYTNASLLVRDDFAFEDGLFS GYDAEKRYDKSSWNYQLDE NGYAKRDETLTHPRCVNLLK EHVSRYTPDVVENICGTPKADF LKVAPDRNTTFLYALGWTQHT VGAQNIRTMAMIQLLLGNMGM AGGGVNALRGHSNIQGLTDLG LLSTSLPGYLTLPSEKQVDLQS YLEANTPKATLADQVNYWSNY PKFFVSLMKSFGDAAQKNN WGYDWLPKWDQTYDVIKYFN MMDEGKVTGYFCQGFNPVASF PDKNKVVSLSKLKYMVVIDP LVTETSTFWQNHAAVSGGKR PGRKRLNLLPMARLTTTIASAT YANISAQWAKRLQTAFR
9100	39468	A	9159	1	2235	
9101	39469	A	9160	1	1821	

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9102	39470	A	9161	14	1785	FDQVEERVSVIEDQMNMKRE EKFREKRVIRNEQSLQEIWDYV KRLNLHLIGVPESDWENGTKLE NTLQDIIQENFPNLARQANIQQ EIQRMPQRYSSRRITPRHILNA HKRK*ERYKIDTLTSQKLELEK QEQTYSKASRRREITKIRAEI.KE IETQKTLQKINESRSCFEKINKID RLLARLIKKKREKNQTDVIKND KGDITDPTETIQTIREYYKHLY TNKLENLEEMDKFLDTYTLPLRL NQEEVESLNRPTGSEIEAHNSL PTKKSTGPDRTAEFYQRYKEE LVPFLLLKFQIEKEGILLNSFYE ASTILJPKAGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHYNQVSFIPGIQGFENICKSIN VIQHINRTKDNHTIISDAEKA FDKIQQPFMLKTLNKLGDGTY LKIMTAIYDKPTASTILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMMIVYLENPVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRKIVVGQLTRDVKDLFKEN
9103	39471	B	9162	1	2025	
9104	39472	B	9163	67	3156	

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9105	39473	A	9164	1	2019	MDTIKNDKGDTTDPTEIQTTIR EYYKHL YANKLENLEEMDKFL DTYTL PRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRK\AFDKIQAFTLKTLNK LVIDGTYRKIIRAICDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVL DRAIRQEKEITCIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLGQLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGRINIMKMAILPKVIYR FNAIPIKLPVAFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSL FN KWCWENWLDIWRKCLKDPFLT PYTKINSRWIKDLNVRPKTIKTL EENLGNLIDIGMGKDFMSKTP KAMATKAKIDNWDLIKLSFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELKQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSLAIREMQIK TTMRVHLTPVRMVIKKSGNNR PPLSKEQPIFRLSILATTRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
9106	39474	A	9165	1	3477	

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9107	39475	A	9166	1	2460	MGDFNIPLSTSDRSTRQKVNDK TQELNSALHQADLIDYRTLHP KSTEYTFPSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNNL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRQKERSKIDTLT SQLKELEKQEQTHSKASRRQEI TEIRAELEKETQKTLQKMNES RSWFFKEINNIDRLRLARLIKRR EKNQIDAIAKHNHKGDTTNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEQUESLNRPI TGAIEIAIINSLRTKKSPGPGGF TAEFYQRYKEE/HVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMTVYLENPTVSAQNLLKLIIS NFSKVSGYKINVQNPQAFLYTN NRQTESQIMSELPFTIASRKIKY LGIQLTRDMKELFKENYKPLLS EIKEDINKWKNIPCSWVGRINVR KMAILPKVIYRFNAIPKLPMTF FTELEKTTFKFIWNQKRARIAK SILSQKNKAGGITLADFKLYYK ATVTKTAWYWYQDRHIDQWN RTESSEIMPHIYNLIFDKPDKN KKWGKDSL FNKWCWENWLAI CRKLKLDPLTPYTKINSRWIK DLNVRPKTIKLEENLGITIQDT GMGKDFMSETPKAMATKDKID KWDLIKLSFCTAKETTIRVNR
9108	39476	A	9167	1	1389	

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9109	39477	A	9168	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIRSLH AKSTEYTFSSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKIKNLTQNRSTTWKLN NLLNDYWIHDEMKAIEIKMFF ETNENKDDTTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGDI TTDPTEIQTTIREYYKHLIYANK LENLEEMDKFLDTYTLPRLNQE EVESLNRPIITGAEIVAIINSLPTK KSPGPDGFTAIFYQRYKEELHI NRAKDKNHMIIISIDA EKAFDKI QQPFMLKTLNKLIGDGYFKIIR AIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMTVYLENPIVSAQNLLKLI SNFSKVSQYKINVKQSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKINPCSWVGRIN IMKMAILPKVIYRFNAIPKLP TFFTELEKTTLKFIWNQKIRARI AKAILSQKNEAGGITLP
9110	39478	B	9169	1	1716	
9111	39479	B	9170	1	3171	
9112	39480	A	9171	1	2952	MLLNQGRKLPVFAEETLKFK GTSNKPQTLEQISTSHAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLFEQTLNVLQEFLLTP QWHLECCQERTVHSPGKAAEA REPSVIDRHLIQESSNWHLVGA ALGQSQRKEQAAIFAVLQPLL VIPRQTGSGVDLQKTPDLOQR GLIVRRKTNKQKGIHVHNSTRE QNWTENEFDKLEGGFKRWVI TNSSELKEHVLQTCKEDKNLEK SAIKLELRKLNLIQN
9113	39481	B	9172	1	2406	
9114	39482	A	9173	1	2307	

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9115	39483	A	9174	3	2776	QRDLDSHTLMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDYRTLHPKSTETFFSAPHH TYSKIDHILGSKALLSKCKRTEII TNCLSDHSAIKLELRITLTQSH STTWKLNNLLNDYVWHNEM KAEIKMFFETNENKDDTTYQNL WDAFAKAVCRGKFIALNAHKRK QERSKIDTLTSQLELEKQEQT HSKASRRQEITKIRAELEKIEITQ KTLQKINESRSWFFERINKIDRP LARLIKKKREK
9116	39484	B	9175	133	3213	
9117	39485	A	9176	284	1689	QNFNGFKDLL*RSW*REKSWI CML*ARNTASRQQRNKAGQR MTLMS*EKKASDDQTSPS*R/Q EVRTHRKEAKNLVKRLDKWLN RITSVEKSLNDLMELKTM/RTR TTT*MHKLQ*PI*SFGKKEIQT IREKHLIYANKLENLEEMDKFL ETYTLPRLNQEEVESLNRPITGS EIEAIINSLPTKNSPGPDRFTAKF YQMYKEELVPFFLKLQFSIEQE GILPNSFYEASIIIPKGRDPTK KENFRPISLMNIDAKIFNKILAN QIQQHKKLIHHDQMGFIPGMQ DWFNIRKSINVIQHINRTKDKN HTIISIDAFAFDKIQCFMLKT LNKLGIDGTYYKIIIRAIYDKPTA NIILDGQKLEAFPLKTSTIQGCP LSPLLFNIVLEVLARAVRQEKEI KGIQSGKEEVKLSLFADDMTV YLENPIISAQNLKLSNFSKVS GYKINVQKSQAFLYTNNREPN
9118	39486	A	9177	1	1515	

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9119	39487	A	9178	3	1601	ESRS*FFEKINKI/D/RLARLIKK KREKNQIDAINKDGDITDPT EIQTITREYYKHLTYNKNLENLEE MDKFLNTYTLPRLNQEEVESLN RLITGSEIAIINSLPTKKSPGLD TFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEAIIILIQKPG RDTTKKENFRPISLMSINAKILN KILANRIQQHIKKLIHHDQVGS PGMKGWFNICKSINVQMGINRT KYKNHMIISIDEKAFQKIQKRF MLKTLNKLSDGTLYLKIRAIYD KPTANIILNGQKLEAFPLKNGT RQGCPLSPVLFNIVLEVLARAI/ RLISCFKSVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLGQLTRDVKDLFKENYKP LFNEIKEDTNKWSIPCSRVGRI NIVKTAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRACIV KTILSKKNKAGGITLPDFKRY KATVTKTA/WSFHELKGTQLAT RTTVSTFQQIPGI*VQLRFDFSR DITLLSLLCR
9120	39488	B	9179	1	2034	
9121	39489	B	9180	1	2088	
9122	39490	A	9181	1	1870	MKAIEKMFETNENKDDTTYQN LWDTFKAVCRGKFIALNAHR KQERSKIDTLTSPKLEKQEQT HSKASRRQEITKIRAEKKEIETQ KTLQKINESRSWIFESINKIDRPL ARLIKKKREKNQIDAINKDGD IITDPTIEQTITREYYKHLTYNKN LENLEEMDKFLDYTLPRLNKE EVESLNRNPTGAIEIVAIINSLPTK KSPGPDGFTAIFYQRYKEELVP FLIKLFQSIEKDGLPNSFYEASI ILIPKP
9123	39491	A	9182	1	1410	
9124	39492	A	9183	1	3996	

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9125	39493	A	9184	281	3030	KPRL ENYMKNAEASRADAINW KKGY/LVMEDKMNMKREGKF REKRIKRNKQSLQEIW DYVKRP NLRLISVPESDRENGTKLENTL QDIHQENFPNLA RQANIQIQEIQ RTPQRYSSRRATPRHIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTA EYY QRYKEELVFP LLKLFQSIEKEGI LPNSFYEASII
9126	39494	A	9185	1	2250	
9127	39495	A	9186	248	2385	RQWAGVVGRC SHLASVWSST SETGAIRSSTEVDAPDDSM LLST CDIDLTAARRAWLGCLPTKKSP GPDGFTA E FYQRCKEELVPFLL KLFQSI/EKEGILPNLFD EASII PKRGRD TT KKENFRPISLMNID AKILNKILANRNQQHIKLIHH DQVGFI PMGMQGWFNICKSINVI QHINRTKDKNHNMIISIDAEKAF DKIQQPFMLKTLNKL GIDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTGRGCLP L LFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKIN VQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKK WKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWY WYQNRDIDQ WNRTEPSEITPHIYNILFDKPE KNKQWKGKDSL FNKWCWENWL AICRKLKLDPLTPYTKIHPRWI KDLNVRPKTIKLEENLGNTIQ DIGMGKDFMSKTPKAMA AKA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKKTNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPSLAIREMQIKT TMRHYL

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9128	39496	A	9187	1	2229	MGKKQNRKTGNSKTQSA SPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKGE VQNFKEKNLEECITRITNTEKCLK ELMELKTKARELREECRLSR CDQLEERVSADEMNEMKRE GKFRERIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLVANKLENLEEMD TFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AEFYQRYKEELVPFLKLFQSI KEGILPNSFYEAIIIPKGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVQHINRAKD KNHMIISIDA EAKFDKIQPFML KTLNKLIGIDGTGYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTTRQ GCPLSPLL FNI VLEVLAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLSNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRIKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AIIPLKVIKGTTLKFIWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWWYQNRDIDQWNR
9129	39497	A	9188	1	2667	
9130	39498	A	9189	1	3033	MADMLTWESCLEESLQESPL VTHCGPSCCISGQSPSSARPSS VSSAISVLMPLPQNRKLPPAWTS PGIFPTDLVVYSMSLPHALARY NCDVCKSMLPPRLYAPEEKAR TSPLCGTWYPSLPLCGAWCKK NEKKRERERERKRQREDILSGA SSYKDTIHQIRPPPYDVLQIQ TTIREYFKHLVANKLENLEEMD KLLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPRPGFT AEFYQRYKEE

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9131	39499	A	9190	1	950	MQAICTGQARALICMGGNFAL AMPDREASAVPLTQLDLAVHV ATKLNRSLLTARHSYILPVLG RSEIDMQKNGAQAATVEDSMS MIHASRGVLKPAGVMLKSECA VVAGIAQAALPQSVVAWEYLV EDYDRIRNDIEAVLPEFADYNQ RIRHPGGFHLINAAAERRWMT SEIQTITREYVKHLYTNKLAENL EEMDKFLDTYSLPRLNQEVEES LIRPITGSEIEAVVNSPPTKNSPG PDRFTAKFYQRY/K/EELVPFFL KLFLAAVPAPSSHGPFCCSRKA LRGSKTGSAYPSSSALRRVTVS EVVCLFAEAQLF
9132	39500	A	9191	1	3470	MASVSSATFSGHGARSLLQFLR LVGQLKRVPRTGWVYRNVQRP ESVSDHMYRMAVMAMVIKDD RLNKRDCVRLALVHDMACEIV GDIAPADNIPKEEKHREEGNK CHKQKAMGKHLKEPHVLGGQET KGLESTDVLLPLAAGQDLGRE KKIREEAMKQITQLLPEDLRKE LYELWEDLEFESPCLDSLCLCC SLKPQSESSPVLPEGCETLIQRL CAVGTGVTAAALATRLCRASGL PAPHQWASELQRSRKKE
9133	39501	A	9192	1	3907	MAAWNLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKLTTRKDIYTENPSV HHHHQRPKVDTTKMGKKQN RKTGNSKMQSAPPPKERSSSP ATEQSWMENDFEELREEGFRRS NYSELRREDIQTKGEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRLSRCDQLEER VSAMEDEMNMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
9134	39502	A	9193	3	3197	

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9135	39503	A	9194	I	3158	MVKGSIQQEELTILNIYAPNTG APRFIKQLLSDLRDLDSHTLM GDFNTPLSTLDRSTRQKVNKD QELNSALHQADLIDYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNYLSDHSAI KLELRKNTQSRSTTWKLNLL LLNDYWRKQERSKTDLTLSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKEKNQID TIKNDKGD
9136	39504	A	9195	I	3285	
9137	39505	B	9196	I	1366	
9138	39506	A	9197	735	3541	RSFPRSRSPPFLLLSRYLRIHMV FSVLPFGLQNP KYLLSGSLQEK FRTPGINSHKTLDPNRVIVKVR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITDATEIQTITREYVKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPTGSEIAIINSL PTKRSPGPDGFTAIFYQTYKEE LVFPFLKLFQSTEKEGILPNSFY EASILIPKGRDITTKENFRPIS
9139	39507	A	9198	I	5356	MGKKQNRKTGNSKMQSASPPP KERSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNEKCL KELMELKTKARELREECRSLRS RCDQLEERVSA MEDEMNMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDYRTLHPKSIEYTFFS APHHTYSKIDHIVGS

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9140	39508	A	9199	I	2491	MGDFNTPLSTLDRSTRQEVNK DTQELNSALHQVDLIDIRTLH PKSTEYTFSSAPHYTYSKIDHIV GSKALLSKCKRTEITNCLSDHS AIKLELRICKLTQNHSTTWKLN NLLNDYWVNNEVKAIEIKMFF ETNENKDTTYQNLWDTFKAIN KIDRPLARLIKKKREKNQIDA NDKWDITTDPEIQTITIREYYK HLYANKLENLEEMDKFLDITYT LPRLNQEEVESLNRPIGTSEIEAI TNSLTITKKSPPGPDGFTAKFYQR YKEELVPFLKLFLQIEKEGILP NSFYEASIIIPKPGRDITTKQKK NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPVQMG LFNICKSINVIHHINRTKDKNYM IIS/I*DAEKAFDKIQPFMLKTL NKLIGDGYTLKIIAIYDKPTAD IILNGQKLEAFSLKTGTROGCPL SPLLFNIVLEVLARAVRQEKEIK GIRLGKEEVKLSLADDMIVYL ENPIVSAPNLLKLSNFSKVS KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD MKDLFKENYKPLLNEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIASLSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIINYLIIDKPEKMSIIDTGGW
9141	39509	A	9200	I	3083	MGKKQNRKTGNSKTQSASPPP KERSSPATEQSWMENDFDEL EEGFRRSNYSSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRLRSR CDQLEERVSAEMEDEMNMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGKLE NTLQDIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQ TIREYYKHLYANKL

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9142	39510	A	9201	1	4201	MRKKQSRKTGNSKKQSTSPPPK ERSSPAMEQSWTENDFDELRE EGFRSNYSKLEIEITKGQEV ENLEKNLKDCKITRITNIEKCLKE LMELKAKARELHEECRSLRSRC DQLEERVSVMEDEMNMEMKQE GKFREKRIRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLRQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
9143	39511	A	9202	715	6193	GQHHIPDTKAWQRJHKKKENF RPISLMNIDAKILNKMLANQIQ QHKKLIYHDQVGFIPGMQGW NICKSINVIIHINRTKDKNHMII SIDAAKAFDKIQPFMLKTLNK LGIDGTYLKIRAIYDKPTASIL NGQKLEAFTLKTGTGQCPLSP LLFNIVLEVLARAIQKEIKGI QLGKEEVKLSLFADDMIVYLEN PIISAQNLKLGINFSKVSGYTIN VQKSQAFLYTNNRQTSEQIMSE LPFTIASKR
9144	39512	A	9203	1	3682	KEGHYIMVKGSIQEEILTILNIY APNTGAPRFKQVLSDLQRDL SHTLIMGDFNTPLSTLDRSTRQ KVNKDTQELNSALHQADLIDIY RTLHPKSTEYTFPSAPHTYSK IDHILGSKALLSKCKRTEITNCL SDHSAIKLELRIRKLTQNRSAT WKVNNLPPGMTYVWVHNGNE GQKLKMFETQWE/HKDTAYQ NLWDTFKAGCRGKFIALNAHK RKAGDKPKLTPLTSQKK/LEK QEQTNSKAS
9145	39513	A	9204	1187	1680	DSPCTIASTRSYFCINRPLSVDI QLRCSCRNVRLSTYC/LYLRLQ LRIEGGNFVFTTKADNGPQQIIT *TNSFPVGNNATVKVRHHILT FFINLFGEIGGPDHFNNGFTQP LPSSGTQPQHILSCVTIDGGNVT MRIHRNQPFINRTKQRLLLT ACDLLWLH
9146	39514	A	9205	3	293	ERSWSQLLFSTEQFWQQLPGTG SGRARQNISRKTPREHAGGYRR DNGNNWAVPHIQCNLVPR**K RPPVRAHRAPETLCASKALQE RYWVFELLR
9147	39515	A	9206	1	4509	
9148	39516	A	9207	1	507	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9149	39517	B	9208	1	3448	
9150	39518	A	9209	1	2652	
9151	39519	A	9210	75	784	
9152	39520	B	9211	1	1968	
9153	39521	A	9212	1	298	LQGHVLVDYVLSCLPFGIMGH GNWPLVWLTAACLVLLC*/WSL RRQ*IQQ*APSDQKRDFLVPHG A/VFDR*ISATCWSSINWPANCS RPSIAGWPKQAS
9154	39522	B	9213	167	362	
9155	39523	A	9214	959	1267	YHWHQLLSMVRQLMVLSSWKK ISSWFMGPPIIRKSILAENSI*KN LV*VILKLTGISTLK*MAPQN TQY*MTVIKLFKWWARQTRLR SIMVCYSSTTTLLT
9156	39524	A	9215	370	555	
9157	39525	A	9216	1	1016	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEFPY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RIFARLSLDSALPDRTTIMNFR HLLEQHQALARQLFKTINRWLA AGVMMTQGLVDAITIEAPST KNKEQQORDPEMHQTKKGNQW HFGMKAHIGVDAKSLTHSLV TTAANEHDLNQLVQNELETAE RFRRQEDTQSKCLLSSIMLYIKN LSGPDVSELISPLSEGNLCSV VVAVIAA VLRRAPIHMPSGWW RSWNAESGAYNVTRSGDSYI/H G*LLYRSRKLDPDADEGALQK WWSVLPPFKRRLWF
9158	39526	A	9217	408	643	PGCGSGHSWHRHQCGPSCQSA TDCLSWSDASPDRAALCSWS SWVPQ*WHR/HKVP*VIMTP ASASQRLMVLNNWRAS
9159	39527	A	9218	626	760	
9160	39528	A	9219	1	2469	
9161	39529	A	9220	1	756	
9162	39530	A	9221	1738	1913	PTAWSPPRPTSMTSISWVICFME RSNLSPMPATKERHSARSWPR WMWTG*SPSVPAR
9163	39531	A	9222	2403	2760	FRGDGILVSCPLVFSSAFSWRA ADGGKNRNVHPSV/VR*AGAL RPRTQSRQ/SQRLNKVEKGGV KQFEHNQSCRQQVGVITIKVVK QLADILPHGHFQFYAEVIGKLF RQRSARDAIRGSS
9164	39532	B	9223	1	3663	

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9165	39533	A	9224	1	1584	MELIEKHVSFGGWQNMRYRHS QSLKCEMNVGVYLPKAAANEK LPVLYWLSGLTCNEQNFITKSG MQRYAAEHNHIVVAPDTSRGS HVADADRYDLGGQAGFYLNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMSG LGALVLA LRNPDEYVSVSAFSP IVSPSQVPWGGQAFAYLAEN KDAWLDYDPVSLISGQQRVAEI MVDQGLSDDFYAEQLRTPNLE KICQEMNIKTIRYQRGAI CSAD AATRGAKRESCRSGCGLLIAER PAKVEPGTASRQDNATINIEYM KASIRARVEHPFRIJKRQGFVK ARYKGLLKN/ETNWRCSRW/P/ HLFRADQMIRNPHDLYAPEVV HQA KAVTTSGYRFLPCCGFAN TFWGKTTADGTLIEHFGRRCCQ WFEDDDGHREQCDFRFRKNC PQCN AENDIAARRCRECDTVLV DPDMDLKAALRLKDALVLRCS GMSLQHGHEKGEWLKITYYD EDGADVSEFRQLTPAQRATAFE QLFIRPHTRTPGI
9166	39534	C	9225	1	2127	
9167	39535	B	9226	1	1917	
9168	39536	A	9227	1671	2198	RAGAWASDPQRGVVRNAALL PPDDRS DGRDAKTQSHRDG/VI SY/RAFDETILASGIVPRTPIDGI DHPKNEADDMLRMGFIEDVETI /IGADPGRSSDRSVLCNHAGSDS SHYPPL YERAAGSAHSVQRDYP SGHQPELLDCLGYARTRSTDTG TPERWSSGHPDCDRRCSPWPGR
9169	39537	A	9228	642	746	
9170	39538	A	9229	1	2031	
9171	39539	A	9230	909	1058	
9172	39540	A	9231	2	268	WRCLLRQLKFIKTVTSWICTG KLMLSTTSP LMMQMMVILLMP VLASKVKPKSTIN*LVSVSGNM NSKATALNLKVPKIKPVLPSL
9173	39541	A	9232	63	463	FPA TCWSSINWPANC SRPSIAG WPK/PGVMMTQGT/LVDAITIEA PSSTKNKEQQRDP EMHQTKKG NQWHFGMAHIGVDAKS/A*P TAWSPRPRTSMTSISWVICCME RSNLSQMPMPATKGRHSARSWP RWMWTG

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9174	39542	A	9233	74	247	RNVMIKRRVLSSTSAS*LPPASA FCRLFTSPARWRSTACFTSGNR YRFLTVRLSGYW
9175	39543	A	9234	3	271	ASYWNRSFSPWGTYNRHPR*N RQCASRHCRGLHKQYQWPRJR S/WLNCTPAPHARDVLLWRPSS LPAGNADGPIRWRPCCVFTACS IGTT
9176	39544	A	9235	1	1048	MCSFRSQTCSSSRFTFARVSVI HSANHRVNLNDRSTIMRTRGQD PTLPEMRRVRLLEMADAMDMF CQGLRYGPLPAPVRQQAIIIPC HRVVRGDGTLSGYRWGVSRA QLVREAEENEERPINRGWPKQP SDDPKHFVMPTHIEAPSSTKNKE QQRDPPEMHQTKKGNQWHFGM KAHIGVDAKSLTHSLVTAA NEHDLNQLGNLLHGEKQFVSA DAGYQGAPQREELAEVDVDW LIAERPGKVKTQKQNPKNKTA INIEYMKASIRARVEHPFRIKR QFGFVKARYKGLLKN/ETNWR CYSWPWTCFGWTK*YPSIPTCLL TTRTASLLKPPGVRTSVCWQQL

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9177	39545	A	9236	I	2493	MTQIFTGLVEADPFHAVTLVA NHDQPLQALEAPVEPWFKPL AYALILLRENGVPSVFYPDLYG AHYEDVGGAGQTYPIDMPIEQ LDELILARQRFAGVQTLFFDH PNCIAFSRSGTDEFFPGCVVMS NGDDGEKTIHLGENYGNKTWR DFLGNRQERVVTDENGEATFFC NGGSVSVWVIEAANNRQYDY GAGHKIPVINYTDVHLRIERSCR FRADPRQQHELQLSSKLAVHD VLTNIYNRRYFFNSVESLLSRPV VKDFCVMLVDINQFKRINAQW GHRVGDKVLVSIVDIQQSIRPD DILARLEGEVFGLLFTELNSAQ AKIIAERMKNVELLTGFSNRY DVPEQMTISIGTVFSTGDTNRIS LVMTEADKALREAKSEGKNKH WYNLSDGAMEDALYEIASMRL FARLSLDSALPDRTTIMNFRHL LEQHQLARQLFKTINRWLEA GVMMTQGTLDATIEAPSSTK NKEQQRDPPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNQLGNLLHGEEQF VSADAGYQGAPQREELAEVDV DWLIAERPQKVRTLKQHPKRN KTAINEYMKASIRARVEHPFRII KRQFGFVKARYKGLLKN.ETN WRCYSRWP/HLFRADQMILCPV FVHHIPRFFGTFFGATDQTFTL TESVIHQPLVLTNFIAIDGNDFA
9178	39546	B	9237	I	3148	
9179	39547	B	9238	I	1680	
9180	39548	A	9239	191	470	

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9181	39549	A	9240	1	1675	MFARVSTTPVTRYEMYRKTRS TRLEDNNALSQSKPLPFSEVT GSKGKADKEKVG DY VFCLKAQ GRYNGEPLTGTGKIGGMLALR GEGTPEFPVQADFRSGNTRVAFD GVVNDPMKMGVVDLRLKFSG DSLGDLYELTGVLDPDTPPFET DGRLVAKIDTEKSSVFDYRGFN GRIGDSIHGSLVYTTGKPRPK LEGDVESRQLRLADLGPLIGVD SGKGAEKSKRSEQKKGESVQ PAGKVLPYDRFETDKWDVMD ADVRFKGRRIEHGSSLPISDLST HIILKNADLRLQLKFGMAGGS IAANIHLLEGDKKPMQGRADIQA RRLKLELMPDVELMQKTLGE MNGDAELRSGNSVAALLGNS NGNLKLLMNDGLVSRNLMEIV GLNVGNYIVGAIFGDDEVRYN CAAANLNIANGVARPQIFAFDT ENALINVTGTASFASEQLDLTID PESKGIRIITLRSPLYVRGTFKNP QSG*WS/GTLLSTKAKTIVAI TTLKVTVMASVSLPMNTKDS VSVQLMRNLIVPTLKLMMQGGKF LKYLLPVKMQKFGPQV
9182	39550	A	9241	72	506	GHVAHLQPRAGGRQPAPRLHHP QGTDRVLHGQRGGQPGP/LLPS LSAWRPSTSLKPA SCGLRGPT SKRMSMQDGGPLPHHRAGAQP PVHPGQEA VG*C/EYWSASSRP VTQPGALMWRLWSAGRPRPY LLSHSQHDPHSGQGGGEHP
9183	39551	A	9242	1	447	
9184	39552	A	9243	70	490	CGCDAETIILRINALAFIWKCGT EWICCFCLALRELQQA VHVAG LPQQA KILFDGSGSEIGKIH*LRC AHCPLSSGKPVVPAALMNRPT RGERRFAYWAPGWFFFPVRR ATADCPSPGPERVAASGRPRWF APAGENPV

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9185	39553	A	9244	1097	1841	ANDGDLRSCVTLSCHMASHASE AADPPATTAFTDEHMSVKLRR TVGVACSVCPGWVTSCHPVNP AAS/GAKVLPGDDIALPGPLPF ILSR\QLRDNTLILSDNGG\RLY FELLFPGEDGYRRCESLWLVRG GVAKL DQGHRLAALWQALSEE LRLTPHRYLATNSPQGPWWLL GWCERVPEADEVLPAPLPPYRV LTGLVDRIWRSEDVSAASGLHH DNRNAPSLSDQTRTDPPIRAH SRYQRQKPDG
9186	39554	A	9245	456	928	EAATEPKHLHLQRHAALAQHR QAPRPQGRPLARPHQQDQPD RLHHLRGGGRHGARGHLHQA GAGESAPAPKG/VTCPASPLGD VTGKPTSAWNTEKGRWAQHR GYSPGPAAPLVLRSWPIPLFRP PPLLPLSSPAWILPSPLCHSLKA QSLVQATI
9187	39555	A	9246	1	1572	

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9188	39556	A	9247	1	2505	MAWRNSVNWQCKQEPGLHR RHGRRKLTNGTTRRSQNKKEE DFYTSQPGFPALALGCCLRVNL LLGHRGISAGSSYRPITSTPCHL CKLGQEVFAKPLNLQDQCCQN LVMQVLKLVNCLNDFFIGSSA DESADDLCTVQIPTTWRTMGL VGCDGVCCRTWCQCLATAV VSGVGGGPWLLPACSSGSPMIS KRKKFVHKWAKDLVEPRHGLE NVWDLPRAMAGSYLMYKQQRK WKIMEFGKWALQHKTMTVKDIE RLQLYNKVKEQPVQVEGSGRA STIFVVLKTFKGGKSPCGAPGE CVAWTQCRILGWVQIHFKEHP ADRVVGLIKMPGLDFYFAADV CYAEKVAQEKGLYRLTSRYR HYAAFERATFEQGSTKLMMML TDKQIADFQKHYTEPERFQILP PGIYPDRKYSEQIPNSREIYRQK NGIKEQQNLLQVGSDFGRKG VDRSIEALASLESRLHNTLLFV VGQDKPRKFEALAEKLGSRAS MEFKRYEYNAAGDLTAVITPD GNRSETQYDAWGKAVSTTQG GLTRSMEYDAAGRVISLTNENG SHSVFSYDALDRLEDEGLVIL WYYDESDRITHRTVNGEPAEQ CQYDGHGWLTDSHLSSEHGRV AVHDGYDDKGRLTGECQTVEN PETGELLWQHETKHAYNEQGL ANRVTPDSLPPVEWLTYGSGYL
9189	39557	A	9248	481	857	PLAYLYRDPHVRCVTASGPAP VYGFQPGFSAPTGI/IRKSVHGD HSYCKYAHSCSRQYRAPEPRLS RTSQCLFSHRSARCPDLLMGR RYRRPECLRLSPLLPAAPVPGLP WTIYPRRLYRNSPR
9190	39558	A	9249	777	1229	GAGYSSARCGKHHARTGGAGR NILWRQLRRRGCRSTVDRSHH NQPGTWHRHQPGRGPAKPAR PWRAGTHLPTGTASVRHPCLG QPLRAEPRPAVPDAPRNQNLFP PAPQTDSALPGAVRG*RAR*YH *SRITTPPPDEHDSHWARACSP
9191	39559	B	9250	1	2681	

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9192	39560	A	9251	933	1828	VSRHVLVWQPRMPAPPAVDW LTY/GSGIL/SGNKLVTPLVEY TRDSLH/RETLRSFASMAGSNA AY/*LTSTDTAGQLQSQH/LNS LVYDRDYGWSDNGL/VRISGP RQTREYGYS/TGRLESVRTLA PDLDI/RIPYATDPAGNRLPDPE/ LHPDMRADGGA TGQKVEPEYT PARKAHLYHWTGDCRWRLSA KTAIRVERGI**MGQPAY*GEPH HVYQPR*TWHRWRQKGRKS ASGRRYLRPINPNVNGRENQRP TSPDGTHTMAPISLMAWQPIQLR YRGHVRQRLSAVGERIYRYLPP
9193	39561	A	9252	I	1409	MECDASALLRYDSRQFIPLAID GLAKDVLGRRFALEGHPRLEAI ARAGDVVRFPADSELDPDYDG LIPGQESLKVHACVGLPLFAGQ NLIGALTLDGMQPDQDFVFSDE ELRLIAA/LAAGALSNAIIIEQL ESQNMLPGDATPF EA VKQTQM IGLSFGMTQLKKEIIVAASDLN VLISGETGTGKELVAKAIEHASP RAVNPLVYLNCAALPESVRKSE LFGHVKGAFGAISNRSGKFEM ADNGTLFLDEIGELSLVLQAKL LRVGQYGDQIRVGDDRCLRVD VRVLAATNRDLREEVLAQRFR ADLFHRLSVFPLSVPLRERGD DVILLAGYFCEQCRLRQGLSRV VLSAGARNLLQHYSFPGNVREL EHAIHRAVVLARATRSRGDEVIL EAQHFAFPEVTLPTPEVAAPV VKQSLREAT*AFQRETIRQALA QNRKRWACARMLETSVANV HRLGKRLVLKK
9194	39562	A	9253	389	799	PQFLIPSVTPCMFIHPLDAK/AR DLRRGDKVKVVSRRGEVISIVE TRGRNRPQGLVYMPFFDAAQ LVNKLTLDATDPLSKETDFKKC AVKLEKACPYDTLKLATLASG LSAGTFYFVARDIPCMECDIPC AKVCPS

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9195	39563	A	9254	588	1500	RHPPIPAKIGLHAVAQDRAWNN MQAGPNINEERMPGWRDPRNF IIVSDPYPTVSALAADL/TPEVSK FPGSELAEDQLNDESRELGFYL QKGLFEEYAWFGRGHGHDLP FDDYHKARGLRWPVNVNGKET QWRYSEGNDPYVKAGEGYKF YGKPDGKAVIFALPFEPAAEAP DEEYDLWLSTGRVLEHWHGTGS MTLRVP*LHRAFPDAGLFIYPL DAKARDLRRGDKVVKVVSRRGE VISIVETRGRNRPPQGLVYMPFF DAAQLVNKLTLDATDPLSKET DWPHFSSTYNGPLQGANGLIL VQQH
9196	39564	A	9255	1	1698	MEREQDSIIIMDAATTRNLEITQ NLGGAENTLASVLDCTVTPM GSRMLKRWLHMPVRDTRVLLE RQQTIGALQDFTAGLQPLVRQV GDLERILARLARTRARPDLAR MRHAFQQLPELRAQLETVDSA PVQALREKMGFAELRDLLE AIIDTPPVLWSWMSGARWLTA IICNYEVDRITRHTKMNVGDVQ RLSVAVVVNYKTLDPGKPLPLS NEQMKQIEDLTREAMGFSEKR GDSLNVVNSPFSNDSDESG
9197	39565	A	9256	590	910	SCSIQLSPWILPRTVMCPVGFTC ELLST*WLAKEPKTVSWITIRS FTAETSTFGPTMTASMTFLPTY CSIIASLLSSFKLAAAILNSLPQI GRYITIGSGVRRNA
9198	39566	A	9257	1	854	MANRMLNETAWFGRGAVGA LTDEVKRRGYQKALIVTDKTL VQCGVVAKVTDKMDAAGLAF AIYDGVVANQHLYCRQDSSDEF AEMSLIEGRRGLRRRPLWEFEI DTARQQLNLQFGRDLVGFV ENAPRGLCAAGCLLQYAKDTQ RTTLPHRSITMEREQDSIIIMDA ATTRNLEITQNLGGAENTLAS VLDCTVTPMGSRMLKRWLHM PVRD/DPRVA*APANYWRIAGF HRRATAGTASGRRPGTYSGTSG FTNCSPTRSGPYAPRPATAGA ACAVRNCR
9199	39567	B	9258	122	868	

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9200	39568	A	9259	2610	2897	PNLYLRFFFFFLRQESHVSTQA GVQWCNLSLQPLPPGFKQFSH LTGALPKCWDRSKRPRPANQT SILDVKEDPY*LHWPRSNRDIK LNLVANP
9201	39569	A	9260	2166	2426	VQPGGCGL*RQHGSYRPESRTA GGRHRG*RRLRRAPIDGGANSS GTGICRDAFNRIHWTGRTGRP DVDSGEHRKTAEQRRDGA VR
9202	39570	A	9261	846	1022	
9203	39571	A	9262	1	1339	MNALSKARQYVEEFDGNIASFI FSGKPGTGKNHLLAAICNELL RERNLGESEIHTTSDHMTATL PGETQTWPEDFRDVEQRQVV FQHLVGCVKVDGKYIQVCTFT VGGNYGGTCLRGDES LVIKKES DIEPLIVTVVQQFHIGNGYVVI TITPSEGERYQGVVGLGRIIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTEVSPVLKKQLVLPNPH YPGNKPNFKRVSVKIIGESASRR LQLSRGDDIADALSDRFVSEAI TAKVEAAIKN*LSQYGILPEEW GGESQFVHVSAGKTGIDELLA DAILLQAEVLELKAVRKGMS GAVIEFPSLDKGRGPVVTVLV REGTLHKGDIVLCGFYGRVRA MRNELQGEVLEAGPSIPVEILGL SGVPAAGDEVTVVRDEKKARE VALYRQGGKFREVKLARQQKSK LENMFANMTEGEVHEVNIVLK ADVQGSVEAISDLLKLSTDEV KVKIIGSGVGITETDATALAAS NAILEGLFTLTSQDEFVIAPGFS TDPLEEQHSVVSGLLHKYIHN ALLLVKGGCAVNCRYCFRRHF PYAENQGNKRNVQTAL EYVA AHPELDEMIFSGGDPLMAKDH ELDWLLTQVVHQHDVGRRVQ RLPFIHDALFHQQFFNQHTTF GQVHLARFFVHREVDSILFRRIS VLKMMMSPHRVKDRCYCAQFI

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9204	39572	A	9263	922	2357	GKGNDEKKI.VSDQ*MGTA*RQ RIHPISIIPL.LW/YPEGPSVSRPE AGGYNSLL.MVTHGK.VINGRRG ILIESD.EPGDAR*SSGSCARHGL VFWLCSRRCMPQTIEAIQHNP A/VAVNKIDRPEADPDRVKYVL SQYGIL.PEEWWGESQFVHGS AGTGIDELLDAIL.LQAEVLELK AVRKGMA SGVIESFLDKGRG PVATVLVREGTLHKGDIVLCGF EYGRVRAMRNELQGQEVLEAGP SIPVEILGLSGVPAAGDEVTVVR DEKKAREVALYRQGGKFREVKL ARQKSKLENMFANMTTEGEVH EVNIVLKADVQGSVEAISDSL KLSTDEVKVKIIGSGVGVIEAES LDLRYYSVIYNLIDEVKAAMSG MLSPCLKQIIGLAEVRDVFKSP KFGAIAAGCMVTEGVVKRHNPIR VLRDNVVIYEGELESRRFKDD VNEVRNGMECGIGVKNYNDVR TGDVIEVFEHIEQRTIA
9205	39573	A	9264	1	748	
9206	39574	A	9265	923	1387	PPNLARCSPSAMARQSPIRSPRR PLAPSPALRAPSPAPPHAARLA VPRQA*GLLLLLALIAVSTHIEMI SNTLAMGWNSPLTTVLALLAC GFACFIEMGKIPFDVAASWIIMI WSQSSTCTAPTLKPLRSVTLMR LTPVSARDLVGYFATAVRLP
9207	39575	A	9266	352	478	CDPTQRKPLYWLQALRRGLPI WRNQRFRKAVR*MAMAPMFS
9208	39576	A	9267	54	811	HTTGGNPLYGI/SRQIAR*QSRV/ GPGFCQDYRDIHKLFKRQEVAP TSSGLMFRMLMPWVLISSMLVLA MALPLFITVSPFAGGGDLITLIY LLALFRFFALSGL.DTGSPFAGV GASRELT.LGILVEPMLILSLVL ALIAGSTHIEMISNTLAMGWNS PLTTVLALLACGFACFIEMGKIP FDVAEAEQELQEGPLTEYSGAG LALAKWGLGLKQVVMASLFV DI.FLPFGRAQELSUACLLTSLV VTLLKRLL

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9209	39577	A	9268	2	627	CGSIIALVAIFKSFSGHYLGTLE GLNGLVLKFGYKGDKTQVSLG KLNTISMIFIMGSTWVYAYANP NILDLEAMGAPIASLLCLLPM YAIRKAPSLAKYRGRLDNVPH AITRVDLKEDGKGLKIVRQSLP YGTASGTHGLYFCAYCARLHNI EQQLSMFGDTDAIKAYQSFLA RSAFAVSQCIPVNTVYRAYSVI QNWIATIRHV
9210	39578	A	9269	2648	3072	LSRTGKTTFAT/LEYAASIIAL VAIFKSFSGHYLGTLEGLNGLV LKFGYKGDKTQVSLGKLNTIS MIFIMGSTWVYAYANPNILDLI EAMGAPIASLLCLLPMYAIRK APSLAKYRGRLDNVFTVIGLL TILNIVYKLF
9211	39579	A	9270	467	614	VPLAVPYGRLWRTIFSPSSFR STRE*YESMLGRFFERTACLQQ KQF
9212	39580	A	9271	1	846	MSYLVVWPFIASLVLSLIPYW NSAVIDQVDLGSALATGHDGILI TVWGGIMSTKVFPLNFPNVFSF GIVSKIRKK*KKDFGRDFTERKC SQIISRASMLMVAVVMFFAFSC LFTLSPANMAEAKAQNPVLSH LANHFAASMTGKTTFSITLEYA ASIIALVAIFKSFSGHYLGTLE LNGVLKFGYKGDKTQVSLGK LNTISMIFIMGSTWVYAYANPN ILDLEAMGAPIASLLCLLPMY AIRKAPSLAKYRGRLDNVFTV IGLLTILNIVYQLF
9213	39581	A	9272	95	456	RAISMSFRMERPCCLSLPSSLCIS STRVTASSPLSGCSSCTLLWISW GRMVRNCNT/MQI.QDLLRA HLRPPKPPMAKLLLEPAEGFPGTS CLLEAEPSTIRDVVLIASQPASQ PASQQGSQI
9214	39582	A	9273	1	1241	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
9215	39583	A	9274	3	1608	SRGFPRRREFSGPSIKKKVDAPTQ AQWVPVHAVITNSTYDGLLYNT DWIKQTLDPVSIHLDSAWVPYT HFHPIYQKGSGMSGERGAGKVI FEPQ*AHRLMLAALSQGSLLIKG EYDQEAFFSEAFMRHSPSSPSYPI GGSVETAAAMLRGNPGKRLIN RSVERALHFRKEVQRLREESDG WFFDIWQPPQVDEAECWPVAP GEQWHGFNDADADHMFDPV KVTLTPGMDEQGNMSEEGIPA ALVAKFLDERGIVVEKTGPYNL LFLFSIGIDKTKAMGLRLGLETF KRSYDLNLRKNMPLDLYAEDP DFYRNMRIQDLAQGIHSRRVTA SVSSGSQANQQVNFIGDQSTAA LTLSPVSGDITVTNTAPQYMTA TLQDKNGNPLKDKETFSVPND VASKFSISNGGKGMTDSNGVAI ASLTGTLAGTHMIMARLANSN VSDAQPMTFVADKDRVVVLQ TSKAEIINGVDETTLTATVKD PSNHPVAGITVNTMPQEGVYA MSLEYIILTFIALNGSRMWINS REKRTQRND
9216	39584	A	9275	106	709	LRS AEDNDTREKNKQTNRSDS KLRLVETSGSPPTSSSQTPDPAF RYPKKYCVEDCS\YRPE*PRITP DNRLLYGGGVVYGARDPDVVE RLVVPKLLKTFPQLKGVKIDYR WTGNFLLTLRMPQYGRDNTNI YYMQQYSGHGVTCNHLAAGRLI AELLRGDAERFDFANLPHYFP PGGRTLRLVPFTTKSAAYYSLR DRLGV
9217	39585	A	9276	140	558	RKPIHRQGEKAGRNRSVDGCC EKAMSVIIVGGGMAGATLALAI SRLSHGALPVHLIEATAPESHA HPGFDGRAIALAAGTCQQLARI GVWQSLADCATAITTVHVS DR GHAGFGTLSRKITTWGL*QRSW ARWIWYPFKNYHLGALTTVV ELQMGGKRLF
9218	39586	A	9277	3799	4086	
9219	39587	A	9278	3017	3184	
9220	39588	B	9279	1	1050	
9221	39589	B	9280	1	1455	
9222	39590	A	9281	374	506	RCIALIAWLTLPVLRVTLK*RW RVARR*RAACW*S*WHHSALA P
9223	39591	C	9282	47	406	

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9224	39592	A	9283	1	4749	
9225	39593	B	9284	507	3568	
9226	39594	A	9285	101	638	RQKYSWSSALVPTAGEPTRH TQTRAGIAHA/EADFAADILFL LCGKDISTAGGFSFV*LADNKQ HLMPCVCFANHLTVKM/PHQSPV PDH/QALISHRIRSSRGSCSRYS DNSVSRTPLSPTPGRSTMVICS PICRRKRKGSRVQAATSLTGD SPANRALQRLFPAPVLPMMPI TGS
9227	39595	A	9286	271	532	
9228	39596	A	9287	643	768	
9229	39597	A	9288	1	1948	MCSHAAGCTIPDVEHWTRINR KVPRLVSVLNPGPDYHPTVRAF LAGGVPEVMLHLRDLGLLHLD AMTVTGQTVGENLEWRPEPGA FRQCLREQDGVPPDDVILPPEK AKAKGLTSTVCFTGNIAPEGS VIKATAIDPSVVGEDGVYHHTG RVRVFVSEAQAIIKIRVVIVA CGFSPTRTAHAASDIDITNTVDL RNRRLQLRRGEIVQF/IPANKYR TSA*GS*LAHPTGSLCD*VGRL DIPLAANFVQR*SPPGISPTPV
9230	39598	A	9289	2166	2426	VQPGGCGL*RQHGSYRPERSTA GGRHRG*RLRRAFIDGGANSS GTGICRDAFNRIHWTGRTGRP DVDSGEHRKTAEQRRDGA VR
9231	39599	A	9290	846	1022	

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9232	39600	A	9291	1	1336	MNALSKARQYVEEFDGNIAEFI FSGKPGTGKNHLAAICNELLL RERNLGESEIHSTSDHMTATL PGETQTWPEDFRDVEQRQQVVI FQHLVGCVKVDGKYIQVCTFT VGGNYGGTCLRGDES LVIKES DIEPLIVVTVVQQFHIGNGYVVI TITPSEGERYQGVVGLGRIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTEVSPVLKKQLVLPNPH YPGNKPNFKRVSVKIJESASRR LQLSRGDIADALSDRFVSEAI TAKVEAAIKN*LSQYGILPEEW GGESQFVHVSAGAGTGIDELLA DAILLQAEVLELKAVRKGMA GAVIESFLDKGRGPVATVLRRE GTLHKGDIVLCGFYGRVRAM RNELGQEVLEAGPSIPVEILGLS GVPAAGDEVTVVRDEKKAREV ALYRQKGFREVKLARQOKSKL ENMFANMTEGEVHEVNIVLKA DVQGSVEAISDSLKLSTDEVK VKIIGSGVGGITETDATALAASN AILEGLFTLTSQDEFVIAPGFST DPLEEQHSVVSGLLHKYHNRA LLL VKGGCAVNCRYCFRRHFP YAENQGNKRNVQTALEYVAA HPELDEMIFSGGDPLMAKDHEL DWLLTQVVHQHDVGRRVQRL PFIHDALFHQQFFNQHTTFGQ VHLARFFVHREVDSILFRISVL KKMMSPHRVKDRCYCAQFICP
9233	39601	B	9292	1	2890	
9234	39602	A	9293	1	822	ITQYCDSTFICLSKGLGTPVGS LVGNRDYIKRAIRWRKMTGGG MRQSGILAAAGIYALKNNVAR LQEDHDNAAWMAEQILRETG A\DVMRQDTNML\FVRVGEEN AAALGEIT*KPRNVLI\NASPIV RLERDVPQRILVLGASGYIGQH LVRTLSSQGHQILAAARHVDR LAKLQLANVSCHKVDLSWPDN LPALLQDIDTVYFLVHSMGEAA IYRSAGVASVSSVERYCLRPSY DPRVFPCLCCRALVLPCLLIY SPLSFALVLSLAPIK
9235	39603	A	9294	1565	1825	SRMCVAIRSNRQSRCEITIAQPG NSSRAFSSARRVSISSLVGSSSS SMLPPTCSSFARCRPRSPPESS PTRLP*STPLKLRPT

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9236	39604	A	9295	236	742	VATRCRSRSPSLSPSLSLRVMIPTTSAYSFMITAKSSPAVLKLSNASERVNVSGTISVLRICPTLFSA RLWLASTFRSRLST*PMMWS ISSLQTRNLECGCSATLFFRLCSSWRSN/TNDVFTAVTLITERDGI PAQRRFQSARVPVYTRPPAH RLPLPRRCHQK
9237	39605	B	9296	1	951	
9238	39606	B	9297	1	666	
9239	39607	A	9298	761	1162	IILGSMIAITILILPIHEQGMFFHL FVTSFILSSGL*FSLKRSFTSLV SCIPRYFILFVAIVNGSSSLVWLVS FLLFVYRNACDFCTLILYPETL LKLLISLRRFWAETLGFSKYTIM SSANRDNLTSFFPN
9240	39608	A	9299	82	160	
9241	39609	B	9300	64	477	
9242	39610	A	9301	408	507	LLPLFQNL LLYVYSGI*LLPGLVW KGCMMHPGIYP
9243	39611	A	9302	1	3141	MILLGLHSLAAFLQRESFSQKQS WGCQLAALLQRRITKMTTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQA VDLIS NVAGDRVITYRITKGEDLREQG YMGLHTVGRGERSPVLLALD YNPTGDKEAPVYACLLGDIITY RNGKKVEVMNTDAEGRVL
9244	39612	A	9303	1	983	MVRASGYLQTLDDFNHIVLKA SENGVPVYLRDVAKVQIGPEM RRGIAELNGEGEVAGGVILRS GKNAREVIAAVKDKLETLKSSL PEGVEIVTTYDRSQLIDRAIDNL SGKLL EEFIVVAVCALFLWHV RSALVAIISLPLGLCIAFIVMHFQ GLNANIMSLGGIAI AVGAMVD AAIVMIENA/R*TAGRVAAPAS* RHAG**NALAGQEGRLFGPLAL HQNVCDGGCGAAGDRSDPD PD GLLDPWQNSAGKQ*PAQSLFDS CLSSAVAESTALAENHAAGG AFGADGSLAAQ*SSPGEFLPQIN EGDLLYMPCDAAQGPQRRR
9245	39613	A	9304	362	436	
9246	39614	A	9305	101	208	
9247	39615	C	9306	1	882	
9248	39616	B	9307	1	822	

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9249	39617	A	9308	668	826	VNSHSQLLQRE*NT*ESNLQGM *RTSSRRTTNHCSRK*KRIQTNG RTFHAHG
9250	39618	A	9309	497	1042	LPRIPTVLTSQVRRDQWYRRFG RRPSG*PGNWSSSPVEKSA TRT LRITG TSAIPSEAITGSSAVVRR VPAGKTTAPTEIKSTPVSANSRS VLSVTLPTDSSSALPLVRLTASR ICSVSKLSSMMISAPAFRASSSS SRFSTSTSTGASGCSQDAFSTA WRTEPAIHWFSLRKASESPRR
9251	39619	C	9310	1	3447	
9252	39620	A	9311	570	647	
9253	39621	A	9312	1071	1323	RPPPHRLSGCYHPSHRRPVHGF HHA*RQRQFRR*TVDTLPADAP LPSPHPAHFRPL/TSIFCPVSTMA DNASM*RNSCCRLSARG
9254	39622	B	9313	1	2585	
9255	39623	A	9314	133	357	SSFFQFCEEIHW*LDGDGIESIN YLRQ*GHFHKIDPSYP*AWNVL PFVCVLFHFIEQWFFVLLLEEV HIPCKLYS

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9256	39624	A	9315	1	2680	MLVLPFLQPFMRILDHDSSID HRPDGGRNATQRHNIGIQSLEV HDNKSNTQPRQRNRHRQRRRA HMPEKQRTDYRRDPLESPKAA AACLFPAIADPNTPPVFTPPASL PTTGM/FDSPPFNRDA*MVMRS LIRSMTVARAVIGVAICNKGGLP ATMMALAAQHNIATVLPVGGGA TLPAKDGEVNGKVQTI GARFA NGELSLQDARRAGCKACASSV RRSCQFLGTAGTSQVV AEGGLG AIPHSALAPSGEPVWREIARAS ARAALNLSQKGITREILT DKAI ENAMTVHAAFGGSTNPLLHIIPA IAHQAGCHIPTVDDWIRINKRV PRLVSVLPNGPVYHPTVNAFM AGGVPEVMLHLRSLGLLHEDV MTVTGSTLKENLDWEHSERR QRFKQLLLDQEQINADEVIMSP QQA KARGLTSTITFPWQYAWIL HPDLDPETLLKLLISLRRFWAET PVGKNRITQMTNARHRTGQFG VTIHHTGVQFMGFITRKDSANS GVKQWTLFQQTHRFRHHIQR FARFQHFLPGFNNGRQLRDVAS VFMEFTTGLMSLD TALNEMLS RVTPLTAQETLPLVQC FGRILAS DVVSPLDVP GFEDNSAMDGYAV RLADIASGQPLPVAGKSFAGQP YHGEWPA GTCIRIMTGA PVPEG CEAVVMQEQT EQMDNGVRFT AEVRSGQNIRRRGEDISAGAVV
9257	39625	B	9316	1	2577	
9258	39626	A	9317	2	772	AFGASLAQDKPNTGTG*KSPSH PLLRLVDIGKICHLARKVGAVS VVDNPFIRPALQNPLALRADLV LHSC TKYLNHSDVVAGVVIA KDPDVVTELA WANNIGVTG GAFDSYLLRLRLTVPRMELA QRNAQAIVKYLQTQPLVKKLY HPSLPENQGHEIAARQKGFGA MLSFLDGD EQTLRRFLGGLSL FTLAESLGGVEKLISHAATMTH AGMAPKARAAAGISETLLRIST GIENGENLIADLENGFPA
9259	39627	B	9318	68	1895	
9260	39628	A	9319	I	636	
9261	39629	A	9320	I	942	

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9262	39630	A	9321	479	969	MPSTSQ*I/ISEDVFELNAARYR DEEIQRTPQRYSSRRPTQRHIV RFTKVEIKEKMLRAAREKGGV AHKRRPRLTADLSAETLQARR EWGPIFNILKEKNFQPRISYPTK LSFISEGETKSFTDKQMLRDFGT TRPPLKELLKEALNMERNRY QPQQKHTKL
9263	39631	A	9322	1	652	MGKKQSRKTGNSKNQASPPPP KERSSSRAMEQSWTENDFDEL REEGFRRSNYSELKEEVQTHGK EDKNLEKLDDEWLARIINAES LKDLMEKTKARELCDECTSL SRFDQLEDGVSVMEDMNEMK SEGKFRKRIKRNEQSLQEIWD YVKKPNLCLIGVPESDRKNGTK LENTLQDIQENFPNLSGQANIH IQENQRTPQRYSLRRATPRHLI VRFTKVEMKEKMLRAAREKG R/VTHGKGPRLTTADLSAETLQ AR/RTWGPINFILKEKNFQPRI SYPAKLSFISEGEIKYFIDKQML RDFCHHGQIPLKELLERKALK HGKGNNQ*PPPKERSSSRAMEQ SWTENDFDELREEGFRRSNYSE LKEEVQTHGKEDKNLEKKLDE WLARIINAESLKDLMEKTKA RELCDCTSLSSRFQLEDGVS VMEDEMNEMKSEGKFRKRIK RNEQSLQEIWDYVKKPNLCLIG VPESDRKNGTKLENTLQDIQE NFPNLSGQANIHQIEPENATKIL
9264	39632	A	9323	403	410	VFLIRWGGKPLKRKLYFLHCSI TQALV*ACQGYLG*IVGAKNI KYIDFFITASRYLRMLAQVFE*I LLLREVTRY
9265	39633	A	9324	174	1252	

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9266	39634	A	9326	1	1049	MHRSDMSPDKVDILDTTAFRI AINEVKHSLTSVTVKVLD MF ISRSSLFPIDDLDDGHSDQVG VLNSPTCYSAHQNGERIERFSR KV FVGGLPPDIDEITASFRRF GPLVVDWPHKAESKSYFPPKG YAFLLFQEESVQALIDACIEED GK\LYLCVS*PLLSKDKPSSKYV PWNLSDSDFVMDGSQPLDPRK TIFVGGVPRPLRAVELAMIMDR LYGGVCYAGIDTPELKYPKA PGRVAFSNQQSYIAAISARFVQ LQHGDIKRVVEKPYVLDDQM CDECQGARGCGKFAPFFCANV TCLQYYCEFCFWANIHSRAGRE VHIPLVTESA VAAPRIHIPWT
9267	39635	A	9327	2	126	IASNSWNASSSPGEAREDGPEG LDKGLDND AEGVWSPDIEQSF QEALAIYPPCGRRKIILSDEGKM YGRNELIARYIKLRTGKTRTRK QVSSHQVLARKKVREYQVGIK AMNLDQVSKDKALQSMASMS SAQIVSASVLQNKFSPPSLPQA VFSTSSRFWSSPPLLGQQPGPSQ DIKPFAPAYPIQPPLPPTLSSYE PLAPLPSAAASVPVWQDRTIAS SRLRLLEYS AFMEVQRDP*TRT SKHLFVHIRHTDRNPRRFFRTPP LGPVVDVRQIYDPNFPEKKGGL KELYEKGPNAF\FLVKFWADL NSTIQEGGAFYGVSSQYSSAD SMTISVSTK VCSFGKQVVEKVE TEYARLENGRFVYRIHRSPMCE YMINFIHKLKHLPEKYMMSV LENFTILQVVTSRDSQETLLVIA VFVEVSTSEHGAQHVVYKLVK
9268	39636	A	9328	1	1327	
9269	39637	A	9329	2	339	TYGCASPRKPRVMPVLTAQVP ITALRVNSSSIPAQSAVETTSNR PPTTGVPFRPVRAAV*AVISPO ISADPTTGGRA*LISAIPSQSVRH GSYSPRLML*RLDSEILLSSQPL TPVKHQRR
9270	39638	A	9330	1505	1876	
9271	39639	A	9331	1	1710	
9272	39640	A	9332	1	1191	

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9273	39641	A	9333	838	1365	STETLSPLPATPGVEVTLRLHLDV VSAEQQMFSGLVEKIQVTGSEG ELGIYPGHAPLLTAIKPGMIRIV KQHGHEEFYLSGGILEVQPGN VTVLADTAIRGQDLDEARAME AKRKAEEHISSSHGDDVYAQAS AELAKAIAQLRVIELTKKAM*H RLEKHKSSQSGNRLAFFCACDPS
9274	39642	A	9334	3	601	MLSAVGYP/TLAEEMGVLOE RIPSTKTGTSITSVQAVVVPADDL TDPSPATTFHAHLDATVVLRSQI ASLGIYPAVDPLDSTSRQLDPL VVGQEHYDTARGGQFILARYQ ELESLLAAILGMNDLSEEDKL VV ARARKIQRFSLSPFFVAEVFTGS PGKYVSLKDTIRGFKGIMEGEY DHLPEQAFYMVGSIEEAWEKA
9275	39643	B	9335	681	1071	
9276	39644	A	9336	203	2189	VASSARRGLPVHGPAPLQGPNG SQDRL/ESGTRNRCGLRPLVKG GKGGFRFPSARLIQTVKKGTPS RDHAIIEPSGYVSVAGVGERTR KGSVFAHEMPDCNVIDKVS LV YGMTEPPGNCMRVALSGLTM AEKFRDEGRDVLVFDNIYRYA LAG*ERFATVGR*ASN/AVGIQP TLAEKMGVLQERITSTKTGTSITS VQAVVVPANDLTDPSPATTTFA HLDATVVLRSQIASLGIYPAVD PLDSTSRQLDPLVVGQEHYDTA RGG*SI LQRFQELKDFMALP/G LSEDLSEEDKL VVARARKIQRF LSQPFVVAEVFTGSPGKYVSLK DTIRGFKGIMEGEYDHLPEQAF YMGDMAMTYHLDVVSAAEQQ MFSGLVEKIQVTGSEGELGIYS GHAPLLTAIKPGMIRIVKQHG EEFIYLSGGILEVQPGNVTVLAD TAIRGQDLDEARAMEAKRASG KVKPSIMQSLTPEKIAAILPLQF FPQPADFTGPYVMLTSRRNNRA LSRCDQTLMPGLAIRGIRHRH QQAGVRI LLNNAIEHVVDGEK VELTLQSGDTLQADVVIYGIGIS ADEPLAREANLDTANGIVIDEA CRTCDPAIFAGGDPVITSSLINV VDEIHDILLTQPVATRYCIVKVI FEAVMILRDSGGAPFCSNGMAT

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9277	39645	A	9337	905	2319	SRQAQWKGVPTFSVINYHSLQ KRTTNLTHRQLNLLSTVLYCS CPSIQKLLMLQTGPSPGVGLV DLPLKAMSRPALPNATAALPTG TRTQPPSTPLLTRLPSHRLLLH SGF*AAALLGVSEMTIRRLDNN HSA PVVLLGGYIVLEPRASHY LLSDQKSRLVEEKRRAAKLAA TLVEPDQTLFFDCGTTTPWIIIEA IDNEIPPTAVCYSLNTFLALKEK PHCRAFP CGATPFSPNPSIFSKRV NNFCRDIAFYYSAGVHVSKGV TCFNLKRWPVKQWAMSAQK HVLVV D HSKFGEVGPVCMGDL KRFDIVVRECCPEDEYVKYAQT QRIKPKD VSRHPV IIRLREPGL E PVMEFHHPVLPQRITESA VVHI AHTRKSWRPEHSA PVLIQTSPV ERGPQYIQCYQLSLTSEENNQP DTQTTTKPAQYSSILFLSKYPKV IVDAPDRSTQRGWSSGLATQSN EQACTTKCNSCTANWHQNTTT FNSTANPSTFKPPTSAALRVLSL WTGNHCDWCFIRYWRLTPNW QRFRRVGRTERATTHNRLQAF GGHTQGLSPGRRRWLHEQRFP TSDTGGHTADDFRKLDPICQGP YGSHRHSVKSEVNFKEKRYAF APAASFRTYTLIRFCAPPNTGRF LLTGTPLMLSYRHSFHAGNHA DVLKHTVQSLIIESLKEKDKPFL YLDTHAGAGRYQLGSEHAERT
9278	39646	A	9338	98	596	YSGIIMAAQSKLYPVVMAGGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQPRFIVAHQMRQLNSENIIL EPAGRTTAPTIAAALANRHS PESAPMLVLATDHVIANEDAV RAPVKINAIPYKKGKLVTFGIG LDGRVPRYNM
9279	39647	A	9339	2	437	LECPGRSTANCSPRARATSLLL LTHVHGESRDRAQEMVDLLAQ YEQHGLQLNSRELPDHLPLYLE YLAQLPQSEAVEGLKDIAPIAL LSARLQQRESRYAVLFDLLKL ANTAIDS DKVAEKIA/VR SAR*Y AAGAGCCLGRRAG
9280	39648	A	9340	152	334	HLSPQYGSIPRVISRMGGKLIIM DHFHYGRDSILLSME*TLALDA NLQFLYVVLNPNYYL
9281	39649	B	9341	1	1401	

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9282	39650	A	9342	86	2063	
9283	39651	B	9343	1	885	
9284	39652	A	9344	1	101	MDDNITYITFCINPLNLSPQRR MLIITGPNMGGKSTYMRQTALI ALMAYIGSYVPAQKVEIGPIDRI FTRVGAADDLASGRSTFMVEM TETANILHNATEYSLVLMDEIG RGTSTYDGLSLAWACAENLAN KIKALTLFATHYFELTQLPEKM EGVANVHLDALHGDTFMFM HSVQDGAASKSYGLAVALAALG VPKEVIKRAQKRLRELESISPNA AATQVDGTQMSLLSVPEETSPA VEALENLDPDSLTPRQALEWIY RLKSLGKTMPS TRYQKINAHH YRHIWVVGDIHGEYQLQSR HQLSFFPKIDLLISVGDNIDRGP ESLDVLRLLNQPWFTSVKGNH EAMALEAFETGDGNMWLASG GDWFFDLNDSEHQE AIDLLKLF HHLPHIIEITNDNIYAITTCVGN ARRAHAVHFCGDVARLLTTCQI NIYRGQFRRLPRTFHRRLTKL RDLILRLSAGNLQCCPDRAWRD NIHPNTFLRDLFCQATAVVQNR RLRSRIGDRFLGAVERRFGNDL PSSPVEWLTDNNGSCYRANETRO FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDYISIMPKPDGLT AAKNLAEA FEHYNEWHPHRAN PITYQAVCANHYRTLNGTMT NTG*QYNVYHYIQLPAESVAA APHVDHHRSEHGR
9285	39653	A	9345	1062	1179	PRFVPILAPYAPVRSVCLR*V*T DLPEYGHILFQPADR
9286	39654	B	9346	1	2439	
9287	39655	A	9347	136	629	RSVTPVTDIVKLLFETRLRLPGY TKSIE*TNITFQCAIAAA*KNSVS TPRGGGTGTNGQALNQGIIVD MSRHMNRRIEINPEEGWVRVEA GVIKDQLNQYLKPFGYFFAPEL STSNRATLGGMINTDASGQGS/ LGVRVLLGGDILDTQPLPVEL AETLGKSAE
9288	39656	B	9348	1	4653	
9289	39657	C	9349	584	819	

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9290	39658	A	9350	1	765	MQEWGRYTILSGCCNSALKGD VCLLYGFRVAGRRQASELQELT IGYRAQKNRVSSWCYCHFRQM AKAQHIKGFNLRLRKTAKK*GF QLVLLPFSANGK\AQHIKGFNL RLRKTAKKTRDFLTRMPKLG TMVGVDPALVLCYRDEYKLAL GEERGEFNVLLEANWLASALES QPVATVSGESWYFFGHCTEVT ALPGAPAQWAAIFARFGAKLE NVSVGCCGMAGTYGHEAKNH ENSLGIYELSWHQAMQRLPRN RCLATGYSCRSQVQRVEGTGV RHPVQALLEIK
9291	39659	A	9351	1	1710	
9292	39660	A	9352	1377	1712	IFRASLNQLFCGLLAGRNHRQ RSVRALSQRKMVPTDRK*RC ARRAAR*PSARVL*SGE*TD RQH AD*PTIR*RRSWYLRPAVYAS V RQSDRLYSDEYHW*PVRLQRY VRR
9293	39661	A	9353	203	1293	VASSARRGLPVHGAPLQGGPN SQDRL/ESGTNRCGLRGPLVK GKGGRRFPSARLIQTVMKGGT PS RDHAIIEPSGYSVSAGVGE/R TR EGNDFYHEMTDSNVIDKVS LV YGMQNEPPGNRLRVALTGLT M AEKFRDEGRDVLVFDNIYRY T LAG*ERFATVGR*ASN/AVGY Q PTLAEEMGVLEQERITSTKT GSIT SVQAVYVPADDLTDPSPATTF A HLDATVVLRSQIASLGIYPA VD PLDSTTRQLDPLVVGQEHYH TA RGG*SLQR/QELKDFMALP/G LSDELSEEDKLVARARKIQRF LSQPFVAEVFTGSPGKYVSLK DTIRGFKGIMEGEYDHLPEQAF YMVGSIEEAWEKAKKL
9294	39662	B	9354	1	505	
9295	39663	A	9355	604	789	TMVASGSRMTST*SRGSVNG CRTILRWKRHSSPLKIKRKQKS L*TMPSF*RLPAENSLFEI

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9296	39664	A	9356	1	1514	SVAVLRE*APKIRIQLATMPLELA DASDQDDNGAEMNLVYDRD TMARLGLDVLAAANSLNNAFG QRQISTIQPMNQYKVVMEVD PRYTQDISALEKMFVINNEGKA IPLSYFAKWQPANAPLSVNHQG LWRALTIWFTLPTGKSLCDPS AAIDRAMTQLGVPSTVRGSAFAG TAIQVFQETMNSQVILIAAIAT VYIVLGLIYESYVHPLTILSTLPS AGVGALLALELFNAPFSLIALIG IMLLIGIVKKNAIMMVDFALEA QRHGNLTPQEAIFQACLLRFRP IMMTTLAALFGALPLVLSGGDG SELRQPLGITIVGGVMSQLLT LYTTPVVYLFDRLLRFRSRKP KQTVTDTRWQLWIVAFGFFMQ SLDITIVNTALPSMAQSLGESPL HMHMVIVSYVLTAVMLPASG WLADKVGVRNIFFTAIVLFTLG SLFCALSSSTIRIILRFVSLHMR WQFRDLTFWQMRFRNTNPITSG GSDDSLMLNQSHQRSYSSSI
9297	39665	A	9357	3218	3337	
9298	39666	A	9358	252	771	RRCQILLSGSLHSSWRTLPGHV *QLASAHRRPRR*LPGLEPGEL FVHRNVANLVIHTDLNCLSVV QYAVDVLEVEHIIICGHYCGCG VQAAVENPELGLINNWLHIRD IIHGWAYGIHDGLLRDLDTAT NRETLEQRYRHGISNLKRDVHF TTGRFIQORTNRQRLRFAQA
9299	39667	B	9359	604	831	
9300	39668	B	9360	1	1104	
9301	39669	A	9361	242	337	LTVIHGVSAKTVILSSAVPIQ*K TVRRVSRR

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9302	39670	A	9362	2208	3411	LAADHRRRNAVQRPCNGGQSV QSTDEAAGRLSHADTHGRPA RALPGDCRPETLLRTAGVAE*T KALYTLRSEKTRERPMDKQQA SDEKHRRFHDKESFLA/FVNL WNY/LGEQQKALSSNAFRRLCR TDYLNLYLRVREWQDIYTLRQ VVKELGIPVNSEPAEYREIHIAL LTGLLSHIGMKDADKQEYTG RNARFSIFPGSGLFKKPPK WVM VAELVETSRLWGRIAARIDPEW VEPVAQHLLIKRTYSEPHWERAQ GAVMATEKVTVYGLPIVAARK VNYSQIDPALHDTIELGTSPAF LITRWGFGRNLSRTSGGPRQEP RRKEIAMELVLKDAQSALT VSE TTFGRDFNEALVHQVVVAYAA GARQGTAPKTRAAVTGGMPT LYAVGRLSRIPMDT
9303	39671	A	9363	79	559	TLSPGSINPFKPN*DSVPMTL/ RRFIEVRVFQIHHMRQRP AHL W
9304	39672	A	9364	1	655	THWER/A/QGAVMATEKVTVY GFRIVAARKVNYSQIDPALCRE LFIRHALVEGDWQTRHAFFREN LKLRAEVEELEHKSRRRDILVD DETLFEFYDQRI SHDVISARHFD SWWKKVSRETPDLLNFEKSM LI KEGAEKISKLDYPNFWHQGNL KLRLSYQFEPGADADGVTVHIP LPLLNQVEESGFEWQIPGL/RRE LVMPD*SCQTVTFEPANSHSY

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9305	39673	A	9365	1	2082	MDIQEFPLDKGTTSLLEILTLTRA GIRLLPSGMCQQLPRLRVLELS HNQIEELPSLHRCQKLEELGLQH NRIWEIGADTFSQLSSLQALDLS WNAIRSIHPEAFSTLHSLVKL.DL TYSQTLTTLPLAGLGLMHLKL KGNLALSQAFSKDSFPKLRILE VPYAYQCCPYGMCASFKAASG QWEAEDLHLDDESSKRPLGLL ARQAENHYDQDLDELQLEMED SKP/TPSVQCSTPCKPCEYL FESWGIRLAVVAIVLLSVLCNG LVLLTVFAGGPAPLPVVKFVVG AIAAGNTLTGISGLLASVDAL TFGQFSEY/GLARWETGLGCRA TGFLAVLGSEASVLLTLAAVQ CSVSVCVRAYGKSPSLGSVRA GVLGCLALAGLAAALPLASVG EYGASPLCLPYAPPEGQPAALG FTVALVMMKLLLSWVFGPLP YHQNWYCDLPRGDFEAVWDC AHGEATWAWPHLRKTGLLYCP VAFLSFASMLGLFPVTPEAVKS VLLVVLPLPACLNPLLYLLFNP HFRDDLRLRLTPRRRTQGGP*PL CCGREDAGERASCDSYPQALV APSLMWISFCEAS*\$WAGPLEL ETYGFPSVTLISCQQFGAPRLEG THCVEPEGNHFGNPQPSLDGEL LLRAEGSTPASGGLSGGWRLSA LWLGLWLHTCKYSPSPFFSSPLF PFLSPSPVNDGCF
9306	39674	B	9366	1	510	
9307	39675	A	9367	88	246	TPMRPMKSPMPTPVSRSGSSSK MG*SSASL*RSIPGLDAGKTPW PAGRSGTWA
9308	39676	A	9368	693	1041	AEGYSQCPNAREGHVDEENED SAPAAQKIP*I*ED*SPHVSQVPV EGEEECVKKQ/GRFSWNTSTS* RQT/TARKLLADQAEARRSKT KEAHKSYEEHLQAKKEEIIKTL SKEETKK
9309	39677	A	9369	1	1911	

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9310	39678	A	9370	1	921	MWRSIFLDSRYLLSSRRKILILIL HVTFSGIRALAVPFRLPVEKMS FIFMGDVIHRLMLTATQYVAPL MANFNPGYSDNSTVVYFDNGQ QIRKLIKDGIIIRKPVTVHSRAR CRKNTLARRKGRHIMGIEFACFC CVFLTPALICMVCAVRLLTRDP YLASGDQPLERATGEHASMHE YVPGELGQPPGLYPSHPPGRA GTLRALSRQDTFDADTPGSRNS AYTEL*DSQVMDMTDPSEGPGL GDPCE/GTPPARQGSWEDEED YEEELTDNRNRGRNKARYCAE GWGPVLGRNKNELEGWGRGV
9311	39679	A	9371	3	740	ELFPFAAAAAAAMSMRLQKRL ASSVLRMWQRTNGLG*TPMRP M*SPMPTPRQIPEAHQRWAD HP/LSLVTGPFPGSMPEKTPLA\ AGEGAGQHGA LGKAGRGTSQ MPGMPGEGQHGLRRIEDFGAG LLQKDTGEI*RRSDRPHVFTAC YLEGEGGMLFQKQGGFFMGTL PQG*RQDKGPQRSFLADQA*RP QGLRTKESTESAEEERLPQQRK EEINQRLYSKEGRPRPNKNLPL GSVHTWPLVIT
9312	39680	A	9372	1	2229	
9313	39681	A	9373	3	1560	SGPNSLKFYDWGETVPQWPPIF GLSPAFGFPLCFPRGLGETIFSSR PHIR/RNYPELQKRLNGWLSAA LKTARILTVCAVVMLLLSAWG LFDWFWNLQNGAGQKNP*NIP D/LRIRNSILFL/LSAVGWTVLA\ SLIENRLASD/HGRPLP/SARTR TLTLFRNALAVIISTITIMIVLS EIGVNIAPLAGAGALGLAISGF SQTLYKDIHTGVFIQFENGMTG DLVTIGPLTGTVERMSIRSVGV RQDTGAYHIIPWSSITTFANFV RGIGSVGANVDVDRHEDADKA NQALRDAVEDDETRFTSESPIL RCCQREGGLKAVVQILLSHGR NGLPGEPASSQGLSASSTPVF HLALQIDSAPDNIDWVEMLFNK NMVTERLQNMVMLEQCFSDSS SLYRFLTYSYLLAFNVWLLAP VTLCYDWQVGSIPLVETIWD RNLATIFLAVVMALLSLHCLAA FKSRVTASIPGCIKAHAVENVL TTKSKTRIYPEVVVQSGLQKQK GKGSVMFIEAAGL

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9314	39682	A	9374	3	276	VRQYR/LGN/MHQQRMAEMID ARQQAFGEAGACWGGCPKHR VMLDASGKPGNDLCAGYQRD VRHLPRYLKAMADLLAIGRPA SDIMHAHLV
9315	39683	A	9375	102	916	RSLLAIFNHW*IKRDLGKFLVW NIK W/AFKFCRSAGQTSGRSVI VEHNGEIIYACDHVYPQYRLG NMHRQRMAEMIDSRQQAFGE DKFKQLPAQCRSCNVLKACWG GCPKHRFMLDASGKPGLNLYLC AGYQRYRHLPPYLKAMADLL AHGRPASDIMHAHKVFKRGT ACSGFQKGGPLFRSTGYCPTL RKKAPCPKTGLLGKWTQRR NSSGKSCAKRRGDPLLENRFN GSRVQRKPQWNSCTGHPENN FPNYGGTYPQRMWPL
9316	39684	A	9376	338	1155	SIFISIGNLAANDLSPSRIARLQK ILHSYVPEIRDGNQVRVTSWD GRKWGELEGDTYDRVLVDVPC TDRHSLHEEENNIFKRSRKKE RQILPVLQVQLLAAGLLATKPG GHVVYSTCSLSHLQNEYVVQG AIELLPINTASRYRWKI*LTSEG FSWTHFVSSQSCPGWGAGNTK TSLANLALCTSAKCVGT*YPP QSLKQEYQRYVSVGCTRNWKL GPVAMHSRSLHPVRVFLQFS AIRSRRFVLLSNCGASAWFPT SLINYPYIS
9317	39685	C	9377	157	453	
9318	39686	A	9378	486	1195	ARPQQYEQVPGKAEASEWERG SSAPTGGGHAAAAAGGVGGG EGSPPALHGRGARAG/GAGICM GLRQQLNR*AMDLTGAGGP AGAAGAVARGGGRHQGPAG GRGRGLGFAAGTAEPGAPHR PLQRALPPIRREPGERHRAPRAG AAPQCGSARPRAPQSLRAG ALPEAHQGGQGPARTHPAEPGP AARRAQSLCRHWD*GRGRPG PPDALRGGAASDFRLSARTPICR
9319	39687	A	9379	10	1278	

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9320	39688	A	9380	1	1305	MECVVCVKEKEREKEGKEEEEE EDEAVAERGGKGERRGERRGE RKREKETYTEKNRYRDTKRDR DRERKEPYEIPSSLIHGDPKDE LDRNLALKQVKTYWVIQFSKSI EVIEKRMAVLNEQVKEAEGSS AEYKKEIEELKELLPEITEKTED AKESQTTGNVAELALKATLGG GSSVS/SIASRKPTDGASSNCV TDISHFVRKKRPPEEQSPWKDD AKKVKQLEVNNGSGDAVPSG NEVLNMEEEAENRVESRAAV EGTVEAGATAESTAYMYDIPA MYQENTAVSKTDEVSDLIHLK AQTDLAQERAGKRASPDGG SAEGQAQSDRQEATKQRHKQE AGDRHYDKQMLEYQGAHELY SSREKRKEKKKKPPHGRLLPPTP VALHGAKRRLTKRLFNASPN KPKGHSTQFSVMSQAEQQPVL
9321	39689	A	9381	67	458	WDMANSCKDVTGPDDEESFLY FAYGSNLLTERIHLRNPAAFFC VARLQ/QEGVKSGMYVIVIEVK VATQEGKEITCRSYLMTNYESA PPSPQYKKIICMGAKENGLPLE YQEKLLKAIEPNDYTGKGSEENE
9322	39690	A	9382	139	710	WDMANSCKDVTGPDDEESFLY FAYGSNLLTERIHLRNPAAFFC VARLQDFKLDGNSQ/GKTSQT WHGGIATIFQSPGDEVWGVVW KMNKSNNLSLDEQEGVKSGMY VIVIEVKVATQEGKEITCRSYLM TNYESAPPSQYKKIICMGAKE NGLPLEYQEKLLKAIEPNDYTGK VSEEDIIKKGETQTL
9323	39691	A	9383	1	731	MANSCKDVTGPDDEESFLYFA YGSNLLTERIHLRNPAAFFCV ARLQLLIESPRMSRLAKFWPRT HAVILSKTERTSFWPLKPKQWE SGSDTPYSQTRKDFKLDGNSQ GKTSQTVHGGIATIFQSPGDEV WGVVWKMNKSNNLSLDEQEG VKSGMYVIVIEVKVATQEGKEIT CRSYLMTNYESAPPSQYKKIIC MGAKENGRLKYQEKLLKAIEP NDYTGKVSEEDIIKKGGTTKL
9324	39692	A	9384	41	333	MFCNTDLGT/LCCTDVVARGLD IPQVNWVIVHDHPDDPKYIHR VVPFVVDLVNNGNEGKQKKRG GGGGFDYQKIKKVEKSKIFKHI SKKSSDSRQLSH

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9325	39693	A	9385	3	1852	SKQKPMNVGLSETQNGGMSQE AVGNIKVTKSPQKSVLTNGEA AMQSSNSESKKKKKKRKMV NDAEPDTKKAktenKKGSEEE SAETTKETENNVEKPDNDEDES EVPSLPLGLTGAFEDTSFASLCN LVNENTLKAIKEMGFTNMTEIQ HKSIRPLEGRDLLAAAKTGSG KTLAFLIPAVELIVKLRFMPRNG TGVILISPTRELAMQTFGVLKE LMTIHVHTYGLIMGGSNRSAE AQLGNGINIIVATPGRLLDHM QNTPGFMYKNLQCLVIDEADRI LDVGFEELKQIHKLLPTRRQTM LFSATQTRKVEDLARISLKKKEPL YVGVDDEKANATVDGLEQGY VVCPEKRFLLFTFLKKNRKK KLMVFFSSCMVVKYHYELLNYI DLPVLAIHGKQKQNKRTTTFQ FCNADSGTLLCTDVAARGLDIP EVDWIVQYDPPDDPKEYIHRVG RTARGVLNRRGHALLILRPEELG FLRYLKQSKVPLSEDFSWSKIS DIQSQLEKLEIKNYFLHKSA/Q EAYKSYIRAYDSHSLKQIFNVN NLNLPQVALSFGFKVPPFVDLN VNSNEGKQKKRGGGGGFGYQ KTKKVEKSKIFKHISKSSDSRQ

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9326	39694	A	9386	1	2703	MAQQATLCSMKGCMRALVAQ LKSESEDLQQTVAQKREVPKSK VPAAEKRESGPKQAAVNAAVQ RVQVLPDVTLLHFATESTPDG FSCSSSLSALSDEPFQIKDVEL RIMPPVQENDNGNETESEQPEE SNENQDKVEKPDSEKDLLDDSD DDDDIEILECIISAMPTKSSRK AKKLAQTASKLPPPVARKPSQL PVYKLLPAQNRLQAQKHVSFTF GDDVPRVYCVGTFPIFSTATS LSDLTIESPPNELATGD/GVRA/S IQSGKSHKPFVRVK/IMDQVQQ ASSTSSGANKNQVDTKKKKPTS PVKMPQNTYRTRLPNEDR VRGSFALDSPHHYPIEGTPYCF SRNDSLSSLDFFFFFFDLSREK AELRKGESKDSKAVTCRPEP NSSQQAASKSQASIKHPANRAQ SKPVLQKQPTFPQSSKDGPDRG AATDEKLQNFIAIENTPVCFSRN SSLSLSDIDQENNNNKESEPIK EAEPANSQGEPSRQLSQQNLTK QASLSKNASSIPRESASKGLNQ MSNNGSGNKKVELSRMSSTKS SGSESDRSERPALVRQSTFIKEA PSPTLRKLEESASFESLSPSSRP DSPTRSQAQTPVLSPLPDMSL THPSVQAESEKAKSEDERHVS SMPAPRQMKENQVPTKGTWR KIKESDISPTGMASQASSGAAS GAESKPLIYQMAPPVSKTEDV
9327	39695	A	9387	2	193	QSSE*NIQGPCNVWSSR*RWER SKGRRLSSASRPLSALSTLRFT SVSQHAAKRVVVRPQGG
9328	39696	A	9388	395	761	SMQKPRPIAHRQRCRAAMAA/ GQQPQIPITITGTGVVYPGAIIM ATTTSPQMSTDCSSSTASPEPS LPVIQSTYGMKTDGGSAGLNQ MINGEDEMAMYDDYEDDPKS DYSENEAPEAVSAN
9329	39697	B	9389	1	477	

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9330	39698	A	9390	167	890	LSGARSSQGRLPWGRGDAVSTSTSRNRNRTGASDERNNHEPGKN SPYLQAQVVRIGGKGFTARRKKK VVHRTATA\DDKKLQFSLKKL GVNHMSGIEVNM\FTNQGTSG STFNPN*KVQAISWAANTFHL PGPCWRPKPADKKWL.PQPSL PSL.GAG*S*LRFKGLARSFLPP NNPVDGKATHLPTG\KDDDDA KVPRSLWRILMRLPKNEGKLEL RSTSR*NLEEVTVGSRVFKIMT AF
9331	39699	A	9391	2	315	GAASLLRAGPGSSGSDP\PLSSR FVERRGALYRSPMNQENPPYP PGPPTAPYPQYQWQGGPQEP KTTVYVVEDQRRDELGPSTCLT ACWTALCCCCLWDMLT
9332	39700	A	9392	263	680	LLLPAVLTSAPLPPAGLATCP RLAQLGIGRAAPQKRSRPRRNP EASRGRPPDGVWRAPLR/VPPT PRETEPQRRGDPGLRNPCLSQL SPGAPQFSGP/PPGSPGTRPVRA* SPPGPSWVGPGPLHLTSLPNRL DNGRV
9333	39701	A	9393	2	537	SGARLLTTCSETGAASLLRAGP GSSGSDP\PLSSRFVESRGALYR SPMNQENPPYPGPGPTAPYPP YPPQPMGPGPIGGPYPPQGY YPRIPTVRLAGWTSGLLKTTV LLWVGRPKKEEMKLGTHLPSQ AGTGCLLLSLGTWFTLTRTRP RPFLFLASSAANLLTGVCPIHLF
9334	39702	A	9394	3	470	PKAKKEAPAPKAEAKAKALK AKKAVLKGVHNHT\QKKKIHTP LTFQRPKSLRLRQPKYPRKSA PRRNKLDHYAIKFP.LTTESAM KKIEDNNTLVFIVDVKANKHQI KQAVQKLYDIDVAKVNTLIRPD GEKKAYVRLAPDYDALDVAN KIGII

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9335	39703	A	9395	1	1144	MLYQVLMVDTCGRGEGAFLK YRK PACPTALGFMFPRSHGLTA DTVLVSSLRWFLWRRLLLLL LLLLNLPLQKAVHRKATPESAI ADCSGRDCAPWVKFAMLELH SFKCPAGEYWSKDVCCNKCSA GTFVKAPCEIPTQGQCEKCHP GTFTEKDNLYDACILCSTCDKG DFYGGKTAVHEALCDNIDTRT VMEEMRALVSQCNLYMAARK AERRRPNRALLENIAMYLTHM LKIFGAIEEESPLGFVPVGGPGTN LNPIENGGMDFLTTSVSLRKT HRVSNQNSVCRSVSYWKPKC TFCSLTHITYIRYLELRLTLESTV MPYLQVLSEFREGVRKIAREKK VLEVLQLSDALRVTSCLSLGSG LKTMKPECLLF
9336	39704	A	9396	1	639	MDGDEKTSFICAVHNGIFREW QTGTCSPKKGQLLRVECHGK IKAQGGQMYIKAALFRAKTW NQPKCPSMIDWIKKMWWHIY/ TCEYYTAIKKKIMSSVETWMEL EAHLSKLTQEQQSKFRFTSLYSS RVFQRTQDVPYHNKLNEADK PTTNKKGLILNLRVNTPIGRK NTGKLSAIEKLLKRPKRKHLS KIYTLKNDSDLIKDKNI
9337	39705	B	9397	1	825	
9338	39706	A	9398	2	285	HEENRPFVCEH/AGCGKT/FAN KPSLTSDAVVH/DPGKKMKML KVKKSRKESRLASHLSGYIPPK RKQGGQLSLCQNGESPNCVED KMLSAPVPLTLG
9339	39707	A	9399	2003	2344	PFVGVFWLFFFFSVFVTFVPP EYYVLPA PPHRSVFLVFGRV VFFFPLPC/CDFRSRLTPPFVCAP PAPPLPFVSVCPVPSLSCGDVC AADKKNKKKFLNTRWKKKT
9340	39708	B	9400	3	113	
9341	39709	C	9401	48	182	

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9342	39710	A	9402	2	752	VWWNSRRRPVKRRRLASPSY ACSGRSAGFLDNCAMCAARLA AAAAAQSVYAFSARPLAGGEP VSLGSLRGKVLLIENVASL*GTT VRDYTQMNELQRRLLGPRGLVV LGFPNCNQFGHQENAKNEEILNS LKYVRPGGGIEPNFIMLFHKSE VNAGAGHPLFAFLREALPAPIS DDATALMTDPKLITWSPV/CRK DPGKIKFFLGPPGNFFKFLGGP CTVLPRLRRYSRRF/QTIDIEPDIE ALLSQGPSCA
9343	39711	A	9403	1	1128	ARCDHPTAFVVCYRFYPWPAG HVDAAVH*YVCARATDSFIAV WRTLLKGTIIILHESSIHDNFNLT SQKLWAFVPNKAPRTSGIICWP EIQSAFQGGNLYFTIPIVDRNS TNYVLRQVRLLGN
9344	39712	A	9404	7	378	
9345	39713	A	9405	318	616	DPAGFPGCWKPLFYDLHYRSQ LHQLCLQAGRTPGQFGHQHRF WWQFCT*EIPALQPLPEGNLV SCNEQSFGAPATGTNPGEVHP AALGTWLYLLPPC
9346	39714	A	9406	1	145	MEYYAVIKKDEFMSFAGTWM KLETHLSKLTQE/QKFTPLMFSL ISGS

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9347	39715	A	9407	1	2052	MVLVVAVVVVVLVAVIVV VVVVVAVVVGAVVVVVVV MVVVVVVVVEEDNQHKTGA INNNNTAKNPQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQWQITKKK YLIYLKKHSGVKNIPRNPTYEG CEGPFQGGELQTTAQQNGGHHK QTEDHSMMLDRKNQYCENGH TAQAVPNPYTLLSQIPDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGF NSPHLFGQALAQDLSQFSYLD LVLRVMDLLATHSETLCHQ ATQALLNFLATCGYKVKPKA QLCSQQVKYLGLKLSKGRTRL EERIQPILGYPHPKTLKQLTAF GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPAEAVAF QALKKALTHAPVLSLPVGGNFS LYVTEKITGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLLSKGTLVKHQE AIKRLLLAVQKPKAVLHWCW GHQKGEREIEENRQADIEARR AARQDPPEMLTEGPLAFELA MATARAELSLIIHCCLP PPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTA WPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEQGPVTVQTHILRSHL
9348	39716	A	9408	2	350	YKVSFKPAQLCSQQVKYLWLK LSKGRTRALSEERIQPIALYPHPK TLKQLRGILGTGFCRIWIPR* SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9349	39717	A	9409	1	749	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNP HLFGQALAQDLSQFSYLDLTLV RYMDDLLAAVSETLCHQATE ALLNFLATCGYKVKPKAQLCS QQVKYLGLKLSKGRDLTTFLP VNEEKIE/P* LSTNSCNKLRCSRG TSRGS LG
9350	39718	A	9410	118	174	
9351	39719	A	9411	577	3018	

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9352	39720	A	9412	310	1964	TFRLTEPTQMRRNQKTNPHNM TKQGSSIPPQKNHTSSPAMDPN QEEIPDLPEKNSGVNKIIPRNPT YEGCEGPFQGELQTTAQQKNG GHKQTEDHSMMLDRKNQYCE NGHTAQAVPNPYTLI.SQIPEDA EWFTVLDPKHAVFCIPVHPDSQ FLFAFEDPSNPMSQLIWTVLPQ GFRNSPHLFGQALAQDLSQFSY LDTLVLRVMDLLATHSETLC HQATQALLNFLATCGYKVSKE KAQLCSQQVKYLGKLSKGTR TLSEERIQPILGYPHPKTLKQLT AFLGITGFCQIWPSILTAKGDL WLSDNHLLKYQVLLLEGVPLQ LRTCATLNPATFLPDNEEKIEH NCQQVIAQTYATRGLLEVPLT DPDLNLYTDGSSFVQKGLQKA GYAVVSDNGILESNPFTPGTST QLAELVALTWALEFGEGKRVN INTGSKYAYLVLHAHAIWRER EFLTSEGTPKHQEAIRRLLLV QKPEEVALVHCWGHKPKGERE IEGNCQADIEAKRASRDPPLE MLIERHLVWGNPLWETNPQYS
9353	39721	A	9413	3	370	RCCPCPRVHHMHISARAIRPPP RPPFLLLLVFLFQTGPCSHPGC SPPPAHSPSCSSWPQWPG/CSSPV SVLLAKPAACLIAAAVSANPRL LFKPCCRRTASNWAHRQVTLQC WSELSSCFWPE
9354	39722	A	9414	191	1375	EWPEGGGRYSSVPSAVHHART CLAAELSGTSRQPEPRALPPETG VATAEAESNQPAAISK/PNGQ GAPLQR/RSPLSPSPGAAQVPA LPMQDMSEGGSSPSPGGHIWL ASLTPCSLALWNSCCQSPGSQP RGRDEGDCLVRATEPSATGPDP RRTRLCSISASLVVRNTDPGIS DRRPGISDRRPGTSDRRPGTSDR RPGISDRRPGTSDRRPGTSDRRP GTSDRRPGTSDRRPGISDRRPGT SDRRPGISDRRPGTSDRRPGISD RRPGTSDRRPGTSDRRPGISRLP RDWIPAAAASRENSNSADARN RCSSPSRKCCQPTPSHRMRGSAG SVGSSAGHTAGGTGLTPSRCS QALQVFPVAVLGKRGFLSWERS LKQRDIRGPDFSSTALI
9355	39723	A	9415	3	523	

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9356	39724	A	9416	1	846	MLCDFQDGSTSRHVNPESSNPS PQPWSEDDQGASATVPCA KSV MHRLLKKFTIEYLVVKFLKAVS HAIQMEMLAPKGPSPIDEDASV KEENICRAFS DALL YKIEDIDNK DWNPNQLCSDY/VKDNAYTSF QIQEMETILKELKFEVGGPLPL HFLRQASKAGKADVEQHTLAK YLMELTLIDYDMMHYHPSKAA TAASCLSQVLGQGWNLKQQ CYTGYTQNEVLEVMQHVAKN VLKVNENLTKFIAIKNKYASNK FLKISMIPQLNSKAIKDLAFLPM GGS
9357	39725	A	9417	72	1340	CPPFSVRVPPWAGLALLPSPSL MALLRRPTVSSDENIDTGVNS KVKSHVTIRRTVLEEIGNRVTT RAAQVAKKAQNTKVPVQPTKT TNVKNQLKPTASVKPVQMEKL APKGPSPTPEDVSMKEENLCQA FSDALLCKIEDIDNEDWENPQL CSDYVVKDIYQYLRLQEVLSIN PHFLDGRDINGRMRILVDWL VQVHSKFRLLQETLYMCVGIM DRFLQVQPVSRKKLQLVGITAL LLAPKYKMFSPNIEDFVYITD NAYPSIQIREMETLILKELKFEL GRPLPLHFLRRASKAGEVDVEQ HTLAKYLMELTLIDYDMVHY HPISKVAAAASCLSQVLGQGWK WNLKQYYHKDTQENEVLEV MQHMAKNVVKVNENLTKFIAI KNKYASSKLLKISMIPQLNSKA VKDLASPLIGRS

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9358	39726	A	9418	I	1875	EPEKQQLYDIPASPKKAGLHPP DSQASGQGVPLISVTTLRGGY STLPNPQKSEWIYDTPVSPGKA SVRNTPLTSFAEESRPHALPSSS STFYNPSPGRSRLTPQLNNNV MQKKLSLPEIPSYGFLVPRGTFP LDEDVSYKVPSSFLIPRVEQQN TKPNYDIPKATSSVSQAGKELE KAKEVSENSAGQIPHGSPDGQ/ RSPSPDPRLSGSSSDSRASIVSS CSTTSTDSSSSSEESAKELSL DLDVAKETVMALQHKVVSVA GLMLFVSRKWRFRDYLEANID AIHRSTDHIEESVREFLDFARGV HGTACNLTDNLQNRIRDQMQ TISNSYRILLETKESLDNRNWPL EVLVTDVSQNSPDDLERFVMV ARMLPEDIKRFASIVIANGRLLF KRNCEKEETVQLTPNAEFKCEK YIQPPQRETESHQKSTPSTKQRE DEHSSSELKKNRANICGQTLPN LEEKDKPILEQRLDENKDLGTM NPGLIPQPSQQTPERKPRLSE HCRLYFGALFKAISAFHGSLS QPAEHTQSKLVIMVGQKLVDT LCMETQERDVRNEILRGSSHL SLLKDVALATKNAVLTYPSPAA LGHLQAEAEKLEQHTQRFRGT

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9359	39727	A	9419	1	2013	MGLKSWGGMGLGTAFGKGLR GEKAWCVSGRYHWRYSQWSG TLTQGPVWVRVHSLSDRVYDV PTQHRGPVVLKEPEKQQLYDIP ASPKKAGLHPPDSQASGGVPL ISVTTLRRGGYSTLPNPQKSEWI YDTPVSPGKASVRNTPLTSAE ESRPHALPSSSTFYNNPSSGRSR SLTPQLNNNPMQKKLSLPEIPS YGFLVPRGTFPLDEDVSYKVPS SFLIPRVEQQNTKPNYDIPKAT SSVSQAGKELEKAKEVSSENSAG IQIPHGSPDGG/RSPPSEPDRLSG SSSDSRASIVSSCTTSTDSSSS SSEESAKELSLDLDAKETVMA LQHKVSVSSVAGLMLFVSRKWR FRDYLEANIDAIHRSTDHIEESV REFLDFARGVHGTA CNLTDNL QNRIRDQMOTISNSYRILLETKE SLDNRNWPLEVLVTDSVQNSP DDLRFVMMVARMLPEDIKRFAS IVIANGRLLFKRNCCEETVQL TPNAEFKCEKYIOPQRETESH QKSTPSTKQREDEHSSSELLKKN RANICGQNPGLIPQSSQQTPE RKPRLSEHCRLYFGALFKAISAF HGSLSSQPAEIIQSKLVIMVG QKLVDTLCMETQERDVRNEILR GSSHLCSLKDV ALATKNAVLT YPSPAALGHLQAEAEKLEQHTR
9360	39728	A	9420	3	645	DFHTN/K/RVCEEIPILSKKLHN RRAGCVTHLTNQIRGPPVRGISI KLQEEEEKERRDNYVPKVSALD QEIIIEVDPTKEMKLKLLDFGSL NLQQQKATRVYAVVQISAPMF LLWALPLSVAPLITDFKMFVTT SYLISLFLIINSSANPIYFFVGS L RKKRLKESLRVILQRALADKPE VGRNKAAGIDPMEQPHSTQH VENLLPREHRVDVET
9361	39729	A	9421	312	694	LTPAPRKNVTEKYVMCLGNDF HTN/K/RVCEEIPILSKKLHNRR AGCVTHLTNQIRGPPVRGISIKL QEEEEKERRDNYVPKVSALDQEI IEVDPTKEMKLKLLDFGSLSNL QVTRPTVGMNFKMPRGAV
9362	39730	A	9422	3	383	

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9363	39731	A	9423	304	1862	RMLEATSKMRKGVPSIQ/SSQ GNSYTLIPSAKSDNLSDDSHSEI SSRSSIVNCSVDMSAALQDE RCSSQALAVPESTGALEKTEHA SGIGDHSQHGPWTLKPSLIK CLAVSSSVSNEEISQEHIIIEAAD SGSWEVGTSCSSSHDNFQSLP NPKSWDFLNSYRHTLDDPIAE VEPTDSEPYSCSKSCSRTCQC KGSLEKSWTSSSLSDTYEPN YGTVKRRVLESTPAESSEGLDP KDATDPVYKTVTSSTEKGLIVY CVTSPKKDDRYREPPPTPPGYL GISLADLKEGPHTHLKPPDYSV AVQRKMMHNSLSRLPPASLSS NLVACVPSKIVTQQRHNLQPF HPKLGDVTDADSEADATLGNK CKLLYMSDVRNPVPAVKDVLV QKYTSFNFFHPQEALDRRREEL ALPEGASGEACLSTRSLKRSV QALAQQTSHRNFLPEKQPFSAQ AAGILHGSINHNRGPCLLEGT KMMTGVLRYRAYLLCIAYSRDLI VDEQIMNGLRKA

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9364	39732	A	9424	1	1335	MTFKNPKYPFVSNLAKQKGMS VIKVNGLQKQSNPNRTTNGPDP SGMKVWVSPQGKNPQPTVLA EGKGNTWVVEEDTRNFGFI QKHTDIGIKYDSSTGIYDLDFN VVLDRASEEGITLTAALAADR ETPSENCLPSPVNPTAQEGEIH PDPHILEQEDPTTAPHQRCLCQ QQCQRPLCRLQPVVPHIVDLT PLTEIGSEEPVGELNFKHIRFEV SEDNMTFDASDQGPFFENYWL LVLATPGDVTWNGALGLHTP KSSSPDTCASQAQSQCWELSPG GRRIGTLPLQESGASWLP TSSLAARVIMNCGDKATPRN GGVRTLKKLSSPLSKAGGKVL YGEINPEQEVQASLSFAALLES YGIFMETEFLVACLISQGGQLR NQDFSSSIYSLAPGLDPSSVRA GAQRTAPPWGISPRSC/PVIKVN GKLQSNPNRTTNGPDPGSMK VWVSPQGNPQPTVLAEGKG NTEWVVEEDTRNFGFIQKHT DIGIKYDSSTGIYDLDFNVVLDR RASEEGITLTAALAADRETPSE NCLPSPVNPTAQEGEIHDPPII VLEQEDPTTAPHQRCLCQQQC QRPLCRLQPVVPHIVDLTPLTEI GSEEPVGELNFKHIRFEVSEDN MTFDASDQGPFFENYWLVL ATPGDVTWNGALGLHTPKSSSP DTCASQAQSQCWELSPGGRRIG
9365	39733	A	9425	56	235	
9366	39734	A	9426	1	515	
9367	39735	A	9427	138	830	AWAQLPSALGSTRVSPPPSARS QPPWRRRHK/CLLETEPLQGT EDAVASADFSMLSEEEKELK AELVQLEDEITTLRQVLSA/KER HLVEIKQLGMNLMNELK/QNF SKSWHDMQTTAYKRTHDTL SHAGQKATAAFSNVGTAKSKF GDMSYSIRHSISMAMPARNSTP KSFEERVETTTSKTKVGGTN PNGGSFEVLSSTAHAASQSLA GGSRRTKEEELQC
9368	39736	A	9428	3	381	LLETEPLQGTDEDALASADFS MLYEEKEEVKAELVQLEDEIT TLRQVLSAKERHLVEIKQLG MNLMLNELKQNFSSKSWHDMQ TTAYKKTHTLTHAGQKATAA FSNVGTAKSKFGDMRRK

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9369	39737	B	9429	79	426	
9370	39738	A	9430	1	570	
9371	39739	A	9431	1	1677	MLESVNVRLLEDLITGPCWEAG WNAGYAFLVVAVEDFTIGKLF DKLEGTKLCLKNALPRVITQTE SHRQRLLEAAAAWHSWLKIV QKMKAVYHILNMCNIDVTQCC VIAEIWFVPADATRIKRALEQG MELSGSSMAPIMTTVQSKTAPP TFNRTNKFTAGFQNVDAVGV GSYREINPAPYTIITFPFLFAVMF GDCGHGTVMLLAALWMILNER RLLSQKTDNEIWNTEFFHGRYLI LLMGIFSIYTGLIYNDCFKSLNI FGSSWSVQPMFRNGTWKTGTH DPHLAVLFKMGHVEGRDCVLR IVLAKIGYRNGFLRKIWNLASN KLTFLNSYKMKMSVILGIVQM VFGVILSLFNHIYFRRTLNIILQF IPEMIFILCLFGYLVFMIIFKWCC FDVHVVSQHAPSILIHFINMFLFN YSDSSNAPLYKHQNFNGDVFV HQAHTIEYCLGCISNTASYLRL WALSLAHAQLSEVLWTMVMN SGLQTRGWGGIVGVFIIFAVFA VLTVAILLIMEGLSAFLHALRL HWWFEQNKFYVGDGYKFSFSS FKHILDGTAAE
9372	39740	A	9432	3	933	GTWFPVSSAASIYAGTGGLGSKI SMSCSTSFWGGLGSGGLATEM AGGLAEMGGIQNEKETMQSLN DHLDYLDVRNLETENWRLES KIQEYLEKRPHVRDWHGYFKTI KELRAQIFANTVDNVHILQIDN AQSSMRQELAMRQSVESNIHG LCKVIDDTNVTLLQLETEMGAL KEELLMMKKNHHEEVKGLQVQ IANSGLAVEVDAPKSQVLAKM EQLNRILLYLESKLAQNWAEG QRKVQEKDLLNIRVKLEAEIA TYRRLLEDSEGLNLGDALDSSN SMQTIQKTTTRQIVDSKVVSSEIS DTKVLRH
9373	39741	A	9433	3	698	

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9374	39742	A	9434	2	479	PRVRESTTVVTTQSAEVGAAET TLTELRRTVQSLIEDLSMRNL KASLENSLREVEARYALQMEQ LNGILLHLESELAQTRAEGQRQ AQEYEALLNIKVKLEAIEA/TTY RRLEDEDGEDFNLDALDSSNS MQTIQKTTTTRRIVDGGKVVSETN DTKVLRLH
9375	39743	A	9435	1	618	AEHLKPLPADKQIETGPFL VSHLPFFDCLGSPVFTPIKADIS GNITKIKAGYDTNQPRFRTLKT ILEGEKEMYGAKGPKVGATLA LMWLKRGRLFIQVFLQSCDGE RDEHNPNLRV NATKAYEMAL KKYHGWIVQKIFQAALYAAPY KSDFLKALSKGQNVTEEECLEK IRLFLVNYTATIDVIYEMYTQM NAELNYKV
9376	39744	A	9436	1	1569	
9377	39745	A	9437	211	368	ERNLSQLQWDNPTTPATRRPS HSSLRGEHAQ*GLLSFFERLST LSRFMPI
9378	39746	A	9438	1435	1703	
9379	39747	A	9439	1	913	MKNYNCWRRVFLFVVTPIPMG HIKHQQGPNKQGRGQKRDQER MRKENRGHRKGCTWCGGGTE GTGWGKYEKSEVERGLVRYER KRRAYSGIQQYAAAAALPTVYN QNLLTQSSIGAAGSQKEACAY AVMSLASRAPVYVSFDSEKAG DREVQRTMLELLNQLDGFQPN TQVKVIAATNRVDILDPALLRS GRIDRKIEFPMPNEEARVARIMQ IHSRKMNVSTDTTLVALQMAL NVYNGKQAPYASCHIFELYQE DNGFLLLEHTGFVSYDNPVSAQ AAIQSMNGFGIGMKRLKVQLK RSKNDSEKPY
9380	39748	A	9440	3	438	
9381	39749	A	9441	1	247	AIAAIDSDDSGSRQSEWFKWK GFTILDAIKNIYDSWEEVKMST LTEVWKKLPI LMSDFDFNEE VTVDVWECTVLQTI

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9382	39750	A	9442	93	726	TSLGLSLCPRQCKRCPHLSLQQ EEDPANLEVDHDFQDKVWP HLALRVPAFETLKVQSAWAGY YDYNTFDQNGVVGPHPLVVN MYFATAFSGHGLQQAPEGIGRA VAEMVLKGRFQTIDLSPLFLTR FYLGEKIQENNIILRHVCSGIG LPLACNPWLCLKSLVCLPIFP KVLCPGLLSPPVSSSSQAGHW HPIWAGQGTGSEAEQG
9383	39751	A	9443	1	849	MSGALDVLQMKEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHS/DPEEIE KEEQAAA EKA VTKEEFQGEWT APAEFTATQPEVADLSEGVQV PSVPIQFPPTDDWSTQPATENW SAAPTAQATEWKMQQQSTILE AESSPHQTPNLPAWRSRTSQPPE
9384	39752	A	9444	1	1575	
9385	39753	A	9445	1	2325	
9386	39754	A	9446	1	1149	
9387	39755	A	9447	85	1041	REIVTMSGALDVLQMKEDVL KFLAAIGTHLGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWEKL LLAAVRAIVAIENPADVSVISSQE ILGQKGAESFAAATGATPICW ARFTPWNLSTLQIGSPSGEPR AFLLVTDQGLNHQPSHGGNL NV*PTLPLALVNPDSPLRRYVD IAIPCNNQGSSSLQWGLMWW/M LASGSFCAMRGTSIREHPWEV MPDLYFYRDPPEIEKEEPCCL RSQVTKEEFQGEWTAPAEFTV VTQPEVADWSEGVQVPSVPIQ QFP/TTEDWSAQATEDWSAAP TAQATEWVGATTDS

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9388	39756	A	9448	1	762	MGKVKVGVNGFGCIGRLVIRT ACNSGKVDIIAINDPFIDLSYMV YMFQYDPTHGKFGHTVKAENG KLIVINGNPITIFQEPDPSKIKWG DAGTEYVMESTGIFTMENAG AHLQWGAKRPQGLQNIIPATT/ GAAKAVRKVIPELNGKLTGMA LRVPTANVSVDLTYHLEKPA KYDDIKKVKQASEGPKLGILG YTGHQVVSDFNSDTHSSTFNA GAGTALNDHFVKLSISWYDNEF GYNNRVVDLMAHMASKE
9389	39757	A	9449	93	660	DTMGKVKVGVNGFGRIGRLVT RAVAFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFGHTVK AENGKLVINGNPITIFQERDPSK IKWGDAGAEIYVVESTGIVFTT MEK/ALGAHLQGGSQKHSSL APSLMPPMFVMGVNHEKDD NSLKHISNASCCTTNCLAPLAK/ VIHDTLVSGEGLKDHRLAP
9390	39758	C	9450	554	715	
9391	39759	A	9451	193	472	RRVGWVRRPQFQQSRCSHGPN QGSAPWLNPTGAFGKETDLLA/ DDSLVSIFGKRRL/KRFSMVG/D RMASKNALNAQPDGPGLTCSL APNIISQL
9392	39760	A	9452	1	864	GTRMGLAGVCLRRSAGIYLV GGAG/WSVLAPRAAAARRCSE GEWASGGVRSFSRAAAAMAPI KVGDAIPAVEVIFEGEPGNKVK PGKSLFKGKKGVLFGVPGGPPP LGCSKTHLAKGLWEQG*RLCK AKGSRVVALF*VVNDALCDW AQWQAPQGGKARFGLLAESP LGPFGLVETDLL/LDESLSVSHLL GIRRLK/RFSMVVQDGI/KAL/ NVEPDGTGLHLAAWAPNIIFTA LEALGPDLLPLPPYSSPCPALC LGPLQFGNVGQISAINTLWVLR PKQKKKKKS
9393	39761	A	9453	1	239	QCCSGGTHGNPAIGDRIMQKQI LPWAPAQMKIRFMAPPERKYS VWIAAPILASLSTSSRMWISKQE YDESGPSIVHRKCF

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9394	39762	A	9454	2	801	ASAPRAQSLAFADPPPVHTRRQ LTMDDDIAALVVDNGSGMCKA GFAGDDAPRAVFPISVGRPRHQ GVMVGMGQKDSYVGDEAQSK RGILTLKYPIEHGIVTNWDDME KIWHHTFYNELRVAPEEHPVLL TEAPLNPKANREKMTQIMFETF NTPAMYVAIQAVLSLYASGRTT GIVMDSGDGVTHTVPIYEGYAL PHAILRLDLAGRDLTDYLMKIL TERGYSFTTTAEREIVRDIK/EE AVLRRPGLRARDGHG\ASSSL EKSYELPDGQVITIGNERFRCPE ALFQPSFLG\MESCGIHETTFNSI MKCDVDIRKDLYANTVLSGGT HQFPLPCRPGC*KKITALEPIAT MKIRIIA\PEEAQSTPLWNRGAP ILASLVHLPKMWQKRSREYD ESGPLPFVHRKICFQLLPGEELR
9395	39763	A	9455	3	108	
9396	39764	A	9456	1	1430	MKFLIFAFFGGVHLLSLCSGKAI CKNGISKRTFEEIKEEIASCGDV AKAIINLA VYGKAQNRSYERLA LLVDTVGPRLSGSKNLEKAIQI MYQNLQQDGLKVVHLEPVRI HWERGEESA VMLEPRIHKIAIL GLGSSIGTPPEGITA EVLVVTSF DELQRRASEARGKIVVYNQPYI NYSRTVQYRTQGA VEA AKVGA LASLIRSVASFISYSPHTGIEYQ DGVPKIPTACITVEDAEMMSRM ASHGKIVIQLMGAKTYPDPT SFNTVAEITGSKYPEQVVLVSG HLDSWDVGGAMDGGGAFIS WEALSLIKDLGLRPKRTLRLVL WTAEQGGVGAFQYYQLHKV NISNYSLVMESDAGTFLPTGLQ FTGSEKARAIMEEVMSLL/QPL NITQVLSHGEGTDINFWIQAG/V PGA/SLDDLYKYFFFHHSHGD TMTVHGQTQMECLLLFWAV VSYVIVADMEIEMLRPS
9397	39765	A	9457	2	631	
9398	39766	A	9458	1	406	PTVCERELCVFAQTLLGVMNE AADEIATGAQVVDLLVSMCRS ALESPRKVVFEPYPSVDPNDP QMLAFNPRQLKFMHTPHQFLL LSPPAKESNFRAAKKLFGSTF AF/HLHGAMYSGGIYLSMSSIS FGYSA
9399	39767	A	9459	7	257	

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9400	39768	A	9460	2	649	
9401	39769	B	9461	50	607	
9402	39770	A	9462	627	1665	EQAGQALSTAPVGDGHELLCE VGSSSFRDVLGTSMGLCGGY/G GAS/GMGGITAVTVNQNVLSPL NLEVDPNMQGMHTQKEQVK TLNKSASFVDKVLFEQQNKM LETNWSLLQQQKPAQSNMDN MFESYINLLGQLEILGQEKLK LEAELGNMQGLCMFFVKEDFK KKYEDEINKPTMENEFVLICK DVEDDAYMNKVELEFRLEGLTD EINFLRLYEEEEPELQSQILDTS VVLSDMNSRSLDMSIIAEIKY EELQTLAGKHWDRLTKTKIS EMNRNISRLQAEIEGLPQRPEQ RASLESVIADAEQRGELAICKDA KTKLSELEAAQRAKQDMAHG
9403	39771	A	9463	2237	2656	LSCSLFSGFAGTRFFGTSILRLPL MYCPVNDSGTAAIASSGSPSATS PP*TPAPGPMISITWSAARIASSS CSTTITVLPRSRRWISVFNRRSL SRWCRPIDGSSSTYITPTRPAPI WLAARRIRCAPSPESVSAERESV
9404	39772	A	9464	3	2790	EFVLIKKDIVDEAYINKVELES LEGLTDEINFLRLYEEIEIRELQ SWISDTSVVLSDMNSRSLDMNS VIAEVKAQYEEIANRSQAEEAS MYQIKDEELQSLAGKHGDNLR CTKTKISEMNRNISRLQANEG LKGQRAFLEAAIADAEQCCELA IKDANAKL/SELEALQRAKQD MAWQLRLMNVRLALDIEIATY KKLLEGEESRLESQMNMNSIHT KTTSGYASGLSSACGGTSPGL SYGLGASSFSRT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
9405	39773	A	9465	2	1516	SAIPTSTPASTMSIRVTQKSYKV STSGPRAFSSRYTSGPGSRISSS SFSRVGSSNFRGLGGGYGGAS GMGGITAVTNQSLLSPLVLE VDPNIQAVRTQEKEIKTLNNK FASFDKVRFLEQQNKMLETK WSLLQQQKTARSNMDNMFESY INNLRRLQLETNLGQEKLETK LIGNMQGLVEDFKNKYEDEINK RTEMENEFVLKKDQVDVDEAY MNKVELESRLLEGLTDEINFRL QLYEEIEIRELSQISDTSVVL DMSRSLDMSIIAEVKAQYEDI ANRSRAEAESEMYQIKYEELQSL AGKHGDDLRRKT*DLRL*TRN ISRLQAEIEGLKGQRASUEAAI ADAEQRGELAIKANDANAKLSE LEAALQRAKQDMARHLR*VTR ELD*TFKLGPGTFEATYRKLL EGEESRL/ESGMQNMSIHTKTT GGYAGGLSSAYGGLTSPGLSYS LGSSVFGSAGSSFSRTSSRAV VVKKJETRDGKLVSSESDVLPK
9406	39774	A	9466	1410	3244	PPCRSRHPRLRGEQKPRPSQP PFAVPAAPAPQV*PQMIDLCNV GFQFYRSLHFHGGKPVKQEPK PSAVWPQPTPTPLPTPYPPYYPK VHPGLMFPFFVPSSPFPFSRHT FLPKQPPEPLPRKAEPQSEET KQKVERVDVNVQIDDSYVVDV GGSQKRWQCPTCEKSYTSKYN LVTHILGHSGIKPHACTHCGKL FKQLSHLHTHMLTHQGTRPHK CQVCHKAFTQTSHLKRHHMQ HSEVKPHNCRVCGRGFAYPSEL KAHEAKHASGRENICVECGLDF PTLAQLKRHLTTHRGPIQVNC ECDKTFQYPSQLQNHMMKHK DIRPYICSECGMEFVQPHHLKQ HSLTHKVLRLWWGGRGLGK RSGALSRLGSRTPVPLCTLPR GGLQGEIQAQSESEFSPVCNHSP GVIAELKQGPSGVPEILPQLNS CPTKGTCRYYPEGSRLPSAGTI NKGPRLGFSRKGDHSLTSGAPL YVGKESKVHFRAYEDPGVKEH KCGICGREFTLLANMKRHLVLIH TNIRAYQCHLCYKSFVOKQTLK AHMIVHSDVKPFKCKLCGKEF NRMHNLMGHMLA/RNGKPLK RLYCPSKFTLKGNLTRHMKVK

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9407	39775	A	9467	1	1309	MRIQQLCGHLWQQKKSLELM SSFHKLKMKMGCGVTPDSKEL LKYLSYCNSTPLTQSPQEA PVS DVPLPVSKCSHCSVQLIMCLRP EHIIPNSPGIKGGQIKQHEEKHPT LLHLDASHLMTCFVVEMLTYV LIAGFKSLCSIHSYPPRTLRLHC EKVWDSLENERRHEKRGAN FLHRLPAEHQWGVQSSNIMAG LSARLQFLFHRFPFVFELTAN GCPTKGLQGEIQAQSEFSPVC NHSPGVQIAELKQGPSGVPEILP QLNSCPTKGTCTRYYPEGSRLPS AGTINKGPRLGFSRKGDSHLS TS GAPLYVGKESKVHFRAYEDPG VKEHKCGIGREFTLLANMKR HVLHTNIRAYQCHLCYKSFVQ KQTLKAHMIVHSDVKPFKCKK SFTAQGNAPQEDAGSQGE/PV CLL/CPNWGQQRKGRAWRLRH
9408	39776	A	9468	3	4804	KRLNIQKTLFVAFSEAVWMQ PSVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIPPNQE QRCEILCNVIKKNLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPFLFANLPIRQRT GILLYGPPGTGKTL
9409	39777	A	9469	2	1844	
9410	39778	A	9470	3	772	VPNPYTLTSQIPEEAEWFTVLD LKDVFFCIPVHPDSQFLAFEDP LNPMSQLTCTVLPQGRDPSPL FGQALAQDLSQLSYLDTLVQ YVDDLLAACSETLCHQATQA LLNFLATCGYKVSKEAQLCS QQVKYLGKLKSKGTALSECI QPILAYPHLKTLLQLREFLGITG FCRIW/NFQALLLERPVQLCTC ATLNPVTFLPDNEEEYNCQHI SQTYATRGDILLEVPLTDPDLNL YTDGSSFVEKGPQKA

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9411	39779	A	9471	1	6504	MWGSDDLGAAGGGGAATVA FTNARDCLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDOGENVAEINRQVGQKL GLSNGGQELHAVSLQHLDDQI RIVFPKAIFFVWVDQQTIFYIQI VALIPAASYGRLETTDKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMLKELQTKLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSQSEKKQETSWG LTEINAFKNMQSKVVPL
9412	39780	A	9472	2	1658	
9413	39781	A	9473	1	617	MCSWTPVSSILTHPNWPVLR MAGLTGCASVAMKKKIEHNCQ QVIAQTFTTRGDLLEPLTDPGL NLYTDGSSFVEKGLRKAGYAV VSDNGILESPLTPGTSQAEL IALTWAPLEEGKRVKRRKAI WRERFLTSEGTPIKHQEAIRRL LLAVQKPKAVVLCRGRH/QE GNCQVDIEAKRATRSQVARGH KICDFPSCSYR
9414	39782	C	9474	587	715	
9415	39783	A	9475	96	269	
9416	39784	A	9476	1	1398	
9417	39785	B	9477	1	1152	
9418	39786	A	9478	3	241	
9419	39787	C	9479	202	534	
9420	39788	A	9480	108	199	
9421	39789	A	9481	125	352	
9422	39790	A	9482	2	325	RRSLALSPRDCQLQWHNLGSL QAPLPGFTFSCSLSPSSWDYRR PPRPANFLYFLVETGFHLVSQ/ SGLDLLTSIDPPASASQSAGITG VSHRARPNQLFFKVRCE
9423	39791	A	9483	184	383	LGLQWRNLGSLQAPLPGFTPFS ICLSLSPSSWDYRRPQRPANFFF FVFFLVKGTGFHLVSQ/GLDLL TS*SHPASAFQSAGIIGVSHRRP AITLQF
9424	39792	A	9484	1	416	MGRSFLGGGSLMLLGGGQLH ILTPSPSWTETGNYTCEFCGKQ YKYYTPYQEHVALHAPIRNSA KDDHRSASILSENRRGSHQ/SHAS CHHHYHCHYYHQHHHCLHHH SYHHHHCHHHHRGMWRNWDTV LWIHQTPQVQD

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9425	39793	A	9485	3	534	GRRQRRSRHLLHRRQDRQSA PGSGKIPQKVKVLADEDDDD DDEEDDFDEETEEAPVKKSIQ DTPARNAQKSDQNGKVKSPSS TPRSKGQESFKQEKTPKPKG PRSVEDIKTKMQASIEKAHGT VIGTTVGNIPLRGGNQEKFHGA GVWFGKFGVQRKIQQKQLQKD VTSGS
9426	39794	B	9486	44	924	
9427	39795	B	9487	41	2197	
9428	39796	B	9488	67	1507	
9429	39797	A	9489	134	311	
9430	39798	A	9490	5	1545	EKIQINTI/KNDKGILPLDPT EIQITIREYYEHL YAHKLENLE IDKFLDIYTLPLRNQEELES NRKPN TACSNLRDGSLLLDG DGHGSSIQAAIEVVGAGSV ATKGRGRQDDTDP SNRYHRPPYSQEEKEQCITL LLSWCLGDSQGPQCRPQLS QELRRFTVSLHLARKLLSE VRGQAHRFVSPNNAAGAGD GQTPNPFWPPLTDLAPQ AESHLPGVNLVYLPL LGEQLPDVSLTFQAWRRLSV KCTAVRAYQITRVVETSS CRLHVKGASNASTHRSPKE VTQGTNKSERRTRETQRA IRERNMAGCCTCATDVL VTLQSLMEGLALQPQ RTRALLGASIKASCAVT IIMSENKKGCKSKSEGM VRRYAKHKKQEIKPY YQRKSPSLERGQEEK KVGREDSSENQYLYG PSNISEARNRLPECGR MGLGYVARLFLGDRS STPSFASYDPSSLVTY GHRRCRVS DIRVPLGPNVGGPCKGT GIDLQCE REKKN
9431	39799	A	9491	32	2123	
9432	39800	A	9492	1	911	MSTLKLGIKIIISVMIASE FILEERIKTGLNAAKHCF AAPSQAASH TISRPI MPIRSASACSTPTH TPQDSL TGVGGDVQEA FAQSSRRNLRNDLL VAADSI NTMSSLVKE LNSEV GSETESNV DSEFARTQF EDL VSPSTSEKA FLAQIHARKPGYI HSGATTSTMRGDM VTGIDANPYVQPE DENYENDSV RQLENELQME EYLKQKLQDEA YQMPLVPTKKEI HMFLLSLPEGA IAQCPRTFIPDC RRKGASYSQTD DES NMKTGDDG EPCGHTTEED SSLAAASPKRG TTPSSS

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9433	39801	A	9493	2	2233	
9434	39802	C	9494	477	737	
9435	39803	A	9495	2	746	GQATHFMAKEV*QWAHAHGHIH WSYRVPHHPEAAAGLIEWWDCL LKSRLLQCQLGDNTLQAWGKVL QKAVYALNQCIYGTVPIDRI HGSRNQRVEVEVEVAPLTITPS DPLAKFLLPGLTTLCSAGLQVL VPEGGMPLPGDTTTTPLNRKLR LPPGHFGLFLPLSKQAKMRVTA LAVVIDLDYQDEISLPLHNGDK EEYARSTGDPRLRLVLPCEVIE VNGKLQHNLRGTTNGPDPLG MKVWVSPPG
9436	39804	A	9496	70	532	HVALLMPLQNSRFSGYGFAYP ARNTFSTTIHGLKECLIHGHI PSSIASDQGRFLPKFV/RKWAH AHGHIWSYHVPHYPEAASP/HS DPLAKFLLPVPTTLCSAGLAVL VPEGGMPLPGDATMIPNLSSR SHLGMPPTSLKVVVMCSKDKY
9437	39805	A	9497	51	408	CVPEPTPSLGFQT/HPAAHAPG AQAPGSAH/DRLSSAGPGSRAA PRAPWRPWTIGYSESQPTVL/RP GQPWPGRGVSGSSAPSVPSALR GPPRSSRPSCTTW/WCLWCRRH RDLGRDINFLL
9438	39806	A	9498	3	618	SSCAFHSRRSPSRCHTVRRSTA PCAAS*HSSRAPKRHWALPGSS G*S/WRETPSTHW*P*TLPRWRT ALRPSQ*PRPRVFRVRKPCSSRP PTITRCALASQA*SCAA'PTSSLA QRKSSSRPRRTATTWGTAARRSR AHAVPAGRSPAPSPAPPQAP RAWSAAPASPSRLSSAGRGRO AAPRAPWRLRGPSPRSCTCT WWCP
9439	39807	B	9499	215	293	
9440	39808	C	9500	1	1170	
9441	39809	C	9501	25	481	
9442	39810	A	9502	27	265	
9443	39811	A	9503	2	326	GRVGGRVGSDLRGDMAKRT KKVGIVGKYTRYGA/SRVRK MVKKIEISQHAKYTCF/CGKT KMKRRAVGIWCCGSCMKTVA GGAWTYNTTSVIVKSAIRRL KELKDDQ

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9444	39812	A	9504	2	1125	RVGRPLPPRPPTHPRRKPLPPNN VTGKPGSAGHSSGPITTPPLRST PRPTGTPLERIEDIKQPTVPAS GELENITDFSSSPTRTETDPLGK PRFKGPHVRYIQKPDNSPCSITD SVKRFPKEEATEGNATSPQNP PTNLTVVTVEGCPFSVILDWEK PLNDTVTEYEVISRENGFSFGK NKSQMTNQTFSTVENLKPNTS YEFQVKPKNPLGEGPVSNVAF STESADPRVSEPVSAGRDAIWT ERPFNSDSYSECKGKQYVKRT WYKKFVGVLQCNLSRYKIYLS DFLTGKFYNGDQGRGHGEDHC QFVDSFLDGRGTGQQLTSDQLPI KEGYFRAVRQEPVQFGGIGGHT QINYVQWYECGTTIPGKW
9445	39813	A	9505	2	385	REAGSGGNDNFARRRNFSGRG G\FGGSRGGVWVWVAVGDGY NGFGINDGSGNF\GGGSY\NDF WENTNKSGLQNFPGHEGGEIFG GQKLLAPYGGWRPNTFAKPTK PQGG\YGG\SSSS\SSYGGKWPEDF
9446	39814	A	9506	945	2313	TRVLLESRAGSQSQSEGEASWQ RGYARPSCQAAISFPEHRRALR ALWAGDCRVADAGPGSSSTPP SPPSLPKTSVSLGFLCFKKSLLAA SCASGRERQLEA*VWASQPLSP TQWSEGLGVVWASQPLSPT QWSEGGQ/PGGPSVGISTSLTYPV EGRT/GWGPECYVFCMLHRLPE QHDCTFDHMGGRGREAIMKM VKLDRKVGRSCQRIEGGQED DVVASILVSMQPHSPRTSPHLP YSKFDFSSCNCARQGWKEMG ACVQRPSAVLGGTRPVSVQAK QPLPCFLLGASALGSCGTGLGV KDRDIDRIVVMSVMKILRGNQR PSGDEQARGQRAREGGLGLGV RRACREQWAVLCPLVHRNWV CVSSFLIASQSNSPQQQHNCY ANNSPQQEEGMVGRQAETFL GGVRNRKPWVGVRGLQGSH QQHIQGA VSSPSPKKGVSKRE
9447	39815	A	9507	3	684	

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9448	39816	A	9508	15	513	RIRLEGLWGSSKTMNLCSKCFADFQKKQPDSDSAPSTNSQSDFSEETSDNNNTSITPTLSPSQPLPTELVNTSPSKEEYSQSENEASPVKRPRLLENTERSEETSRSKQKSRRCFQCQTKLELVQQELGIMCRCGYVFCMLHRLPEQHDCTFDPHGAVAGR
9449	39817	A	9509	818	1455	SDYITRDGASFTKALLTWKNPVPNFFWKDFTKLWGEVIRSTMWKT/DQSPSAAWGGFGAQQPQQGAPPVIPPNNQAGYGMASYQTQILPSPHILAVFMLPERGPNPDPKRGFLDLARKNLGNWVSTITFLSRFGVQVLQEFVVPGTMLPLRPLELPMHFNPHFSTALASLIADELYLLPQLSVSQMGESFPSPDMMMAICAQASTNRLWMP
9450	39818	A	9510	1	1132	MMEDDGGQRTLYVGNLSRDVTEVLILQLFSQIGPKCKSMITEHTSNDPYCFVEFYEHRDAAAALAAAMNGRKILGKEVKVNWATTPSSQKKDTSNHFHVFGDLSPEITTEDIKSAFAPFGKISDARVVKDMATGKSKGYGFVSFYNKLDAENAIVHMGQWLGGRQIRTNWATRPPAPKSTQENNTKQLRFE DVVNQSSPKNCTVYCGGIASGLTDQLMRQTFSPFGQIMEIRVFPEKGYSFVRFSTHESAHAIVSVNGTTIEGHVVVKYWGKESPDMTKNFQQVDYSQWQQWSQVLGNPKPSDRIYMANGWQVPPYELYGQPWNQQAQGVDDQSPSAAWMSGFGA/QPP/QGQAPPVIPPNNQAGYGMASYQTQ
9451	39819	B	9511	1	1212	
9452	39820	A	9512	1	1032	

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9453	39821	A	9513	17	976	SGRP/GGPGGPGMGKPRCF/RGE VFGIVIRGPGFPFGRGRGRVGR GARGGKGPRIKGLGCPSTKLGL RLVKDH*RSKFPWRRSIYSYSG PLKESEIDFGLGGLLSKDEVFE RLCQVQEPEPVPQGRHQGSRHF VATGNVQWPTVGSGLKCSQE /VWPTAHPVGPILAKLLHSSPC AEGYWGEQSIGKAP/HTVPCQ/ VWTGRGCSVLVRPHPWHPGRS GIVSAPVAKKLLMMAGIDDCY TSARGCTATLGNFAKATFDAI SKTYSYLTPLWKETVFTKSPY QEFTDHLVKTHTRVSVQQTQA PAVAYNIGLVYKKNKVN
9454	39822	A	9514	1	866	
9455	39823	A	9515	1	1793	MAAAAVSGLGRAGWRLLQL RCLPVARCRQALVPRAFHASA VGLRSSDEKQKQPPNFSQQHS ETQGAEKDPDESSHSPPRYTDQ GEEEEEDYESEQLQHRILTA LEFVPAHGWTAIAAEGAQSLG LSSAAASMGKDGSELILHFVT QCNTLRLTRVLEEEQKLVQLGQ AEKRKTDQFLRDAVETRLRMLI PYIEHWPRALSILMLPHNIPSSL SLLTSMVDDMWHYAGDQSTD FNWYTRRAMLAAYNTTEL VM MQDSSPDFEDTWRFLNRVND AMNMGHTAKQVKSTGEALVQ GLMGAAVTSRPRRGGWVPLG EMPYANQPTVRITELTDENVKF IIENTDLAVANSIRRVFAIEVP AIDWVQIDANSSVLHDEFIAHR LGLIPLISDDIVDKLQYSRDCTC EEFCPECSVEFTLDVRCNEDQT RHVTSRDLISNSPRVIPVTSRNR DNDPN DYVEQDDILIVKLRKGQ ELRLRAYAKKGFGEHAKWNP TAGVAFYEYDPDNALRHTVYP KPEEWPKSEYSEDEDESQAP YDPNGKPERFYNNVESCGLSRP ETIVLSALSGLKKKLSDLQTQLS HEIQSDVLITIN
9456	39824	A	9516	3	176	FFFFFAETNSK*ITYQNIHIMVEI FQNSIFWDLTYTKDKQIRGQEA RREKRGLGRPL
9457	39825	A	9517	1485	1679	RVGDAGHDDPGKPGPPGAGHR PEG*TAHSLRAGLPACRAEPA GPGRAREGSKAPGHCABELLQ

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9458	39826	A	9518	1	232	FFFETESCVAQAGVQWCDLG SLQTLPTG/SSRHSPASAFRVARI TGARYHVRLLFVFLVQGLHHL GQADFLLTS
9459	39827	A	9519	1	2408	GTLVTKVAPVSAAPPKVSSGPRL PAPQIVAVKAPNNTTTIQFANLQ LPPTVLIKSNSGPLMLVSPQQT VTRAETTSNITSRPAVPANPQT VKICTVPNSSQLIKKVAVTPV KKLAQIGTIVVITVPKPSSVQS VAVPTSVVTVTPGKPLNTVTTL KPSSLGASSTPSNEPNLKAENSA AVQINLSPTMLENVKKCKNFLA MLIKLACSGSQSPMGQNVKK LVEQLLDAKIEAEFTRKLYVE LKSSPQPHLVFLKKSVVALRQ LLPNSQSFQCCVQQTSSDMVI ATCTTTVTSPPVTTTVSSSQSE KSHVSGATAPRTSVSVQTLNPLA GPVGAKAGVVTLHSGVPTAAT GGTTAGTGLLQTSKPLVTSVAN TVTTVSLQPEKPVVSGTAVTSL LPAVTFGETSGAAICLPSVKPV VSFCWDHICKPVIGTPVQIKLA QPGPVLSPAGIPTGSSSKQLFS LFHVQQPSGGNEKQVTTISHS STLTIQKCGQKTMVNTIPTSQ FPPASILKQITLPGNKILSLQASP TQKNRIKENVTSCFRDEDDIND VTSMAGVNLNEENACILATNSE LVGTLIQSCKDEPFLFIGALQKR ILDIGKKHDITELNSDANLISQ ATQERLRLGLEKLTIAQHRMT TYKASENYILCSDTRSQLKFL KLDQLEKQRKDLEREMLLKA AKSRSNKEDPEQLRLKQKAKE
9460	39828	A	9520	1	637	MLSNVVRGRKLPNGTWAHDL VTPPTASLLLLTEPAMPSPAFC HSILIVTKGGVKRTRVPPPNSS GARTGNPLKVKHISFKTGDELIF LDPHITQTTFVDTEENGTDNDQT FHCLQSPQRMNINLDPVSALG FFCKEEKDFDNWCSLVQKEILK ENLRMFELVQKHPSHWPPFVPP AKPIEVTTTGAEFNDSTEQLAEF DLAEEDFEILSV
9461	39829	A	9521	3	176	
9462	39830	B	9522	1	792	

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9463	39831	A	9523	2	486	NGHVGLGVKCSKEVATAIRGAI ILAKLSIVPVRGYSWGNKIGKP HTVPCKVTGRGCVLVRLLPAP RGTVISAPVPPKLLMMAGIDD CYTSARGCTATLGNFAKATFD AISKTYSLTPLLKE\TVFTKS P*QELTDHLVKTHTRVSVQRT QAPAVATT
9464	39832	B	9524	1	2991	
9465	39833	A	9525	3	263	KHENWSTARQSLHACSRVTWQ NRLRLSNKWMPSHVLCLLP/S MTLQPANLSSLLITPPEFGPKIA SPICTSCSVNFRRLISPFSHC
9466	39834	A	9526	1022	1201	
9467	39835	C	9527	1	924	
9468	39836	A	9528	2	837	WKNCLEKRSM\TMHRILES*D* RQE/ILERHDAKYHSPKAEKQ MKHKAGSQIVKKEEAKLALAL EGFCRFRNHHQTGFSPAGATQR GPLVAILSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGFTGKRAWPPFRL FLPHKGFADWGPTINQDFRLLG QPSVARFLNFSQGPAGEGQSAV ARLPGHFFITQPYPLPGYAAAAG MQALARRRRPLMFDSLSSNFCH SSAYYHLFRRSNQAFKGTNNCL KKITPRPATHRSTVVIH
9469	39837	A	9529	3	1137	APAPSPVSGSGCCLSHMFFHPPS RANRAFDVYAPMDEIQNAEIN SQVRRYLEGLTDEIDVRNPSVT TMLSQGPSPGHTPTHALLAS EPHVNGCKTVSTVEDYSGSSE SSNDESDSED\TSDSSIPRNL QSVVAVPKNSTLPMETSPCSS RSSQSYRHYSDHWEDERLESRR HLYEKFESIASKACPQTDKFFL HKGTEKNPEISFTQSSRKQIDNR LPELSHPQSDGVDS\TSHTDVKS DPLGHPNSEETVKAKIPSRQGE ELPIYSSDFEDVPNKS\WQQTTF QNRPD\SRGLKTEL\SFSSSC\IPH VDGLHSSEELRNLG\WDFSQEK STTYQQPDSSYGACGGHKYQQ NAEQYGGTRDYWQANGLLGS
9470	39838	A	9530	1	1857	

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9471	39839	A	9531	1	989	MEDWKVRGHQEKTLAEVQSF SCSERETTLVLRLSPAVPQLLL HGLCGPDLSTKAAQCHFKAIW QSLGNTLGAUSDQATPGHVKS LPPGALISRQGRGQFCSVDAVF LLHDSPELPSSLPHGASLPASS DKQAEQTLWGA VGS VQCTSIT ACPRDLED RPHLTEHPAGVHC GQNPCPCHLIFTLYSKSLPLDLA CRIWDVFCRDGEEFLFKTALGI LKLFE DILTKMDFIHMAQFLTIR LPEDLP AEELFGPSIATIQMQSR NKKWAQEPGHELEWPD RSFRP RVLACPMGSRHRLQPA CSGST GQGHTKALFPETCCQSP IQDA
9472	39840	A	9532	2013	2270	
9473	39841	A	9533	3	744	
9474	39842	A	9534	190	991	SVLSNKQNHCSQTAPPPPPAA SGSRGWVWGLFWGLAAILEGS TGADWSQLPHSCCPSLLVPHVL SVVPLRPPHRDFPVEDVFTLPV YFSSDWLNEFDALD VDDYRF VYAGPAGSWSPFHADIFRSFSW SVNVCGRKKWLLFP PGQEEAL RDRHGNLPYDVTSPALCDTHL HPRNQLAGPPEITQEAGEMVF VPSGWHHQVHNLD DTTISINHN WVNGFNLANMWRFLQQELCA VQEEVSEWRDMPDWHHHCQ VIMRSCSGIKL
9475	39843	A	9535	1	885	MKRRAVMGPQVQAWKALDL WESSQVMEGKAVVPMGRNPM MRKATQGQLENSPALEKLLPPL QGNVGFATKEDLTEVRDLLL ANKVPAATRAGAIGPCEVTVPA QNTGLGPEKISFFQALGHTTKIS RGTTILSDVQLIKTGDRVGAS EATLLNTPNISPFSGFLVIQQVF NNGSIYNPEVLDITEETLYSGFL EGVRNVASCLQTGYPPVASVP PSII/NGYKGCLALSVETDYTFPP AEKIKTFLADPSAFVAAA PVAT TATAAPAAAAA PTKFENEESSE LDEDMGFGLFD

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9476	39844	A	9536	65	988	RTAVMPREDRATWKSNYFLKII QLLDDYPKCFIVGADNVGSKQ MQQIRMSLRGKAVVLMGKNT MMRKAIRGHLENNPALEKLLP HIRGNVGFVFTKEDLTEIRDML LANKVPAARAGAIAPCEVTVP AQNTGLGPEKTSFFQALGITT SRGTIEILSDVQLIKTGDKVGAS EATLLNMLNISPFSGLVIIQVVF DNGSIYNPEVLDITEETLHSRF LEGVRNVASVCLQIGYPTVAS VPHSHINGYKRVLALSVETDYTE PLAEKVKAFLADPSAFVAAAPV AAATTAAPAAAAAPAKVEAKE
9477	39845	A	9537	1	993	MREIALTQTQCCKGKIGAKVGI RGSEVPAPAYWVAREDVSGSGS GLGGGWYVPCAVLVLDLEPVT MDSLRSRGPGLIFRPTTSSLKLE NADKTFICIDNEALYDIYSRTLK LPPTYGDMNHLLSATMSGVT MCLGFPQQLNADLQKLSVNMV PFPRLHFFMPGFAPLTSRGSQH YQALTVaelTQMIFYAKNMM AARDPRHGRYLTAAlFQGRM PMREVDEQMFNIQDKNSSYFA DWFPDNVKTAVCDIPPRG/LKM SGSFIGNNAIQELFQCVSEQF TAMFRKA/FLHWYTGEG/MDE IMEFTAEASNMDLVSEYQQY QDATAQGGGG
9478	39846	A	9538	231	881	SSLGKTVGSLPFRLLHWMPVS YSSVTTRYHHRAGAEKGKDRII FVTKKDHETPSSAELVADDPND PYEEHGLILPNGNINWNCPLG GMASGPCGGEQKSAFSCFHYST EEIKGSDCVDQFRAMQECMHK YPDLYPQDEDEEEEREKKPAQ QAEETAPlEATATKEEEDQVNE GHKALSTSPFGVLLQKALSSP SKKVSFCCPVHNIQNNLF
9479	39847	A	9539	1	804	

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9480	39848	A	9540	2	3337	SSLLEKMTSSDKDFRFMATSDL MSELQKDSIQLEDSESRKVVK MLLRLLLEDKNGEVQNLA VKW LGVPLGAFHASLLHCLLPQLSS PRLAVRKRRAVGALGHATACS TDLFVELADHLLDRLPGPRVPT SPTAIRTLIQCLGSVGRQAGHRL GAHLDRLLVPLVEDFCNLDDDE LRESCQAFAFLRCKPKEMGP HVPNVVTLCLQYIKHDPNYYN DSDEDEEQMETEDSEFSEQESE DEYSDDDMSWKVRRAAA
9481	39849	B	9541	1	3178	
9482	39850	A	9542	190	284	LNAQPGTRRLWPAEIRPPRRRL GKGGQQVSHHPPISCFYCECEE KRLCVNTHVWTK*T
9483	39851	A	9543	62	280	
9484	39852	A	9544	1	1452	
9485	39853	A	9545	2	998	ITAGATPEERVICFVEYYLTAFI EGRKGALAKKPYNPIGETFHC SWEVPKDRVKPKRTASR/PLLP AVMNTQWMTLPKSYKLRFA EQVSHHPPISCFYCECEEKRLCV NTHVWTKSKFMGMSVGVSMI GEGVLRLLHEGEEYVFTLPSAY ARSILTIPWVELGGKVSINCAKT GYSATVIFHTKPFYGGKVHRVT AEVKHNPTNTIVCKAHGEWNG TLEFTYNNGETKVIDTTLPVY PKKIRPLEKQGPMEARNLWREV TRYMRLGIDIDAAEQKRHLEE KQRVEERKRENLRTPWKPKYFI QEGDGGWGLQSPLESTLMGLEV
9486	39854	A	9546	12	740	HFFLYKKLIPFVLKNCMFHFSF VRGTVVTNDRWGAGSICKHGG FYTCSDRYNPGHLLPHKWENC MTIDKLSWGYRREAGISDYLT EELVQPLVETVFSAGNPLMDIG PHLDGTVSVVFEERLRQMGSW LKVNGEAIYETYTWRSQNDT VTPDVVWYTSKPKKLVYAIFLK WPTSGQLFLGHPKAILGATVEV KALLGHGQPLNWIFFGDKMGIM VELPQLTJHQMPCKGWG\WAL A\LTNVI
9487	39855	B	9547	1	627	
9488	39856	B	9548	47	504	

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9489	39857	A	9549	2	379	VDLVREFIERQ/HAKNRYYYYH RQYRRVPDITECKEEDIMCMEY AEMQWKRDRYKVDQEIINIMQD RLKAFQQQSYRA TQQGHPQAA SGGGSWRPLLQIFSLA ASSASV RPGTSWQNCRRPPGPDILGKQ
9490	39858	B	9550	49	707	
9491	39859	A	9551	3	1162	
9492	39860	C	9552	342	581	
9493	39861	A	9553	3	513	LLPHKPLAGFFKAYLPSEPPRV YVSSFWPQ/EYKPDTHQELFLQ EEIS/LLEDLNQVIENRLENKI/A FIRQHAIRVRIHALLARGLDPF IGPRRDWLVPVAVTGAVAFGF VEGLDPSQEHPRFQGTQDNVSK DESTRKEQSVRLVCGGADDRK PRDLQILDRDRKGPFLVQ
9494	39862	A	9554	1	1365	
9495	39863	A	9555	771	1536	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLPTGSPQSLPPYAS IPPTSPSTIK/DPPSTQM/VQKET DKGVNNEPKSGNIPQLCRLQAV GGGEFGPARVRVPFSLDLKQI KIDLKGFSDNPDGYIDVLQGLG QCQDLTWRDIMLLNQLTLPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPSGTYDTKE CKIVQSVEMSMVMIAVMSVQ RQQKGQTQQQPLL VVVRSAEP AEESVPHKSSTRGAS
9496	39864	A	9556	220	249	P*N**PSTLTGTGTTT*QIRM KVN*MGN/DSQKNTPKMYS GEFSPVRVHVPFSLDLKQIKID LGKFSDDPDGYIDVLQ
9497	39865	A	9557	2	385	
9498	39866	A	9558	84	849	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLPTGSPQSLPPYAS IPPTSPSTIK/DPPSTQM/VQKET DKGVNNEPKSGNIPQLCRLQAV GGGEFGPARVRVPFSLDLKQI KIDLKGFSDNPDGYIDVLQGLG QCQDLTWRDIMLLNQLTLPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPSGTYDTKE CKIVQSVEMSMVMIAVMSVQ RQQKGQTQQQPLL VVVRSAEP AEESVPHKSSTRGAS
9499	39867	A	9559	66	197	RQWKG*KFVFQKM*DLGKYLQ RQLFCLSSLVQPPWPVPTEIYP
9500	39868	A	9560	1	2340	
9501	39869	B	9561	1	1776	

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9502	39870	A	9562	1	1349	
9503	39871	B	9563	107	769	
9504	39872	A	9564	329	2042	
9505	39873	A	9565	511	1631	HFGNHERTSKVMGNVPRKTKT PLRRILENWEQFDPTLRKKRLI FFCSAAWPEGSINYNTILQLD LFCRKKGKWEVP*VQTFSLRD NSQLCKKCDLCPTGSLQLPPY PSIATPSPLNKDPPSTQMVQKEI DKRVNSEPKSANIPQL*PLQAV GGREFGPARGVHVPFSLPDLKQI KTDLGKFSNDPDGYIGVLQGLG QFFDLTWDRDIMSLLNQTLTPNE RSATITAARELGDLYWLSQVN DRMTTEERERFPTGQAVPSAD PH*DESEHGDWCCRHLCTCVL EGLRKRTRKAVNFVSMSTVTQ GKEENPTAFLERLREALRKHTS LSPDSIEGQLILKIFITRSAADI RKQTSKVHLRPGAKLKTPY
9506	39874	A	9566	15	178	
9507	39875	A	9567	3	826	RQLGTRNFLNGTKAKAFELSYL EKVPEGKDTVHKQSLHHVGT MGGENFPDSSDLYSEIGAITRSA KDDFDQLQDNLCQMERRCIAS WDHLKAIKHEMKPLLKQKMS ELLKDCAERIIILKIVHTRIINRF HSFLFMGHPPIAIREVNINKFC RIISEFALEYRTTRERVLQKQK RANHRENRKTRGKMITDSGKF SGSSPAPPSPQGLSYAEDAAE HGEHEGCAENLVPLQESPAHTF SIVSAVFLIP*HPVY*FKSVTPF LGKEQPL
9508	39876	A	9568	1	670	

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9509	39877	A	9569	1	2426	MPKPSLEAGSCPRLEFPVEDAQ PVIKGEETPPPPNSYLALGDIST EEWDLEVAQEYQERMPQRAA LICVFSWNLGRSLPAPAMRRPC QNFCVALSTFAGDPEPESEAE EAEAGAGQVADEAGQDIASAH EGAETEVEQALEQFPEERASLS EKERQNEGVRNDRNCSASSVSS SSSTLEREEKEDKLSRDRITGL WPAGVQDAGVNGQCGDILTNK RFMLDMLYAHNRKSPDDEEK DGEAGRTQEEAEAVASLATRIS TLQANSQTQDESVRVDVGCL DNRGVSVAFAEKFSGDLGRV FNAPQGLGWSQVPRGQPTFTK KKKTIRLFWNRN/VGLLTGH/G KNNRRCREFLWSKLEPIKVDTS RLEHLFESKSKELSVSKASKLV RPLFILTSACPLSFPWKAPLHS STRQLHRGLSAQERWRCSGIRG MECLNGKGPLESRNPAYRKSE GTRQTGAGDMKDVWQGVPA TPDTQGMCTVCTVSFAIMDGL NVNSVGPLPFHEVAEPLDLKE GIDQLDYLTLGFFFLVSMISGGG LLGGSASAKAFELSYLEKVPEV KDTVHKQSLHHVCTMVVENF PDSSDLYSEIGAITRFHSFLFM GHPPYAIREVNINKFCRISEFAL EYRTTRERVLOQKQKRAHRE RNKTRGKMITNCVRHCVRMFS GSSPAPSPQPGQLSYAEDAAEH
9510	39878	B	9570	164	346	
9511	39879	C	9571	160	339	
9512	39880	A	9572	54	212	SFSPVVLWKDLQNLKIQVPLI LLGVGLISVPGGRI*LLRTGSRK PISQVCP
9513	39881	C	9573	48	185	
9514	39882	A	9574	2	551	ADRRGAVYPRSRDGGGVGRGP AMATSVLCCLRSCKDRGTGHIP LKDMLSVHMDTQHMGTDVVI VKNGRKIFGTGGCLASAPLHQ KSYFEFKIQSTGIWGIGVATQK VNLNQIPLGRDMHSLVMKNDG ALYHNNEEKNRLPANSPLQEG D/VVDDSAILDCCQSEFYHTPPP GFEEKLFEQQIF
9515	39883	A	9575	3	655	

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9516	39884	A	9576	131	1066	SHSSAAAHPLGLLPAAQSLA VFIEPWSQASSRGQLQVSAPGI WGIGVATQKVNLNQIPLGRDM HSLVMRNDGALYHNNEEK NRL PANSLPQEGDVVLCSNNGHS LCKEESLPILPTSDGEERRRKR KKRRKKRKKQKQQQQEAAA PAEADAEATAAEAAVEEAAAR KEEEEEEGEEGEGEEEEEKAA AAARGDWSQQEKACKSSLQAI LFGHAKLEPGRLPRPTQCRVEA TVLVGTNSPLDNPLWSISWSLW QKPVGTSQQPLGLWTREFFLE GHILTRNETTFEATPLIPEIGML SQMMSEEH
9517	39885	A	9577	1	2363	ELQRDIEKHSTGVASVNLCEV LLHDCDACATDAECDSIQQATR NLDRRWNRNICAMSMERRLKIE ETWRLWQKFLDDYSRFEDWLK SSERTAAFPSSSGVIYTVAKEEL KKFEAFQRQVHECLTQLELINK QYRRLARENRTDSACSLKQMV HEGNQRWDNLQKRVTSILRL KHFIQREEFETARDSILVWLTE MDLQLTNIEHFSECDVQAKIKQ LKAFFQEEISLNHNKIEIIAQGE QLIEKSEPLDAAIIIEELDELRR YCQEVFGRVERYHKKLIRLPLP DDEHDLSDRELEEDSAA LSDL HWHDRSADSLSPQSSNLSLF ASLQPLRSER/SGRDTPG/SVDSI PLAEWDHDDYDLSDLESAMSRA LPSEDEEGQDDKDFYLRGAVG LSDVMIPESPEAYVKLTENAIAK NTSGDIHSALESQIRQLGKALDD SRFQIQQTENIIRSKTPTGPEDT SYKGYMKLLGECSSIDSVKRL EHKLKEEESLPGFVNLHSTET QTAGVIDRWELLQAQALSKEL RMKQNLQKWQFNSDLNSIW AWLGDTEEELEQLQRLELSTDI QTIELQIKKLKELPESCWDHR/K AIIISINLCSPEFTQADSKESRDL QDRLSQMNGRWDRVCSLEE WRGLLQDALMQCGFHEMSH GLLLMLLENIDRRKNEIVPIDSNL DAEILQDHHKQLMQIKHELLES

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9518	39886	A	9578	2	3248	ENAVGSWTDDLTLQLSLKDLT SAYISADDISILNERVELLRQW EELCHQLSLRRQQIGERLNEWA VFSEKNKELCEWLTQMESKVS QNGDILIEEMIEKLLKDYQEEIA IAQENKIQQLQMGERLAKASHE SKASEIEYKLGKVNDRWQHLL DLIAARVKKLKETLVAVQQLD KNMSSLRTWLAHIESELAKPIV YDSCNSEEIQRKLNQEQELQRD IEKHSTGVASVLNLCEVLLHDC DACA TDAECDSIQQA
9519	39887	A	9579	2	194	CSTSLMIREMQIKTTVRYHLTS ARMAIIKKSKNSRCWHGCGEH GTL LHCCNLWKERNVSYVSA
9520	39888	C	9580	105	215	
9521	39889	A	9581	1	210	MNSHFLKEDIQMANHKMEKCS VTL MIREMQIKPTVRYHLTSAR MPIIKSKNSRCWHGCGEHGT LLHC
9522	39890	C	9582	48	182	
9523	39891	A	9583	3	225	
9524	39892	A	9584	1	549	
9525	39893	A	9585	367	971	GVCLLGAPAGRRGSLLSLGLSR GQGSYLSKNVA VPSEATTVREL HP**\TSLQRPSPDPGGWVVLGF PCNQFGHQENRQNEIILNSLK VRSGPGGGFEAQLHGSSRKCEV NG\SGAHLPLFAFLRLEALPVPS DDGPRAL*PTPKLITWFGSVFA TIVAWNFFEKFLVGPDPVPLR RYSRAVQTIDIEPDIEALLSQGP
9526	39894	A	9586	1	129	
9527	39895	A	9587	1	406	PTVCERELCVFAFQTLGV MNE AADEIATGAQVVDLLVSMCRS ALESPRKVVFEPYPSVDPNDP QMLAFNPRQLKFMHTPHQFL LSSPPAKESNFRAAKKLFGSTF AF/HLHGAMYSGIYLSPMSSIS FGYSA
9528	39896	A	9588	2	634	SSNRSHIVKLPVNRRLKFMHTP HQFLL LSSPPAKESNFRAAKKL FGSTFAFHGSHIENWHSILRNL VVASNTRLQLHGAMYSGIY SPMSSISFGYSGMNNKKQVSAK DEPASSKSSNTSQSKKKGQQS QFLQSRNLKCVLACEVITSSDL HKHGEIWGCPPI/SDHVCTRFFF VYEDGQVG DANINTQEGGIHK EILRVIGNQTATG

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9529	39897	A	9589	3	3623	FGVCARGCLDSAGPWMTSRAL RPPLPPLCFFLLLLAAAGARAG GYETCPTVQPNMLNVHLLPHT HDDVGWLKTVQYFYGIKNDI QHAGVQYILDSVISALLEDPTR RFIYVEIAFFSRWWHQQTNAATQ EVVRDLVRQGRLEFANGGWV MNDEAAATHYGAIVDQMTLGLR FLEDTFGNDGRPRVAWHIDPFG HSREQASLFAQMGGDGGFFGRL DYQDKWVRMQKLEMEQVWR ASTSLKPPTADLFTGVLPNGYN
9530	39898	B	9590	1	3839	
9531	39899	B	9591	1	513	
9532	39900	A	9592	1	233	KQELNEPPKQSTSFVLQEILES ENKGDPNKPSGFRSVKAPVTK VAASIGNAQKLPMDCKGTVL QQASAAAFSLV
9533	39901	A	9593	3	469	LTVARSEHKVWSPLVTGEGKR HPYKMNLASEPQEVHLHIGSAHN RSAMPFNASPASSTTARVITNQ YNNPAGLYSSENISNFNNVASSL VIDKESEVYKMLQEKQELNEHP KQSTSFVWLQEILESEEEKGDPN KPSGFRSVKAPVTKVAASIGNA
9534	39902	A	9594	1	1146	MTTQQIDLQGGPWGFRVLVGR KDFEQPLAISRVTPGSKAALAN LCIGDVITAIDGENTSNMTHLE AQNRIGCTDNLTLTVARSEH/ KKVWSPLVTEEGKRHPYKMNLA ASEVPQEVHLHIGSAHNRSAMPFT ASPASSTTARVITNQYNNPAGL YSSENISNFNNC/ALESKDWLPA GVEANSRPLDHA/QPPSSSLVID KRILKVYKMLQEKQELNE/PPK QSTSFVLFQCEILLES/EEKGDPN KPSGFRSVKAPVTKVAASIG KCSRKFACVDKCVHLGFLGV FLKLRDRHRHP*VFMCCTDC GHQT*KQKGPFLWMDQIYCE ESMAPGSEVNTHPGYESGST VFPPSGAQDLDPLFLPAGLLL KLFLKCKSGPLSL
9535	39903	A	9595	65	353	

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9536	39904	A	9596	1	1974	MNGVPVGAQKRVDKEEVKNG AIAELFSEDWSDCAYKANEVSR IRPLEESELLYPILGQSKLFVLSG EWSQSSEASEEVAVTLIYQLA ESPTVICAQIWQGCQAKQALEKL EEKRTSQGDPKESPTMLPTFL MNL LSLAGDVAIQQLVHLEQA VSGELCQRRVLRREEQEHKTKDP KEKNTSFETTMEEELGLVGAA DDTEAELIRGFCKMELLDGKQT LAAFVPLLLKVYNNSGLYSNPD LSAAASPTLGKFCMISTTFCNSQ PHLLFTMLEKSPLPIVRSLI VA TGDLAIHFNLVDPWTPHLYAH LQDPAQPVWKTGVLVMTLHL KDMVKVKGQSKAL/RKMLGNF DCFQDKLSDSEIFSSFLSVMGKL QHGAKEGKAIIDFEQKLQAC HARGLDGIEELINQAGSQRAP TAKKPSTVCRHQPLASAASDN DFVTPEPRRTTHRPNTQQRAS EKKPKVVFSSDESSIKTEVEGLG YNIKL RVATQRLSFVWVMNIA EGESAVLVTVAWPECEVAVMG SLGSAARGTGKRLQEGNLQL NFVTIATKLEVSWTELGCGCVS ALFASVGTGREKAGFYQGCSE ASNIMKRGVKEVEDVQKRLI KMTVEFNLAWSLPPHMA MDQGGDRVTHTSFLRCMTLMR
9537	39905	A	9597	785	5049	ACRSRMAPQMYEFHLPSPLEEL LKSGGVNQYVVQEVLSIKHLPP QLRAFQAAFAQGPLAMLQHF DTIYSLHHFRSIDPGLKEDTLEF LIKGVYSGVSVSRHSQELPAIL DDTTLSGSDRNAHLNALKMNC YALIRLLESFETMASQTNLVDL DLGGKGKKARTKAAIHGFDWE EERQPIQLLTQLQLDIRHLW NHSIIIEEFVSLVTGCCYRLLEN PTINHQNRPTRAITHLGLVA LTRYNHMSLATVVKI
9538	39906	C	9598	134	382	
9539	39907	A	9599	117	235	KIAAPQLHVLPFLFFCMRPFAP WQPLPEPLELRPLSLD
9540	39908	B	9600	1	732	
9541	39909	C	9601	1	420	
9542	39910	B	9602	110	928	

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9543	39911	A	9603	1	868	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSLRLSEMPRKQGD YRTRIWKFEDGLSNVLVIQLNK LIICVMCLDLAIKGLRVLLVEG NDPQGTASMYHGWWPDLHIHA EDTLPPFYLGEKDDVTYAIYFT CWPGLDIIPSCLAHRIETELMG KFDEGKLPTDPHMLRLAIETV AHDYDVVIDSAPNLGIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRLDKNVDLKGFEPDD PTGNRTVQLTWQPLPEPLEL/C*
9544	39912	A	9604	1036	1119	
9545	39913	C	9605	1	513	
9546	39914	A	9606	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLDTCVV MRDPNTKRSRFGFVITYATVE EVDAAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYQKIE VIEIMTRDGSKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQGRS GSGNFGGGRGGGFGGNDNFRG GGNFGSGRGGFGGSHGGGYYGG SGDGYNGFGNDGNSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGQYFAKPRNQ/ GGYGGSSSSSYGSGRRF
9547	39915	A	9607	1	286	
9548	39916	A	9608	1	1674	
9549	39917	B	9609	531	744	
9550	39918	A	9610	1	818	YNRAMFHFAVNVKIALSLNNK NPARSKVLFLELLAAVCLVRGG HKLFLYLAFDNFKEVCGEKQRFE KLMEHFRNEDNNDIFMVASMQ FINIVVHSVEDMNFVRVHLQYEF TKLGLDEYLDKLKHTESDKLS/ VQIQAYLDNVFDVGALLEDAAE TKNAALERVELEENISHLSEK LQDTENEAMSKIVELEKQLMQ RNKELDVVREIYKDANTQVHT LRKMVKEKEEAIQRQSTLEKKI HELEKQGTIKIHKKGDDGDIALLP VVASAHCPWGQKW

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9551	39919	A	9611	1	937	MALLTLKQQQNEDLQDISHFTT TRTPRQGTTPVQKEKSEETRLEW ARRMLRRDQHSTKGKVVKRM RGFLVGLVYCDKQSGALESLLC LWNVSGNTTLSSLVEIGSKAAL GLVCGEKQRFKLMHEHFRNED NNIDFMVASMQFINIVVHVSVD MNFVRVHLQYEFTKLGLDEYLD LLDTKSTDRKQTLLHYISNVVK EQYHQVSLFYNELHYVEKAAA VSENVLLDVKELQRGMDFTK REYTMHNDHTLLKEFILNNEGK LKKLQDDAKIAQDAFDDVVVKY FGENPKTTPPSVFFPVFVRVKA YKQAEFE/NMELRKKQEALM EKLLEQALMEQQDPKSPSHKS KRQQQELIAELRKQRQVKIDNR HVYEGKDGAIEDIITVSENVLL DVKELQRGMDFTKREYTMHND HNTLLKEFILNNEGKLLKLQDD AKIAQDAFDDVVVKYFGENPKT TPPSVFFPVFVRVFKAYKQAE
9552	39920	C	9612	47	286	
9553	39921	A	9613	1	423	

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9554	39922	A	9614	1	2015	MPSVSKAAAAALSGSPQTEKP THYRYLKEFRTEQCPLFSQHKC AQHRPFTCFHWH/FPQTRRRR PLGRRDGTFNYSPPDVYCSKYNE ATGVCPDGDCEPYLHRTTGDT ERKYHVIRYYKTGTCHETDAR GHCVKNRLHCAFAHGPLDLRP PVCDVRELQAQALQNGQLGG GEGVPDLQPGVLASQAMIEKIL SEDPRWQALLPVALLRHRVAH FSDANFVLGSYKTEQCPKPPRL CRQGYACPHYHNSRDRRRNPR RFQYRSTPCPSVKHGDWEGEPS RCDGGDGCQYCHSRTEQQFHP EGPVRESGVRGVFCVQSRRPW LQTPVSGTQLKWSWHVGHHSR TINPEGDKPSRLGAPENIKRGN DFACDGRADAAGMAPHVCVFP IYKSTKCNDRMQTGYCPRGPFC AFAHVEKSLGMVNEWGCHDL HLTSPSTSGSQPGNAKRRDSP AEGGPRGSEQDSKQGVRAHGV YVFEQNHAAVFAAVHPPAPSVS SSVASSLASSAGSGSSPTALPA PPARALPLGPASSTVEAVLALE PTPSSPTSSAVQGVAGELGMGS GGQGCWSHVVGALAAVPAWT HSGDLEWDPSTIRTVNVGGGGP AARPAMTLAREPQLLVGGGCP TRNCSGPAASPQLLDDAGQG GRGERDSSQRLRPQTTHRQDT
9555	39923	A	9615	2	609	IHSLCVSPCLSPCHCLSLSPASLL VSFFCCLFLMTLFPCLCVCGSLP VHLLPSL/HFLSQVLNEYFHN CELDLVFNFYKVECFPLKSPVV PESKEIGSQVDGQSRMEQRSPA HTNRENDIAREGGSEETHSKPG KGNLEFRFRCSHLQLGECPIPP WQKERTIAQGPEPEARAAVPA GRHDTRHAVNAGCALIGSLRRP WGGA
9556	39924	A	9616	60	277	
9557	39925	B	9617	43	354	
9558	39926	A	9618	3	309	GGGQGRPGAGGQGRSDGGGQ GSPGGGSGQSPGGSGGVGGGS RGGQKPGGGGGGQSPDGGGR PLAGGASRRGRSGQAQ/CPISV SATHLAF
9559	39927	A	9619	36	363	

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9560	39928	A	9620	1	512	MLMPGLSACVRDCVAFQLQAVV LGDPSAAQCQDWTWLAASAD GTCKAVGTEDGSVYFISVYDKE SPQVVHKAFLSESSVQHVVYD QQGIFLLVGTAEKGVFIINANSS SSFQIIGFT/DGGQRHFTDIHSVS FRNRHSGSDGAFLASRSREKQV GDVHTAYITATSFHNL
9561	39929	A	9621	1	822	MKLG/VQVVITDHEKLDQIRQR ESD/ITKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVRR VLK/RIAKASGATILSTLANSKA HTSASIIIRGANDIMCGEMERSL HDALCVVKRV/LESKSMVPGGG AVEAALSILYENYATSMGSQKE LAIAEFARSLLVIPNTLAVNAA QDSTDLVTKFRAFHNAAQVNP EHKNLKWIGLDLSNGERGDNK QAGMFPEPTIVKVKSLKFATEAA ITILRIDDLTKLHPESKDDKHGG YEDAVHSGALND
9562	39930	B	9622	625	1162	
9563	39931	A	9623	202	402	
9564	39932	A	9624	350	652	SAGGYPDGGQGVHPGPPELFAAL GRLGHTLREHGHLLRYHRPG HMGRRPLPCRMGHREPGSLH* QDCPRAWQWCWPHRPGHLQD VPPPGIHLQRLSQPGP
9565	39933	A	9625	83	1503	SWNTPYNHWATKQ/LSSHSYR GGAKYEGEAVKQSLVESYTHP NSNETERSANIDTVMNWFKE DFDFVTLCYREPNDVGHFRPE AENRKLMIQIDRTIRPWDHR EETQCCQDPLSNYIKFMDLVK FDIVGYGGFGMPLPKLGQEEAL YQALKNAYPHLHIYKKEGFPEH FHLAKHDRVLPIVMYANFGYSI NGISLLYFYTHLCDKYFNVHFF HEPLSLWRAQTTPSLSHRYISLV RHMDATNLDASEAQLPGSPYP DSAPGANLSTQDLQORRLSW PYPRPRFPNAHGPALQAPRTL LLTLPPGPAPSLPPRTALGPPL QSRPGFRPVSQRRCGAHFMAP EENAGTELLQSFERRFLAART LRSFPWQGGGGAERAPAGLAG VQQTGWVSVLKPALLPREFL GSPRSGPRDPVPVPGAWPKSLA PLLPRELAAEDGVSTALGGQT RARCGVQFTIITFTF
9566	39934	B	9626	1	1177	

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9567	39935	A	9627	1	283	
9568	39936	A	9628	1	708	MPKGKEAKGKKLALAPAFVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTCFVKWPRYIRLQW QRSILYKQLKIPETKQEKKWRL LAQAE/SVGKGDLPMKRLPVFR AGVNTVTTFVDNKKAPLVVTT HDMPIELTVFLPVLCHKMGA TCCIIKGKARLGLVHRKTYTT VDFTVQNSDEKGAALVEAI GTNYNARYDETHCHWDGNVL GPKSVAHIAKLEKAKAKELAT
9569	39937	A	9629	1	836	GTRPKMPKGGKAGKKVAPAP AVVKKQEAKKVVNPLFEKR/PK NFGIGQDIQPKRDLTRFVKWPR YIRLQQRRAILYKRLKEPPAIN QFTQALADRTATQLLKLAKH YRPETKQEK/KQRL/LARAEEK AAIGKGDVPTKRPPV/LFRAGV KQSPPLVEWKEFSFVVISHD VDIELVVFLPALCRKMGVPY CIIKGKARLGRSLHKKCTTTVA FTQVNSDEKGAALVEAIRTN YNDRYDEIRRHGGNVLGPKS VARIKLEKAKAKELATKLG
9570	39938	A	9630	3	119	
9571	39939	B	9631	1	711	
9572	39940	B	9632	97	942	
9573	39941	A	9633	1	588	
9574	39942	A	9634	1	1029	
9575	39943	A	9635	1	1031	MADQKEARHSASQWKFVGF SFRGHMQVAWEADRCCKGPRP LLAEALQDLWSPRRSQDPVP ERPCRRPQQSPLPRFGSLAPLH RENNFIKDFQLADGLLVIPLPV EEQCRGVLSEPLDLQLLTGDIR YDEAMGYPMVQQWVRVSNLY RVKLSITLAAAGFTNVLKILTK SSRELLSFIQHYGSHYIAEALY GSELTCTIIHFPSKKVQQQLWLQ YQKGFLGEPKKILGSSLPRTQF LWKNHNLITKQTVSILSCGEAFI LRKGQQISFSDSLLSEFLR PGAGDQSLPTHLVKVIFPPQFS L/LCEMGTFFILFCNNINCAWGRG RGERYSQSC

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9576	39944	A	9636	3	4091	FASASAVSAAASSSSFATAATA AAARSTAAPPMAAAAGARLSP GPGSGLRGRPLCFHPGPPLLP LLLLLFLLLPPPPLLAGATAAAS REPDSPCRLLKTVTVSTLPALRES DIGWSGARAGAGAGTGAGAA AAAASPGSPGSAGTAAESRLLL FVRNELPGRIAVQDDLNTLP FFTLEMSGTAADISLVHWRQQ WLENGTLVFHVMSSSGQLAQ ATAPTLQEPSEIVEEQMHILHIS VMGLIALLLLLLV
9577	39945	A	9637	2	398	SDARVDALNKKIWERIKKHLE GHSTNLSLDIAKLKEQIFEASQA HLTLMPTGVLEGAADRLSAS NPLKWIKTLGSSVISMMIVLLIC VVCLCVVCRCS*LLREVAHRD KAAFAFIALQIKEGEHVGNST
9578	39946	A	9638	201	495	WKKTLMPGTGVLEGAAN/GLA AINPLKWIKTLGDSVISMMIVLL IC/VCLCIVCRCSRLREVAHC DKATFAFIIEKMWYGFQFCFN NSLRVIASSCIH
9579	39947	A	9639	3	409	GIYILHQKKTWEKILLAAACAIV AIENPADVSVISSRKTGQKATPL FAAVTGATLVAGCFTPTFSNQ ISAAFREPQLLVVTDPRADHQP LTEASYINLPTIALC/TDSPLHYV GLAIQCNNKGAHSGGLTCNLS
9580	39948	A	9640	3	438	
9581	39949	A	9641	288	489	SFRPLSVLGDVVRGPTKPSGK CSPASRSLFVRRHILLHPQGLH NLDQNKATPPQPL/GHQTCAC
9582	39950	C	9642	23	411	
9583	39951	A	9643	1	209	SPSTTAVCCPPRPSIDFHSSGSSR VSAALLIQ/QRFPLPWIGLKAR HCSCGLRQRQSVSQETEDGK AG

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9584	39952	A	9644	28	925	PEAGTRSWREPDPEDLRRFLLS AACRSFPQWLPGGGGGQVSSC SDTDVPYLLAVKSEPGFAER QAVRETRRKPTS\GIRLLFLLS PVGEAGPDLNSLVAWESRRYS DLLLWDFLDVFPNQLTKEP/VL WLPGWAGPCPTGSFVLRQDD AFVHTPALLAHLRALPPASARS LYLGEVFTQAMPLRKPGGPFY VPESFFEGGYPAYASGGGYVIA GRLAPWLLRAAARVAPFPFED VYTGLCIRALGLVPQAHPGFLT AWPADRTADHCAFRNLLLVLP LGPQASIRLWKQLQDPRQC
9585	39953	A	9645	1	1612	MIFVVIIMVVLSPGGSGLDSS PFLSEANAERIVQTLCTVRGAA LKPYPTGPNFYSHGVPPHLF AYFPFGSTVSQDNSFISPLQHI FERVRSADFMPRWQMLRVLE EELGRDWQAKVASLEEVFAA ASIGQVHQGLLRDGTAVKIQ YPGIAQSIQSDVQNLALVKMS AALPAGLFAEQSLALQELA WECDYRREAACAQNFRLAN DPFFRVPAVVKELCTTRVLGME LAGGVPLDQCQLSQDLRNQIC FQLTLCLRELFEFRFMQTDPN WANFLYDASSHQVTLDDFGAS REFGTEFTDHYIEVVKAAADGD RDCVLQKSRDLKFLTGFKAF SDAHVEAVMILGEPFATQGPYD FGSGETARR\QDLIPVLLRHRL VSP\PEGDLWPWHRKL\AGAF ACAHLRDHIACRDHKPGHLPPL LGQSPARRSHCRQPPHQGTGP WIPHDSLHGGFSPQSRPYAVV PLIPSPSALGQRSPLGLPSLAWL SSLAQELRIPGAGELPTSCPRSC TS\PESEVSEN
9586	39954	A	9646	930	1123	GVRRDGSSASVTVGQPCRDTSL AFETVAGPYLA*K*T*TSQKPGS D*RASKVAGGVQNGTRTTAT
9587	39955	A	9647	719	1346	

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9588	39956	A	9648	1	823	MKKVLIAALIAGFSLSAATAETI RFATEASYPPFESIDANNQIVGF DVDLAQALCKEIDATCTFSNQA FDSLIPSLKFRRVEAVMAGMDI TPEREKQVLFTTPYYDNFALFV GQQGKYTSVDQLEGKKVGQV NGPTHQKFIMDKHPEITYVSDE SYQNAKLADLQNGCAARAAPG SRRYGGWTIQASTARPSDVLLT ADSVSFAVRSRGAAATAYHRC CLSGVMVNAATACEHSTASQG RASRTVTDSDPHPRSVRRRAS FRRSGRGFCGTVR
9589	39957	A	9649	583	730	
9590	39958	C	9650	333	439	
9591	39959	A	9651	2	171	
9592	39960	A	9652	1	826	MGGLFWRSALRGLRCGPAPG PSLLVRHSGGTIMGVFAVGTI PVPSRVPCIEADTLKPGGPSWT RERTLVAVKPDGVQRRVLVDV IQRFERRGFTLVGMKMLQAPE SVLAEHYQDLRRKPFPPCPSSR YMSSGPVVA MVWEGYNNVRA SRAMIGHTDSAEAAPG(TIKGV DFS VHSRNVIHADSVEGAQR EIQLWFQSSSELVSWA/DGGQH SSIHPLRLRAALTTPSPQTQDPT YPPLARTSPSTKPAISPPLTS PVSPLAPPQAQREF

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9593	39961	A	9653	144	1650	NCETTTKGSAILRNVDPSLLPL RRAGSSPGLMPVEEEMEIDEK QMKGFLDDSERMAFLVSLHLG AAERWFILQMEVGEPLSHENKS FLRRSQGIYDSLSEIDILSAVLC HPKQGGKSVRQYATDFLLAR HLSWSDAILRTRFLEGLSEAVT TKMGRIFLKVAGSLKELIDRSL YTECQLAEKDSPGNSSQVLP ACKRNNEEAMGNELSSQQQTE EHQHVSRCYLYLKEHGDPOEG LHDHLQSTGHHQKAHTNNVA ATKKVVQQLQLEAGLNSVKVS QAAETPQTIIISPPNALQEPSGIE WEQFPKAIQSEPOENLCPFVST MNSIKGLHEDYQGNAGKVLST VPGRRYALQNLGTAIVQGEER KQSSLCPGEEGRHLELRSGSHS LVMKHAMVLFNVGFETKDQIH LPTRLGMAEVEITLCYAKQLPH KLIAKLRLLLKGRPLSLNNEHIL THPGLGWLHTEFFRILSINNKY HLSAYLVQSVLHVMOGFHRT
9594	39962	A	9654	8	440	VFERSTPPTLETVRSKQEWETR LNGVRIMKKNVDRDQFNHIQL VRNGAKLSSLQIPTPTLPPPPSE TSCFRCFNPVPLWLLGCPSPLG RQTGEDPGEAADPVPTVQ*GPD DQHSSADQDSTYHHGRPDHGG TYPVGCCTTGRT
9595	39963	C	9655	89	389	
9596	39964	A	9656	1	184	
9597	39965	B	9657	1	942	
9598	39966	A	9658	424	614	NDGPDWGGRRRETVDNKRKRGF KISKTLYLSDIYSCHVHFYIG NVCIESLYSNVRK*NYVYY
9599	39967	A	9659	1	717	
9600	39968	A	9660	103	374	
9601	39969	A	9661	1590	2051	SYPVSEERSQAEQSSNPYSHT STPIRDLHASGVSTQSLSGSSD ALLHWAGHNAHGVAQCRSPLL VFPNPEPCFPAPQAFLLTPSWLP WQK*PWLGFCPPRSTHAPCR LHPTSPGLGGVKASAEPRPQP VD/ETGEDPGEAADPVPTVQ

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9602	39970	A	9662	1	2912	MAQALPWLLWMGAGVLP AQHGIPLRLSGLGAPLGLR LPRETDEPEEPGRGGSFVEMV DNLRGKSGQGYVEMTVGSP QTLNILDVTGSSNFAVGAAPHP FLHRY YQRQLSSTYRDLRKG VYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAITESDKFF INGSNWEGILGLAYAEIARPD DSLEPFDDSLVKQTHVPLNLS LQLCGAGFPLNQSEVLASVGG SMIIGGIDHSLYTGSLWYTP
9603	39971	A	9663	1	902	MSAKEKGFENMAKADKVHY VREMKTYPKQETKKKFKDPN APKRPPFS/SEYCPKIGIEHP GQSTGDAKKLGEMRTNSAADK WPKKAAKLKEKYRKDTAV YRAKGKPDAAKKGDVKAES KKRKNKEDEDEDEDEDEDE DEEDDDNEVADNCTGSGFVY KTFNSPVHNSLFLNVEIHAG FDELLESIFCILLVEVFSLQK GVAMLEEVVNGERSGRSLPWL PAAPSLPVVPLGLRHPPSQSD NHSLQLTFLTALRLRLPRLG AVLEETVEDGRTKTNLPDENS VPFSPET
9604	39972	A	9664	146	733	LNMKGDKPKPRGMSSYAFF VQTCREEHKKHPDASVNFSE FSKKCSERWKTMSAKEGKFED MAKADKARYEREMKTYIPPK GEDTKKKFKDPNAPKRPPSA FFLFCSEY/RAPKIGEPGLSIG LDVAEETGEEMWNNNTAADK QPYEKKAALKKEKYEKDIAAY RAKKGPDAAKKGVVKAERSTR PRIPDL
9605	39973	A	9665	30	359	
9606	39974	C	9666	418	555	
9607	39975	B	9667	550	1717	
9608	39976	B	9668	1	1705	
9609	39977	B	9669	328	484	

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9610	39978	A	9670	5	1215	IIVLPKMSMPVVSQAQLTITSIPP WAVE/WGNVTLVSQGIPQNLIS YNNWLRGATTNQVTRILNFFFS HGVTLGPAHTGRETGRADGSLI IIDVRASDNGIYTLHLISSGEKV AIMLCYLSLLVAPWHFHKTPR WRFPGWPRAASQRASCSPQS WSSGCSK/VSQAALYIQKIQEPQ QKNQDLLLLSVQGVDPDTFQDFN WYLGEETYGGTRLFTYIPGIQR PQRDGSAMGQRDIVGFPNGSM LLRRAQPTDSGTYYVAITINSE WTMKAKTEVQVAEKNKELPST HLPNTAGILAAIIGSLAAGALL ISCIAVLLVTRNWRGQSHRMAT TEKPELGPAHDAGDNNIYEVN PSPVLLVSPIDTRINPARPLPT PPHLQAEPEHQYQQDLLNPDP APYQCLVPTS
9611	39979	A	9671	1	558	EGGLRTPSNPYHVDISQTKPCH *TNHCIOKEYSKNYGKYEEN MFFKEFNQVLTSLNITLESSIL LQIKHIIRNCLLSVEPAISTKHL YQSFQFLFGDFMVDEELKVWL IEVNGAPACAQ*ACTSLCFYKW EVGSAGVIVCGYKCSHFDCCEG GCHSDRRPLGGLYLAGGFAESL PFLFPRV
9612	39980	A	9672	1	534	MVGVDVTFKVISREERQTQRL GSSSPKRCPLQEFEEHYSSFFG RNCLLSVEPAISTKHLPYQSFQL FGDFMVDEELKVWLIEVNGA PACAQSPAKSL/CATSSSLFLSPP PWTCQQHSRQPTALAEILLSCH GWTRGAGQACLWAFVLSVTC VWNPHHHYHHHHQPYRGWLL LYQNIL
9613	39981	A	9673	624	805	SGGHPGHWLPNPMASPGATT PVGEG/ELQYASLSFQMVKPWD SRGQEATDTECEIKIHR

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9614	39982	A	9674	1	1005	MENRRKVKGEWIAVPQPVKEL RGVLNAATTLSTREILRGKCF QLTSPGTGNEPSHLSWTPRKRSR DGHFGCPDPLAASGARPLRSS AFAAAAADSGSTVQVWDKGV LRVADVWSTIEPVTHVNLGWA AKVGPIISHGSAVSAFSGEGMF RIFSERKTLAKLRDFQNTQLR KLFSEMEKAAGRSQSGVSGFG KGLGDRACEEMSENPKGRKK PKAPQEVSFRENGNWKTPSIF SPKTPRKKKSFSKEELMS/SD/L EETRWQAPSPKPKKSTPKEET VNDPLEAGHK/SGSKKKRKF KVEEPVSSGPPEEAAAGKSSSKK KFKHKASQED
9615	39983	A	9675	1	2742	
9616	39984	A	9676	1	405	MADIPQEARQYRHKQAYAYS QGEGVEDDDERIVRFHTRWPL QNADGTVAEYNGYHVVFALA GSPKADDDTSIMFYQKVGDN SIDSWKNAGR/VLKSDDKFDAN DPLKDKQTEWSGSATFTGSVF LAFGCYSK
9617	39985	A	9677	3	642	GKGLFDDDEESDLFMEAPQD RQAGASVKESSSKPGKKIPA GAVSVFLGDTDFVGAASVPSLK EPQKPEQPTPRKSPYGPPTGLF FFSAPHSKPSKTRKVQSTADIFG DEEGDLFKEKAVASPEATVSQT DENKARAEKKVTLYSKNLKP SSETK/TQKGLFSDEEDSEDLFS SQSASNLKGASLLPGKLPTSVS WFDDEEEDNLLGVQ
9618	39986	B	9678	175	1422	
9619	39987	A	9679	1	3096	MVTHQQAARKPNMTSKPKPK MGPKAHGIFSGTRKNNLEIYMD QTRTGIKTKLSKNKSGGMT LPDFKLYYKAIKACGSGMY NSDTDEDEETEPSSGQIIENSI TMNKMKLLKAKMKNMNLKSK HITQVSEDEEDDDGCDLFADSE KEEKDIEDIEENTPRKSRPTSF ADELAARIKGDVGRVDEEPTT VSYEDDRRGKNQDAYTEGGLS TIKTVNCSSSLPSGEAKLRKTL/ KEKKERRTPSDDE
9620	39988	A	9680	1	2925	
9621	39989	A	9681	2	688	
9622	39990	A	9682	1	1005	
9623	39991	B	9683	1	588	

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9624	39992	A	9684	1	2763	
9625	39993	A	9685	2	1075	NSDEELLFSHKLQKNDNDPVDL FAGTKKTKLLEPSVGLFGDDE DDDLFSSAKSQPLVQEKRRVV KKDHSVDSFKNQKHPESIQGSK EKGIWKPETPQAHQVSLHLKP NEPSTRIGKIQANLAINPAALLP TAAASQISIEVKPVLPIELAFPS EHRRSHGLIESVPVLPGSGEAG VSFDLPAQADTLHSANKSRVK MRGKRRPQTRAARLAAQESS EAEDMSVPRGPIAQWADGAISP NGH*PQLRAASGEDSTEEALA AAAAPWEGGPVPGVDTSPFAK SLGHSRGEADLYDSGDIFSRAP GSQ/SVERPNPRQSRDLPPPGW KQRPSPGKQPRKRPSP*QPKHP LPKGRITSSPW
9626	39994	A	9686	1	4086	VTTPRAAWLGLGFRGSVAVLGLC WQPRSPPSRAAGMMNRITPDQ ELVPASEPVWERPWSVEEIRRS SQSWSLAADAGLLQLQEFSSQ TISRTHIEKKQVDGLIRETKATD CRLHNVFNDFLMLNTQFIENR VYDEEVEEPVLKAEAEKTEQE KTREQKEVDLPKVEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVLELLEPKDLYDRPLP YLIGSKLFMEQEDVGLGELSSE EGSVGSDRGSIVDTE
9627	39995	A	9687	1930	5781	RAKSPANIIMTGSNSHITILTLN VNLGNSPIKRRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQAADLIDYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
9628	39996	A	9688	1	3654	
9629	39997	A	9689	1	5127	
9630	39998	A	9690	1	3663	

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9631	39999	A	9691	1	3210	MVKGSIQEEELTLNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRIKNLTQNRSTTWKLNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTTHSKASRRQEITKIR AELKEIETQ
9632	40000	A	9692	1	3489	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKREITITNYLSDH SAIKLELRIKNPTQSRSTTWKLN NLLNDYWVHNKMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIPNLNAHKRKQERSKIDTL TSQLKELEKQEQTTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKTRPLARLIKKR EKNQIDTIKNDK
9633	40001	A	9693	1	3235	
9634	40002	B	9694	1	3300	

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9635	40003	A	9695	1	2563	MKAEEKMFFETNENKDDTTNQNLWDAFKAEVEESLNRPIGTAEI GAIINSLPTKSPGPDGPTAEFYQRYKEELVPFLKLFQSEKEEI LPNSFYEASIIIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISDAEKAADFQIQPFMLKTL NKLGDGTFFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLSNFVSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPTYTKINSRWIKDLNVRPKT IKTLEENLGITQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNPNPKKWEKDMNRHFSKED IYAAKHKMKCSSSLAIREMQI KTTMRIYHLPVRMAIHKSSGNN
9636	40004	B	9696	1	3420	
9637	40005	A	9697	1	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSASEPPSAIPKAQV SSTEKLRLNCIDDLKFPALASEL SRRAKALQIAGFPPMKVPRDTI SKVCLDKTVGKLCHSGEESRK CTLICNNKHYPIDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAKYSSLEAKLCQIESKYL ILLQEMKTPVCSDDQGPTRVVI AQLLEDALQVESQEQPEQAFV KPHLVSEYDIYGFRTVPEDDEE EKLVAKVRLDLK
9638	40006	A	9698	1	4371	

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9639	40007	A	9699	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRLDLSHTIIM GDFNTPLSTLDRSTROKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFPSAPHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTONHSTTWELNNLL LNDYVVHNEMKAEIKMFFETN ENKDDTTYHNLWDTFKA VCRGK FIPLNAHKRKKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLARLIKKKREKNQI DAIKNDKGDITDPTEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPIGTAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLKLFSIEKE GILPNSFYEASILIPKPGRDITK KENFRPISLMNIDAKILNKKLA KRIOQHKKLIHHDQVGFPGM QGWFNIRKSINVIQHNRAKDK NHMIIISDAEAKAFDQIQPFMLK TLNKLGIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNI CSWVGIRINIVKMAILPKNILITL QLLLVLPSTLIPLWLPALAGO
9640	40008	A	9700	1	4449	
9641	40009	A	9701	824	3693	AWKGTDDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHITYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNLLLL NDYVVHNEMNAEIKMFFETNE NKDDTTYQNLWDAFKA VCRGK FIALNAHKRKKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
9642	40010	B	9702	1	2858	
9643	40011	A	9703	1	3354	
9644	40012	B	9704	288	3301	
9645	40013	A	9705	1	3457	
9646	40014	A	9706	1	4794	
9647	40015	B	9707	1	3384	
9648	40016	A	9708	1	3345	
9649	40017	A	9709	1	3780	
9650	40018	A	9710	1	3720	
9651	40019	A	9711	1	3894	

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9652	40020	A	9712	1	3335	MVKGSIQQLTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSLDRSTRQKVNK DTQELNSALHQAADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEITNYLSDHS AIKLELRKIKNLTSRSTTWKLN NLLNDYVVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQKLELEKQEQTHSKASRRQE ITKIRAELEKETQ
9653	40021	A	9713	1	3780	
9654	40022	B	9714	1	3855	
9655	40023	A	9715	1	3345	
9656	40024	A	9716	965	4362	TWKGTTSTRCKIMPKYRSTRQ KVNKDTQELNSALHQAADLIDY RTLHTKSTEYTFSSAPHHTYSKI DHIVGSKALLSKCERTEITNYL SDHSAMKLELRKIKNLQNCSTT WKLNNLLNDYVVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRQERS KIDTLTSQKLELEKQEQTHSKA SRRQEITKIRAELEKETQKTLQ KINESRSWFFERINKIDRPLRLI KKKREKNQIDT
9657	40025	A	9717	1	3921	
9658	40026	A	9718	1	3988	MTGSNSHTILTLNINGLNSAIK RHRLASWIKSQDPSSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKAGVAILVSDKDFKPT KIKRDKEGHYIMVKGSIQQL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAAD LIDYRTLHPKSTEYTFSSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAILKLELRKIKNLTS RSTTWKLNLL
9659	40027	A	9719	32	583	GPHGAFTHGRR/FRGRDPYEGP RRTGKRKQKSARGCIVDANLSI LNLVIVKKGKIDIPGLTDTMVP CHLGPKRASRICKLFLSSEDD VHQCVVRKALNKEGKKPRTKA PTTKYLVTPHVLQHEWWHIAL KKQRIKENKEVAEYAKLLAK RMKEAKEKHQEQIAKRRRLSSL RASTSKSESSQK
9660	40028	A	9720	318	605	

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9661	40029	A	9721	1	649	MGLKGQGVVEGGLLRQSGSVSL QPLSREDLGRSQSESLGPEFQGL WEWLPVVERVERENLSDYCVLG QRPMHLPNMNQLASLGKTNQ SPHSQIHHSPIRNQVPALQPM SPGLLSPQLSPQLVRQIAMAH LINQQIA/S*PAGSPASSSHQPA VPEPS/IPSPEQLSQSQPTLPWKS LQISTSKSEMS*RGVPVCPKLSLQ EWHSTAHRLNLTWKD
9662	40030	A	9722	15	272	KPQWPGIPSGPPPGSCFKC*K GHWAKECLQPRIPKPCPICAGP HWKSDCSTHLAATPRAGTLA QGSLTDSFPDLLGLAAEG
9663	40031	A	9723	96	531	VQPADLLRPLHTDTCNIWCQRP GTEGLLRETGPLSS/PLTP/MRRS TYDLRSSDQPKHELTDFKSGSC FKCRKSGHWTKCQQRIPPKP CPICAGPHWKSDCPSCPAATPR APGTLAQDSLTDSPFDPKGSLL DYFPDLLCLVAED
9664	40032	A	9724	3	567	GRLQTGADPAWRVHGTWRSTS AADAIDQMVPWPVMTWRLNE RHYGGTLTLGKAETAAKHGEA QVKIWSNISKDRRYADLTDDQL SSCESLKDTIASALPFWNKEIVP QIKEGKWVLIAAHGNSLRGIVK HLEGLSEEAIMELNLLTGPIVC KLDKSSKPIRCMEFLGDEGTL KAMEVAQAQKAKK
9665	40033	A	9725	2	801	GGVPHQPAAAMAAYKLVLIRH GESAWNLENRFSGWYDADLSP AGHEEA KRGGQALRDAGYFED ICFTSVHLYAIRTLWTVLEML SEMWLVPVVRTWRLNERHYGG LTGLNKAETAAKNGEAQVKI RRSYDVPPPMPEPDHPFYSNISK DRRYADLTEDQLPSCDRLKDTI ATALPFWNIEIVPQIKEGKRVLI AAHGNSLRGIVKHLEGLSEEA MELNLTGPIVYELDKNLKPI KPMQFLGDEETVRKAMEVAQA QKAKK

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9666	40034	A	9726	3	573	VAPVVQVWKEMHKLLPFSPDS VVTHGDISIDSGIFDQDKLIGRI DVGRVGIACGCQDVAIVWNYL AACSVDRNTRCIRMPNCRPEVE ETPGLKEEKELSQPKEGEATDL KKEVEKISSSEEEETVNLKEEVE KIPPPPEETMDLKEEKEIIPPEL RDQKLHVLKDLPEVSAVPHK DSLFIIGQLTTVPV
9667	40035	A	9727	2	685	TLYCRVFLLDGTEVSVDLPKHA KGQDLFDQIVYHLDLVETDYF GLQFLDSAQVAHWLDHAKPIK KQMKIGPAYALHFRVKYYSSEP NNLREEFTRPKITKMDFFKSKL TLVVVEDDDQGREQHTFVFR LDSARTCKHLWKCAVEIHIAFF RLRTPGNSKSNRSDFIRLGSFR FSCFS/ERENAHSTGNSPALRER PGDGSVSREGRWVDEGWQP RP GGRGQNALCSVP
9668	40036	A	9728	1	419	MSKFGGRATRGLRKPEVGDVIRT IVRAGLAMPGPPLGPVLGQRRRA SINQFCKEFNERTKDIKEGIPLL TKIFLKPDTFEEKIGQPTVSYF VKAAAAGIEKGARPT/DLSSEFEA AFQKEQAIFLAAQKKADLATQ EEAAKK
9669	40037	A	9729	97	826	SQLPRIMSKLGRAARGLRKPEV GGVIRAIVRAGLAMPGPPLG'N VLGQRGVGSINQFCKEFNERTKD IKEGIPLPTKILAVKPDRTFEIKI GQPTVSYFLKAAAAGIEKGARQ TGKEVAGLVTLKHVYIARIKA SGLRAFAIQDVPLSSV'VRSIGS ARSLGTSRGERTSSSEELAAAFQ KERAIFLAAQK'EA'DFGLPKKE AAKEIDPLPHQLPDFQKEVSLQ KLCPMRGRRSHQYDDGFHDFE
9670	40038	B	9730	273	418	

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9671	40039	A	9731	69	1565	RRRRFQASGAAAMLSSRAEAA MTAADRAIQRLRTGAAVRYK VMKNWGVIGGIAAALAGIYV JWGPIITERKKRRKGLVPGLVNL GNTCFMNSLLQGLSACPAFIRW LEEFTSQYSRDQKEPPSHQYLS LTLHLKALSCQEVTDDEVL ASCLLDVLRMYRWQISSFEEQP HFQDGLVQLRVGVVCRHYPEK WEAASWTSQNCGADDAHELF HVITSSLEDERDQPRVTHLFD VHSLEGHPLTLDHCLHHF/TQSE SVRDVVCNCTKIEAKGTNG EKVEHQRTTFVKQLKGLKPQ CLCIHLQLRLSMVQPGTPLKRHE HIVQFNEFLMMDIYKYHLLGHK PSQHNPKLNKNPGPTLE/HAGW AGSPHTSSSESARGPQNTDFYEW RLLPIFIANA VSADALPSPCSR LQLLHPLPADGQLSSTMGDMA LWDTLFIYRSPPSARNPLSTSN QWLWVSDTVRKASLQEVLS SAYLLFYERVL SRMQHQSQEC
9672	40040	A	9732	1	1393	PLQLQPRHIGAIQLGPLLQRV QAIRLGSFHMVLSLW/VMQSAR VEILEPPRLQRMYGKAWRISL CPQGLSTVMRSELTASSTPQVQ EILPPQSPEYLGPKGITERIHKIM HVKGKLAKLPANRNQSPGVSG KRLVNCVSASAVDSEPAAVPEP DVCAGIVIKKQCFPIARCNKT KQVDSIPHRAAYAKSPFFFAVV VVTSESKDPRVKQNPHTHLLAE GSNAAHFHKT KISQSLKWLVPV YLNSTTYEYRDLTKGLSLCSL LLGVEADIPSMAGLHVRHLMQ VPQPCIAFAVSSPLHQGGKET EDAWSFHIPSTIHRWPTSPVQL SSLRASTQLLCLHINLAKCFIWG ILAQVLSCHHHRITQFVGM LTF VCAGDSSKLSPDIRTLVRR LTS YLVSA SVLLKSKQMALCSASRI LDVSVSPGDHVASEARARCAP DLVAPRPMPIHQNGSLEWTEE
9673	40041	A	9733	44	282	FSCLILHDAFPCLILHDAFPCL CSVTGSLVLSRVPLRGTHQKSA IATSTKIALSNM/KILKHHTDAY FKKQQLFFDVSKK

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9674	40042	A	9734	3	381	EQQGQR/SQWWRGAAARVSRTV KRVLCV/VVECP.LKSACPDVDM YWAALQRLASLLKADGNLVT MAALHSHYMGSKKFFGLHPE KETVEKAMQEAGCQVQRCA/SI SCSETCSINDGICFVAACKGPSV
9675	40043	A	9735	2	209	CRHSTQHCVS/HHGHSQYK/DS HQHYSHYHHHHNPHHHHQSPY LHHHHYDCHLHHHHNDHYH RHISVYDI
9676	40044	A	9736	197	3348	RVVQTDMIKGMLETSLKISLD QAFIRJCLNSTCFRPKGKLVK/C EKSINSASLVSTSQRI SCRPKTHI SKNYGNFLNSSLLTQKQEVH MREKSFQCNESGKAFNYSSVLR KHQIIHLGAKQYKCDVCGKV NQKRYLACHRRCHTGKPKYK NDCGKTFSQELTLTCHRLHTG EKHYKCSECCKTFSRNSALVIH KAIHTGEKSYKNECGKTFSTQ SYLVYHRRLLHTGEKPYKCEEC DKAFSFKSNLERH

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9677	40045	A	9737	1	1665	MAGACWLMAFQYWVLKLLVV KSA/SWPRQSSLKWNWNFKGC QDLETWGKKETRKFYGYRRNE EAQKYScriPRKPD*WCHCWO W**WLMAFQYWVLKLLVVK AYGLVKALSNIGISKVAKTW KPGGKKRLNFMAIEEMKKHR STHVGFENLTNGATAGNGDD GLIPPKSRTPEQQFPDTEEN YHRDFSKLCLGSAANGVVHVE VKMCVYNGKGERQEEKMKGLI SMNLVVEEMKKHESNNVGLL ENLTNGVTAGNDNGLIPQRKS RTPENQQFPDNESEYHSLGDK SKTSFQNSNNNNKQEQQQQ NPTFSNTRKLTLYKAPIPPSIL SGCPNINDSNWQIEHGMQTA GLPTRPLSHGLQKQGAARCLG CKCSEPFQSLILQKAKTNTQK WQATYPKSQNEQLVPSVGKSY RCSTPAQPMKTAUGHKPKCAT GAELPKALGAQPLHPCALDVG QGFKKGNFGAVGLNLLGLEF HGVSGVLLVPGDGGISEGVV REDLMCGVWSAGTWSVGTA RCLEKPGALHVEGPLDSWDGP VMPNGPVKSRQSSCLDGPGR CSEILTGQSHGNKKPARASSKS SQSINDRPLAVLTNQYQCEQLA SERQSSNSCSIRIDSA
9678	40046	A	9738	1	115	RRTARGPQQTSDGLGTSPCRN ASEHTADILELSTLIV*RRQ*ICL CLDFLYY/LIPEGRFCRCADLV HNFDTIILQQHRTLTSGQVDDF LKAKATFKASDFIDALVLSKVA SPRILIQGGRMGA*DQVSDQAS VYGRCSGAEAAKRPKSAWL LLGYDSRASGLY*ILYNLTKHP D/YRECCQPMQES*S*RRAR GPQQTSDGLGTSPCRNASEHT ADILELSTLIV
9679	40047	A	9739	1	506	MVIVGLAAGVLLVPGDGGILS EGVVRDELTCGVWSAGTWSV GTAERCLEKPGALHVEGPLDS WDGPVMPNGPVKNHKGQQE VPSKHPQMALEICLCLDFLYY/L IPEGRFCRCADLVHNFDTIILQ QHRTLTSGQVDDFLKAKATFK ASDFIDALVLSKVASPGS

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9680	40048	A	9740	1	380	KFSRSPVNMRLRIVKPCITRG/YP NLKSVNKL IYKHGRGKINKKRI ALTDNTLIDQSHGGYGIICIEDLI HELYLWPKLSSPQSGMKKKT THFVENGAAANREGQIHRLLIR MNCGVYRDYFSLVS
9681	40049	A	9741	3	279	
9682	40050	B	9742	23	197	
9683	40051	A	9743	2	402	CGDRGALRPPSCAGRSRGPGR PPRPPRLPWHAPPAHGA PLARPGARARRSEKPPSEKPLRRSS PRAQEEGPGPEPPPELALLPPPP PPPTPA/PRRPRP/PGPRAAG ALGDVPEAAEAYLERVPPSSC
9684	40052	A	9744	1	660	
9685	40053	A	9745	1	1035	
9686	40054	A	9746	1	2575	MRAAGGAMLCGKQGRWDPEG EGAHPGFIPLKACSSQGVFRQL HLRTAVTAAVSRHFPQPSWRY DPGPQFLGEKSGFKPRCPGVAV CQFQSMNAFIHWFNRKAWASS CDRIKIPVPEATFVEPNCLPGEI GQLLRQLQSGRNLKEWLREQF CDHPLEHCEDTRLHDAAVYVD LQTLRSLQEEYSRINEKSV WCCGWLPCTPLRIAATAGHGS CVDFLIRKGAEVDLVDVKGQT ALYVAVVNGHLESTQILLEAGA DPNGSRHHRSTPVYHASRVGR ADILKALIRPAACDRSVSITADT HFRYLKVVPAEFRSRKAIPFLS SCTAWRCADQLQIPVPLVDT SGSGKTVSNVITESHNSDNEED DQFVVEAAPQLSEMSEIEMVTA VELEEEKHGGLVKKILETKKD YEKLQSPKPGKPSATGWHG ECLGTRNRAQALVGWGLY SERHSGMLRAITLKYKGGGRQ GIQA/AWKSEIFRSRAAPENPL GRWGFALLSKIIIS*ROVLKLFH SLSPQARVNSRFPGSGKAGLGL WMEGARPSGHVPKERVVAGK RPQVPTKAHHTCVRETAGNQE GNGEGALQQEQRLGVAEAGSN GEGALQQEHRITDCAVEPLKAE LAELEQLIKDQDKICAVKANI LKNEEKIQKMERSLFSAWKKE KDIVSKEIEKLRTSIQTLCKSAL

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9687	40055	A	9747	2	1739	MKGLYTDAEMKSDNVKDKDA KISFLQKAIDVVVMVSGEPLLA KPARIVAGHEPERTNELQLHIGK CCLNKLSSDDAVRRVLAGEKG EVKGRASLTSTRSQELDNKNVRE EESRVHKNTEDRGDAEIKERST SRDRKQKEELKEDRKPREKDK DKEKAKENGGRHREGERERA KARARPDNERQKDRGNRERDR DSERKKETERKSEGGKEKERLR DRDRERDRDKGKDRDRRVKN GEHSWLDREKNREHDKPEKK SASSGEMSKLSDGTFKDSKAE TETEISTRASKSLTTKTSKRRSK NSVEGDSTSDAEGDAGPAGQD KSEVPETPEIPNELSSNIRIPRP GSARPAPPRVKRQDSMEALQM DRSGSGKTVSNVITESHNSDNE EDDQFVVEAAPQLSEMSEIEMV TAVELEEEKHGGLVKKILETK KDYEKLQQSPKPEKERSLFES AWKKEKDVSKEIEKLRTSIQTL CKSALPLGKIMDYIQEDVDAM QNELQMIVHSENRRQHAELQQ EQRTIDCAVEPLKAELA/ELEQ LIKD/QQDKICAVKANILKNEE KIQKMVYSINLTSRR
9688	40056	A	9748	93	800	RANLPTQPYCHCLGAPAAALTRI VGGSAAGRGEPWPQVDLWLR RREHRCGAVLVAERWLLSAAH CFDVGDPK/QWAAFLGT/HVP ERRGGAVERVARIYKHPFYNL YT/FDYDVALLELAGPVRR/SL VRPCLPEPA/HATPDGTRCVIT GWG/YGS/GAQLQKAAVRLLS EQTCRA/LYPVQISSRMLCAGF/ LQGGVDS CSGDAGGPLACREPS GAPVPGQPRTCTAPARWPRRSA LSPAPL
9689	40057	A	9749	107	378	NLVP*LRSGD/SPLGDQSPVLLIF TP*ERSTYNLKSDD*PAQETS/PP ISNPDPDEN/PDCSTHLAATPRA PGTLAQGSLTDSFPDLLSLAAE D
9690	40058	A	9750	2	286	

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9691	40059	A	9751	215	631	GTQSCNQKVLNSANNLQELGIG PKFQMRLLKPQLAPMQPNRGTS LGRSIPCPPVLCMRKIHLPQV LRPTSPRNISPILNRVSEVSDHA GTPALVLHP*RVPLFWGRGK YPNPFSLCLYPFSAFLGGKKHP TPSPSP
9692	40060	B	9752	1	933	MLPNRLGSSSETITDAELRVTLT VEELNGLRAVQDMFVKQILKA ARSLRVITIPNLKYPGTQTLRKA AAPDPNTTGLIFLEKLCEIAAAI ASYVAVPSLEINHRKKANPNLL LRRSGSGSVSLQLLAEKIWEGV REPWARVVLVWEWLPDQNPPLS GLTKSNSTRHELPHGRAIQLH LSGWELWSEPSNLLDLVVTGDI ENTSLAPEDPTFLTTPSGSHCPE SPSDGPGLLSSVALVWFLVED WLSRKRLSEPAELPLGKAGEV VFDTLPLPSRRTHFSGFLGHFCY SFSDBGYSTNRAAPDGSSTKAKE HGSCRKQPPLYTLQCRDKAGLR VHGNSPVSAYGWLFSEERPGKP TRTPFSWEGDPPGLLTADETSL VVHLELPVFPFLKRAGNSRHS GMGSPLEAEEAYSTVVMADVS QYPVNEPLVAAVVCQEPERAQ PDVHFFQ/CLRLGGHAGGVAAR PLPAAETPPLQRRPSVRA*SAP* SGARAADDPRTTHS/QAEEAQR PEPDILNHVFDDVESF/VRLQK SAEAAARVLEHR/KRGRSRRRRA AGEGLLTLR/AKPPSEAEYTDV LQKIK/HAFSLLARLRGNIADPS/ SSELLHFLFGPLQMIV/QPSGGP EFASSVRRPHLT/RDAVALLRD NVTPRE/RLWTSLGDSWTRPG LELSP EEGPPY/PEFFSGWEPPV TDPQSAAGRTOLRNSYSTSGGA
9693	40061	A	9753	1	2283	
9694	40062	B	9754	1	930	
9695	40063	A	9755	76	247	QLKTDTAQLPRKLFVESHNYH CSWPGQLQSGLPHYSGYHTSS* LYLSDPADIHPIPS
9696	40064	C	9756	95	301	
9697	40065	A	9757	352	545	DILNHVFDDVESFVSRLLQKSAE RPGCWRRRTRPQKPA PGVAG* RGTW RGI*TPPDLFQMSPSLP
9698	40066	B	9758	406	602	
9699	40067	A	9759	1	543	

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9700	40068	A	9760	2	138	LDDFVGRMLTLMGCPPEPC/PRVPSPLREGRKTQAALSVRRGRSHRR
9701	40069	A	9761	1	417	
9702	40070	A	9762	830	1029	YLPHLSLRLLPCCPPLPLSKPNSLP*LRPSLLQRDYL SIFILINMPSISSTTLLLYGQKEISSLH
9703	40071	B	9763	40	980	
9704	40072	C	9764	419	700	
9705	40073	A	9765	271	1185	
9706	40074	A	9766	2	1655	RGRSRRRRAAGEGLTLTRAKPPSEAEYTDVLQKIKYAFSLARLRGNIADPSSPELLHFLGQLQMI VNTSGGPEFASSVRRPLVTSDI AVALLGNNVTPRENELWTSLGDSWTR/LRA/EELSPEEGPPYRPEFFSGWEPPVTDQSRAWEDPVEKQLQHERRRRQSQAPSGRCQWVTGDLPESEPEQLESETAGKWVLCNYDFQARNSSEAVRSSSGDVLAEVLDDSR:KWWKVRDPAGQEGYVPYNILTPYPGRLHH SQSPARSHDSTPPPPAPAP/VP/LPPALARPRWDRPRWDSCDSL NGLDPSEKEKFSQMLIVNEELQARLAQGRSGPSRAVPGPRAPEPQLSPGSDASEVRWLQAKGFSSGTVDALGVL TGAQLFSLQKEELRAVSPEGGARVYSPVTVQRSLLEDKRESSELEAVMEKQKEEGRRGGNGGHLTCQAPFAKSDEAPWENGPPQTLPNSGRSSEGWPICSGPGLPPLPVDRLNDPCCSPSGEDLDWLGVGRAWRQSTESASRPGRCSGALSIVILRPSINMPPCLAKKKKK
9707	40075	C	9767	565	762	
9708	40076	A	9768	1	401	SPLRPLLLALALASEPCAQGACPASADLKHSDGTRTCAKLYD/CSDPY YENCCGGAELSLESADLPYLPSNWANTASSLVVAPRCELTVWSRQGKAGKTHKFSAGTYPRL EEEYRRGILGDWSNAISALYCRCS

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9709	40077	A	9769	1	1489	MPQLLQNINGIEAFRRYARTEG NCTALTRGELKRLLEQEFADVI VKPHDPATVDEVLRLLDEDHT GTVEFKEFLVLVFKVAQACFKT LSESAEGACGSQESGSLHSGAS QELGEGQRSgtevgragkgqh YEGSSHRQSQQSGRGQNRPGV QTQGGATGSAWVSSYDRQAES QSQERISPQIQLSGQTEQTQKAG EGKRNQTTTEMRPERQPOTREQ DRAHQGTGETVTGSGTQTQAGA TQTVEQDSSHQTGRTSKQTQEA TNDQNRGTETHGQGRSQTQSA VTGGHAQIQAGTHTTPTQTVE QDSSHQTGSTSTQTQESTNGQN RGTEIHGQGRSQTSAVTGGHT QIQAGSHTETVEQDRSQTVSHG GAREQQTTQTQPGSGQRWMQ VSNPEAGETVPGGQAQTGASTE SGRQEWSSTHPRRCVTEGGD RQPTVVGEWVDDHSRETVILR LDQGNLHTSVSSAQGDAAQS EEKRGITARELYSLRSTKP
9710	40078	A	9770	2	3031	
9711	40079	A	9771	6288	6584	TAVSLPAPLFSDLQIPPRKRSK ETVMAPENLTN*RAPPOSSARV FQ*EALYVPGP*ALDPPEVCSSY SSVCGLHLQLSHSSSESSSTLGL LGSFQML
9712	40080	A	9772	884	1032	ESRPNTTTLRKTSSWSFQS*TA TQTKGPRDPGASMTKPGATSER SASG

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9713	40081	A	9773	1	1457	RSAQKEKTAAKEQQGEKTEVL SSDDDAPDSPVILEIPSLPPSTPP STPTYKKSLRLSSDQIRRLNLQE GANDVVFSVTTQYQGTCTCKA TIYLWKWDDKVVISIDIGTTTK SDALGHILPQLGKDWTHQGITS LYHKIQLGQLVMPDARPERP MDGMKVRAFMERLLFVRRGT DKRWSVRMYVTCSSSNLNEE IYINQVVIQANMKLQLWAMRT DDARGLSSLGDTSPSPSVVP GLQPKPAPVCAGDALLQAQIPG VLLGTLFSGAAFYSGLYGGSEQ FLDHLLHPARAAPPPPLVGP APRVPGSPSAPELAGPAVWRFA AAASRGVVVAASGWGRGGEA SQTFTQTKPEGGTRHPTRMPLG STGCIFFGTLEKSQGYERYNAM RADPALCFLEKVGMPDEKSLSA EQGVTDGTSIPERARQNEEQ TSFGLLWPTPQGSTDHIDNHP RYPERMWELDVLPDIDYMEI PVDWDDA
9714	40082	A	9774	3	4804	KRLENIQKTELVAFSEA VWMQ PSVVLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSVALIATSQSQSLHPL LVSAQGVHIFQCVQHIPPNQ QRCEILCNVIKNKLDKDKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLV TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYELFANLPIRQRT GILLYGPPGTGKTL
9715	40083	A	9775	1	897	
9716	40084	A	9776	486	800	CLQLSWLSLQQAQVHWLGRA VHTAF CMD*VLLFGESFGFLVR LTPGILLGLL*P*KQGHCHSVSL GEVRI/CGHS*TFITSWAFSVLQ GKASAPVKVSTQNSRY
9717	40085	C	9777	332	497	

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9718	40086	A	9778	1	6504	MWGSRLAGAGGGGA AVTVA FTNARD CFLHPRRLVAQLHL QNQAIEV VWSHQPAFLSWVEG RHFS DQGENVAEINRQVGQKL GLSNGGQELHVAVSLEQLLDQI RIVFPKAIFFVWVDDQQT YIFIQ VALIPAASYGRLETDTKLIQPK TRRAKENTFSKADA EYKLLHS YGRDQKGMMKELQTKQLQSN TVGITESNESEIPVDS SSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKV VPL
9719	40087	A	9779	1	5421	
9720	40088	B	9780	124	273	
9721	40089	A	9781	84	493	IHANNC S*L*K AALNFVLLLQ KRL*GEKHLTLSETGREGNKVG GVGS*VTGTGQETELGSLGRCH SPLSVLHLLPFFS/LLGRTHLNA LLIRDYFASSCKYL*EVLLSLSD GSG*NLMSVVMAGNSSAEYVR
9722	40090	A	9782	1	5954	MDGMT EACIKGGIEAC YAAVS CVCTLI.GALDEL SQQGLSEGG VQLLLRLLEELKDGA EWSRDS MEINEADFRWQRRVLSSEHTP WESGNERSLDISISVTTDTGQTT LEGELGQTT PEDHSGNHNKSLK SPA IPEGKETLSKVLETA VDPQ DVVQSRSHTV PYPDITNFLSVDC RTRSYGSRYS ES NFSVDDQDL S RTEFDSCDQYSMAAEKDSGRS DVSDIGSDNCSLADEEQTPRDC LGHRSLRTAALS
9723	40091	A	9783	1	2217	
9724	40092	A	9784	1	1360	
9725	40093	A	9785	1	777	MNIKNPIAAQHLDNLP IVKASSI GMTWGLVRNGVSAPTQKSCIRI HILARCTGAVAF EKL YFKSPAN QAHARKVGKQVQDCYIGR DIV AKAGAIHHLNVGKGTPVCCPLL EEGINSEVWTT EGQYGRAK'NA RPVQVKLKDSTSPFYQRQYPLR PKA/LTKGFQKIVKDLKAQGLV KPCSNPCSTPILGVQKPNRQWRJ EAL.KLQIVLQMEPQM QSMTKI YHGPI.GRPASPCSDVNDIEGNP TKEISTAPPLLCPSAGSS
9726	40094	A	9786	1	415	

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9727	40095	A	9787	1	451	MVHFISRLLYSDGLDVPGDPIQ DSDDAALSVSPHCSPDSRVSTT KHLWVSPRLLRVAVRVKNIDIT NFSWWNDGLAFCALLHTYLP AHIPYQELNSQDKRRNFMLAFQ AAESVGIKSTLDINEMVRTERP DWQNVMLFVIAIYKYFET
9728	40096	A	9788	3	605	DEWPPERIIQYNEPTTWH/EDGL WGYRTRFYMINQIIW/LQAILEH TNKTDRAITLAQQETQMRNAI NQNRALADYLPAAEGGICGKF NLNCCLVHDDQGGQVVEDIVR DMIKLSHVPMQVWHGFDPGA MFGKWFPVLGGFKTLIGVILVI GTCLLPCLLPVLLQMIKSFAT LVHQNASEQLYYMNHYRSVLQ EYMGS
9729	40097	A	9789	3	876	GAGGGFGSPMDIFDMFF/GGGG RMHRERRGKNVVHQLSVTLED LYNSATRKALQKNAICDKCE DRGGKKGVEYCPNCRGTGM QIRIHQIGPGKVQIQSVCECQ GHGEQISPKDRCESCNGRKILR EKKILEFHIDKGMKYGQKITFH GEGYQEPGLEGEDIIIVLDQKD DAVFTRQGEDLFMCQIVKHGDI KCVINEGMPYIPRYPEKGRLEIE FKVNLPENDFLSPDKLSLEKL LPKRKEVEETDEMDQVELVDF DPNQERWHHYNGEAYEDEH
9730	40098	A	9790	199	410	
9731	40099	A	9791	134	1369	KMVKETTYDVLGVKPNATQE ELKKAIRKLALKYHPDKNPN EGEKFKQISQAYEVLSDAKKRE LYDKGGEQAIKEGGAGGGFGS PMDIFDMFFGGGGRMQRERRG KNVVHQLSVTLEDLYNGATRK LALQKNVICDKCEGR/SGRFKE QGAVRSACPNCRGTMQIRIHQ IGPGM/VQIQSVCEMECQGHGE RIRPKDRCKSCNGRKIVREKKIL EVHIDKGMKDGGKITFHGEGD QEPGLEPGDIIIVLDQKDHAVFT RRGEDLFMCMDIQLVEALCGF QKPISTLDNRTIVITSHPG/QIVK HGDIKCVLNEGMPYIRRYPEAK GRLEIEFKVNFENGFLSPDKLS LLEKLLPEIRKEVEETDEMDQV ELVDFDPNQERRRHNGEAY EDEHHPRGVQVQCSDLLMGVP

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9732	40100	A	9792	3	337	GYSQAPRRK/GGECSSLSQPFSSK AQPDAAASLEPPSLETPAGRTPA TLTQGSPPAAVREPLSPGHNAK ARLRSRPARPPWIPDPDPFGHFV TDFCAPESLQGETRTSRSFQLL
9733	40101	A	9793	1	346	SGS*QLQMCISGLPAHTQDETHI SSCGQLDLALPPLLPLPPSLN TLPPQGLCTC
9734	40102	A	9794	1	1110	MEGEEAAGAAGDPVGHRRKCC GFHPVCEREAPSTFAAVMIHLV VQYIGEICRYLLKQPVREAERR HRVRLAVGNLRPAIWEEFTER FGVRQIGEFYGATECNCSIANM DGKVGSCGFNSRLPHVYPIRL VKVNEDTMELLRDAQGLCIPC QAGEPGLLVGQINQDPLRRF NGYVSESATSTKIAHSVFSKGD SAYLSRDALMMDELGYMYR DRSGDTFRWRGENVSTTDVEG ELSRLLGQTDVAVYGVAVPGK LGLQGVVLRHGVGKAGMAA VADPHSLLDPNAYQELQKVLA PYARPFLRLLPQVDTTGTFKIQ KTRLQREGFDRQTSRDLFFLD LKQGHYLPLENAVYTRICSGAF
9735	40103	B	9795	28	376	
9736	40104	A	9796	3	461	VRQCRGIRDPIYRFFKRTLEFIA AEGIHGTGQFVYCGKKAQLNIGN VLPVGTMPGTVCCLEEKPGD RGKLARASGNYATVISHNPETK KTRVKLPSGSKKVISSANRAVV G/VVSGSS*MLRAVGEHAVSAG GQPVARLGPWNSITCCSKTWV
9737	40105	A	9797	1	701	MQEVPMGFERNYPHAIITFKPS VPVSRSLDYAPLPGGVFRDPYW FKKRTLEFIAAEGIHGTGQFVY GKKAQLNIGSVLPVGTMPGMI VCCLEKPGGRSKLSWASGNY ATAISHNPETKKTRVKLPSGSK KVVSSANRAVVGVVAGGGRT DKPILKACQAYHKYAKARNW WPRVVDVAMNPMHEHPGGGN HQHIGIPSA/SRDDPAGCKMGL IAARQTGRLGWTKTQKEKEN

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9738	40106	A	9798	1	910	QCGGIRRTGPPVAMGRVIRGQR KGAFSVFRAHVKHRRGAARLR AVDFAERHGYIKGIVK/DAERW PGREGKGRPAGTPHSRRLCPQD IIHDRGRIGAPLA/RVVFRDPYRF KKRTELFAAEG/IHTGQFVYC GKK/AQ/LNIGNVLPVGTMP*IG TIVCCLEEKPGD/RGK/LARASG NYATVISHNPETKKTRVKLP GSKKVISSANRAVVGVAAGGIG RIDKPIFEGWPGRYHKYKAKR NC**PRIRGVAMNPVEHPF/GGG NHQHIGK/PSTIRRDAP/AGRKY GLIA/ARRTGRLRGTKTVQEKE
9739	40107	A	9799	1	405	LEISIMAAISISGYTFSVACFHSA NSNADHEGFLGGEVRQEETFSS DSQISNTEFLQV/KVIGWYFR RNTQQQMSYREQVLHKQLTRI LGVPDLVLLFSFISTANNSTHA LEYVLFRRNRRYNQRISLAIPN
9740	40108	A	9800	1	232	
9741	40109	A	9801	1	420	
9742	40110	A	9802	3	1272	EISIMAAISISGYTFSVACFHSAN SNADHEGFLGGEVRQEETFSSID SQISNTEFLQVIEIHNHQPCSKL FSFYDYASKVNEESLDRILKDR RKKVIG/WYFRFRNTQQQMSY K/SEQVLHKQLTRILGVPDLVFL LFSFISTANNSTHALEYVLFRRN RRYNQRISLAIPNLGNTSQQEY KVSSVPNTSQSYAKVKEHGT FFDKDGVMMKDIRAIYQVYNAL QEKVQAVCADVEKSERVVE QAEVNKLRRQITQRKNEKEQE RRLQQA/VLSRQMPSES LDPAFS PRMPSSGFAEGRSTLGD AEAS DPPPPYSDFHPNNQESTLSHSR MERSVFMPPRPQAVGSSNYAS TSAGFEVFLGSGADLPPQRAA GDSGEDSDSDYENLIDPTEPS NSEYSHSKDSRPMAPHD EDPRN
9743	40111	A	9803	3	513	GAYGGGYGACDNYNGYGYGF GSDRFGRDLNYCFSGMSD HKY GDGGSTFQSTTGHCIVVH IEIGP DGRVTGEADVEFA THEDAVAA MSKDKANMQHSYVEPLN CAA GASGTA YGSQMMGGMGL SIQS SYGGPASQLSGGYGGGYGGH SSMSGFDQVLQENSCDFQSDIA
9744	40112	B	9804	73	1127	

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9745	40113	A	9805	1	3647	MRVRHVGGAALELLTSVRESR ATSAFQVSPYEDEPCRPCNCDP VGSLSVVCIKDDLHSDLHNGKQ PGQCPCKEGYTGEKCDRCQLG YKDYPTCVSCGCNVPVGSASDEP CTGPCVCKENVEGKACDRCKP GFYNLKEKNPRGCSECFGVS DVCSSLWPVGVQVNSMSGWL VDLISPRKIPSQQDALGGRHQVS INNTAVMQRLAPKYWAAP EAYLGNKLTAFGGFLKYTVSYDIP VETVDSNLSMASHDVIK
9746	40114	B	9806	141	236	
9747	40115	B	9807	66	266	
9748	40116	A	9808	1	330	
9749	40117	A	9809	1	792	
9750	40118	A	9810	129	311	
9751	40119	A	9811	3	538	
9752	40120	B	9812	96	536	
9753	40121	A	9813	1	2090	MSSNQKSPITKTSKSPGTANVLD VNNSTLMFVGGGQIKKSPA VKVTHFGKCLGEALNGKSI GLWNYIEREGKCRGCGSSQ NEDPSFHFDGSGYSVVEKSL PATVTQIIMLFNTFSPGGLL LYLGSYGT KDFLSIELFRGR VKVMTDLGSG PITLLDRR YNNGTWYKIAFQR NRKQGV LAVIDA YNTSNKETK QGET PGASSDLNRDKDPIYVG GLPRSRVVRGVTTKSFVGC IKNLEISRSTFDLLRNSYGV RKGCLLEPIRSVSFLKGGY IELPPKSLSPESEWLVTFA TNSGIIAALG GDVEKRGD REEAHVPFFSVMLIGGNI EVHVPDGTGLRKALL HAP TGTCSDGQAHSISLVRNRR IITVQLDENNPVEMKLGAL VESRTINVSNLVYGGIPEGE GTSLLTMRRSFHGCINKLIF NLDHGFVD SVEQKRFCGVP SCARESARGRAQAQDTAQE LQSESACDKRSPQPGKGK HMYGGVLPQPSLFQKNLL LFYDEVLDLPNGKEKFSV GANHNAMFVVHVGVCFC LFPSEGLASPCFVHPQIT IHPDDR FQASVTDEGYL FLAKPTQPAPACPLDPIR PLLGHAQQPLLTQDHTD AAVTPSSAVTARAANYCA GGRNERKKTGREKRHLTG GPCVALRTFTVLHISHHQV DGIRAGYVQRDGLQPTNRQ IVM

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9754	40122	A	9814	1	8705	MRGGVLLVLLLCVAAQCRQRG LFPAILNLASNAHISTNATCGEK GPEMFCKLVHVPGRPVRNPQ CRICDGNANPRERHPISHAIDG TNNWWQSPSIQNGREYHWVTI TLDLRQVFQVAYVIIKAANAPR PGNWILERSLDGTTFSWPQVYA VSDSECLSRYNITPRRGPTTYRA DDEVICTSYYSRLVPLEHGEIHT SLINGRPSADLSPKLEFTSAR YIRLRFERIRTLNADLMTLSHRE PKELDPMLPR
9755	40123	A	9815	1	564	MGDLEDKLVFFIGELPRHLDQN SEQLKQVQRELKELHETCQQ HQLCQASTSGEPKERDKEEGK DSKPRSLRFTWSMKTTSSMDPN DMMREIRKVLDAANCDYEQKE RFLFCVHGDARQDS/LPCQWG DGKSCQVGPRLSLNGVVRFKRI SVGTSYCPKLNIA\SKIA\NELKP VKKSQIQVQGGRIHI
9756	40124	A	9816	2	451	ANAHGFIMELQDGYSTETGEK GAQLSGGQKQRVAMARALVR NPPVLILDEATSALDAESEYLIQ QAIHGNLQKHTVLIHARLSTV EHAHLIVLDKGRVVQQGTHQ QLACPRAGFYGKLVRQRMGLGL QPAADFTAGHNEPVANGSHKA
9757	40125	A	9817	1	498	MVKY/YLGQGVLRSSW/DQVV PA/FWQRYRNPVQRYLTEDIVH RENQMTTFTWNINHARPMVV EERCYVCVNSDNGWTEIRREA WVSSSLCGVSRAVWEFGLAQF KSNVTKLKGFEYILAKLQGEA ASKTLIKTAREAKEKAKETALA ATEKAKDLASKAATKKQQQ
9758	40126	A	9818	3	231	
9759	40127	B	9820	94	375	
9760	40128	A	9821	45	439	

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9761	40129	A	9822	304	1557	DRQNVMEQFNPLRLNLNLGK NYEKAVNAMILAGKAYYDGV AKIGEIATGSPVSTVELGHVLEI SSTHKLQRESLMENFKKFKH EIIHELEKKIELDVKYMNATLK RYQTEHKNKLESEKSAELK KIRRSQGSRLNALKYEHKEIEY VETVTSRQSEIQQSIADGCKEA LLERERGASCFPLNKHCGFA/ NTHIHYYHLQSAELLNSKLPR WQETCVDIAIKVP/EKIMNMIEI KTPASTPVSGTPQASPMIERSNV VRKDYDITLSCSPKMPAPSGR AYTSLIDMFNNPATAAPNSQR VNNSTGTSEDPSLQSVSVATG LNMMKKQKVKTIFFHTAGSNK TLLSFAQGDVITLLIPEEKDGL YGEHDVSKARGWFPSSYTKLL EENETEAVTVPTPSPTPVRSFSG
9762	40130	B	9823	1	1128	
9763	40131	A	9824	1	434	
9764	40132	A	9825	92	319	SIPYPPIPPVDRKEID*LEGMQT SGLFQQTSG*EEGVGSIMASGR PPHPEPLKADFICKREVRLAFSI ACIWMR
9765	40133	A	9826	1	851	
9766	40134	A	9827	227	305	LVFISIFNLVG*NISDCIILICQLK
9767	40135	A	9828	66	808	YCWQSQGAKPRDLLGPDLIPLN HSPRVSHLLCHRRIRKAGGVFV ADEIQVGFGRVKGHEFAQLQ GKDFVPDIVTMGKSIGNHPVA CVAATQPVARAFAEATGVEYFN TFGGSPVSCAVGLAVLVLEK EQLQDHATSVGSFLMQLLGQQ KIKHPVGDVRGVGLFIGVDLIK DEATRTPVELKRHHVYLVSRLE NYVL.LSTDGPGRNILKFKPPMC FSLDNARQVAKLDAILTDM EKVRSCEMR
9768	40136	A	9829	3	597	

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9769	40137	A	9830	1	3281	MGFHHVQGAGLKLLTSGTPQL LALVQHWVPGARLVEELPHEL VLVLPTYGAHDGSFATLFRELD TRLAELRLTGYGSDTSEIEIFL KVVEECAADTDMEDG/TLRAA PMHRHCWPRRNPTAQDAATGD SAGDGEPAAGSAPETDQSGPD AVGRVQGWALTRQQLQALL KRFLARRSRRLFAQIVLPALF VGLALVFLVPPFGHYPALRLS PTMYGAQVSFFSEDAPGDGR ARLLEALLQEAGLEPP
9770	40138	A	9831	1	684	RTRGPPQSRSGRRRRIPLYLP TSCIKELVAGGVAVESWPGRD AAQLLLCSCLSPPPVMTETRE PAETGGYASLEEDDEDLSPGE HSSDSEYTLSEPDSEEEEEEEEE EEETDDPEYDPGYKVK*RLGG GRGGPSRRAPRAAQPPAQPCQ LCGRSPLGEAPPGTPTGTSCC MPGVRCRQSPHTGSLAEGVGW EEGAEIGVVTVMGDLVLPV CIVLEVDV
9771	40139	A	9832	1	670	MESDIGRKGKDPDPEAGPEHSSD SEYTLSEPDSEEEEEEEEEEEEE TDDPEYDPGYKVKQLRGGRG GPSRRAPRAAQPPAQPCQLCGR SPLGEAPPGTPPCRLCCPATAPQ EAPAPEGRALGEEEEEPFRAGE GRPAGREKEEEEEEGTYHCTE CEDSFNGLGELATGTSCCMPGV RCRQSPHTGSLAEGVGWEEGA EEIGVVTVMGDLVLPVCVVL
9772	40140	A	9833	3	512	
9773	40141	A	9834	3	815	MLYSRGPQPMGHGVLVCGLL GTGCTAGAQLREAYTSISSQID QAEERISEIEDKLNEIKREDKITE KRMKRNEQSLQEIWYVVKRPN LRLIGVPKSDVENGTKLENTLQ DIUQENFNLARQANVQIEIQR TPQRYSSRRATPRHIIVRFTKVE MREK/MLRAAREKGRVTHKGK PVRLTADLSAETVQARREWGP FNILKGKNFQPRISYPAKLSFISE GEIKYFTDKQMLKDFVTI/RPA LKELLKEALNMERNWYQPLQ KHAHL

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9774	40142	A	9835	1	561	MVNGRIPQAPSQFSHLARLHPA PSPNSDSPFLAELLMPVIGL TPSYSPRFSSESTFLQEAFFDLC QAEDPVYANGGLNYSYRGYGA LSSNLQPPASLQTGNHNSGPTD LSMKGGAAFTTSTTPTPTPSSTST SRPVPTAQLSPTEISAVRQLIAG YRESAAFLRLSADELENLILQQ NRPRRHL
9775	40143	A	9836	2	226	KGVQFQFSSYG*PVFPPTFIK*G VLSPLFVFLRFLKDQMVVDV*H YF*GLCSVPLVYISVLVLVPCCF FFTVAL
9776	40144	A	9837	2	350	YKVSQPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIPR*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9777	40145	C	9838	213	365	
9778	40146	A	9839	1	1923	

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9779	40147	A	9840	1	2091	MVLVVVAVVVVVLVVAIVVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLLKKHSGVKNIPRNPTYEG CEGPFQGELOTTAQNKGGHK QTEDHSMMLDRKNQYCENGH TAQAVPNPYTLTSLQIPEDAWEF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTLPQGFR NSPHLFGQALAQDLSQFSYLDL LVLRYMDDLALATHSETLCHQ ATQALLNFLATCGYKVSCKPA QLCSQQVKYLGKLSKGTRTSL EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNF LYVTEKITGIALGVLT/PGTSAQ LAELIALTRAPELGEGRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQPKPEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPEMLTEGPLAFELA MATARAELSLAIHCCLP PPPQ TRCWLP SLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPQV REHEACHHLGSLPPFWKWPT TILGALGARTPGNTGSTYTFIGY TYTSPVIFILSWQYVYFHLGY
9780	40148	A	9841	1	1284	

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9781	40149	A	9842	1	1522	MVAPGVSITRLGVSFPFLVLVY DLQYEGAECGVNADVEKHLEL GKKLLAAGQLADALSQFHAAV DGDPDNYIAYYRRATVFLAMG KSKAALPDLTKVIQLKMDFTA ARLQGRGHLCLKQGGKLEAEDD FKKVLKSNPSENEEKEAQSLI KSDQMRLRSQALNAGSGDY TAAIAFLDKILEVCVWDAELRE LRAECFIKEGEPKAIISDLKAAS KLKNDNTEAFYKISTLYYQLGD HDCSFSEFRDVLNLDQDHKRIC FAHYKQVKLNKLIESAEELIR DGRYTDATSKYESVMKTEPSIA EYTVRSKERICHCFISKDEKPV EARNVCSEVLQMEPDNVNALK DRAEAYLIEEMYDEAIQDYETA QEHNENDQIIRGLEKAQRLLA KQSQKRDRYAKILGVKRNACK QEIIKAYRKLALQWHPDNFQNE EEKKAEKKFIDIAAAKEVLSL PEMRKKFDDGEDPLDAESQQG GGGNPFHRSWNSWQGFNPFSS GGPFRFKFHN
9782	40150	A	9843	5	519	LTCQEEHKKHPDSSVNFVEFS KKCLERWKTTSAKEK/SKFEEK AKSDKARC Dreiknyippkckk GRPPSAFFLCSEHRPKIKSGHP GLFVVETAKKLGEMWSGQSAK DKQPYEQKAVKLQERYEKGIA AYRAKKGSEAGKKGSKKNKPE DEEEEEKEDEEEEEGEDEE
9783	40151	A	9844	1	3140	YSIATVLAEEKLDPRRDEAKR LRPQRNFNITFTGTVFRPLTLE STFFNSALLFTTIKQDLPLPKTI ITNAFHRFRNHHQTGFKLSAAN QRGPLAATLSGPGGEGQSAVA RLTGEKKNHPGAQYANRLSPR VGRFINAAGTTGFPPTGKRARSD SSLAKENNQKAYKETYGVSHT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFY

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9784	40152	A	9845	2	604	FLELPAAAAAVLSASPGALER EARSRSPQTADTSPRPAPAC APSRARAMPSPDRPFKQRRSFAD ARCKEVQQIRIDQHPSKIPVIER YKGEKQLPVLDTKFLVPDHV NMSELVKIIRRLQLNPTQAFLL LVNQHSMVSVSTPIADIYEQEK DEDFGLYMYVYASQETFGF*ASS PCLSAHLPLTHPRLCPPGPAHP
9785	40153	A	9846	3	303	RDQHPSKIPVIERYKGEKQLPV LDKTKFLVPDHVNMSELVKIIR RRLQLNPTQAFLLVNQHSMSV VSTPIADIYEQEKDEDFGLAYM VYGLPGKPFPGF
9786	40154	A	9847	254	2110	
9787	40155	A	9848	234	1904	
9788	40156	A	9849	5	189	
9789	40157	A	9850	1	1546	MASASSQPSLAVGFSSFDPGAP SCTASSASGILSPTASEVPYASG MPIKKTGHRGVDSSGETTYKKT TSTALKGAIQLGITYTVGSLSTK PERDVLMDQFYVVEIFFPSEGS NLTPAHHYNAFRFKTYAPVAF RYFRELFGIPDDYLCCLCEPLI ELCSSGASGSLFYVSSDELIK TLQHKEAEFLQKLLPGYYLNLS QNPRTLCLKFFGLYCVQTGGKN IRIVVMNNLLPRSVKMHKIDYD KGSTYKRRASQKEREKPLPTFK DLDFLQDIPDGLFLDADTYNAL CKTLQRDCLVLQSFKIMDYSL WLSIHNIHDAQREPLSSDTLQV SIDTQRLAPQKALYSTAMEFIQ GEARLGDTEADHMGGIPAQ NSKGERLLLYIGIDILQSYTFLK KLEHSWKA VVHDGDAVSVHR PGFYAERFQHFMCNAVFKKIPL KPSPSKKFRSGLSFLHTGSSGN SCITYQPLVSEEHKSQVIKVVQE PGVHLGRSDVLPQTSEIPPLEEIT

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9790	40158	A	9851	233	2051	AGPGAGSTCLREARRGRGGGP QNAGSVKRRWEDSIPRRGR7GL KESQAAEGEGAAMASASSGP SSSVGFSSFDPAVPSTLSSASGI KRPMASEVPYASGMPIKKIGHR SVDSSETTYKKTTSSALKGAI QLGITHTVGSLSTKPERDVLMO DFYVVESIFFPSEGSNLTPAHHY NDRFRKYAPVAFRYFRELFGI RPDDYLYSLCSEPLIELCSSGAS GSLFYVSSDDEFIITVQHKKEE FLQKLLPGYYMNLNQNPRTLLP KFYGLYCVQAGGKNIRIVVMN NLLPRSVKMHKIDLGKSTYK RRASQKEREKPLPTFKDLDLQ DIPDGLFLDADMYNALCKTLQ RDCLVLQSFKIMDYSLMSIHNI DHAOREPLSSETQYSVDTRRA PQKALYSTAMESIQGEARRGG TMTDDHMGGIPARNKGERL LLYIGIIDILQSYRFVKKLEHSW KALVHDGDTVSVHRPGFYAER QRFMCNTVFKKIPLKPSPKKF RSGSSFSRRAGSSGNSCITYQPS VSGEHKAQVTTKAEVEPGVHL GRPDVLPQTTPLEEISEGSPIDP SFSPLVGETLQMLTTSTLEKLE
9791	40159	A	9852	30	298	EPFIFLFIYLFYLFETESRPVIO AGVQWCNLSLQPLPTGFKQFS VCLSPLTSDYRHPPPCPANFCS FSRDGVSPCWPGWSQTPDLR
9792	40160	A	9853	3	938	
9793	40161	A	9854	208	870	LGMAGRLFTVNLQSPNPLSTLL AEVCVEQCTLMSKMKPLWIM YSNEEAGSGRVSLSKRDDD LWQDMLTMQTIRLMDVPDTIA NIQLNNRNMDDGNEFTLSA GYCVATYVLGIGDRHSDNIMIR ASGQLFHIDFCHFRQRPFILTY DFVHVIEQGKTN/SEKFERFRG YCERAVTILRRHGLLFLHLFAL MQAAGLPFLSCSKDIRY/LKDSL VHPL

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9794	40162	A	9855	1	790	VEELSKKLADSDQASKVQQQK LKVGQGLGEWWPI.DKGGKLF KLWGRGGLVYKWFLLIYKISY ATGIVGYMAVMFTLFGLLNF KIKPEDAMDFGISLLFYGLYYG VLERDFAEMCADYMASTIGFY SESGMPTKHLSDSVCVCGQOI FVDVSEE/EDH*EHRC/CFHEF CIRGWCIVGKKQTCPCYCKEKV DLKRMFSNPYPPLGSLGVGCG KKVLA SVTCIWWLLGPSLLPPT RTCQTMMNNKKIMKVMRIKR MMTDTMAS
9795	40163	A	9856	1	1005	FRGRAVKMAAVVEVEVVGGA AGERELDEVMSDLSPPEQWR VEHARMHAKHRGHEAMHAEM VLILIALTVVAQLLL VQWKQRH PRSYNMVTLFQMWWVPLVFTV KLHWWRFLLVIWILFSAVTAFTV FRATRKPLVQTTPRLVYKWFLL IYKISYATGIVGYMAVMFTLFG LNLFLKIKPEDAMDFGISLLFYG LYYGVLERDFAEMCADYMAST IGFYSESGMPTKHLSDSVCVC GQQIFVDVSEEGDHETTYRLSC NHVSHEFCIRGWCIVGKKQTCPC YCKEKVDLKRMFSPNWPWRPHV MYGQLLDWLRYLVAWQPVIIG VVQGINIYLGLE
9796	40164	A	9857	28	267	LNIGKGDSSKKPRGKMSSYAFFV QTCREEHKKQHPDASVNFSEFS YKKDIAAY*AKGKPDAAKKGFI KAEKSKKKKEEEEED
9797	40165	A	9858	1	194	MGKGDPKRLRGKMSSYAFFVQ TCQEEHKKQPPDASVNFSEF/S KKCSERWKTMSAEKSEDM KL
9798	40166	A	9859	241	958	HQIFILFFRKITKHGQRRSLRSPR GKMSSYAFFVQTCREEHKKRH PDASVNFSEFSKKC/SRQGWKT MS/SKEKGKF*RYGQKRDKAR YEREMKTYYP/SGGDKRSF KDPNAPQGGPPGFSFLF/CSEY RPKIKREDHPGLSIGDVAKKLG EMWELTLQ/SDKQPYEKKAA KLKEKYEKDIAAYRAKGPDA AKKGVVKAESKKKKKEEEEDE EDEDEEEEEDEDEDEDEEDD

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9799	40167	A	9860	2536	2909	KSGVPGSRFSSSDKSDTGV TGL FSTYFLKSDFLQLIDISASTAS KSLFSA VLFQ EYILS FGLSEIISIL SSAVCWREAPKLSMVGCLAAG GKLTGC* AAGCLATDGR TETL DAAPAAAALSAV
9800	40168	A	9861	5	1752	KCTICLRNS/AVCCGCGQLSG YLN GEGADGAERGGGSGV E C LRAPVCGQAASSI.AASQLAAG GQAANHAQLRCLSPADCALML FIQVEVL TNSIAMVSVHLEKQP LKLVLGELGFRSPAGEEQATPV VGEGELGCIEDSAAVAEGGIAI GGIVGINTALQEV LKPHTIKMQ RNNAQLSRRKEPK EGLCGERG QDRMSRAKGS SSKGKELPPGCR RVTM KPLL VRETQEGQA AERG AEEQLQTLGPFAVYRDSPSKNF YKRDKMLKGL EEA KVN FVWR TNEG FLEEDAGQ EFGIQA VTP ALCPSRKA EVPLSCLTLK LSED GKAKKAPYNTG PLGLLHLSMC SHSRKGFEQLWQLNSGKLLQG PRDSVEGSARRAETA VHCPAVL HFAPALLLAALRCQRDLESAAA PSHTRSCQHPRLLSGAVQTAGF SNPPKVVIIQIKWNFLVM L NFP GSTKLIARLKQQMNYKEMASQ RLTQSM LPHRSRLIGAGPCNRC VHPEPVIVTLFGQKV FARIKK N QTCLCSQIWCAHYQQGWICA WLAGFGKIYIFSTIGVIDTLSSG HIHLQPNC TARD SASWESPA
9801	40169	A	9862	1	668	MWRLVIQDAKDENGVLVGNR VLAHSSLAVLSCLALNNRRISG WTP/CGPSGSPPGFMGRRGTST/ RLPTG**CPEGQPPRCPCG*ASG CASSPAECRMPATHLPNGSGRV FPFPGPVNYSPLRLQAPEQVTG S/SPWPFS/RPV LGLPLEGS/PPP F/RLPPRPRPAGVAAGSSWGHS AASVRRSPGRRPEGESIHP RPPA SRLPWL RATREEEAGAPKLGED SYNPF

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9802	40170	A	9863	2	624	FMGRRGTSTPFLADNAPRGSP PGAHVVGWDPDLRRAPVTGF SCSGSCSQRGAAWESFPRSP CRASGCASSPAECRMPATHLPG NSGRVFPFPPGVNYSPLRLQAP EQVTGS/SPWPF/SPVLG/PLPLE GS/PPPF/RLPPRP/PAVGAAGSS WGHSAAVRRSPGRRPEGESIH PRPPASRLPWLRAATREEEAGAP KLGEDSYPNF
9803	40171	A	9864	51	225	
9804	40172	A	9865	1	276	AFAAIPNTLLLEQKALDEPAE TESVSKDNTL*PPVETPTTLPR AGRETKYANLSSPTSTVSESQ/P D*AWSNSPSTCKIQNITEKRGG SL
9805	40173	A	9866	3	441	QTNFKGCSKVTSKLNMSLLW TPTGR*GCDRKVEQGP/PGDLGT AAVRPKSLAISSLSV/ACSASK TQGTDLKTSSHPPEMLHGMAPQ QKHGQQYKTKSSYKAFASIPYK HIAFGTEDS/STLPRAAAGRETK YANLSSPTSTVSESQAD
9806	40174	A	9867	123	417	SLDLDLFTVSGLLSDSSGILTR NLEYSAN*VWVGSLTVGTNV KIRGLASEPPAETVSFSSKFLFN KLLFSRFSSSILKENEKERKNR HRGNSV
9807	40175	A	9868	153	1624	TTRRKSMNP/TLGKYLEDN/SDL FSEQALDEPAKTESVSKDNTLE PPVELYFPAQLRQTEELCATID KVLQDSL/SMAPSLPTKQASS LAYMNVERTP/PTLKSNT/MLSL LQTSTSSSVGLPPVPPSSLSL SKQDGDRLGPENPRNIHTYPST LASSALSSLPINQRATFSSEK CFHPSPALSSLINRSKRASSQLS GQELNP/SLP/VSADFA/SLP NL/SSS/A/PSQSAHPG/PAQSL SSA/PT/CGSGTL/PSRLGKSESTTP NHRSPVST/PSLSISL/RTTEELIS CALSMSTGPKNKKSKTPTTLPR AAGRETKYSKNDYLT/LNAGS QQERDQAKL/TCPEVSGTILQE REFEANKLQGMQ/SSDLFKA EYVL/IVDSEGEDEAASRKVEQGP GGIGTA/AVRPKSLA/ISSLSV DVRPKTQGTDLKTSSHPPEMLH GMAPQKHGQASAYKGEESNEE DWTILKSSRMTNPRK/LSDNKI
9808	40176	A	9869	1	762	

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9809	40177	A	9870	1	537	
9810	40178	A	9871	490	681	MGLVLLHVGKLGSSWLRNGSQ ETAGQIISPLSSWHDGTGAGAAL DFSPLGSLCPVR*GSRRAAPH
9811	40179	C	9872	258	527	
9812	40180	A	9873	1	2865	MLPAFEHQTPSSSAFGLNLQQL WVVRGSRAFGHRLLKAALSGSL LLKFSDDSWLPCSSACRGPVIG LHLVIVYVKSHQNA YRHKNQIL KQTLSCNTTKVRSFIEVSETR NPPAGTNSGHILGTCPGYRYAK GKETGKEIKGPQNPPGYRLCPL QAVGGGEFGPTQVHVPSLSDDL KQIRVDLKGFSDDPDRQYPLRP EAHEGLQDILRYLKVQGLVRK CSSPCNTRILGVQKPKGWRLV QDLRFINEAVIPL
9813	40181	A	9874	3	177	
9814	40182	A	9875	255	1299	AAVFPLWCWRTRGKCHSLEWR PCTVCSWDPSPPKVSAGQALCG SETLPLTQTDPDQVPA TLES GHP ANLLVSAAWKSRKSLFSSWTW GTVISLGRPTPHFSEITIPLPWS HGSSITFQVTFPRFHVTTMTIQ LNVSSPVALENATSLSVLKNQS LRFVYVTDSDNPPARLSWTWEG QALNLSQSSSAVLELPPVESC DGGEFVCQAQHPLGSQHVVISIL SVQSDSVISIEEGVLQTLGFTLIR GILMGTSCTFCGFTWICCTSPVI PKPGTQSCSFTRDSATLPDAG SPGPKRVWMCSESHQPLCAVP DEDEQELHYAVLHFHKVQPQE PKVTDTEYSEIKIHK
9815	40183	A	9876	27	385	ASTTTGSGTSTAARCTAWSPG PLVTAVEKEFAEAAALGQRIST LQKGSFPLQVRMLNDQLMLL ERTFLNPRAFPERYYSYHVLWA /PSHGLRSHIPGLSNACSRARDT ASGSEA WAEG
9816	40184	A	9877	160	480	
9817	40185	A	9878	19	433	GLDHGWAGDRWRTRPVVGAG EGRAPRLNSPGQIRSPGPGDLS IYDNWIRYFNRSPVYGLVP.GF SSHQAVARTAGSVILRLSDSFFL PLKVSDDYSETLRSFLQAAQDDL GALLEQHSISLGPLVTAVEKFE AKAAAL

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9818	40186	A	9879	1	996	MALSKERSTVTRTQWARKTML QGETIQISEVSTYLRPYSVSGT VLGTNMSKTSARIPTYHTAFD TFDYVDKFLDPGFSSHQAVART AGSVILRLSDSFPLPKVSDYSE TLRSFLQAAQQDLGALLEQHSI SLGPLVTAVEKFEEAAALGQR ISTLQKGSPPDHVLWA/PSHGLRS HIPGILSNACSRARDTASGSEA WAEVQRQLSIVVTALEGSVEAL HEVLQLPAALRACPPLRKALAV DAAFREGNAARLFRLLQTLPLYL PSCAVQCHVGARREALARFA RAFSTPGQTLPFGFMVNLLA WMDSGKHGTCARPTGCPWTER RELCS
9819	40187	A	9880	66	744	RAHEDRERSGVQIRTQSWNGG KREKDFLHQSGVLETLMLKGC WRKSKTSARIPTYHTAFDFTD YVDKFLDPGFSSHQAVARTAG SVILRLSDSFPLPKVSDYSETL RSFLQAAQQDLGALLEQHSISL GMHSPDPEVRMLNDQLMLLER TFLNPRAFPEERYSHVLWA/PS HGLRSHIPGILSNACSRARDTAS GSEAWAEVQRQLSIVVTALEG AAATLRPVADL

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9820	40188	A	9881	2	2241	PRVRRMQWTKVLGLGLGAAALLGLGIILGHFAIPKANSIAPQDLDEILEITVMGQLDAHRIRENIRELSREPHLASSPRDEDLVQLLLQRWKDPESGLDSAEASTYEVLLSFPSQEQPNVVIVGPTGGIIHSCHRTEENVTEGQGGPDVVQPYAAVAPSGTPQGLLVYANRGAEEDFKELQTQGIKLEGTIALTRYGGVGRGAKAVNAAKHGVAGVLVYTDPADINDGLSSPDFTFNSWYLPSPGVERGSYYEYFGDPLTPYLPAPSSFRVDLANVSGFPPIPTQPIGFQDARDLLCNLNGTLAPATWQGALGCHYRLGPGFRPDGDFPADSQNVSVYNRLELRNSSNVLGIRGAVEPDRYVLYGNHRDSWVHGAVDPSSGTAVLLELSRVLTLLKKGTWRPRRSIVFASWGAEFGLIGSTEFTEEFFNKLQERTVAYINVDISVFANATLRVQGTTPVQSVFSATKEIRSPGPGDLSIYDNWIRYFNRRSPVYGLVPSLGLSAGSDYAPFVHFLGISSMDIAYTYDRSKTSARIYPTYHTAFDTFDYVDKFLDPGFSSHQAVARTAGSVILRLSDSFFLPLKVSDYSETLRSFLQAAQQDLGALLEQHSISLGPLVTAVEKFEAEAALQQRISTLQKGSPPDLQVRMLNDQLMLLERTFLNPRAPFEERYSHVLWAPSHGLRSHIPGLS
9821	40189	A	9882	1	1962	
9822	40190	A	9883	1	166	MEYYAALKKDEMFMSVGTWMKLETIILSKV/CQQQKVKKHMFSLTGALLVRGPWA
9823	40191	A	9884	1	378	
9824	40192	A	9885	1	681	
9825	40193	A	9886	1	3174	MEYYAAIKNDEFMSFVGTWMKLETIILSKLLQGQKTKHRMFSLIGSHIVKVPSSLQAHLQLSGKEVDVNSEVHVQEMAEARKDDVVTVTDAAEKALDKIHLFMVKTLSKIGIQGTYLNVKAIYDKPTANII LNGEKLFAPLRNRETQGCPLSPLLNTVLKVLARAVRQEKEIKGIQIGKEEVILSLFADDMIVHLENPVISAQNLKLIDNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSELPFTIASER
9826	40194	B	9887	1	352	

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9827	40195	A	9888	3	430	FFFLPVAGLRRPRRLGPVPPR PRVPPQDRAATMKKFFQEFKA DIKFKSAGPGQKLKESVGEKAH KEKPNQAPRPPRQGPTNEGTD GSRCCQP/WLEQKQSRAWGPH IAGHHPKPGEKGTSSRSHRQRE PRGPRDQIRGI
9828	40196	A	9889	1	1062	MKKFFQEFKADIKFSAGPGQK LKESVGVWGRPNGLMSVKGN CECGNLWLLYPEVAALAAEAE GPEVGSVEDQRRQQGYFVRLG SLSARIRHLAYEHSVGLRQSK HRAQDTLAQLQETLELVDHMP CGVTPPTAPARPGKVHELWGEW RQRPP/REPPPEIQAELETLVLAR SLTHELQGTVEALEFSVWGLPA GAQEKVAEVRRSVDALQTAF DARCFRDVPAAALAEGRGRVA HAHACVDELLELVVQAVPLPW LVGPFAPILVERPEPLDLADLV DEVIGGPDPRWAHLDPAAQQR AWAEHRDGSNGDGDGRMGV AGDICEQEPETPSCPVKHNPDA RAGLLTHGPFVEAG
9829	40197	A	9890	11	285	
9830	40198	A	9891	2	138	FFFLGFHVFSIPLIPRDNFS*GV FSSLDLITAVFVTLAELRSVT

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9831	40199	A	9892	121	2320	EMAFQKAVKGTILVGGGALAT VLGLSQFAHYRRKQMNLA YVK AADCSIEPVNREPPSRE AQL LTL QNTSEFDILVIGGGATGSGCAL DAVTRGLKTALVERDDFSSGTS SRSTKLIHG GVR YLQKAIMKLD IEQYRMVKEALHERANLLEIAP HLSAPL PIMLPVYKWWQLPYY WVGKILYDLVARKANCLKSSY VLSKSRAL EHF PMLQKDKLVG AIVYYD GQHND A RMNLAIALT AAIRYGAATANYMEVVS L LKK TDPQ T GKVHVSGARCKGCPST GQEF D VRAKCVINATGPFTDSV RKMD D KDA AANCOPSAGVHIV MPGYSPESMGLLD PATSDGR VIFFLPWQKMTIAGTTDTPTDV THHPIPSEEDINFILNEV RNYLS CDVEVRRGDVLA AWSGIRPLV TDPKSADTQSISRNVVDISESG LIT IAGGKWT TYRSM AEDTINA AVKTHNLKAGPSRTVGLFLQG GKDWSPTLYIRLVQDYGLESEV AQHLAATYGDKA FEVAKMAS VTGKRWPVGVHLVSEFPYIEA EVKYGIKEYACTA VDMISRRT LAFNLVQA AEEALPRIVELMGR ELNWD D YKKQEQL ETARK/FL YYEMGYKSRSEQLTDRSEISLL PSDIDRYKKRFHKFDADQKGFI TIVDVQRVLESIN VQMDENTLH EILNEVDLNKNGQVELNEFLQL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \=possible nucleotide insertion)
9832	40200	A	9893	1	2020	MLKPLMGGGAHRRAAAGARK WDGTAHASTSGLEVLWVTTSR SKTVESVGLAKPGQHNDARMN LAIALTAARYGAATANYMEVV SLLKKTDPPQTKGVRVSGARCK DVLTTGQEFVRAKCVINATGPF TDSVRKMDDKDAAA/CQA/SA GVHIVMPGYSPESMGLLDPAT SDGRVIFFLPWQKMTIAGTTDT PTDVTHHIPSEEDINFILNEVR NYLSCDVEVRRGDVLAAWSGI RPLVTDPKSADTQSISSRNHVVDI SESGLTIAGGKWTTYRSMAD TINAAVKTHNLKAGPSRTVGLF LQGGKDWSPPLYRLVQDYG ESEVAQHLLAATYGDKAFAVEAK MASVTGKRV/WPIVGVRVLSDF PYIEAEVKYGIKEYACTAVDMT SRRTRLAFLNLQAAEEALPRLL ELMGRELNWDDYKKQEQLT ARKFLYYEMGYKSRSEQLTDR SEISLLPSDIDRYKRRCHKFDAD QRGFMTVVEVQVRVLESINVQM DENTLHEILNEVDLNKNGQVEL NEFLQLMSAIQKGRVSGRLAI LMKTAENLDRRVPIPVDRSCG GLYFCVRNWWVLGLTDFKNE AADPSGVKLQTTFTVSVTLAKV ARLELFVSPGGLVVLGSGVKL QIFAPNMAMHNKAAPPQIPDTR RELAEVLKRRQELAAATLAKFG
9833	40201	A	9894	2	593	ISSAVEFETSQLSGLWTEQSAA RSRGENIVCGPQGPGR/GPWVP AEPTGSPVVSSEPLDLLPTDLDR QEMPPPRVFKSFLSLLFQGLSVL LSLAGDVLVSMYREVCSIRFLF TVVSLNLNLSAFWLGLLYLVS PLENEPKEMTLSEYHERVRSQ GQQLQQLQAELDKLHKEVSTV RAANSERGAKLVFQRLNEGFV

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9834	40202	A	9895	1	1105	MRRSSRPGSASSSRKHTPNFFSE NSSMSITSEDSKGLRSAEPGPGE PEGRRRARGPSCGLLFQGLSVLL SLAGDVLVSMYREVCSIRFLT AVSLLSLFLSAFWLGLLYLVSP LENPKEMLTLEYHERVRSQG QQLQQLQAELDKLHKEVSTVR AANSERVAKLVFQRLNEDFVR KPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPP TVILEPHVFPNCWAFEGVQGG VVIQLPG/HECTLSIDLQHPPPS VEHTGGANSAPRDFAVFLLSF FTHQGLQVYDETEVSLGKFTFD VEKSEIQTFLQNDPPAAPKV KIQILSNWGHPRFTCLYVRRAH GVRTSEGAEGSAQGP
9835	40203	A	9896	10	395	VEPGKRLIDRIVETICSCFOGPO TDEGVQLQIIKALLTAVTSPHIEI HEGTILQTVRTCYNILASKNLI NQTTAKATLTQML/NHARSDSG KVSTENGDAPRERGSSLSGTN DGAQEVVKDILEDVVT

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9836	40204	A	9897	1	1698	MLGTSVEDIAQFLHQEERLDST QVGDFLGDSARFNKEVMYAYV DQLDFCEKEFVSALRTFLEGFR LPGEAQKIDRLMEKFAARYIEC NQQTFLFASADTAYVLAYSIM LTTDLHSP/PDLEMHQAPAGARS ADRNRCEDALPVWIA*KRRE PEGPHIGRRRVHGPWPR*FGEW RSG*KTDGQLPRIGW*DQLAEC GCSCGQDFYVWYQTGWKNS* LCPLAVCCVHG*TGFPSSHV QLAEDCGDILQHESDPTIVVS NMACDWRSLQ*DKL*MLGTSV EDIAQFLHQEERLDSTQVGDFL GDSARFNKEVMYAYVDQLDFC FKEFVSALRTFLEGFRLPGEAQ KIDRLMEKFAARYIECNQQTFL FASADTAYVLAYSIMLTTDLH SPQILKCISQLELAQLIGTVKT RYLSGSGREREGSLKGHTLAGE EFMGLGLGNLVSGGVDKRQM ASFQESVGETSSQSVVAVDRI FTGSTRLDGNAIVDFVRWLCA VSMDELASPHHPRMFSLQKIVE ISYYNMNRIRLQWSRIWHVIGD HFNKTSCDRLRELHVSEVFTVI TETRETKGPRDTPIFIETLVKVK DAEDQLGARVGYIELDLNSGKI LESFRPEERFPMSTFKVLLCG AVLSRIDAGQEQLGRRHYSQN DLVEYSPVTEKHLTDGMTVRE LCSAAITMSDNTAANLLTTIG
9837	40205	A	9898	1	492	
9838	40206	A	9899	1	3555	
9839	40207	A	9900	1	4145	MFVLKVGCSLLLRDPRRSLLH YTCFTSVPLVQVGCNPNEVDV AIFAVIDSLRQLSMKFLEKGELA NFRFQKDFLRPFEHIMKKNRSP TIRDMAIRCIAMVNSQAANIR SATIFQHHPAIDSFQDAVKCL SEFACNAAFPDTSMIAIRLIRF CGNYLISERPRVLLEYTSDDMN VAPGDRVWVRGWFPILFELSCI NRCKLDVTRTGLTVMFEIMKS YGHITFEKHWQDLFRIVFRIFD NMKLEPELSEKS

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9840	40208	A	9901	1	5477	MQESQTKSMFVSRALEKILADK EVKRPQHSQLRACQVALAWK LLLIAPLAVGKATPVKMWSNK VEQLTVMNMHSAEQETDEIKA EIEKQRLGTAAPPKANFIEADK YFLPFELACQSKSPRVVSTSLDC LQKLIAYGHITGNAPDSGAPGK RLIDRIVETICSFCFGPQTDEGV QLQIIKALLTAVTSPHIEHEGTI LQTVRTCYNIYLASKNLINQTT AKATLTQMLNVIFTRMENQVL QEARELEKPIQSK
9841	40209	A	9902	2	740	TGWEGRAAEAEVPQDDRRREPRH S/IEVEEEDQKLVSASLEPIGG/P PDCPQKQ/PQCPLSPSKKWGC DLCL*QHKLAQKWRREISTSVP SQPLGPGRTADTGPSLPT/TPA GQEAGRTPAPPAWSAFDL.DST VVKMEKGWICS*KYTRSQASC SELPRRLGRAOPTTEELGMPTQE VAPLPARG*GPESLPL/ASRQEF LSGRTRVRVKGLPLPLTEGKIV LPGGEGGSPHVCPSPWIIERRTA DQGVVAE
9842	40210	A	9903	1	1376	MPSSSVGPAPPSLRGSSEQLAW LRGIFSYRSSPPSPQOSSPNQTR SRQHYAPSVFEKYTASVTVGSK EVTNLNYDTAALAGPWPALHS WRPLRGAGCGALEAKPYTKQ WAALGPPMVPGLRLRYLLWSLQ TLATPGQRPREGPHAHTPRAEA TAGQEPARDPKGSARNPEPQRP RGKGVRAAPKQGVGRGMSIPAQ PHASTRAGSERSE/QRRLSSF TGSCDSDLKFNQLKFRKKKLLK FCKSHIHDWGLFAMEPSGDPLE SAWIHARNAPTTTPSQTPHPPPR EAGNPNNPPRAPEARGPGHDKA AQKACVHGGPNTQHPRPQPEP AVPPAALAPPPKHQLSSQASSPS RLGRAAERPHKTQQRQTPTHT GPRAAATAEHAPQALPPAPAP HYNRTRPAQLRNPTPKKGSEE PAQPTKHTPATPAKRDPKGGG ARRRPARPLQPHSGGEEDKES

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9843	40211	A	9904	724	2076	KLCPCLYHFFHTNVQRHAPFVA NPFLLTHIQISTKHPAIVGTTELL LCVGGVQRVLQLAPQRLQLLA QVPALLRLGPGHTLRLQVLLG LGQGCLSLPQGFQQLGPGPTLV FCPLPELLEEDAVGEALATDAD ALQDPVAAKL VQHQPWLQLPG LGKQPPPLPVSQLLEVGRAVPLH HPQGALLLALLEGLQSLPRV HSPFLHDTFRHRPVPASQLN SFEQLCITTPQKLQQLFNHTMF VSPPAVNVAQNPAGLLALDEE CWFPKATDKSFVEKVAQEQQG HPKFQRPRLHRDQADFSLHY AGKVDYKANEWLMKNMDPLN DNVAALLHQSTDRLTAEIWKD VEGIVGLEQVSSLDGPPGGR RRGMFRTVGQLYKESLSRLMA TLSTNTNPSFVRCIVPNEKRAG KLEPRLVLDQLRCNGVLEGIRI CRQGFNRLQFEFRQ
9844	40212	A	9905	2	480	VGCMGCSKGPWRQAFQVDVH VSDALPQCRQLQTGMRGAFGK PQGTVARVHIGQVIMSIRTKLQ NKEHVIEALRRAKFKFPGRQKV CSAAAPFSHLCPRPDSVLSIAP *IHISKKWGFTKFNADEFEDMV AEKRLIPDGGGVKYIPSRGLD KWRALHS
9845	40213	A	9906	1	485	SDEYDQLCSEALVGAQICAKK YIVKCCGKNGFHIRVRLHPFHV ICINRMLACAGTDRLQTGMGG AIGKPQGTVARILIGQVIMSIRT KLQNKHEHVIEALRRAKFKFPGR QKIHISKKWGFTKFNADEFEDM VAEKRLIPDGGGVKYIPSRGLD DKWRALHS
9846	40214	A	9907	198	452	DYYLEGLNHIVVHHDHFLNLQN HSSNLPVAEICYR*RYRKVQQ RIIAKDYTTLEFSNR*LFN

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9847	40215	A	9908	2	1968	SYLHCKWATMEELEKDPRIAQ KIKRFRNKQAQMKHIFTEPDED LFNPDYVEVDRILEVAAHTKDAE TGEEVTHYLVKWCSPYEEST WELEEDVDPKVKEFESLQVLP EIKHVERPASDSWQKLEKSREY KNSNQLREYQLEGMNWLLFN WYNRKNCILADEMGLGKTIQSI TFLSEIFLRGIHGPFLIAPLSTIT NWEREFRTWTEMNAIVYHGSQ ISRQMIQQYEMVYRDAQGNPL SGVFKFHVVITTFEMILADCP KKIHWSCVIIDEAHRKKNRNCK LLEGLKLMALCHKVLLTGTP NSVEELFSLNLFPSQFPSETA FLEEFGDLKTEEQVKKLQSILKP MMLRRLKDDVEKNLAPKQETII EVELTNIQKKYYRAILEKNFSFL TKGANQHNMPLINTMMELRK CCNHPLYLINGAEEKILED HSPDAPDFQLQGMIAVAGKL VLIDKLLPKLIAGGHKVLIFSQM VRCLDILEDYLIQRRYTYERIDG RVRGNLRQAIDRFCKPDSDRF VFLLCTRAGGLGINTAADTCII FDSOWNPQNDLQVPEGRIQKV WEQMSWPRAQPDNAAAACL QDFGSQLGVQSEETGPFHNRQK QDSGNSHTAPRGRESFIKPPSSR DLLPLKIQKEGPATNYNS
9848	40216	C	9909	223	402	

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9849	40217	A	9910	1	1710	MFEKAARQEWIQVAKSVTRVA MSSYTFQKNPDLSVGEDVEKK LELSYAAVTMAWGQYGDYGY PYQQYHDYSDDGWVNLNRQG FSYQCPQGQVIVAVRSIFSKE ADSVSRASATGPDSGQFFLLER VGCTKTTAEAQPORDDPYLVLT RTVEGLSRTVEGVGRGLTQAA AGEGAGAVEAAWNSLCGPFSS TPMASDEETEAIIRGHETRPDDT AKNSGAIQHQSCSWPLY/RA PHSVKRYQTCSNNGLVAGFQS RYFESVLDREWQFYCCRYSKR CPYSCW/LSLAADQTLMTPGVG EAPRKCSSFRKGNRTIEPALTGP KSPTYSVGMPSLKLRPNDSHPS AVLLLPNFWLTTEYPGHYGE MDMISYNYDYYIRGATTTFSAV ERKEERRERKIGDKKHTEPTV LVWAAIPHYLRLGNLRTIEYFH SSGSWKVQDQVDPPEEPARQN HRDRVPCHTTPPLGGQEGDSQPV VMRAKDHYELEKQKALGQVE DEEDLCQQQLPEQTYGSEEP QEAKKNLGSPEPNSQAGAQQPI SMATNRAVFDVTCNFSPHWLQ CLQSRSLSPEDPGL
9850	40218	B	9911	101	1237	
9851	40219	A	9912	1	622	NLSDRHRGSHLESQHFORLQOE DLLSPRIQDQPGQHWETLSHINI VVIGHVDSGKSTTTGHLIYKCG GIDKRTIEKFEKEAAEMGKGSF KYAWVLDKKAER/ERGITIDIS LWKFETSKYYVTIIDAPGHRDFI KNMITGTSQADCAVLIVAAGV GEFEAGISKNGQTRHALPG/ YSQKRYEEIVKEVSTYIKKIGYT PDTVACVP
9852	40220	A	9913	1	762	VVQTQISKTADELISYWGTSFPP PFAASLTLYELCYCITIDISLWK FETSKYYATVIDAPGHRDFIKN MITGTSQADCAVLIFAAGVGEF EAVTFAPVNVTTTEVKSVMHH EVLSEALPGDNVDFDVKNVSV KEVHHGNVAGQISAGCAPVLID CHMAHIAACKFAKLKKKTGSTS GKKLEDGPTFLKSGDAAIIVDM VPGKPMCVEFSVYPLSRFAV CDMRQTVAVGVIEAMDKMAA\ GAGKVTMSAQKAHNAK

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9853	40221	A	9914	1	618	MVQARPGAHPITLLPGPTAAWV SGFSGGSDLTGAREAQERGR WSPTESSASVSPVAKVSKFTLS SELEGGDYPKERERTGGGPRGP PDWTPHGTGA\LQSPHPRTAPA PHPTPCGPRPDAGQRSPGAPA WSPRVHRPTPSLLPPRRWTA LWAAWQRPPLASQPGRGTSPG NPGPGRTPSPQEVGSPGHHIS LRTGFPPTL
9854	40222	C	9915	3	406	
9855	40223	A	9916	1379	2096	NGGGCGAARGGAAPGEGTRRG ACWATRGPLGTGRSAAAPARR GERQQLAMDVFLMIRRHKTTF TDAKESSTVFR/ELKRIRRGQSS KRPPDEQRL\YK\DDQLLD\DG\ KTLGECGF\TSQNRHRPQAPAT VGSLPASSAASSTDDTFEALCI EPFSS\PEL\PDVDGRPGGFEG SAQLNKAVQVETPQEGPIFPQL KGDGLSLPGCCLFFPPLPGMGP TPCGLLLGLVLGSSCAVLSPRS
9856	40224	A	9917	1	695	MAHAGRTGYDNREIVMKYIHY KLSQRGYEWDAGDVGAAPPG AAPAPGIFSSQPGHTPHPAASRD PVARTSPLQTPAAPGAAAGPAL SPVPPVVHLALRQAGDDFSRRY RGDFAEMSSQLHLTPFTARGRF ATVVEELFRDGSVNREMSPL\V DNIALWMTEY\LNRLDHTWQD NGGWPWDFLIGATTPTVTIPYLP YHSTEECLINVKGTAEFKIPFA KPDEMIQAIIIDGC
9857	40225	A	9918	3	422	CSLKNWREVLALLTYSGTEKF PELC\DLMEKVMVNLNRSLEQLR GPH/GGS\AVLGQQSPFPFPRIV VGATLHSEKTSYRLGSQPSHQ VPTSPRPRVFTPQSSPAMPLAP SHPSPYQGPRTQNISDYRAGP QAIQPLPL
9858	40226	A	9919	1	849	

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9859	40227	A	9920	3	868	NSSPPFPFRIVVGATLHSEKTS SYRLGSPSHQVPTSPRPRVFT PQSSPAMPLAPSHSPYQGPRT QNISDYRAPGPQAIQPLPLSPGV RPGPQDSWKEAPAPRGNLQRN KLPETFMPPAPITGPS/IM/RPHP* ATRDSSLTAPLSPV*VMLPQEF QENSPAGDKDNVFPGLGKPPSP PCVQVMVDGPHSSR/PCAEGD WVQVPGVLTAEKGRLLISPILL *WEQCDCESLGTS*GSHEKDS LPLWPFSLLLYQQLQHLPEKMK ERKELPPEHQLKSSFEALLQRC
9860	40228	A	9921	1	307	MKLKELERPAVQAWSPASQYP LYLATGTSAAQQLDSSFSTNGTL EIFEVDFRDPSLDLKHGVLISA LSRFHKLWVGSPGSGLLSSGV IVGGDNGMLILYNVTHILSSG KEPVIAQKQKHTGAVRALDLN PFQPPEDIKALSNNRQAQHILSS AHPSGKAVVWDLRKNEPIKVS DHSNRMHCSGLAWHPDIATQL VLCSEDDRLPVIQLWDLRFASS PLKVLESHSRGILSVSWQADA ELLLTSAKDSQILCRNLGSSEPC PRLVFISQVTTESEFLMRSALQ EALGSGNLLNYCQNKSSQALL QSEKMLWQFLKVTEQDSRMK FLKLLGYSKDELQKKVATWLK SDVGLGESPPQKGNLNSDRQ QAFCSQASKHTTKEASASSAFF DELVPQNMTPEWIPITKDIDGLL SQALLLGELGPAVELCKEERF ADAILAQAGGTDLKQTQERY LAKKKTISSLLACVVQKNWK DVVCTCSLKNWREALALLTY SGTEKFPELCDMLGTRMEQES RALTSEARLCYVCSGSVERLVE CWAKCHQALSPMALQDLMEK VMVLNRSLEQLRGPHGVSPGP ATTYRVQYANLLAAQGSLAT AMSFLPRDCA/PAARDIYAPSTN YCSSYEPHP*ATRDSSLTAPCLQ SASAPAT*EDGKEGAAPRASVL EEQL*GASPTLLPVCN*LKDKK

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9861	40229	A	9922	3	2751	SVSWSQADAELLTSAKDSQIL CRNLGSSEVVYKLPQTSSWCDF VQWCPDRPSVFSAAFNQWISL YSVMGRSWEVQHMROADKISS SFSKGGQPLPPLQVPEQVAQAPLI PPLKKPKWIRRPITGVSFAGGG KLVTFTGLPSTPAHLVPQPCRL VFISQVTTSEFLMRSaelQEAL GSGNLLNYCQNKSSQALLQSE KMLWQFLKVTLEQDSRMKFLK LLGYSKDELQKKVATWLKSDV GLGESPOPKGNDLNS
9862	40230	A	9923	363	543	
9863	40231	A	9924	2	737	EAETEYFVRICKHMTNHNIVFQ LFHLLTFQFDCNTLNDQLEK VTVQMPESSEYEVLSICIPAPSLP YNQPGICYTLVRLPDDPTAVA GSFSCMTMKFTVRDCDPNTGVPD EDGNDDEYVLEDELVTVSDHIQ KVLKPNFAAAWEEVGDTFEK EETFALSSSTKLEEA VNNITFL GMQPCERSDKVPENQD/SHSL YLAGIFRGGYDL/LVRARLALA DGVTMQVTVRCKHRTFVDIILA
9864	40232	A	9925	327	464	GSPTTRPAKPLTLSSGHLSRPR WAEGPQYHLP*ISAPRAKLG VMM
9865	40233	A	9926	2	1179	WQPDIGPYGGLLNVVVDGLFI GWMYLPHPDHPVDDPMRFKPL FRHILMERKAATVECMYGHKG PHHGHIIQVKKDEFSTKCNQTD HHRMSGGRQEEFRTWLREEWG RTLEDIFHEHMQELILMKFIYTS QYDNCLTYRRIYLPSPRPDDLK PGLFKGTGSGHGLEIVMLSFHG RRARGTKITGDPNIPAGQQTVEI DLRIIRIQLPDLENQRNFELSRI VLEVRERVRQEQEGGHEAGE GRGRQGPRESQPSAPRAEAP SKGPDGTPGEDGGEFGDAVAA AEQPAQCGGQPFVLPVGVSSR NEDYPRTCRMCFYGTGLIAGH GFTSPERTPGVFILFDEDRFGFV WLELKSFSLYSRVQATFRNAD APSPQAFDEMLKNIQSLTS
9866	40234	A	9927	287	537	TGKFPSC/CLLSFYGTGLIAGH FTSPERTPGVFILFDEDRFGFV WLELKSFSLYSRVQATFRNAD APSPQAFDEMLKNIQSLTS
9867	40235	A	9928	1	3651	

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9868	40236	A	9929	1	3720	MEEMFGGGAADDYKAGPPE DEGDPKAGAGPPGPPAYDPY GPYCPGRASGAGPETPGLGLDP NKPPELPSTVNAEPLGLIQSGPH QAAPPPPPPPPPAPASEPKGG LTSPIFCSTKPKKLLKTSSFHLL RRRDPPFQTPKKLYAQEYEFEA DEDKADVADIRLNPRLPDV SSCRSRPALSPGLDIDFCPPNPG PDGPRRRGRKPTAKRDPGRPR RGRPRIRPLEVPTTAGPASASTP TDGAKKPRGRG
9869	40237	A	9930	503	739	QGWRRRRPISKISESRNMQNFL HALSNCLPEGGA*DRCSSRLEE GRQLPPLLLGSLQVAKKSGGTG WMVRCSCQLFLG
9870	40238	A	9931	1	1148	MGGKGGDSWVISATPLGKCCA AVPLGGNPTLRVDQLWRKQRP PLQQCTASAPGGWVTSMLGAG THAANTGFQLVWSSKRPMYKV LQAFFGVQRSDRSAMNGQGS KCVGMPITHTRQQADLGRGPE ETEDKKQQSRGSDLRSEGE EPYLLRTSKVKDKERILKAARE MKQIIYNGAPIHLAADFVSVEL QAKKEWCDIFKVLKKKTFYPK MVLTAGPSHPQSVISVSFTGLA NAASLTMSPDHLHGQPGFAGLSS VAAVDWQWALLRPSPPQGRM GLLPICQATQGPQLCVASPSDK EGFLLLFGEIARLTNKGGARL YKCDIVQGVCCEDPLATLDWE LRPDLEQGERPTPERHKPFLG KSFSAPLIKICRYEQWFMF
9871	40239	A	9932	333	689	NSFLTCLPPVSI*TDLLQPSAQ WKQLSLARRNVHSTRLAGARR CAASGPSVVAACHYHPVSGHSR LLHGCGHGWGSWQVPEVPPG SPFSLAPVWKKRRQTALPAILHL PVEHYYPEL

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9872	40240	A	9933	84	933	PLTSPEAFSNRCGLRGPP/PCVP VGRLLQFNDVSSLLGICLPDSSCC SSWHGPHSLHH/HVQACKASIR ASGTAASANCAFSRYHVHCSIA FQIKVLHNLIVLTVIIPAAEHMA WGPGLAQPNPPHRSAGSHSSWGP EVGPKLSTTALVGTYPQVPPV GLETGPPSLFQPLPISTHTAWNT ENCPANATVIAHPTLAAQGTKN PPTLLVHHCHYQHLKDDGT RRRENSLKLGEKGVILQTEGIQK GMDPTMEYATNYWKKLQWLK RRQTALPAIHLHPVEHYYPEL
9873	40241	A	9934	1	627	MESLDTETSTWGECHRKIRGM VPQVKELAEAAAAPPDGA VAE YRREKQKYEALRKQSKKQTS REDQQIINKLPCTNHCIWQSTH EHIPALSDLSGKRAKQVIPVKG GEHYERTLALLNQFKSKLTQAI AETPENDIPETEVEDEDEGWMS HVLQFEGKSRKSGKVPMSQDS DTEIYDPRNP/LVNKRREGKK AKSLMREKKERRLK
9874	40242	A	9935	1	371	PMRPAFTRVEMARVLMERNQY KERLMELQEA VRWTE MIRASR EHP SVQEKKKSTIWQFFSR LFSS SSSLPRKRPYPSPVNIHYKSPTE GCSVAAGFSPPPCHLHCDVCPL PRLFPQDLEVTGP
9875	40243	A	9936	2	186	
9876	40244	C	9937	109	408	
9877	40245	C	9938	161	341	
9878	40246	C	9939	303	439	
9879	40247	C	9940	201	419	
9880	40248	C	9941	122	307	
9881	40249	A	9942	3	80	YNPAPYKEKTITL/PCPRKLGGP QGS/S*NGPPSSSSSQCSVSFND PHLPEGQVQAAR*WAPPGL
9882	40250	C	9943	249	427	
9883	40251	A	9944	90	244	TVVPHDPCGTD AHCETHMD MCPSHSVMLCGWLTF AEF RGA MGEGG RESFLLNQASFCY*CSQ AGFSSNLWRCSRAGRGN TADE LWCHMTLV AQMPYV KHTWT CVPATVLC SVAGSP LSSGVQW GREGGKASS
9884	40252	C	9945	4	204	
9885	40253	C	9946	340	497	
9886	40254	C	9947	158	184	

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9887	40255	A	9948	200	386	LFYTM*IMAFLLSSSSSPGRPF* RILGGAKVYAGMQRYSFFLIGS RIITYLGIFGRELYFC
9888	40256	B	9949	47	622	
9889	40257	A	9950	1	630	
9890	40258	A	9951	1	782	
9891	40259	A	9952	1	677	MHGLGRWDACPDDEMESGQ SSAAATPSTTGKSNPTSSVPS AAVTPLNESLOPLGDYGVGSK NSKRAREKRDNRNMEVQVTQE MRNVSIIGMGSSDEWSDVQDIID STPELDMCPETRLDRTGSSPTQ GIVNKAFGINTDSLYHELSTAG\ S*VIGDVDEGADLLGNNDKCK VYTSVQTRPPQACTFSVRLVES THAELVGIEGRLYHKIHLPLRVH GAVGVSVLT
9892	40260	C	9953	202	366	
9893	40261	A	9954	1	2429	MKEGGWGDPCVGRGVTSGHV LQMKLLPFRQKKAHIMEIQLNG GTVAEKVAWAQARLEKQVPV HSVFSQSEVIDVAVTKGRGVK GVTSRWHTKKLPRKTHKGLRK VACIGAWHPARVGCISARAGQ KGYHHRTELNKKIFRIGRGPHM EDGKLVKNNASTSYDVTAKSIT PLGGFFPHYGEVNNDFVMLKGC IAGTKKRVTILRKSLLVHHSRQ AVENIELKFIDTTSKFGHGRFQT AQEKRAFMDGLSLSPAASDS DYPGEMFLDSDVNPEDPGAD GVLGITLVGCATRCNVPRSN SSRGDTPVLDKGGQGEVATIANG KVNPSQSTEEATEVDPGPG SEPETATLRPGPLTEHVFTDPAP TPSSGPQPGSENGPEPSSSTRP EPEPSGDPTGAGSSAAPTMLWG AQNGWL YVHSAVANWKKCLH SIKLKDSVLSLVHVKGRLVAL ADGTLAIFHRGEDGQWDLN HLMDLGHPHHSIRCMV VYDR VWCGYKKNKVHVIQPKTMQIEA SAGQGPGEGRLLASSPASSI RKSTRPTHDSKSFDAHPRES QVRQLAWIGDGVVVSIRLDST LRLYHAHTHQHLQDVVDIEPVVS KMLGTGKLGFSFVRITALLVAG SRLWVGTVNGGVVISPLTETVV LHRGQLLGLRANKTSPTSGEGA RPGGIHVYGGDSSDRAASSFIP

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9894	40262	A	9955	9	452	KIKVL SKNSQVTFDFPVPTLLND GQCLGYNSTPYKEKAITL/PCPR KLGPQGSFKTA/APSSSSPSFNF FNGSQNSVTNFWSSCFH*KVLI LKTNNLKLPHAKKKT KV/LQ NILLSF*RFYDALLSLTLLLN LNGQLQTVMRPFHH
9895	40263	A	9956	1	3223	ATATPSTTGKSNTPTSSVPSAA VTPLNESLQPLGDYGVVSKNSK RAREKRDSR/NMEVQVTQEMR NVSIGMGSSDEWSDVQDIIDST PELDMCPETRLDRGTSSPTQGI VNKAFIGINTDSLYHELSTAGS\ EVIGDVDEGADLLGEFSGMGK EVGNLLENSQLLETKNALNV VKNDLIAKVDQLSGEQEVLRG ELEAAKQAKVKLENRIKELEE LKRVKSEAIARREPKEEAEDVS SYLCTESDKIPMAQ
9896	40264	B	9957	176	658	
9897	40265	A	9958	2	5671	AGGPCVRSSRELWTILLGRSAL RELSQIEAELNKHWRRLLEGLS YYKPPSPSSAEKVANKDVASPL LKELGLRISKFLGLDEEQSVQLL QCYLQEDYRGTRDSVKTVLQD ERQSQALILKIADYYYEERTCIL RCVLHLLTYFQDERHPYRVEY ADCVDKLEKELVSKYRQFEE LYKTEAPT WETHGNLMTERQV SRWFVQCLREQSMLEIIFLYY AYFEMAPS DLLVTKMFKEQG FGSRQTNRLHVDETMD
9898	40266	A	9959	1	404	MVDQEAIFGCKNRNNCSHLEPP VSRLEGGAFVRDLLSPQTQYLLA SCPYYDGSFVIQIPSSNLFMV VVDSSCLCESAPITMAPIEIRYI LLCEVHSLPRKPENARECGGA PSL\QAQTVLLLLPLLLMLFSR
9899	40267	A	9960	1	1374	
9900	40268	A	9961	102	205	

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9901	40269	A	9962	1	1527	MVPDAAVLAQLAIRARVNRRW PTGLSAPHLCGAACSRCHAAI AKYFGDALPACAGKGDHCQNP TAVRRRLLEALERSSSWSKTCIG PSQGNQFDPPELYEGGRKGYGG FSRYDEGSGSGDEGRDEAHK REWNLFYQKQMLRKGDPKI EEFVPPDENCLKEASSRRIPRL TVKAREHCLRLLEALSSNRQS TRTADADAFRAKAVELEHETF RNAKVANLYKASVLKKVADIIH RASKDGQPYDMGGSAKSCSAQ AEPPEPNEYDIPPAHVYSLKPK RVGAGFPKGSCFPQTATELMET TRIREQAPQPERGGEHPPSRPC GLLDEGSEPLPGPRGEVPGGS AHYGGSPPEKKAKSSSGGSSLA KGRASKKQQLATAAHKDSQS IARFFCRRVESPAALLASAPAEAG ACPSCEGVSGTPDWPQRSTQGR KMEPGDIRLPLRLRSASGRGQ APARPETRAPLKSSPPLQRTHG KGKRPFRPARRTQASLRRGHA PQPIPPS
9902	40270	A	9963	2	99	
9903	40271	A	9964	115	1360	ENGQLHMVNALDGVRSLSLQK PRPFRLLFPKGFSELVCMNREDD TARKEKTDHFIFTYTREGNLR YSAKSLFSLVLGFSIDNVHDIDSLI GFPEQIAEKLFSAAEARQKFTPEP GAGUARALQKFTGGLWEVWVL CSLCFLWLKLPDICCKLGDEHE LLEHLTNEALSRY*PVTTCT*IV SVLF*RLIQDYRVVMKRGLENL TLDDLCKFSKSL*ILMLEEWP *RSCSSFSGTGLKVRLLVPSLIFL DSTI*YFACANWEFDHSNCKTE GWADQVLQIFLPCG*CSFSS*FQ VSYPTSRETAESCFRSTLSLVQN MHDEAAQRFCEKFPFL*SFLPFI CILKAVRLF*KLQFYKEKAPDC HGPVLKHEAISSQESKSKKRP FEESETEQNNSQPSKQKYVCL AVEDWDLNLSY

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9904	40272	A	9965	3	1026	DNVDHIDSLIGFPEQIAEKLFFA AEARQKFTEPGAGLRALQKFTF AYGSLVLCSLCLRNRYLVISEK LEEIKSFRELTCLDLSCCKLGDE HELLEHLTNEALSSVTQLHLKD NCLSDAGVRKMTAPVRVMKR GLENLTLADLSCNPEITGGRA LGYPFLFRGNLNCFRDISGDR GSRDIKTLKHKLQTHIGLVHSH VPLKEFDHSNCKTEGWADQIV LQWERTVAEAVKPRETSEPIAA AQRFYGKRSRAEAPL/CPLAD THMNSSVEKLQFYKEKAP/DCH GPVLKHEAISKPRSPKSKSRP FEESETEQNNSQPSKQKYVCL AVEDWDLNSY
9905	40273	A	9966	1	289	VKCHLHRPILWDPWKTSGIQQ VLTPL*KAMEKLEAILLICSLE AIGLITLPSLSMTQFLQLHVECC YVSPDQTPYFIDVETAMKDEV TVHNPHG
9906	40274	A	9967	1	1413	MVVPPIAELKNLEVLNLFNNQ IEKLPTQISRLQKLKHLNLGFLS PCNSMNRNLNISPQGFSLPALE VLDLTYNNLNENYLPGNFFYLT TLCALYLSNDNFILPPDGKLT KLQILSNRDNLISLPKEIRVLT QLKELHIQGNRLTVLPPELGSR GGSGSRFSAETA TGGAQNAPP VLSAGTIFKQRRNPSPAALRG GSVAA*PSPAAAYGKDQREH LPTAAGDGVGWEPTRDIQVGS ATAQALSQANAARGRLSTAQA AGSLHVECCYVSPGQTLFYTDV EIEAMKDESRGISILYKHRHLK VPLDQKLPKSGHQPDGYGQH DHKPMQMTSLRNATLR
9907	40275	A	9968	1	619	MNRLNISPGFGSLPALEVL TYNNLNENYLPGNFFYLTLCAL LYLSNDNFILPPDIGKLTQLQ LSNRDNLISLPKEIRVLTQLKE LHIQGNRLTVLPPELASSRCGP LSHPYAGKRIPRNAVFKFEQNT PWHTPPKKAGREMLLDVGTGP EAATSKPPAFLHRRRGSGWNP RSRSSSLQRTWPFGSREAEYPP ASGA

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9908	40276	A	9969	810	1672	GLPSVTMSKSLKKLVESREKN QPEVDMSDRGISNMLDVNGLF TLSHITQLVLSHNKLTMVPPNIA ELKNLEVLNFFNNQIEELPTQIS SLQKLKHLNLGMNRLNLTLPRG FGSLPALEVLDTYNNLSNSL PGNFFYLVTTLRALYLSDNDF EILPPDIGKLVTKLQILSLRDNDL ISLPKEIGELTQIKELHIQGNRL TVVPPPELGNLGF*LGQKQVFK AENNPVWVTPIADQFQLGVSHVF EYIRSETYKLYLGRHMQANPEP PKKNNDKSKKISRPLAANNR
9909	40277	C	9970	120	347	
9910	40278	A	9971	2	10018	LCVSPVTAGRPASRLREMEVEQ EQRRRKVEAGRTKLAHFQRQK TKGDSHSEKKTAKRKGSAYD ASVQEEPSVTKEDSALCGGGDI CKSTSCDDTPDGAGGAFAAQF EDCDGEKREDLEQLQKQVND HPPEQCGMFTVSDHPPEQGHM FTVGDHPPEQGRGMFTVSDHPPE QHGGMFTVSDHPPEQGRGMFTISD HQPEQGRGMFTVSDHTPEQRGIF TISDHPAEQGRGMFTKECEQECE LAITDLESGREDEAGLHQ
9911	40279	A	9972	2	5196	APLDGEVELLQKLEKLDEFN ELAIQKESADQVLMQEEIKR LEEMNINIRKKVAQLQEEVEKQ KNIVKGLEQDKEVLKQKMSS LLASTLQSTLDAGRCPEPPSGS PPEGPEIQLEVTQRALLRRESEV LDLKEQLEKMKGDLESKNEIL HLNLKLDMQNSQTAVSLRELE EENTSLKVIYTRSSEIEELKAIE NLQENQKRLQKEKAEIEQLHE VIEKLQHELSLMPVVHEVSDS QAGSLQSELLC
9912	40280	A	9973	1	8277	GEFGSEKKTALHEKEETLRQS AAQPFHQEEKESLSQLQKKN HQVQQLKDQVLSLSHEIECRS ELEVLQRRRERENREGANLLS MLKADVNLSHSERGALQDALR RLGLGFGETLRAAVTLRSRIGE RVGLCLDDAGAGALSTAPAL EETWSDVALPELDRTLSECAEM SSVAEISSHMRESFLMSPESVRE CEQPIRVFQSLAVDGLMEM ALDSSRQLEEARQIHSRFEKEFS FKNEETAQVVRKHQ
9913	40281	A	9974	1	393	

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9914	40282	A	9975	2	153	
9915	40283	A	9976	184	790	KFTKHISMNQEDLDPDSTTDVG DVTNTEELIRECEEMWVKDME ECQNKLSLIGTETLTDNAQLSL LIMQVKCLTAELSQQWKKTPPE TIPLTEDVLITLGKEEFQKVRGQ DLEMVLSTKESKNEKLKEDLER EQRWLDEQQIMESLNLVHSE LKNKVETFSERIFNELKTKML NIKEYKEKLLSTLGEFLEDHFL
9916	40284	C	9977	23	217	
9917	40285	A	9978	25	100	
9918	40286	A	9979	1	2850	
9919	40287	A	9980	108	1132	HPHQVETSRDVAGEQSHAVAF MSTGISQADVCRLEWFSAPNLK GRPRKKKPCPQRDSFSGVKDS NNNSDGKAVAKVKCEARSALT KPKNNHNCKKVSNEEKPKVAI GEECRADQAFVLVALYKYVMK ERKTRIERIPYLGFNQINLWTMF QAAQKLGGYETITARRQWKHI YDELGGNPGSTSAATCTRRHYE RLILPYERFIKGEEDKPLPPIKP RKQENSQENENKTKVFGTKRI KHEIPKSKKEKENAPKQDAAE VSSEQEKEQETLISQKSIPEPLPA ADMKKKIEGYQEFSAPLASR VDPEKDNETDQGSNSEKVAEE AGEKGPTPLPSAPL
9920	40288	B	9981	177	3543	
9921	40289	B	9982	63	374	

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9922	40290	A	9983	1	2023	MGGGSWAPTGLCPQLSLLAMS PEKRKLA AQEGQFTPEPRPEEP KEKLHTEEFSEYFFRAPEKDM VSM AVLPLARARGHLWAYSC PLRQPLLKRVHANVDLWDIAC QIFVDILPHQACTSAVVGVSV YQSVSAWSCPSTVLDSTHIL RYMGDYPSRQAWPTLELTDQIF TLALQHPALQDEVYCQILKHLT HNSDRHSEERGWQLLWCTGL FPPSKGLLPHAQKFIDTRRGKLL APDCSRRIQKVLRTGPRKQPPH HVEVEAAEQNVSRICHKIYFPN DTSEMELVVANTRVRDVCDSI ATRLQLASWEGCSLFIKISDKVI SQKEGDFFFDSLREVS DWVKK NKPQKEGEEASVELGEGVAGW VEGALAASVRPMPIHPSIRSRVS LGCNNQALGPGGAPVTLPLYQ VYFMRKLWLNISPGKDVNADT ILHYHQELPKYLRGFHKCSRED AIHLA GLIYKAQFNNDRSQLAS VPKILRELVPENLTRLMSSEEW KKSILLAYDKHKDKTVEEAKV AFLKWICRWPTFGSAFF/EGEG KPCPTGPGPTQAASAQSPSPRPS VNQHTSWQTSESPYDPVILIAIN RHGVLLIHPKTKDLLTTPFTK ISSWSSGSTYFHMALGSLGRGS RLLSETSLGYKMDDLTSYVQ QLLSAMNKQRGSKAPALAST

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9923	40291	A	9984	428	2502	VSKEIVYNKLLPYAERLDAESD LQLAQIKCNLGRAVQLQELWP GGLFWTRKLS/TRAQPLALSSLE LSPSGDPRVVTPEVKYSSRPPCH FPTGLPGSLPSLYVLRICFSRSV RVVVFPPGGPWVAQGP RPGR ETWGFTMLLRIRLYGRKFSKE DHVLFKLLYELVSIPKLEISMM QG FARLLINLLKYFPADATAEM LEEWRPLMCPFDV/TMQAITY FEIFLPTSLPPELHHKGFKLWFD ELIGLWVSQNL PQWEGQLVN LFARLATDNIGYIDWDPYVPKG GPSKLVQKHLA GLFNSITSFYH PSNNGRWLNKLMKLLQRLPNS VVRRLH RERYKKPSWLT PVPDS HKLTDQDVTDFVQCIQPVLLA MFSKTGSLEAAQALQNLA LMR PELVIPPVLERTYPAETLTTEPH QLTATLSCVIGVARSLVSGGRW FPEGTHMLPLL MRALPGVDPN DFSKCMIT/FQIATFSTLVPLVD CSSVLQERNDLTEVERELCSAT AEFEDFVLQFMDRCFGLIESSTL EQTRETE TEKMT HLESVELG LSSTFSTLTQCSKEIFMV ALQK VFNFSTSHIFETR VAGRMVADM CRAAVKDWGKPGDLWNLGIQ WHVPSSEEVSAFYLLDSFLQP ELVKLQHC GDGKLEMSRDDIL QSLTIVHNCLIGSGNLLPPLKGE
9924	40292	A	9985	2	5396	AESDLQLAQIKCNLGRAVQLQEL LWPGGLFWTRKLS TYRILYGR KFSKEDHVLFIKLLYELVSIPKL EISMMQGFARLLINLLKKKELL SRADLELPWRPLYDMVERILYS KTEHLGLNWFPNSVENILKTLV KSCRPYFPADATAEMLEEW RP LMCPFDVTMQAITYFEIFLPTS LPPELHHKGFKLWFD ELIGLWV SVQNL PQWEGQLVNLFARLAT DNIGYIDWDPYVPKIFTRILRSL NLPVGS SQVLVPR
9925	40293	A	9986	1	477	VREFFGRRFRGCCGALRPYKR LVDNIFPEDP/GYVCIAMEALDQ LLMACHCQSINLFVESFLKMVA KLESEKSNLQILGTNSFVKFA NIEEDTPSYHRSYDFFVSRFSEM CHSSHDDLEIKTKIRMSGIKSLQ GVVRKTVNDELQANWDPQH

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9926	40294	A	9987	1	2371	AGGARLRPARGRPPRLPPRP PCRPPVPAPTVNERRAPPRAG WERKSDAGLSRGARPAEMYGV CGCCGALRPRYKRLVDNIFPED PEDGLVKTNMEKLTIFYALSAPE KLDRI GAYLSERLIRDVGRHRY GYVCIAMEALDQLLMACHCQS INLFVESFLKMVAKLLESEKPN LQILGTNSFVKFANIEEDTPSYH RSYDFFVSRFSEMCSSHDDLEI KTKIRMSGIKLQGVVRKTVN DELQANIWDQPHMDKIVPSLLF NLQHVVEEAESRSPSLQAPEKE KESPAELAERCLRELLGRAAFG NIKNAIKPVLHLDNHSLEWPK VFAIRCCKIIMYSIQPQSHLVIQ QLLGHLDANSR SAATVRAGIVE VLSEAAVIAATGSVGPVLEMF NVTLLRQLRLSIDYALTGSYDGA VSLGTKIIEHEERMFOEAVIKT VGSFASTLPTYQRSEVILFIMSK VPRPSLHQAVDTGRTGENRNR LTQIMLLKSLQVSTGFQCNM MSALPSNFDRLSTALMEDAE IRLFVLEILISFIDRHGNRHKFTI STLSDISVLKLVDKCSRQDTV FMKKHSQQLYRHIYLSCKEETN VQKHYEALYGLLALISIELANE EVVVDLIRLVLA VQDVAVQVNE ENLPVYNRCALYALGAAYLNLI SQLTTVP AFCQHHIEVIETRKKE APYMLPEDVFVERPRLSQNLDG
9927	40295	A	9988	1	662	IPGSTISWSPAAARGLSVCRCCR LHPASAMDLFGDLPEPERSRP AAGKEAQKGPLLFDLPPASST DSG/SSLQALPGSGGPLLFDLDP PASSGDSGLATSISQMVKTEG KGAKRKTSEEEKNGSEELVEK KVCKASSVIFGLKGYVAERKGE REEMQDAHVILNDITEECRPPSS LITRVSYFAVFDGHGGIRASKF AAQNLHQNLIRKFKPKGDVISVE

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9928	40296	A	9989	3	1145	KEAQKGPLLFDDLPPASSTDSA VAALGTTTPSPVTLWFLQTRRGS KIWRNSLDYQSKVGAEPWCHE RQQKADRFLGKRGRVPASSVIF GLKGYVAERKGEREEMQDAH VILNDITEECRPSSLI TRVSYFA VFDGHGGIRAKSFAAQNHLQN LVRKFKPGDVISVEKTVKRCLL DTFKHTDEEFLKQASSQKPAW KDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLS KEHNPTQYEERMRIQKAGGNV RDGRVLGVLEVSRSIGDGQYK RCGCHLCAPTSSRCQLTPNDR FILVWPCDGLFKVFTPEEAVN FILVSCLEDEKIQTRGKSAADV RLRSSPATRLANKAVAAGARP DNVTVMVVRIGH
9929	40297	A	9990	2	419	
9930	40298	A	9991	2	1842	CLRLIAAAPPI/AIEPATTSLSLAF LLLQRDQSSRTGLPEEKEEVT MDTSENRPENDVPEPPMIADQ VSNDDRPEGSVEDEEKKESSLP KSFKRKISVVSATKGVPAGNSD TEGGQPGRKRRWGASTATTQK KPSISITTESLSLIPDIKPLAQOE AVVDLHADDRISEDETERNGD DGTHDKGLKICRTVTQVVP AE QGENGQREEEEEKEPEAEPPV PPQVSVEVALPPAEHEVKKVT LGDTLTRRSISQKSGVSITIDD PVRTAQVPSPPRGKISINIVHISN LVRPFTLGQLKELLGRTGTLVE EAFWIDKIKSHCFVITYSTVEEA VATRTALHGVKWPQSNPKFLC ADYAEQDELDYHRGLLVDRPS ETKTEEQGIPRPLHPPPPPVQPP QHPRAEQREQERAVREQWAER EREMERRERTRSERWDRDKV REGPRSRSRSDRRRKRERAKSK EKKSEKKEKAQEPPAKLLDDL FRKTKAAPCIYWLPLTDSQIVQ KEAERAERAKEREKRRKEQEE EEQKEREKEAERERNRQLEREK RREHSRERDRERERERERDRGD RDRDRERDRERERERDRDTK RHSRSRSRSTPVRDRGGR
9931	40299	A	9992	1400	2959	
9932	40300	C	9993	169	430	

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9933	40301	A	9994	2	199	STSR/KMTELEEVTLNGKPLQALRV/TDLKAALEQRGLAKSGQK SALVKRLKGVRSSRCWGVGGERTR
9934	40302	A	9995	1	4033	MWRRKHPTSGGTRGVLSGNGR GVEYGSGRGHLGTFEGRWRKL PKMPEAVGTDPTSRKMAELEE VTLDGKPLQALRVTDLKAAL QRLAKSGQKSALVKRLKGAL MLENLQKHSTPHAAFQPSQIG EEMSQNSFIKQYLEKQQLLRQ RLEREAREAEEEAESAESSEDE MIHPEGVASLLPPDFQSSLERPE LELSRHSRPRKSSSISEEKGDSDD EKPRKGERRSSRVQRAAKLS EGSQPAEEFEEDQETP
9935	40303	A	9996	3	6305	ELEEVTLDGKPLQALRVTDL KAALEQRGLAKSGQKSALVKRL KGALMLENLQKHSAPHAAFQP NSQIGEEMSQNSFIKQYLEKQQ ELLSSRLEREAREA ALEGGKSS SISEEKGDSDDDKPRKGERRSS RVQRARAALAEQSPAEFEED QETPSRNLVRADRNLTETEE EEEEEEEEDDEEEGDDEGQK SREAPILKEFKEEGEEIPRVKPE EMMDERPKTRSQEQEVLERGG RFTRSQEEARKSHL
9936	40304	B	9997	99	332	
9937	40305	A	9998	3	236	YIFTILNTLQGVFILLFGCLMDR KIQEALRKRFCRAQAPS/SHHLP GELLPSDPQLCIEHVRHSMAL LRGHGHSQKL
9938	40306	B	9999	1	3099	
9939	40307	A	10000	355	858	RASSAAGWPSRKTSASSAFSS CWSS*QS*SYSSSSLS/HGQGE RERQEGPEGRPAAVPHREQRG AEERLEHHPG*DAMLWCH*LH RLVPSAGGEHGSRLPHGELPG LRAQRHHAFVENGLL*KGEDV VR*Q*ARAGHGGDVHPPHADP GHGLLDPLPAHPPDW

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9940	40308	A	10001	3	1478	GRALTSRRRACQGAEEAAGSPA QVTTSTGHHQHRSQHRSPPA QVTTSTGHHQHRSQAATTSTG HHQHRPPPAQVTTSTGHHQHR SPAQATTSTGHHQHRSVHTGH HQHRS/HTSTGHHQHRSQAAT TSTGHHQHRSPPAQVTTSTGHH QI/GIIQHRSPPA/HGHHQHSSPP A/HGHHQHRSPPA/HGHHQH/H HHQHSSPPA/HGHHQH/HQ/P GHHQHRS/P/HSTAHHQH/HGHHQ HSSPPA/HGHHQH/HGHHQH SSPYQH/HGHHQHRSPPA/HGHH QHRSVHTAHHQHRSQH/HGHH Q/PGHHQHRSQAATTSTGHTS TGHHQHRS/HTSTGHHVHTGHH QHRSQHRSPPAQAATTSTAHH QHSS/HTSTGHHQHRS/P/HSTGH HQHSSPPA/HGHHQHSSPPAQA TTSTGHHQHRSPPA/AAAADPS ALSAARRGSPGA/AAAPQSRGTR GGGAPAKW/GSALGLG/WAGR ARARLGRPLRPILGAMPPAPRT PRERREHGEVE
9941	40309	A	10002	5	341	PPRRRGQKRRQK/REEGERERG ERKRPRDRKEERKG/RRTKRQG GTETRESRPNQDGPQAKRKKQ TAGQREEREQGRSSRQGA ERERGRETTHTCLLVPCW/WEP NGRLCL
9942	40310	A	10003	1	582	MLAQRGGRSVVQCIASVSKLSV TQRSFVTLMDEEALGNCGSS GSQTCEKAVCIHNLPLTSHAF QSGFPFPHQSPEASLPKMVSQAQ TARLSLESMLRELGFHISEAGFP APVSGYEHNSPSRPGVMPGSGT HWWKORSQKVEDNRTMVKGIO GDTVKHQQLPRINGN*LAYM TAKSRTWL/PVQDQDGPQT
9943	40311	A	10004	1	332	MEYYAAIKNDFMSFVGTWM KLETILSKLSQGGQKTKHHIFSLI EAQAQVSPPPYPAPQELTQPL LQQPRAPEAPAQ/PPGSLLTAT VRLSASPGPLGIFDQLLPRCGF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
9944	40312	A	10005	1	1108	MLAQRGGRSVVQCIASVSKLSV TQRSFVTLMDEEALGNCGGSS GSQTCEKAVCIHNLPLFTSHAF QSGFPPHQSPASLPKMVSDAQ TARLSLESMRELGFHISESAGFP APVSGYEHSNPLSTTNLSGSPSR RRQPPVSPLTLSFGPEAHQGFSR QLSSTSLAPYPTSQMVSSDRS QLSFLPTEAQAVSPPPYPAPQ ELTQPLLQOPRAPEAPAQPPQA ASSLPQSDFQLLPAQGSLLTNFF PDVGFDQQSMRPGCLSSGTAS GATGSRRELQDSFHLRSPYSNC GSLPNTILPEDSSTSLFKDLNSA LAGLPEVSLDVTFFPLEELQI EPLSLDGR/HMLSDSSMGLLDP SVEETFRADRL
9945	40313	A	10006	1	691	MRERARPPRGCLAPPLPPG/E/S GADGQAPPRGRGTAGG/ELAA AGCGARAAMHRGAVPSAEPVP ASP/DGRWQWAGEGRPCNAAG GSR/TGAGCGWPAPAGWGPAP SSAASCPASGGATHRGASAAPG GGGGGRAP/GPDALQRRAGAP PNAPGTPGSPSESSLRMRRESA AGAPAVGMAAATSLGQALGPR VPRSPYRTAVVLSRSSAFGYFSL ITLARYTLGCLSHSDITLFECL
9946	40314	A	10007	1	1065	MADKRAGTPEAAARPPPLAR EGDARTVPAARAREAGGRGSL HPAAGPGTAFFSPGRGEAASTA TTPSLENGRVRDEAPETCGAEG LGTRAGASEKAEDANKEEGAIF KKEPAEEVEKQEGEEKQEVA AEAQEGPR/PPEPWCPN/CMDP LEAIQWEAEAVSAQADRAYLP LERRFRGRMHRLYLARRSFIIQNI PGFWVTAFLNHPQLSAMISPRD EDMLCYLMNLEVRELHRSRTG CKFKFRFWSNPYFQNKVIVKEY ECRASGRVVSIAIRIRWHWGQE PPALVHRNRDTVRSFFSWFSQH SLPEADRYAQIHKDDLWPNPLQ YYLLGDRPCRARGGLARWPTE TPSRPYGFQSG
9947	40315	A	10008	2	433	
9948	40316	A	10009	125	289	TRKSGCLKIRFHVFLFLYRNPG MDVADAYVTVFVRHSQDVLRD KVNEEMYIERLF
9949	40317	A	10010	1	774	
9950	40318	A	10011	1	1749	

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9951	40319	A	10012	1	1175	MFASCYMRNIPKRVIEFGTCLW RTCKNCLSSLEFKMPFPHPHRSV TYNLKQERCRLSLDASLSCMLS IEDSQIPNTRLECKGLSRCTSV ASTCPLVTFSFCLFSPKMEQYS KDDSEKTLKGWFSFGQVFLD EYCARNGVRGCHRHLCYLRLD LERAENGAMIDPTLLHYFAFC ASHVHGNSQMQMHVYLSGLPPN TDPEGSKTPSPPEAKKDTKK ESKKRDKSKTQANQELKRLTS NLP/ICEPTQW*TFPKYQIYQLT SL*ASHKCLLFRHRHG WLLY/D ADNGSGTSEDFLWKLDALQTFI RDLHWPEEEFGKHLEQRKLKLM ASDMIESCVKRTRIAFEVKLQK TSSIQQIFRVQFNMPCFNVM GLMAKGSIQPKLCSMEMMQE
9952	40320	A	10013	1	3951	MLDPSSSEESDEIVEESGKEV LGSAPSGARLSPSRTSEGSAGSA GLGGGGAGAGAGVGAGGGGG SGASSGGGAGGLQPSRAGGG RPSSPSPSVSEKEKEELERLQK EEEEERKKRLQLYVFMRCIAYP FNAKQPTDMARRQKQISKQQL QTVKDRFQAFNLNGETQIMADE AFMNAVQSYEYFVLKSDRVAR MVQSGGCSANDSREVFKKHIE KRVRSLEIDGLSKETVLSSWM AKFDAIYRGEEDPRKQQ
9953	40321	A	10014	1	457	VAAVAATALKGGGARNARVL RGIFAGATAINKASHNRTRALQ N/HTASPEGKEEPIEPLIPGTGKY IPQKRGAKNPHENCGNLPWAIG FPCGILLDFSPKR/RKLDKDRV KQMKARQNMVRVNTG/EYESQ RFRASSQSAPSPDVGSGVSGV QT
9954	40322	A	10015	464	863	TPAAVESSPSIPLAPRLLYTG*PL QP/GRGQGC/PRIVPCCPKP/V CAPRPPWPQRSQRLRSAGLSPL CAAAAAPPVPAGSHGTPGRVWA PLSNSACCTCCRHP*/LHPGTL D PGRWQAR*GPALPRGPLPGSPP
9955	40323	A	10016	1	300	PKILVGASKVLLLSAHLKLGFIG DTLSRQAKAVDVASRVTHYSN LL/CDFLQIGIVATTKAALQYP IAFPQPKDMVERVKELGHSITQ QFRRLVGLQLAAA

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9956	40324	A	10017	3	291	ARI/VFAISFYFMPCCLTA/SSF YLLSGLLDAFDGHALALLIKFC VRGSESHKMIDLSGNP/VLRIYY TS/RVGSVGLFR/MGLWVTAPIA LLKSLISVIT
9957	40325	A	10018	1	344	VLIRARLSDNPAVRGSESHKMI DLFCYPVLRIYYTSRPAFLTCA GNELFYCLLYLFHFSEGLVGS VGLFRMGLWVTAPIALLKSLIS VIHLTAARNMAIALGRQQDRA KKK
9958	40326	A	10019	1	469	MVRSCFVDRRKRCNFNRQAS EVLNEYFYSHVSNPYHSEAKE ELAKKCGITVSQVSNRFGNKKI RYKKNIGEFQEEANIYAVKTAV SVTQGGHSSTSISPTPPSCAGCG GSFNISGSGDMFLGMPGLNGDS YASQALES GDASPAQSEMPK MGT
9959	40327	A	10020	232	1728	PGGGRGGAGRGPQGGPPAMDE RLLGPPPPGGGRGGLGVSGEP GGPGEPPGGGDPGGSGGVPG GRGKQDIGDILQQIMTITDQSLD EAQGQKTPLNCPARKKPV/LFS GRGEIKEKTGLSIRSSQEEEPVD PQLMRLDNMLLAEGVAGPEKG GGSAIAAAAAAAAAAGGVSPDN SIEHSDYRSKLAQIRHIYHSELE KYEQACNEFTTHVMNLLREQS RTRPVAPKEMERMVSIHRKFS AIQMQLKQSTCEAMMLRSRF LDARRKRRNFSRQATEVLNEYF YSHLSNPYPSEEAKKEALAKKCG ITVSQVSNRFGNKKIRYKKNIG KFQEEANIYAVKTAVSVTQGG HSSTSPTPPSSAGSGGSFNISGS GDMFLGMPGLNGDSYASQ/V WESLRIISMARGVIGG*TFGG RARCYSPRIMRANGSWQEA VTPSSVTSPTGPGSVHSDTSLI LPLRVTVGVGALTRREEDAGFQ RTNPNTGEAQDREGPMGSSPP
9960	40328	A	10021	337	830	IPRLPGSIQLSFVGAFGQTSKSLF FLCVFILLLLFQFLCSVYVPMCT E/RRINIPGPGCGMCLSVKGRC EPVLKEFGFAWPESLNCSEKFP QNDHNHMCMEGPGDEEVPLPH KTPIQPGEECHSVGTNSDQYIW VKRSLNCVLKC/GYDACLYSRS AQEVTDIWMA

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9961	40329	A	10022	1	1561	MAWRGAGPSVPGAPGGVGLSL GLLLQLLLLLGPARGFGDEEER RCDPIRISMCLNGYNVTKMPN LVGHQLQTDALQLTFTPLIQ YGCSSQLQFFLCGGYVPMGTEK INIPGPGCGMCLSVKRRCEP LKEFGFA/WPESLNCSE/YPHP QNDHNPVHPWKGPGEDEVPLP HKTPIQPGEECHSVGTNSDQYI WVKRSLNVLKCGYDAGLYSR SAKEFTDIWMAVWASLCFISTA FTVLFTLIDSCRFSPERPIFLS MCYNIYSIAIYVRLTVGRERISC DFEEAAEPVLIQEGLKNTGCAII FLLMYFFGMASIWVILTLT WFLAAGLKWGHEAIEHSSYF HIAAWAIPPVKITVILIMRLVDA DELTGLCYVGNQNLDAITGFV VAPLFTYLVIGTLFIAAGLVALF KIRSNLQKDGTKTDKLERLMV KIGVFSVLYTVPATCVIACYFY EISNWALFRYSADDSNMVAVEM LKIFMSLLVGITSGMWIWSAKT LHTWQKCSNRLVNYT
9962	40330	A	10023	496	664	FYKAVPSIHQLDVPQTHQP*ST GLVQKVYSRSKHVSL*PKYYY VQLVPKLDHLIFY
9963	40331	A	10024	1	954	
9964	40332	A	10025	127	481	GRTREATWRVYSVAVGVSRSQ IIRIAREFADNADKTHGRSMIIV GAGLNHWYHLDMMNYRGLINM LIFCGCVGQSGQ/GWAHYVGQ EKLRPQTGWQPGVCLDWQRP RHMNSTSYFLLVP
9965	40333	B	10026	161	234	
9966	40334	A	10027	3	199	DDFLDLAESPNASDTESSDEIPL KAGPGTLIMATGVQDFNRTEFD RLNAIKGHELEIALEKHFFT
9967	40335	A	10028	37	455	LRTHLLPRLSQSSPVSSLPALL RPPGQLELWAVPAGPGPLIAA DASQNLQHMALASQSRGRV DMSDGHVLAVSPIEEELRKLRE ETNAEMLRQELDRERQRMEL EQKVQEVLKARTEEQMAQQPP KGQAQASNGA

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9968	40336	A	10029	1	1721	DKIRFRGHKRDDFLDLAESPNA SDTECSDEIPLKVPRTSPRDSEE LRDPAGPGTLMATGVQDFNRT EFDRLNEIKGHLEIALLEKHFLQ EELRKLREETNAEMLRQELDRE RQRRMELEQKVQEVLKARTEE QMAQQPPKQQAQASNGAERRS QGLSSRLQKWFYERFGEYVED FRFQPEENTVETEEPLSARRLTE NMRLKRGAKPVTNFVKNLSA LSDWYSVYTSIAFTVYMNVA WHGWAIFLFLAILRLSLNYLI ARGWRIQWSIVPEVSEPPVEPPK EDLTVSEKFLVLDVAQKAQN LFGKMADILEKIKNLFMWVQP EITQKLYVALWAAFLASCFFPY RLVGLAVGLYAGIKFLIDIFIK RCPRLRAKYDTPYIIWRSLPTDP QLKERSAAVSRRLQTTSSRSY VPSAPAGLKEEDAGRFHSTKK GNFHEIFNL TENERPLAVCENG WRCCLINRDRKMPPTYIRNGV LYVTENYL CFESSKSGSKRNK VIKLVDTIDIKYKVL SVLPGSG MGIAVSTPSTQKPLVFGAMVH RDEAFETILSYIKITSAASGG
9969	40337	A	10030	18	573	
9970	40338	C	10031	71	205	
9971	40339	C	10032	190	243	
9972	40340	A	10033	18	283	
9973	40341	A	10034	1	190	
9974	40342	A	10035	1	135	
9975	40343	C	10036	90	137	
9976	40344	B	10037	272	560	
9977	40345	A	10038	3	422	
9978	40346	A	10039	205	1090	
9979	40347	A	10040	1	2142	

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9980	40348	A	10041	15	1524	FPGRFRFAEGERTCEAEPPRDEP PADGALKRAELKTQANDYFK AKDYENAIKFYSQAIELNPSNAI YYGNRSLVYLRTCEYGYSL*D ATRAIELDKKIYIMGYRRAVAS NMALGKFRAALRDYETVVVKV KPIIDKDAKMKYQECNKIVKP KAFAERIAAGDEHKRSVVDSLDI ESMTIEDEYS*PKLEDGKVITIS MKELMQWYKQDKKLHRKCAY QILVQVKEVLSKSLTLVETTLK ETEKITVCGDTHGQFYDLLNIFE LNLGPSETNPYIFNGDFVDRGSF SVEVILTLFGFKLLYPDFHILLR GNHETDNMNQIYGFGEVKA KYTAQMYELFSEVFEWLPLAQ CINGKVLIMHGGLFSEGDVTLTD DIRKIERNRQPPDSGPMC/DLLW SDPQPQNGRSISKRGVTCQFGP DVTKAFLEENNLDYIIRSHEVK AEGYEVAHGGRCVTVFSAPNY CDQMGNKAS/YIHLQG/SDLRP/ QFHQFATAVPHPNVK/PMAYAN
9981	40349	A	10042	94	188	VIEHLVSQDGLDFL/NLVICPPR PPKVLGLQA
9982	40350	A	10043	419	495	EPTNENSPIALSR*VNSQKISMK AV
9983	40351	A	10044	1	265	EMESRSIA/RMECSGSISAHCKL RLPGSHHSPASVSRVAGTTGTC HHARLIFLYF/LLETGFHCVSHD GLHLL/NLVICPPRPPKVLGLQA
9984	40352	A	10045	3	706	ADAWAWPHC/CTVLL*CLGFA GVLFGWPSLVFVKNEYFKD LCGPDAGPIGNATGQADCKAQ DERFSLIFTLGSFMNFMFTFTG YIFDRFKTTVARLIAIFFYTTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIKLLYEK GISLR/VLLHLHLCLQYLACSTH FPDPAGAHPIPTAPQLQLWPV PWEVHHKREGNS

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9985	40353	A	10046	1	1413	MKRGNGSRRRRLLENNGVVF HIESFAQIPKDEKSRKLLGPIEH WTFVVEKGGKPEETGTVSMV LEDGEVEADIKQGSVVGCCNV PPDAARERAEKAYMDGEQPTLI LLWLWLKKQIPVHKGTHSVGR HQTELLPNNGGGVVRFFYTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIKLLYEK GISLRASFIFISVCTWHVARTF LLMPRGHIPPYPNYSYGLCP GNGTTKEEKETAHENRELQSK EFLSAKEVSTYTNAFAFTQFGV LCAPWNGLLMDRLKQKYQKE ARKTGSSTLAVALCSTVPSLAL TSLCLCGFALCASVPLPLQYL.T FILQVISRSFLYGSNGRFLTAF PSEHFQKLFGLVMALSAVVSL LQPFITLIKGSIQNDPFYVNV MFMLAILLTLPLPSGISGMPYL
9986	40354	B	10047	316	395	
9987	40355	A	10048	1	1614	RMQQQAVMHHYMQQQQQQQQ QQLGGPPTPAINTPVHFQSPPPV PGEVLKVGVPVLACPPCPH*SQ PPLEPLPYLSETYGNKFAAHIS AQALRNPHQPPQGCELDTC PPPLATVLP/ISPMAMLHIGSNPE REVSEELASGHAACRARAHC ASETMPNTVLLARVGWVCKGS REGGTHCGSEPGESGVTSSSCP ADLTQKRELGTASLYPCAF PTPPSFSPSLPAAPLPASFLVLT WAG*KANDL*VRFRLGRVMG LGGQQLTRLALLQKSRELEN HSRRLEMTNKQLWLRQVWS* TWTSVLTLNLAPGPKGQYFR MFCFGNKQSSASLNTYQLEVL FCETLILAPTLAPSSMAHLEL ALKAIVTLKVPHTSVQWAWP MQAHSTSTLTSLAQVVKQEL PSEEGPGEALMLGAEPDPEPL PALPPQAPLPLTPQPPFHHLD FSHLSFGGREDEGPGYPEPLA PGHGSPPFSLSKDLMLLDD SLPLASDPLLTMSPEASKASS RRSSFSMEEGDVL

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9988	40356	A	10049	1	1651	GGVTAGARAPARGSVTAEEAA RAGRGSGRGADGGREGRTGRA SLVARGSRPGAGGGHSLRAR HPNLRQVAGA/GGARAADRLT FRAREPAPAATMASRIGLRMQL MREQAQQEEQRERMQQQAVM HYMQQQQQQQQLGGPPTP AINTPVIHFQSPPPVPGEVLKVS YLENPTS YHLQSQSHQKVREY LSETYGNKF AAAHISPAQALR NPHQPPPGCELDTCPPPLAT VLPISPMAMLHIGSNPERLEDD VIDNIMRLATMSLGYINPEMQM PNTVLLARLPLSSSHLNVYSSDP QVTASLVGVTSSSCPADLTQKR ELTDAESRALAKERQKKDNHN LIERRRRFNINDRIKELGMLIPK ANDLDVRWNKGITLKASVDYI RRMQKDLQKSRELEHNSRRLE MTNKQLWLRIQELMQARVHG LPTTSPSGMNAELAQQVVVKQ ELPSEEGPGEALMLGA/EGP/DP EPLPALHRQAPLPLTPQAPSPFH S/HWDFSHSL/SFGGRVDDWSP GLPRTPGAGAWLPQPQVQEGS GPHAPGRLTATAGL
9989	40357	A	10050	2	76	TPLAPPPKPVRRRLKSRR*IKAR S
9990	40358	A	10051	3	206	
9991	40359	A	10052	1	492	

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9992	40360	A	10053	2	2395	KQTELRSSGSRDVTGALLVAA AVASEAVGSLRVAEGGPNTLL QVLRISWAPWCNKATQTMEERK VKRRSPKSFSAHCTQVVNVQK KMSIPVSKS/TGFSNPASQVNFT SRPKVKKEVMK/VEKTKPQGLEE GQRHSSQLPIQHSFLTDDVSRCS RKMERGLLSLNDFFHSWK/TFK HFGMECS/VEQMEHVSSELQEK LARLNLLEYGELELPEDKRKT ASDS/NDRL/SLDCREMPAFRT FLKRHDKTIVTKMLSLPELLLY PSRRFEYLNLLYAVRLHTPAE HVDRGDLTTAIDQIKKYGYID QTLSEVNRYLIRVQDVAQLHCC DEEISFSLSVACRSVDSASPESL PEMQNSQATLALLNQNLHFNKI TRLYEHIHDL/SLFLNDALLVSS RGTSHTPFERTSKTTYQFIASVA LHRLIENIPDSKYVKNAFILQG PKYKWICATEIEDDKFLWLSVL RNAIKSSMEKACGLVFTGQFMF DTMGMTNILNNQDTAQAALADG LMELSKEDSKCGKKIKDVEGN VIPTKCDPKTTFSLFMKERNVV EDNSWDTKSRLSKNDLNFEALI NLERILQKDSAEKRARVVRELL QSERKYVQILEIVRDVYVAPLK AALSSNRAILSAA/NIQIIFCDILQ ILSLNRQFLDNLRLQEWGPA HCVGEIVTKFGSQNLNTYTNFFN NYPVILKTIEKQWETFSERSSSS
9993	40361	A	10054	2	296	
9994	40362	A	10055	2	369	
9995	40363	B	10056	82	2483	
9996	40364	A	10057	2	3343	YDVVLDAIDTMQRVAWHIND MKRKHEHAVRLQEIQSLLTNW KGPDLTSYGELVLEGTFRIQRA KNERTLFLFDKLLITKKRDDT FTYKAHILCGNMLVEVIPKEP LSFSVFHYKNPKLQHTVQAKSQ QDKRLWVHLKRLILENHAAKI PAKAKQAILEMDAIIHHPGFCYS PEGGTKALFGSKEGSAPYRLRR KSEPPSRSHKVLKTSETAQDIQ KVSREEGSPQLSSARPSPAQRNS QPSSSTMISVLRAGG

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9997	40365	A	10058	32	483	LKGHADAVLAAGTEAVKCHLL LGRHLLRLMASSGIHHKIVN*R QYAKFSHG*IQKF**WQHRQQF RGKETEMASAVDLPVTLTETEA NFPPEYEFKFWKTVENNPQDFTG WVYLLQYVEQENHLMMAARKA FDRFFIHPYCYGYWKYADL
9998	40366	A	10059	1	1090	MRQKRKEEKELFHNDCEKKE KNSWERMRTGTTEKMASESET PTGAISQYKERMPSTHSPHIM DLSELRFPSKPEIALTEALRLA DED/WDKQLHALEQLLASCYS GTRHTTSSFHCGHQGMWWHPE AWRC/LATAEPQREPGKSTISSH SSLWN*Q/LHSHKLQSVPLKV KNLRSGVSRAAVVCLSDLFTYL KKSMDQELDTTVKVLHLKAGE SNTFIREDVDKALRAMVNNVT PARAVVSLINGGQSHLHIAVRR CTAQHLSDVLEFMEPERILSAA KDMAERILPAAAKFAQDSSQET RYYGRKMLFFMMCHPNFEKM LEKYVPSKDLPLYIKDSVRNLQ KVCCKSLFYKQLYKQSLFLHP
9999	40367	A	10060	36	203	
10000	40368	A	10061	1	798	MKFQYKEDHPFEYRKKEGEKI RKKYPRDVPVIVEKAPKAR/RA *SGQEEVPSAL*PYCCLP/DGAG LGTCS/HAMPEPPTHSMGTCAA RASPTSTTPCSTAPSPIDRE/EQT TQGLRNASARRGTGRQLHLQ/S PVWDPLEASWAPESGNVESI SSSGIVNIPISTLCLAQGFSRFVN APIDTLYLAALVGPWRTFMSSS GIVNTPIGTLYLAQGMVHYHKS PFPTCLVQMSKIESLPKEGAQ GVAAGLPSLAPTCTPPDPMSK LHNN
10001	40369	A	10062	164	605	ALLKQHLRTVHRSAPPIRGHCC VSSSWT*G/AGKLSLEHTEEPSD VPSHLLYRWSISSAITEVFQALA SSNPPRSQ*MSTPRRINESTRHSP GPSIEEVKECMQDDN*YLQGTS YAPAGSQSYAKLCFQVLKRN TCPPEKPNPASER

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10002	40370	A	10063	3	2480	RPITGAEIVAIHNSLPTKKSPGLD GFTAEFYQRYKEELVFPFLKLF QSIEKEGILPNSFYEASIIIPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHINRT KDKNHMISIDAFAFKIQQ/R LHAKNS/RIN*VLM/ETYFKIIRA IYDKPIANILNGQKLEAFPLKT GTRQGCPLSPLFNIVLEVLR AIRQEKEIKGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLVTN NRQTESQIMSELPFTIASKRIKY LGQLTRDVKDLFKENYKPLLK EIKEDTNKWNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRAHIA KSILSQKNKAGGITLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEITPHTYNCLIFDKPEK NKKWGDLSFNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK DLNVRPKTIKLTLEENLGITQNI GMGKDFMSKTPKAMATKDKID KWDLIKLSFCTAKETTIRVNR QPTKWEKIFATYSSDKGLISRIY NELNQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTMRVHILTPVR MAIIKSGNNRCWRGCGEIGTL LHCW/DCKLVQPLWKS/VRF
10003	40371	A	10064	317	582	STVCCFLRFIGGGFRHPLSVD LWIHYIKILKETLDPGDPETNNT IRGYVEH*Y*NVFYDINNYSDV DNRAHES*AGSLTSIPLKK
10004	40372	A	10065	41	434	GDLQPTAALWEPLSGLAKAGA RSLSLQGGVGGEARARTRAAR GACGPAAAPGGHGLGGHALGA AGR/LLALGRLGTCSLPCLSLP PSPWAPVPPPEPR*VPHPAGRP VPSATQRLRSAGAQRRTRGRL
10005	40373	A	10066	67	459	LRDCKYTHRHCVSSRFINTPIN TLCLAQGL*VHQSTLCI*LLWV GGLGGNFCQYYSVSN*SDGDV ENLCI*LRDCKCTNQHPVKTG FGSTNQDVGWGGQIKRIKAGLP EPASGNSLGSPTLWELCSLQ

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10006	40374	A	10067	2481	2882	IPQGNRYRVIARNAKTQRGGNLT LTKPS/GIGRRGENSSISSWQRQ QKGGKKTGSQRKRQRGRDKKL ERKRDHRHSQREGKKERKRQR RSQRERWK**RKNSVPIPLKAR VNFSLPTQGNLLDLNPLYPLK QLKK
10007	40375	B	10068	52	5199	
10008	40376	A	10069	1510	2454	
10009	40377	B	10070	97	3414	
10010	40378	A	10071	164	620	PPTGCGTGPIGCSGPGTGPVVPV VAPFPFQEGARTQPGSAGAIPG ARGLRRRAETLVALGAVGPGLP TPPPPPPPAPQSQAPGGPEAQPF GSRVVCVLASCCAHRPRPAPSAP PAPPAPPESTVRPAPPTRPGESS YSSISHAFTATNPFPGTA
10011	40379	A	10072	1	513	MATLAGEGRPAGWVPWISLLA VGVLIWKLWPAPPIGGELQFA FVCFLGNNVYEAFAHWKRLN LLCRSEAAAMKK/HATRLWINLI SILHHQLGEIPADFFVDIVSQHN FLTSTLQVFSSACSIAVDATLR KKAELFQAHLTKKFRWDFAE PEDCAPVVEELPEGIEMG
10012	40380	A	10073	1	1642	MDYIRTDLTAAAPSPRRLGPP PGEQPPSGSGHVRPPGARPPHR GGGRGGGGGDPAAPARGGGG GGKARPPGGGAAPCEPGCQR APMVSVSSERHPLYNRVKGTQI ANCALPCHNPFQSDERAFTVF WIGLWSVLCFVSTFATVSTFLID MERFKYPERPIIFLSACYLFVS GYLVRLVAGHEKVACSGGAPG AGGAGGAGGAAAGAGAAAGAG AGGPGGRGEYELGAVEQHVR YETTGPALCTVFLLYVYFGMA SSIWWVILSLTWFLAAGMKWG NEAIAGYQYFHAAWLVPSV KSIAVLALSSVDGDPVAGICYV GNQSLDNLRGFVLAPLVIYLFIG TMFLLAGFVSLFRIRSVIKQD GPTKTHKLEKLMIRLGLFTVLY TVPAVVVACLFEYQHNRP EATHNCPCLRDLPDQARRPD YAVFMLKYFMCLVVGITSGVW VWSGKTLESWRSCLTRCCWAS KGAAVGGGAGATAAGGGGGP GGGGGGPGGGGGPGGGGGSL YSDVS/TGLTWRSGTASSVSY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
10013	40381	A	10074	3	475	HSSLNSVDKARALEADNGELE VNIRDWYQKQGPASRDYSHY YTTIQDLRDKILGATIENSRIVL QIDNARLAADDFRTKFETEHAL RMSVEADINGLRRVLDLTLAR IDLEMHIEGLKEELAYLKKNHE EEISTLRGQVGGQVTV*VDSAP GTDL
10014	40382	A	10075	39	1323	NGMWSNWNPLIPQRWEEKFQS PSRHRGSSSRGVSLSS\SGGYSGI LSGSNGLLAGNEKLTMHNLNN CLASYLDKVHALEAANSKLEF GLSVVWLDVTLARTDLEAQI KGLKEELAYLKKKHEEEINALR GQVGDQVHILSDRQSQYEIMA KQNWKDAEAWFTSWTEELNQ EVTGHIEQLQISRSEVTDLQCTL QGLEIELHSQSVKAPLEGTLA ETEACFGAQLVQIQALISSIEAQ LGDVRADGEWQNQEYQRLLE QEIATYRSLLEGQEDHYNNLST SKVQIPECTVSNVPVASVCLQT LEPHSLASNPGSSTYSVTFGQYI NLSVSPFLLLEATIAGAKKAAT GNNSTQFSPAERQLCIFTCPRT IPLTTASHAGSYGPKLVKYTSL RPLPMAAPTESNPALPSSRATA HRLLPAPGHFPSGL
10015	40383	B	10076	133	180	

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10016	40384	A	10077	1	2182	MSVDKAEELCGSLTLTWLQTFHV PSPCASPDLSGLAVAYVLNQ IDPSWFNEAWLQGISDPGNW KLKVSNLKMLVRLSLVEYSQDV LAHPVSEELPDVSLIGEFSDPA ELGKLLQLVLGCAISCEKKQDH IQRIMTLEESVQHVVMEAIQEL MTKDTVPDSLSPETYGNFDSQS RRYYFLSEEAEEGDELQQRCLD LERQLMLLSEKQSLAQENAGL RERMGRPEGEGTPGLTAKKLLL LQSLEQLQEENFRLESGREDE RLRCAELEREVAELQHRNQAL TSLAQEAQALKDEMDELQSS ERAGQLEATLTSCRRRLGELRE LRRQVRQLEERNAGHAERTQ LEDELRRAGSLRAQLEAQRRO VQELLGQRQEEAMKAELWFE CRNLEEKYESVTEKERLLAER DSLREANEELRCAQLQPRGLTQ ADPSLDPTSTPVDNLAAEILPAE LRETLRLSLLENKRLCRQEAA DRERQE/EKLQRHLEDANRAR HGLETQ/HLRNQQAAYSELRA QVEDLQKALQEQQGKTEDAISI LLKRKLEEHQLKLEADLELQR KREYIEELPPTDSSTA/RRIEEL QHNLQKKDADLRAMEERYRR YVDKARMVMQTMPEKQRPAA GAPPELHSLRTQLRERDVRIRH LEMDFEKSRSQREQEKKLISA WYNNMGMALQQRAGE/EPAPA
10017	40385	A	10078	1	687	
10018	40386	A	10079	1	1104	
10019	40387	A	10080	1	677	MAAAGGGGGGAAAAAGRAYSF KVVLLEGCGVKTSVLRYCE NKFNDKHITTLQASFLTCKLNI GGKRVNLAIWDTAGQERFHAL GPIYYRDSNGAILVYDITDEDSF QKVKNVVKELRKMLGN/ETCL CIVGNKIDLEKERHVSQIEAESY AESVGAHKHYHTSAKQNKGIEE LFLDLCKRMIETAQVDERAKG NGSSQPGTARRGVQIIDDEPQA QTSGGGCCSSG
10020	40388	A	10081	1	1467	
10021	40389	A	10082	2	244	
10022	40390	A	10083	1	257	
10023	40391	A	10084	1	558	
10024	40392	B	10085	41	618	
10025	40393	A	10086	1	591	

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10026	40394	A	10087	128	851	KMEKEKGNDDGIPDQENSLDFS EHFNQLELLETHGHLIPTGTQSL WVGNSDEDEEQDDKNEEWYR LQEKKMEKDPSRLLWAAEKN RLTIVRRLSEKATHVNTVRDE DEYTPLHRAAYSGHLDIVQELI AQGADVHAIVTDGWTPLHSA CKWNTRVASFLLQHDADINA QTKGLLTPHLAAAGNRDSKDT LELLLMNRVYKPKLKNLEET AFDIARRTSIYHYLFEIVEGCTN
10027	40395	A	10088	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEDP NCHEQIILSNTATHLGTQEAIVI DGRKKPEESRTTSHICRCS
10028	40396	A	10089	2	461	
10029	40397	A	10090	2	749	
10030	40398	B	10091	1	1077	
10031	40399	A	10092	1	1114	MPQNSLEECALGLGKSLQEN VNNFPKTKLFQFLKLTNWILPKI TKFKPIEGAENVFTDGSSNGKA SYFGLKGKVFQTPYTAQKVE LVAVIEVLTAFDMPVMSISDST YVVHSTQLTENAQLRLHTDEQ LMTLFSQLQTAVR/CFAVMGIP ASRKTDNVPGYTIQTLATFFSM WNKHITGIPYNSQGGAIIVGRIN LSLKQRLQKQKEGNNREYRTPQ MQLNLALLALIFLSLSKGQMLS AAEQHLQKPPAKTEAEQLIWW RDTKTRSWIEGKIITCGRGYAC VSPGQNZQPIWTPSRHLKPYHE PDAK/KRFREDPEDPFSCSHVKT DAEEDPNCHEQHPNTAIHLRS DQEAVTDGRRKPEESGTTSHNE
10032	40400	A	10093	239	783	RRAPGTAPDAGPELRS/LIHL GPACIFLRKGFAENRQPVQLRE AFREFDKDKDGYINCRDLGNC MRTMGYMPTEMLIELSQQIN MNLGGHVDFFDFVELMGPKLL AETADMIGVKELR/DAFREFTD NGDGEISTSELREAMRKLGLHQ VGHRIEIEIRDVDLNGDGRVD FEAPFPGSSN
10033	40401	A	10094	1	304	
10034	40402	A	10095	3	154	
10035	40403	B	10096	126	251	
10036	40404	B	10097	122	2916	

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10037	40405	A	10098	3	2433	LAELSSLVRLRLSHNSISHIAEG AFKGLRSLRVLDLDHNEISGTIE DTSGAFSLGLDSLKLTLFGNKKIK SVAKRAFSGLEGLEHLNLGNG AIRSVQFDAFVKMKNLKEHIS SDSLFLCDCQLKWLPPWLGIRML QAFVTATCAHPESLKGQSIFSV PESFVCCDFLKPQIITQPETTMA MVGKDIRFTCSAASSSSPMTF AWKKDNEVLTNADMFNVHV HAQDGEVMEYTTILHLRQVTF GHEGRYQCVITNHFGSTYSHKA RLTVNVLPSTKTPHDIITIRTTT MARLECAATGHPNPQIAWQKD GGTDFFPAARERRMHVMPDDD VFFITDVKIDDAAGVYSCTAQNS AGSISANATLTVLETPSLVVPLE DRVVSGETVALQCKATGNPP PRITWFGDRPLSLTERHHLP DNQLLVVQNVVAEDAGRYTCE MSNTLGTERRAHSQSLVLPAA CRKDGTTVGIFTIAVVSSIVLTS LVWVCIIYQTRKKSEESVTNT DETVPDPVPSYSSQGTLSDR QETVVRTEGGPQANGHIESNGK ASVTVKQSSAVTVSLGAGGGL QVFTGQVPGIRWGKLGEVEGG VCPDRDASHPEPDTHSVACRQP KLCAGSAYHKPWPAMEKAE GTPGPHKMEHGGRVVCSDCNT EVDYCSRGQAFHPQVSRDSAQ PSAPNGPEPGSDQEHSPHHQC
10038	40406	A	10099	1	164	
10039	40407	A	10100	368	566	

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10040	40408	A	10101	3	1160	RDQRGYRDDRSPAREPGDVSA RTRSGGGGGRSATTAMPPVPVN GNLHQHDPQDLRHNGNVVVA GRPSCSRGPRRAIQKQPAGGR RSRGPAAGGLCLQPPDGGTC VPEEPPVPPMDWEALEKHLAG LQFREQEVNRNQ/QARTNSTSA QKNERESIRQKLALGSFFDDGP GIYTSCKSKGKPSLSSRLQSGM NLQICFVNDSGSDKSDAADS KTETSLDTPLSPMSKQSSSYSD RDTTNEESES LGWTWDFLYKG KRNLQAEAKMALAMAKPMAK MQVEVEKQNRKKSPVADLLPH MPHISECLMKRSLKPTDLRDLI MGQLQVIVNDFISQIKSLNEEW VQLLLAQDELHTEQDAMLVDIE DLTRHAESQQKHMAEKMPAK
10041	40409	A	10102	1	506	RGRPRTEPDPCCPRAAAGARPS GPG/QDLPRRLPGSPGAPGAG GGAGTAAGRKGPGLEEEAAD GAWRLGEGWAAASEEPAPPGP HTSQRGASPPQPGWARAAGLS NQPTKDRIFGGSHKAA PQASAD SPTSLQCGAAGHCPKASRRALG DNPETEATSSLSPTEWLQ
10042	40410	A	10103	1	429	MGSRLNWMEVIEQCTYLHLVLI KCMFFWNRQHRGGIQEKAALK QRTPRIFHEKNTPCYLLVQE*H RSNAFGEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EETLFSNM
10043	40411	A	10104	4	122	
10044	40412	A	10105	53	619	ILVWSIVPEGKILWGTKQQRD SRTQRLLLKSPWRAKQSVWEE/ ERKKKNKEEKEEKEKEKEK EKEKEKKRKKRKKKKKKKK KKKKKKKKKKKKKEEEEE EDEEEEEEEEEKKEEKEKVK EKKKEKK/QEEKEEN/EEEEK EEEEKEKSSSKYSLDSVPTL LISLVVILNTPELLQPA
10045	40413	A	10106	2821	4680	
10046	40414	A	10107	18	1535	
10047	40415	A	10108	3	1494	
10048	40416	A	10109	3	617	
10049	40417	A	10110	3	1142	
10050	40418	B	10111	1	2151	
10051	40419	B	10112	1	1461	
10052	40420	A	10113	1	1248	
10053	40421	A	10114	2	1624	

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10054	40422	A	10115	1	1416	
10055	40423	A	10116	1	2262	
10056	40424	A	10117	1	1791	
10057	40425	B	10118	1	1497	
10058	40426	B	10119	1	1599	
10059	40427	A	10120	1	1722	
10060	40428	A	10121	1	3168	
10061	40429	A	10122	1	1083	
10062	40430	A	10123	1	589	MGAIYDKPTANIILNGQKI.EAF PLKTGIRQGCP.LS.LLFNIVLEV LARAIRQEKEIKVIQVGVKEEVK LSLFADDMMIVYLEDPIHAPNLL KLISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RKYLGIQLTRDVKDLFKENYK PLLKEKEDTNKWKNI PCSWVG RINIVKMAILPKPYVES
10063	40431	A	10124	1	1566	
10064	40432	B	10125	1	2406	
10065	40433	A	10126	1	2478	
10066	40434	B	10127	69	1259	
10067	40435	B	10128	225	997	
10068	40436	A	10129	2	1124	
10069	40437	A	10130	1	2058	
10070	40438	A	10131	258	823	TLMQKSSAKYWQTESSTSKSL STMIKWASSLGCKAGSIYANQ* M*SSI/YTNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFK E NYKPLLKEIKEDTNKWKNI PCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTELEKTTTLKFIRNQ KRACIAKSILSQTKEASRYLTS NYTTRLQ
10071	40439	A	10132	1	1512	
10072	40440	A	10133	1	992	
10073	40441	B	10134	1	2019	
10074	40442	A	10135	1	1203	
10075	40443	A	10136	1	1578	
10076	40444	A	10137	1	2956	
10077	40445	A	10138	1	1983	
10078	40446	A	10139	1	3156	
10079	40447	A	10140	1	3325	
10080	40448	A	10141	1	1870	
10081	40449	A	10142	1	1446	
10082	40450	A	10143	1	2310	
10083	40451	A	10144	1	1293	
10084	40452	A	10145	1	1038	
10085	40453	A	10146	1	1713	
10086	40454	A	10147	1	2271	
10087	40455	A	10148	1	3654	
10088	40456	A	10149	1090	1647	

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10089	40457	B	10150	1	1248	
10090	40458	A	10151	1	1884	
10091	40459	A	10152	1	1140	
10092	40460	B	10153	1	1545	
10093	40461	A	10154	1	3300	
10094	40462	A	10155	1	1824	
10095	40463	A	10156	1	1023	
10096	40464	A	10157	1	2169	
10097	40465	A	10158	1	2661	
10098	40466	A	10159	1	1104	
10099	40467	A	10160	1	1668	
10100	40468	A	10161	1	1945	
10101	40469	A	10162	1	3303	
10102	40470	A	10163	1	1382	
10103	40471	A	10164	1	399	MPPVDASRDRLRLNPLSSVKAK PNEYLLLVQVLFLNRNTKEGLI RLARYPDDLQQTESQIMSELP FTIASKRIKYPGIQLTKDVEDLF KENYKPLLSKIKEDANKWKNP CSWIGRINIVKMAVLPKKKIIV
10104	40472	A	10165	1	2218	
10105	40473	B	10166	1	2562	
10106	40474	A	10167	1	3169	

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10107	40475	A	10168	1	2105	MKAIEIKMFETNENKDDTTYQN LWDAFKAVCRGKFIALNAHRR KQERSKIDNLTSQLKELEKQEQ THSKASRRQEITKIRAELEKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK WDITTDPTETITIREYYKHLA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPTGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLLKLFQSIGKEGILPNSFYE ASIIIPKPGRDTTKKANFRPISL MNIDAKILNKILAKRIQQHIKKL IIHHDQHINKAKDKNHMIISIDAE KAFDKIQQFFMLKTLNKLIDG TYFKIIRAIYDKPTANIIILNGQKL EAFPLKTGTGRCPLSPLLNFIV LEVLAIRAIQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKVE NYKPLLEKEIEDTNKWNIPCS WVGRINIVKMAILPKGFCRFRN HHQTGFSPAGANQRGLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINAAGTT GFPTGKRAVSATQLMDFADFG TTIKQDFRLLGQTSVDRLLQLS QQQAVKGNQLLPVSLVVRKTT LAPNTQTASPRALADSLMQLA RQVSRLESGQ
10108	40476	A	10169	1	1689	
10109	40477	A	10170	425	1333	
10110	40478	A	10171	1	2274	
10111	40479	A	10172	1	3828	
10112	40480	A	10173	3	3130	
10113	40481	A	10174	1	960	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 50,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, V = possible nucleotide insertion)
10114	40482	A	10175	746	2470	TLMQKSSIKYWQNESSTSKSL STMIKWASSLGGCAWPNIRKSI KVIQHINRAKDKNHMIIISDAEK AFDKIQQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANILNGQKLE AFPLKTGTRQGCLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDIMIVYLENPVSAQN LLKLIRNFSKVSQYKINVQKSK AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLLKEN YKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKNWKKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPTYTKINSKWKDLNVRPK TIKTLEENLGITIGDIGMGKDFM SKTPKAMATKAKIDKWDLIK KSFCTAKEATIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIY KKKKTNNPIKKWKDMNRHFA KEDIYA AKKHKMKCSPSLAIRE MQIKTTMRYHLTPVRMAIIKKS
10115	40483	A	10176	1	3492	
10116	40484	A	10177	1	3139	
10117	40485	A	10178	637	2760	
10118	40486	A	10179	2	3932	
10119	40487	A	10180	1	1865	
10120	40488	A	10181	1	5754	
10121	40489	A	10182	959	1615	
10122	40490	A	10183	701	6973	
10123	40491	A	10184	3	3319	
10124	40492	A	10185	1	3296	
10125	40493	A	10186	1	2296	

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10126	40494	A	10187	1614	2615	TLMQKSSIKYWQTESSSTSKSL STMIKWASSLGMQGWFNICKSI NVIQHINRTKGKGMHMSIDA AFDKIQQPFLUKTLNKLIGDGT YLKIIRAIYDKPIANIILNGQKLT FEKFPCLKIGTRQGCPLSPLLFNI VLEVLRARIRQEKEIKIGIQLAKE EVKLSLFADDMIVYLENPVSV QNLLKLISNFSKVSGYKIYKIDV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQTRDVKDL FKVENHKPLLEIKEDTNKWKNI IPICSWVGGRINLVKMAILPKVI YRFNAIPKLPMTFFTELEKNYF KVMHEPKKEPVLPSQS
10127	40495	A	10188	141	401	
10128	40496	A	10189	1	156	MQFPKTKTKKKEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEGEE EKEEII
10129	40497	A	10190	1	1446	

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10130	40498	A	10191	272	2722	ETSCLPLVRVHYAEAITGRCTAP EDEGSLGQKPPARRSNNRTEGA WGKRQLMSSP/STEPVCLTIEG QEIDFLDGTGAASFVLSICPGRL SSTSVTIQILGQPVTYFSHLL SCNWETLLFSHAFLLMPERPTG LLGRDILAKAGAIYMNMGKNL PICCPLEEINPEVWALEGQFG RAKNAHPVQIRLKDPPTFFPYQR QY/PLRPEAHKGLQNIVKHLKA QGLVRKCSSPCNTPILEVQRPRL VQDLRLINEAVISLYPVVNPYPT LLSQIPEEAEWFTVLDLKDAFF CVPLHSDSQFLFAFEDPTNHTS QLTWMVLPQGFDRDSPHLFGQA LAKDLGHFSSPGTLVLQYVDDL LLATS*EALCQQA TLDDLNFLA NQGYKVSMSKAQLCLQQVKY LGLILAKGTRALSKE*IQPILAY PRPKTLKQLREFLGITSCRLWI PGYSETARPLYTLIKDTQRANT HLVWESEAEAFKTLKQALV QAPGLSLPTQQNFSLYVTERAG IALGLVTQTRGTPQVAHLSK ETDVVAKGWPHCLRVVAAVA VLVSEAIKIQGKDLIVWTTHEV NGILGAKGSLWSDNCLLRYQ ALLLEGPVLIQICTMALNPATF LPEDGEPIKHDCQIIIVQTYAAR DDLLEVPLTNPDLNLYTDGSSF VENGIRKVSVDVTILESKPLPPGT SAQLAELVALTWALELGKGR

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10131	40499	A	10192	1	2529	MTQEPSAIMREVPEMVNLIKGT GDIHNTEIQNDNGKVGMTKCM AKPKDELRLNLKILSESLESAQR QGVSKQEKVLQCRRAQDLQPT MPEPPIPSMGSCAARASPTSATP CSRAPSPIDHPTAAKCRMRMAR YWQAAPPAALVLDQLGEASW APESANLVGKWRTFVSSSGTA NAPISTLSKQTTGLYQSAGCGW GQNLGAKYRAPVGQLKATSTA ARLKT RVSGFLGKGLTTPDSS ELGPLDPTDHTSQLTWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLLIQYVDDLLLATSEALCQ KATLDLLNFLANQGYKVSRLK AQLCLQSEIARPLYTLIKETQR ANTHLVVSEPEAVI/AFETLKQA LVHAPALSLPIGQNFSLYITERA GIALGDLTQTCGTPQPVAYLS KEIDVVAKGWPHCLRVVAAVA ILVSEAIKIMQGKDLTVWTTHD VNGILGAKGSLWLSDNHLLRY QALLLEGLVLQICTCVALTAT FLPEDGEPIDHCQIIIVQTYAT RDDLLEVLPTNPDNLNYTDGSS VVENGIRRAGYAIIVSDVTILESK PLVPGTSAQLAELVALTRALEL GKGKIIINVYTD SKYAYLILHAH AAIWKEWEFLTSGNPHGCHRE VMELLHVMVQETKEVGVLYHYS HQNGKERGEQQRKQLAEASAA FLWGRALDLQPTMPEPPIPSMG
10132	40500	A	10193	1	197	
10133	40501	A	10194	1	259	
10134	40502	A	10195	1	295	
10135	40503	A	10196	1	439	
10136	40504	A	10197	1268	1420	
10137	40505	A	10198	1	389	
10138	40506	C	10199	1	298	
10139	40507	A	10200	2	90	
10140	40508	A	10201	3	1252	
10141	40509	A	10202	2	82	WMKLETSKLT*EQKTKHCMFSLISGS
10142	40510	A	10203	149	244	
10143	40511	A	10204	485	668	
10144	40512	B	10205	1	598	
10145	40513	C	10206	422	784	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
10146	40514	A	10207	3	899	IYNHLIFDKPKDNKQWGWK\DSL FNKWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMGKDFMTK TPEAMATKAKIDKWDLIQLKSF CTANETVIRVNRQPTEWEKIFAI IYPSDKGLISKIYKELYEKKTN LIKKWAKDMNRHFSKEDFYEA KKHEKSSLLQGQVTKGGCCLP MNL LGTYRSEENPSEYQRRQLI KTLRVCKPSSSYFLTSDFLDTPS FSCEPTQNELQGCSLRFRVAT AAGPVQVRGARLPFAAPERGL AQIPRQMDSKI
10147	40515	A	10208	3	352	APGRRRLCQPAAGPGAWPGS AVPGSVSPAPDARSPISGPSRAL RRHLRPSAAGPGLEIPHTDPH LPGVDYKEGRP/PSGKAGRGGP/ PGKGSASGARALGVAAAA TPRSTL
10148	40516	A	10209	1	510	
10149	40517	A	10210	73	327	
10150	40518	A	10211	1	957	MWSTCKLHGQAKYILCAAE SWGAAASCLHGSTMSTTVVSMA CVGAWPLMGGQDKP/FLSARP STVVPRGGHVAE/RCHYRRGFN NFMLYK/EDRSHVPIFHGRIFQE S/FIMGPVTPAHAGTYRC/RGSR PHSLTGWSAPSNP/LVIMVTGN HRKP/SLLAHPGPLLKSGETV/L QC/WLSA/PSDPLDIVIT/GWENP CLSHVL*S*SHS*ELPADDGEKH GQMQRPEKPTG*NPSSWSPSTE/ PSSKSGICR/HLHVLIGTSV VIFL FI/LLFFLLYRWCSNKK\DSDE QDPQEVITYAQL/NHCVFIQRKIS RPSQR/KTPLTDTSVYELPNA
10151	40519	A	10212	351	637	AWIGDMGLDWRYGLRVEISA WSGDMGLEWRYGL/REGMFN DTLRLIGEHHGVS KANFSISR MKQDLAGTYRCYGSVTHSPYQ LSAPSDPLDIVII
10152	40520	A	10213	1	1314	
10153	40521	A	10214	1	1008	

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10154	40522	A	10215	3	1080	GQDKPLL SAWPSLVVPLGHVIL RCHSYLGFNNFSLYKEGVHRRKP SLLAHIPGRLVKSEETVILQCWS DVRFEHFLHREGKFKDTLHLI GEHHHDGVSKANFSIGPMMQDL AGTYRCYGSVTHSPYQLSAPSD PLDIVITGLYEKPSLSAQPGPTV LAGESVTLSCSSRSSYDMYHLS REGEAHERRFSAAGPKVNGTTFQ ADFP LPATHGGTYRCFGSFRD SPYEWSSNDPLLVSVTGNSTRY LHALIGTSVVIIPFAILLFLLHR WCANKNAAVMDQEPAGNRT VNSEDSDEQDHQVESYA*L.DH CVFTQREITRPSERPKTPPTDTS MYIELPNAEPRSKVVFPCRAPQ
10155	40523	A	10216	3	1379	
10156	40524	A	10217	352	1825	
10157	40525	A	10218	1	1497	MGLEWRYGPGGADM DLEWRY GPGVEMVWWSGDMGLEVEIR AWSGDMGLEWRYEPGDGDMG LEWRYGPGGGQDKPLLSTWPS LVVPPEHVTLRCHSNLGFNNFS LYKDDGVPVPELYNRIFWKSLF MGPVTPSHTGTYRCRGSHTHSP SGGSAPSNPLVIVVTGFRRKPSL LAHPGPKVKSEETVILQCWSDV MFEHFLHREGTFNHTLRLIGE HIDGVSKGNFSIGRMTQDLAGT YRCYGSVTHSPYQLSAPSDPLD IVITGLYEKPSLSAQPGPTVLG ESVTLSCSSRSSYDMYHLSREG EAHERRLPAGPKVNRTFQADFP LDPA THGGTYRCFGSFRDSPYE WSKSSDPLLVSVTGNSSNSWPS PTEPSETGNPRHLHVLIIGTSVV KLPFTILLFLLHRWCSNKKNA SVMDQGPAGNRTVNREDSDEQ DHQVESYA*L.DHCVFTQRKITP PSQRPKTPPTDSSMYIELPNAES RSKAVFCPRAPQSGLEGIF
10158	40526	B	10219	114	1944	

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10159	40527	A	10220	20	1138	AGARPPVCTGSTMSLMVIMAC VGFFLLQGAWPQEGVHRKPSF LALPGHLVKSEETVILQCWSDV MFEHLLHREGKFNNLHLIGE HHDGVSKANFSIGPMMPVLAG TYRCYGSVPSPYQLSAPSDPL DMVIIIGLYEKPSSLAQPGPTVQ AGENVTLSCSSRSSYDMYHLR EGEAHERRLPAVRSINGTFQAD FPLGPATHGGTYRCFGSFRDAP YEWSNSSDPLLVSVTGNPSNSW PSPTEPSSKTGNPRHLHLVIGTS VVKIPFTILLFFLLHRWCSDKKN AAVMDQEPAGNRTNVSSEDSDE QDHQEVSYA*L DHCVFTQRKIT RPSERPKTPPTDSMYIELPNAE PRSKVVECPRAQSGLEGIF
10160	40528	A	10221	1	1334	MSLMVVSMAVCVGLFLVQRAGP HMGQDQKPFSLAWPSAVVPRG GHVTLRCHYRHRFNFMPLYKE DRIHIPHFHGRIFQESFNMSPVTT AHAGNYTCRGSHPHSPTGWSA PSNPVVMVTGNHRKPSLLAHP GPLVKSGERVILQCWSDIMFEH FFLHKEGISKDPSRLVQGIDHG VSKANFSIGPMMQDLAGTYRC YGSVTHSPYQLSAPSDPLDIVIT GLYEKPSSLAQPGPTVLAGEV TLSCSSRSSYDMYHLRGEAHE ERRFSAGPKVNGTFQADFPLGP ATHGGTYRCFGSFRDSPYEWSN SSDPLLVSVTGNPSNSWPSPTEP SSETGNPRHLHLVIGTSVVIIIFI LLLFFLLHRWCNNKNAAVM DQESAGNRTANSEDSDEQDPQ EVTYQLNHCVFTQRKITRPSQ RPKITPTDIIIVYTELPNAESRSK
10161	40529	A	10222	50	492	RARHRVTRPSIRKHSGHIRRLC LTCSSGVFLQGLRAGSRGTGPG LRTGWRSLSPAPRRRLHTPSAS SP*CSQ*RGPSAGTAAGARRRW RCRGQLRHPAGTSPPGRRWTG TACGPPAAPAPWHSSWSCPHS GAGPPWSPACRTASL

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10162	40530	A	10223	3	3159	QAEFAAASTTPALGSDGVRVT MDSALTARDRVGVQDFVLLN FTSEAAFIENLRFRFENLIYTYI GPVLVSVNPNYRDLQIYSRQHME RYRGVSFYEVPPHLFAVADTV YRALRTERRDQAVMISGESGA GKTEATKLLQFYAETCPAPQR GGAVDRLLQSNPVLEAFGNA KTLRNDNSSRFKYMVDVQDFD KGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEETL RRLGLERNPQSYLYLVK
10163	40531	A	10224	1	2810	MLNGCAHAHPIFPTRILSECPRG MLRAGFHLLNRREALPPSRSHIS AAVLAPGALLSWGPDHPLELY GLHSHQDPPTYEGVKGAPVG GHILSYLLEKSRVVHQNHGERN FHIFYQLLEGGEETLRLGLER NPQSYLYLVKGQCAKVSSINDK SDWKVVVKALTVIDFTEDEVE DLLSIVASVLHLGNIHFAANES NAQVTTENQVKYVLRLLSVE GSTLREALTHRKIIAKGEELSP LNLEQAA YARDA
10164	40532	A	10225	1	416	FRGVARQLRTSAMTPVNGAH KDADLWSSHDKMLAQPLKDS VEVYNIKKESNRQRVGLELIAS ENFASRAVLEALGSLNNKYSE GYPGQGSPANFAVYTALVEPH GRIMGLDLPDGGHLTHGFMTD KKKISATSI
10165	40533	A	10226	135	840	GSPANF/AVYTALVETHGCMG LDLPDGGHLTHGFMTDKKKIS ATSIFFESMPYKGGPHNHTIAG VAVALKQAMTLEFEVYQHVV VANCRALEALTELGYQTVTG CSDKHLILVDLHSIKGTDGRRRA EKVLEACSIACNKNTCPDDRNT LRPSGLRLGNPALTSGLLEKQ FQKVAFHFIHRGIELTLQIQSNAG IRATLKEFKERLAGHKYQGCV QALQEEVESFTLPLPLPDF

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10166	40534	A	10227	2	1355	QLRTSAMTMPVNGAHKADADL WSSHDKMLAQPLKSDSDVEVYN IHKESNRQRVGLLEIASENFAS RAVLEALGSLNNKYSEGYPG QRYYYGGTEFIDELETLCQKRAL QAYKLDPPQCGVNVQPYSGSP ANFAVYTALVEPHGRIMGLDLP DGGHLTRGLMTDKKISATSIF F*SMPLYKANPETGYINYGGLEE NARLFHPKLIAGTSCYSRNLEY ARLRKIADENGAYLMADMAHI SGLVAAGVVPSPFEHCHVVTIT THKTLRGCRAGMIFYRKGVAV ALKQAMTLEFKVYQHQQVAN CRALSEALTELGKIVTGGSDN HLILVDLRSGKTGGRAEKVL EACSIACNKNTCPGDRSALRPS GLRLGTALTSGLLEKDFQKV AHFIHRGIELTLQIQSDTGV RAT LKEFKERLAGDKYQAADVQALR EEVESFASLFLPLGPDF
10167	40535	A	10228	2	243	GTACNPAWPPGLAPHLTHYA DLLPGSPFHVALPPESELWETP DVSLITGPRLGQTPVTEAVSGR RGIAIAYEDEGSG
10168	40536	A	10229	1	1194	MESMFSSPAEALQRETGVPL LTPLPDLGVYELERVAGFVRD LGCERVALQFPDQLLGDAVAV AARLEETGSKMFILGDTAYGS CCVDVLGAQAGAAQLIHFGP ACLSPPARPLPVAFV/LSSFTCG LGALCQGL*GPEPRPQSACGAA GEPACAHALDTGKTQDEGAR AGRLRARRRYLVERARDARV GLLAGTLGVAQHREALAHLRN LTQAAGKRSYVLAIGRPTPAK LANFPEVDVVFLLACPLGALAP QLSGSFQPI LAPCELEAACNPA WPPGLAPHLTHYADLLPGSPF HVALPPESELWETPDVSLITGD LRPPPAWKSSNDHGSLALTRP QLELAESSPAASFSSRSWQGL EPRLGQTPVTEAVSGRRGIAIA
10169	40537	A	10230	35	429	KEKRYLVYLGCDCLEK*ESV* TNPVQPIELSAMMAYPVAALSP HVA/RLNT*MTNVTEKLSF*S*L T*I*V*PHVFSGYCTGQCRSS*A SSSSSSSSSSSSSSSSSSSSSS SSASDK*WAEASPRVR

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10170	40538	A	10231	73	393	RTQAPKLSQGGPRCIPPPKLCLE MESMFSSPAEAAALQR/ETGVPG LLTPLPDLGRSVALQFPDQLLG DAVAVAARLEETTGSKMFI/LG DTAYGSCCVDLGAEQAGAQAQ
10171	40539	B	10232	191	367	
10172	40540	A	10233	131	1681	RTQAPKLSQGGPRCIPPPKLCLE MESMFSSPAEAAALQR/ETGVPG LLTPLPDLGVYELERVAGFVR DLGGERVALQFPDQLLGDAVA VAARLEETTGSKMFI/LGVD AYGSCCVDLGAEQAGAQAQ HFGPACLSPPARPLPVAFVLSST FCGLGTLCDLWGPKPRPQSAC GAA/GEPACAHAEALATLLRP RYLDLLVSSPAFPQPVGSLSEP MPLERFGRRLPAPGRRIEEYG AFYVGGSKASDPDLPDLSRL LLGWAPGQPFSSCCPDITGKTQD EGARAGGLRARRRYLVERARD ARVVGLLAGTLGVAQHREAL AHLRNLI/VQAAG/KCSYVLAAG RPTAKLANFPEVDVFLVLA LGALAPQLSGSFFQIPAPCELE AACNPAAWPPG/LVWPHLTH/Y IADLLPGSPFHVALPPPESELWE TPDVSLITGDLRPPPAWKSND HGSALATPRPQLEAESSPAASF LSSRSWQGLEPRLGQTPVTEAV SGRRGIAIAYEDEGSG
10173	40541	A	10234	3	605	AAAREAAAGRDMLAADLRCSLF ASALQSYKRDVSLRPPFASAYR GDCKDFEALLADASKLPNLKEL LQSSGDNQTPGDLVSLDFYP QKVLTNPQVQ/WECSRFEKDSK S*LGLLTRLFLHRTSCLKLS/SD PANAKFYETKGERDLIYAFHGS RLENFHSIIHNLHCHLNKTSFL GEGTYLTSDSLALIYSPHGHG WQH
10174	40542	A	10235	197	895	LGLLTRLFLHRTSCLKLS/SDP ANAKFYETKGERDLIYAFHGS LENFHSIIHNLHCHLNKTSFLG EGTYLTSDSLALIYSPHGHGW QHSLLGPILSCVAVCEVIDHPD VKCQTKKKDSKEIDRRRARIKH SEGGDIPPKYFVVTNNQLLRVK YLLVYSQKPPKRASSQLSWFSS HWFTVMISLYLLLLLIVFCGLL ALQDRGLPQVCPQIPCGWRPPS EGSQVFETQPG

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10175	40543	B	10236	1	1059	
10176	40544	B	10237	226	522	
10177	40545	A	10238	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNPQKEHLTNFKSAA ED
10178	40546	B	10239	101	397	
10179	40547	A	10240	2	253	LQEFGRKDPPTTSGPQTDQAR EHLTNFKSSA/CQIPWNSGPRLS E*LLPRSSRLSS*RLT/RAQSPW KPTGQSQMLWVTLTVEGT
10180	40548	B	10241	1	409	
10181	40549	C	10242	1	462	
10182	40550	A	10243	1	861	
10183	40551	C	10244	1	140	
10184	40552	B	10245	1	1773	
10185	40553	B	10246	1	320	
10186	40554	C	10247	1	420	
10187	40555	A	10248	273	485	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQPKHLTNFKSG PTENRTVQLTWQPLPEPELW PKAL
10188	40556	A	10249	508	558	
10189	40557	B	10250	76	358	
10190	40558	C	10251	83	414	
10191	40559	B	10252	1	1111	
10192	40560	C	10253	1	411	
10193	40561	B	10254	1	1054	
10194	40562	B	10255	57	229	
10195	40563	B	10256	1	222	
10196	40564	A	10257	230	1272	LLCSSACKCLMLGLHFVIVGNI CATLKEKYSSMLHLDVTMKKN GEKRTLQKRKKGMPPHPAYE DLNIAAITLPANVVLHQPSGFRT SGQLDPVWWSLDTDAHEIWCQ DPGLSGGDFPWEITPLSSYSLLH EKDPPTTSGPQTDQPKHLTNF KSKTKETGFIHGPKTPAPVTDW EGSLPLVFNHCRDTSLIHPCFK GVRPRRDACLGPSPLAASPAFL EKGQDLINLAFKVVYNNRKKLQ FLASTVRQTAATSPAHKNFQMP EPQRPVGPPEPPPTGACYMCRK SGHIWTRNAGSPGFLLSRVPSV WDPTENRTVQLTWQPLPEPEL WPKALCLTDSFPDLLGLAA

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10197	40565	A	10258	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSKIDSLILCLKKKIM NRHFSKEDIYAACKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIIKSGNNRRCRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DLADPAIPLGLIYPKDYKSCCYK DTCTRMFIALFTIAKTWNQP
10198	40566	A	10259	1	1947	MNIDAKILNKILANRIQQHIKLL IHHDQVGFIPGRQGWFNCKSIN VIQHINRAKDKNHMISIDAEGA FDKIQLFMLKTLNKLIDGTY FKIIRAIYDKPTANILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLIISNFSKVSQYKINVQKQS AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLEKEIKEDANKWKNPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSITPHIYNYLIFD KPDKNKQWKGKSLFNKWCWE NWLAIKRLKLDPLTPYTKIN SRWIKDLNVRPKTTKLEENLG ITIQDIGMGMDFMSTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFTTYSDDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAACKH MKKCSPLAIREMQIKTTMRYH LTPVRMAIIKSGNNRCWRGC GEIGTLLHCWWINWMKKTWH IYTMYYASIKKNEFMSFAGA* MKLETH
10199	40567	A	10260	1	347	TNKIDRPLARLIKKKREKKQID AIKNDKGDITDPTETQTITKEY YKHLIYANKLENLEEMDKFFDT YTLPRNLQEEVSLNRPIAGSEI EAIINSLPT/KKSPGPDGFTAKFY QRE

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10200	40568	A	10261	31	809	KPRLNYYVKNAAEASGADAINW KKGY/LVMEDEMNEMKREGKF REKRIKRNEQSLQEWDYVCRP TLHLIDVPETLNAHKRQERSK TDLTSQLKELEKQEQTSHKAS RRQEITKIRAELEIETETLQKI NESRSWFFERINKIDRLARLIK KKREKNQIDAINDKGDITSDP TEIQTITREYYKHLIYANKLENL EEMDKFLDTYTLPRLNQEEVES LNRPIITGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
10201	40569	A	10262	209	3816	QGRPTFRFRKYREHHKDTFREE QLQDT*SSDSPKPK*KKC*GQ PERKVKLPTKGSPD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTIEQITIREYYKHLIYANK LENLEEMDKFLDTYTLPRLNQEE VESVNRPIITGSEIAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLLKQPIEKEGILPNSFYEASII LIPKPGRDTTKGNFRISLMNI DAKIL
10202	40570	B	10263	1	2265	
10203	40571	A	10264	1	2832	
10204	40572	A	10265	1	2757	

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10205	40573	A	10266	1	2114	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPFI NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTTRPVLK ELLKEALNMERNWYQPLQKH AKNMPNSIILPKGRDITTKEN FRPISLMNIDAKILNKILANRIQ QHKKLIHHDQVGFIPGMQGW NIHKSINVIQHINRTIDKNHMIIS IDAFAFKIQQLFMLKTLNKL GIDGTYLKIRIKYLGQLTREV DLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAISNKLPMFTFTELEKTTL NFIWNQKRARIKSIKSNKA GGITLPDFKQYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWGDLSF NKWCWENWLAVCRKLKLDPP LTPYTKINSRWIKDLNVRPKTIK TLEEILGITQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKS CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AACKYMKKCSPLAIREMQIKT TMRVHLTPVRMAIKKSGNNR QTESQIMSELPITIAKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWGRINIVK/T WPYCPSQMYMSPTWQPKTLQ LWRQPKYPWKGTHRRKK
10206	40574	A	10267	1	2952	MLLNQGRKLPVFAEETLKFK GTSNKPQTLEQISTIAAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLEFQTLNLYLQEFLETP QWHLECOQERTVHSPGKAAEA REPSVIDRHLEQESSNWHLVGA ALGQSFQRKEQAIFAVLQPLL VIPRQTGSGVDLQKTPDLQQR GLIVRRKTNKQKGIHVNSTTRE QNWTENEFDKLTGGFKRWVI TNSSELKEHVLTCQCKEDKNLEK SAIKLELRKLNLIQN
10207	40575	A	10268	1	1797	

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10208	40576	A	10269	1	1751	MIISIDA EKAFDKIQPFMLKTL NKLIGDGYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIMKMAILP KVIYRFNAIPIKLPMPFFTELEK TTLKFIWNQKRARIKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTDKIDKWDLIK KSFCTAKETTIRVNRQPTKWEK IFTTYSSDNLISRIYNELKQIYK KKTNNPIKQWAKDMNRHFSIE DIYAAKHKMKCSSSLAIREM QIKTTMRYHLTPVRMAIKKSG NNRNHLDFKHILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA
10209	40577	A	10270	1	4729	
10210	40578	A	10271	1	1428	

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10211	40579	A	10272	1	2718	MALFRVGMITRRLLGHANKFTR DLLVKRLLLYEFVVEIIPGLRTK TTLVGPLETGYTSSDVNSPHF MLDIALSHNVKSTQLLLRPWR NIDCSRNHKNAKKEEQMGDDE INRQQECSSPAMEQSWTENDF DELREEVFRRSNYSELQEEIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQETKIRAELEKIE TQKTLQKINESRSWFFKINKID RPLARLIKKKREKNQDTIKND KGDITDPTEIQTITREYYKHLV TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPTGSEIAIINSL PTKKSPGPDGFTAIFYQRYKEE LVFPLLKLSQSEIKERILPNSSYE ASIIIPKPGRDTTKKNFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGWFNIRKS INVQIHNRKTDKNHMIISIDAE KLISKFSKVSCHKIN/VKQSQAF LYTDNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIIPCSWVG RINIVKMALLP/RFSAIPIKLPMT FFTELEKTTLKFIWN/QKRARIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNYLIFDKPDK KKEWGWKDSLFNKWCWENWLA ICRKLKLDPLFTPYTKMNSRWI
10212	40580	A	10273	396	1227	SLGRNSTSQKRVGANIQHS*RK EFSTQNFISSQTTLHK*RRNKIL YRQANAERFCHHQACPKTAPE RSTKVLERNRRLPARLIKKKKREK NQIDATKNDKGDITDPTEIQTIT IREYYKHLVANKLENLEEMDK FPDTYTLPRLNQEEVESLNRPT GSEIAIHKSLPTKKRPGPDRFTA EFYQRYKEELVPFLLKLFQSTE KEGILPNSFYEASIIIAKPGRDT TKKENFRPISL/NIDAKILNKILA NRIQQHIKKLIHHDQGVFIPGM QGWFINI
10213	40581	A	10274	1	2168	
10214	40582	A	10275	1	1845	

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10215	40583	A	10276	1	2877	MENDFDELREECFRQSNYSER EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMFLKTKAQELR EEWRSLRSRCDQLEERVSAE DEMNMKGEGKFKREKRIKNE QSLQEIWYVVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIVRFTKVEMKEKML RAAREKEIQTTSIYKYKHLTYN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPTGAE
10216	40584	A	10277	1	1689	MIFSIDAEKAFDKIQPFMLKTL NKLIGIDGMYLKIIRAMYDKPA ANIILNGKLEAFPLKTGTROG CPLSPLLFNIVLEVLAIRAEK EIKGIQLGKEEVKLSLFADDMI VYLENPITSQNLKLSISYSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYTFSAIPLPMTFFTELEK TTSKFIWNQKRARIASILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM PHIYNILFDKPKDNKQWGKDS LFNKWCWENWLDIWRKLKLD PFLTPYTKINSRSIKDLHVRPKTI KLEENLGDITQDIGMGKDFMS KTSKAMATKAKIDKWDLIQLK SFCTAKETTIRVNRQPTWEKIF AIYSSDKGLIFRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEAI YAAKRHMKKCSSLAIREMQIK TTLSLPAQVSVV/RHGLSFCWD SRGICGKSGFLAYSINFPQSH WDQEQVM
10217	40585	A	10278	1	2142	

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10218	40586	A	10279	1	1722	MIISDAEKA FDKI Q QRF MLK TL NKL GIDGLYL KIIRAIYDKPTAN IILNGQKLEALPLK TGTR QGCPL SPLQFNIVLEVLARAI RQEKEIK GIQLGKEEVKLSLLADD MIVYL ENPIVSAQNLLKVISNFSK VSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWYQKRARITKSILSQ RNK AGDITLPDFKLYYKATV NKTA WYWHQNRHIDQWNRTK PSEIT LHIYNLYFFDNPDKNKKW GKD SLFNKWCWENWLAICRKL KLD PFLTPTYTKINSRWIKDLNIRPK TI KTLEENLGITIQDIGMGKYFMT KTPKAMATKAKIDKWDLIK LK SFCTGKETIIRVN RQPTK WEKIF ATYSSDKGLISRIYNELKQI YKK KTNNPIKKWAKDMNRHFSKED IYA AKKHM KK CS PSLAIREMQI KTTMRYHLTPT/RLIVIGIEECL R GKEKLETLYYWNSD TDH QV*W LGWP*WKS DHK EQPSF

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10219	40587	A	10280	1	2076	MDKFLNTYTIPLRNQEEVESLN RSITGSEIEAIHNNLPTRKSPGPD GFTPEFYQRYKEELVPFLKLF QSIKVEGFLPNSFYEGSILITKS GRDTTKKENLRPISLMNINAKIL NKILANQIQHHKLLHHEQVDF IPGMQGWFNIRKSINVIQHNR NDKNHMIISIDAEKAFDKIQQLF MLKTLNKLGDGTYLKIIRAIYD KHTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAI QEKEIKGIGLKEEVKLSLFAD DMIVYLENPIVSAQNLLKLIGNF SKVSGYKISVQKSQAFLYTNKR QTESQIMSELPFTIVSKRIKYLGI QLTRDVKDLFKENYKPLLNEIQ DETNRWKNCSWVGRINIVKM VILP/KELEKTTLKFIWNQKRAR IAKTILSQKNKAGGITLPDFELH YKATVTKTACYLYQNRDIDQR NRTEPSEIMPHIYNYLIFDKSDK NKKWGKDSLFNKWCWENWLA ICRKLKLDPLPPYTKINSRWIK DLNVRPKTIKLEENLGNTIQDI GMGKDFMSKTPKAMSTKAKID KWDLIKLSFCTAKETAIRVNR EPTWEKIFAIYSSDKGLISRIYN EFKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAANRHMKKCSSS LAIREMQIKTTQVGGSEKSSAS ELGNKLIELDQSEEWROKED

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10220	40588	A	10281	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRINKLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLEKEKQEQTSHKASRRQ EITKIRAEKIEITQKTVQKINES RSWFFERINKIDRLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHLANKLENLEEM DKFLDYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAEFYQRAIRQEKEIKGIGLK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFTELKKTTLNFIWNQK RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD
10221	40589	A	10282	1	1996	

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10222	40590	A	10283	1	1778	MIISIDAEKAFDKIQPFMLKTL NKLIGIDGTYLKIIRAIYDKPTAN IIPNGQKLEAFPLK TGT TQGCPF SPLLFNIVLEVLARVIRQEKEIK GTQLGKEEVTLSLFADDMIVYL QNPVSAQNLLKLIGNFSKVSQ YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFKWNQKRACIAKSILSQKNK AGGIMLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPDQNKQWGKDS LFNKYYWENCLAI CRKLKLDLP FLTPYTKINSRWIKDLNVRKTI KALEENLGNTIQDIGMGKDFMS KTPKAMATKDIDKWDLIKPK SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRNYNELKQIYK KKTIGPIKKWAEDMNRHFSKE DTYAAKKJMKKCSSSLAIREM QIKTTMRYHLTPVRMVIKKSG NNRCWRGCGETGTLSHCWWD CKL/IQPLW/RFLRD*GPKTGGD S*MIQVKY*PQKKKGCPNA
10223	40591	A	10284	3	2875	

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10224	40592	A	10285	1	1838	MIIPIDAEEKAFDKIQPFMLKTL NKLGIHGMYLKIIIRAIYDKPTA NIILNGQKLEAFPLKGTGRQGC LPPLLFNIVLEILARAIQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGDLSLF NKWCWENWLAICGKLLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNLELKSFC TAKETTISVNRQPTWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPICKWAKDMNRHFSKEDIY AANRHMKKCSSSLAIREMPIKT TMRVHLYTPVRMAIHKSGNNRC WRGCGEIGTLSHCWWDCLNVQ PLWKA VWRFLKDLEIIPFDP ISLLG/TYPKDYKSCCYKDTCTQ STFTCRQHLPL
10225	40593	A	10286	1	2046	

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10226	40594	A	10287	1	1700	MEDEMNMKQEGKFREKRIKR NEQSLQEIWYVYKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIQEIQRMPORYSS RRATPRHIIVRFTKVEMKEKMS RAAREKEIQTIREYYKHLAYAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAIFYQRQSESI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTFFTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNIRPKTI ETLEENLGITQDIGMGKDFMS KTSKAMSTKAKIDKWDLIKLS FCTAKETTIVNRQPTKWEKIF ATYSSDKGLISRIYNELKQIYKK K'TNNPIKKWVKDMNRHFSKE DIYAAKRHMKKCSSSLAIREMQ IKTTMRYHLTPV
10227	40595	A	10288	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFPSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRKKNLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRRQERSKIDTLTSQ KELEKQEQTHSKASRRQETKIR AELKEIETQ

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10228	40596	A	10289	1	2019	MDTIKNDKGDITDPTEIQTTIR EYYKHLKYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRKAFDKIQQAFTLKTNLN LVIDGTYRKIIRAI CDKPTANII NGQKLEAFPLKTGTTRQGCPLSP LLFNIVLEVLDRAIRQEKEITC LGKEEVKLSLFAADDMIVYLENP IISAQNLKLSNFSKVSGYKIN VQKSQAFLYTNNRQTSEQIMSE LPFTIASKKIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGJRNIMKMAILPKVIYR FNAIPKLPVAFFTELEKTTLKF WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTTKTA WY YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSL KWCWENWLDIWRKLKLDPLFT PYTKINSRWIKDLNVRPKTIKTL EENLGNITLIDGMGKDFMSKTP KAMATKAKIDNWDLIKLSKFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSLAIREMQIK TTMRYHLTPVRMVIKKSGNNR PPLSKEQPIFRLSILATRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
10229	40597	A	10290	1	3144	MGDFTNPLSTLDRSSQKVNK DTQELNSTLHHDLDIYRTLHP KSTEYTFPSAPHHTYSKIDHVV GSKALLSKCKRTEHTNCLSDHS AIKPELRIKLTQNRSTTWKLN NLLNDYVWINKMKAIEIKMFF ETNENKDTTYQNLWDTFKA VSRGKFIALNAHKKQKRCIDTL ASQLKEVEKQEQTSHKASRRQ EITKIRAELEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
10230	40598	A	10291	1	2274	
10231	40599	A	10292	1	2250	
10232	40600	A	10293	1	822	

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10233	40601	A	10294	1	2605	MKA EIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAYKR KQERSKIDTLTSQLEKEKQEQ SHSKAGRRQEITKIRAELEKET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTNPTETIQTIREYYKHLA NKLLENLEEMDTFLDYTLPRLN QEEVGS LNTPTTGSEIVAIINSLP TKKSPGPDGFTA EYQRYKEEL PGRVPTKKENFRPISLMNIDAKI LNKILANRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHIN RAKDKNHMII SIDA EKA FDKIQ QPFMLKTLNKL GIDGTYFRIIRA IYDKPTANILNGQKLEAFPLKT GTRQGCSPLLFNIVLEVLAR AIRQEKEIKGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYNFYVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKNPICSVWGRIN IVKMAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEIMPHIYNLIFDKPEK NKQW GKDSL FNKWCWENWLA ICRKLKLD PFLTPYTKINSRWIK DLNVRPKTIKLEENLGITQDI GVGKDFMSKTPKAMATKAKID
10234	40602	B	10295	111	2440	

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10235	40603	A	10296	I	1795	MIISDAEKAFDKIQQPFMLKTL NKLSDGTYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTGRQCPL SPLLFNIVLEVLARAIQKEIK GIQLGKEEVKLSLFAHDMIVYL ENPIVSAQNLLKLI SNFSKVSQI KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRKYLGQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSGVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKGACITKILS/QKNK VGGITLPDFKLYYKATVTKTA WYWYQ\NRDIDQWNRKPSEIM PIINYNLIFDKPEKNRQWGEDS LFNKWCWETWLAIWRLKLDLP FLTLYAKIN*RWIKDLNVRPKTI KTLLENLGITIQDUGMGKDFM SKTPKAMATKAKIDKWDLIQL KSYCTAKENTIRVNRQPTKWE KIFATYSSDKGLITRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAACKHMKKCSSSLAIRE MQIKTTMRYHLTPVRMAIIQKS GNNRTKRTIYRRNDDDDNDD NDDDSLMSLSRTEIPFSSYSELN VVLHKPRPEPSASTILLHTA
10236	40604	A	10297	I	2851	
10237	40605	B	10298	I	3220	

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10238	40606	A	10299	1	2047	MENDFEELREEGFRRSNYSER EDIQTKGKEVENFEKNLEECITR ITNTQKCKELMELKTKARELR EECRSLRSRCDQLEERVSA MED EMNEMKREGKFREKRIQRNEQ SLQEIWDYVVRPNLRLIGVPET LHPRDEAHLKNLDAIKNDKGD ITTDPTIEQTTIREYYKHLYANK LENLEETDKFLDTYTLPRLNQE EVESLNRPTGSEIVAIINSLPTK KSPGPDGFTAIFYQRYKEEL/PD KQLQQLRIQNQCITKI'SILIHQ QQTNRPNHE*TPHNCFKENKI PRNPTYKGCEGLQGELOTTAQ GNKRGYKQMEHSMMLGRKN QYHENGHTAQGNLQIQCHPH* ATNAFLHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT *LQTHLQGYSNQNSMVLVPKQR YRSMEQNRALRNNAAYLQLSD L*QT*EKQEMGKGPI**MVLG KLASHM*KAETGSLPYTLKYN QFKMD*RLKR*T*NHKNPRRKP RHYHSGHRHGQGLHV*NTKSN GNKSQN*QMGSN*TKELLHSE KKKNY*QTEQATCKMGENFHN LLI*QRANIQLQ*TQTNLQEK KNQPHQKVKGHEQTLLKRRHL CSQKNHEKMTITGHQRNAN QNHNEIPSHAS*NGNH*KVRKQ VLERMCRNRNTFTLLVGL*TSS

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10239	40607	A	10300	1	2704	MYSHVITVCRHVKNCDILLNR QPTLHRPSIQAHRAIRILPEEKVL RLHYANCKAYNADFDGDEM AHFPQSELGRAEAYVLACTDQ QYLVPKDGGQPLAGLIQDHMVS GASMTIRGCFFTREHYMELVY RGLTDKVGVRVKLLSPSILKPFPL WTGKQHINRTKDKNHMISIDA EKAFDKIQPFMLKTLNKLGD GTYLKIIIRAIYDKPTASIIILNGQK LEAFPLKTGTGQCPLSPLLFNI VLEVLARAIRQEKEIKSIQLGKE EVKLSLFADDMIVYLENPTVSA QNLLKLSMNSFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSGLP FTITSKRITVYLGILTRDVKDLF KENYKPLLEIKEDTNKWKNNIP CSWVGRINIVKMAILPKVIYRF NTIPIKLPMTFLTELEKTTLKF WNQKRAHIAKSILSQKNKAGGI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMPHI/Y YNYLIFDKPEKNKQWGKDTLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKT PKATATKAKIDKWDLIQLKSFC TAKETTRVNRQPTWEIEIFAIY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMVIHKSGNNRRC
10240	40608	B	10301	1	3345	

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10241	40609	A	10302	248	2623	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMMLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAEFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASII PKRGRDITTKENFRPISLMNID AKILNKILANRNQQHKKLIHH DQVGFIQMGQWFNICKSINVI QHINRTKDKNHMISIDAFAKAF DKIQQPFMLKTLNKLGDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTGRQCPLSPLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDIMVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKWKNI PCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFK LYLQGLQ*PKTAWYWYQNRD IDQWNRTEPSEITPHIYNYLIFD KPEKNQWGDSDLFNKWCWE NWLATCRKCLKDPFLTPYTKIN SRWIKDLNVRPKTIKTEENLGI TIQDIGVGKDFMSKTPKAMAT KAKIDKWDLIKLSFCTAKETA IRVNRQPTTWEKIFATYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAANKH MKKCSPLAIREMQIKTMRHY

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10242	40610	A	10303	1	2467	MGDFNIPLSTSDRSTRQKVND TQELNSALHQADLIDYRTLHP KSTHEYTFSSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNLL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRQKERSKIDTLT SQLKELEKQEQTHSKASRRQEI TEIRAELEKIEITQKTLQKMNES RSWFFEKINNIDRLLARLIKKKR EKNQIDAINKHKGDIITNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEQUEVSLNRP TGAEIEAIIINSLRTKKSPGPGGF TAEFYQRYKEKLIVLEVLARAI RQEKEIKGIQLGKEELKLSLFAD DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYSNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEV KEDTNKWKINPCSWIGRINIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTLKFIWNQKRSRIAKSIL SQKNRAGGITLSDFKLYYKATV TKTAWYWYQNRDIDQWNKTE PSEIMPHIYNYLIFDKPDKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLLPYTKINSRWIKDL NVRPKTIKLEENLGITQDTGM GKDFMSETPKAMATKDKIDKW DLIKLKSFACTAKETTIRVNRQPT
10243	40611	A	10304	2	2480	
10244	40612	A	10305	1	4793	MGDFNTPLSTLDRSTRQKVND DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRKNTQSRSTTWKLN NLLNDYWVNNEMKAEIKMFFEI ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRQKERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKIEITQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
10245	40613	A	10306	1	4320	

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10246	40614	A	10307	1	3229	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIIDYRTLQ PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAV CRGKFIALNAHKRQERSKIDTL LTSQKLEKQEQTHSKASRRQ EITKIRAEKKEIETK\TLQKINE SRSWFFERIKKTDRPLARLIKKK REKNQIDTI
10247	40615	A	10308	1	3392	MGDFNTPLSTLDRSRQKVNK NTQELNSALHQVQLIDYRTLH PKSTEYTLFSAPHHTYSEIDHVV GSKALLSKCKRTEIITNCLSDHS AIKLELRINKLTQNCSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTYPNLWDTFKAVC RGKFIALNAHKRQERSEIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFEKINKIDRPLARLIKKKRE KNQIDSIKNDK
10248	40616	A	10309	1	4137	MGKKQNRKTGNSKKQRASPPP KEHSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VENFEKNLEECITRITDIEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSADEMDNEMKQ EGKFREKRIKRNEQSLQEIWDY VKRPNLPPIDVPESDRENGTKL ENTLQDVIQENFPNLARQANQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKMLRAAREKAFKQ ASRREDDIKVTSG
10249	40617	A	10310	1	5195	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIHIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQKLEKQEQTHSKASRRQE IMKIRAEKKEIETQKTLQKINE\ SRSWFFERINKIDRPLARLIKKK REENQID\AI

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10250	40618	A	10311	1	2958	MKQEGKFREKRIKNEQSLQEI WDYVKRPNLHLIGVPESDREN GTKLENTLQDIIQEDFPNLARK ANIQIEIQRTPTORYSSRAATPR HTIVRFTKVEMKEKMLRAARE KGRVTHKGKPIRLTADLSAETL QARRELNQEEVESLNKPVGTGSE VVAIINSLPTKKSPPGDTAEF YQKYKEEPVPFLLKLFQSIEKE GILPNSFYEASIIIPKPRDRTK KENFRPISLMNIDAKILNKILAN RIQQHINKK
10251	40619	A	10312	5211	7687	TDTSQKKTFFYAAKRHMKKCSS SLAIREMQIKTTYHAGPDGFTA EFYQRYKEELVPFLLKLFQSIEK EGILPNSFYEASIIIPKPRDRTT KKENFRPISLMNIDAKILNKILA KRIQQHIKLIHHDQVGFIPGM QGWFNIRKSNVQIHNRKADK NHMIISIDAFAFDKIQQPFMLK TLNKLGDGTFFKIIRAIYDNPT ANIILNGQKLEAFPLKTGTRQG CPLSPLLFNIVLEVLAIRQEK EIKGIQLGKEEVKLSLFADNMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQTE SQMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNI PCSGIEGRINIVKMAIL PKNWKKTTLFIWNQKRARIA KSILSQKNKAGGITVPDFQLYY KATVTKTAWYWYQNRDIDQW NRKEPSEIMPHIYDSLIFGKPKD NKQWKGDSL FNKWCWEDWLA ICRKLKLDPLTPCTKINSRWV KDLNIRPKTIKTEENLGNITQD IGMAKDFMSKTPKAMATKAKI DKWDLIKLSFCTRIAKEPTIRV NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKHKHMK KCSSLAIREMQIKTTMRYHLT PVRMAIIKSGNNRCWRGCGE TGTLHCWWDCKLAQPLWKS

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10252	40620	A	10313	1	4525	MGDFNTPLSTLDRSTROQVVK DTQELNSALHQADLIDYRTLH HKSTETFFAAPHHITYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN LLLNYYVWHNEMKAEIKMFFE TNKNKDTTYQNLDWTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKQLEKQEQTTHSKARRQEI TKIRGELKEIETQKTLHKINESR SWFFERINKIDRLARLIKKKRE KNQIDAIINDKG
10253	40621	A	10314	1	1185	MEDIKRTQNKLESEMKAELAEM KNTLDGINDHGRDSRRKIRKLQ DNGGDDPTGNTQRKKNLINGP SLSVHIGEKRGRRSWAETLTP LQTKALRLGPTTPSARRKCGIV PNLQTRKTEAYRYPDTHPGETP VGTAVLSIQPKLESVIDVRVN MSSFHPEPELQPTQTSVLPDQD ATVAGSTTKFPEEQEARQGRVR ERPATRERPVPGGVSVPLHHI HFLRGPSPLASLTRITVLEAVV CFFSVWSIVGLSGFHTYLISNSQ TTNEDIKGSWSNKRKGKENYNP YSYGNIFTNCCVALCGPISPRT/ LSHTGQRPTPIECEPHNLVTSA ETLLASKPD/PTEEGTSSPTRRS QQHPPMASPTGPRSHRVCTCL EKREEEGVGQRLSPLCKPRL
10254	40622	A	10315	44	302	GLLGPGPTAC*CGPHCGIHPES SPQSWCLCHSHRSSRAPPLARL SGDRHPGWRTWGGRDARSVA RGQWWCLVEPVLFPFSTRSAFW

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10255	40623	A	10316	3	2182	IRDPGKKPVMFLFHGGSYMEG TGNMFDGSLAAAYGNVIVATL NYRLGVLGLSTGDQAAKGNV GLLDQIQALRWLSENIAHFGGD PERJITIFGRYSQPGLSYHIAFGPV VDGDVVVDDPEILMQQGEFLN YDMLIGVNQQGEGLKFVEDSAE SED/GAFDFTVSNFVDNLVGYG EGKDVLRETIKFMYTDWADRD NGEMRRKTLALFTDQWVAP AVATAKLHADYQSPVYFYTFY HHCAEGRPEWADAAHGDPEL YVFGVPMVGATDLFPCNFSKN DVMLSAVVMYWTNFAKTGD PNQPVVYDTKFIHTKPNRFEV VWSKFNSKEKQYLHIGLKPRL WSRFRGVLYQVFHDICEKEAP KSSLLRKQTQPKKQSSPAVHL RCTMDPVMMTVSPPAHRHRR RGSPTRCAHCPVAVAPDTDDE KPHQYPAICSYHWDVPEDWEG FQHTQGTWVPWSQDAPESPQ TIRFQPTVEERPLKTGIWSELGL RAYVYPVNPVPPSPPEAPSHKNG RIVYDARDMRRRLRELTREVE ALSGCYPLASGSSAEETSKNW VYRSLTGSQKMSQLHRVFPFD QEDPDSYLEEEDNLPFPYKYP RRGWGFGFYQRAGLPSNVGLW GHQGGILASLPPSLYLSPELRC MPKRVEARKCQDLGDSILLLLG SFILLNVWINVVTLLWKHLKSS
10256	40624	B	10317	37	241	
10257	40625	A	10318	2	815	
10258	40626	A	10319	1	943	RAGGQGVG*GWGPPSVPCSVH GGKGL/PPEEGPQVTHLEFGR GDGLLTPWPLTGDGRGPSA/S LASQRTCSQ*GMWLPAAQPSPS HPGPAGTVGQSHLHL*GLLGP PPHCLLMRPTLRDSSRVFTSKL VSPVQPVQVQGPTRTKTVWRS ASWMENLGRKGCVCSTWPM VVPGGACTSIWEWEADRVTPG GHRGSSCSHAAGGANAAAPHG PRGRPGGHAAAGGRHSTDGRS SCSPRPDPGAARPQSAVHTDY RSPSLGTFLAQPFGESKSDQSA PGIRGQKAPLAVARRGQQTFRP RGQARGRGRTFRP

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10259	40627	A	10320	39	621	SCPEEESSLLSPGTSWPLHAW ACSAAQVTGRERVVADWPGY HPGGPTAPHWRAGPLSDKTRPS RDVGTWDTGRAGCPPPPGRNP GPPDQRKALGVVTSFGSQLG NGTPNSCLSPRCQWIQLRGSS RTGPPPPGSVPEAAVSCPGIHT LFLRSGAGKIQG*LLGPGWEL GQAGTEPPLPLAPPPHRSCG
10260	40628	A	10321	1	496	AAATYVQNQSEDCLYNLNLYVP TEDGPLTKKRDEATLNPPTDI RDPGKKPVMFLHGGSYMEGT GNMFDGSVLAAYGNVIVATLN YRLGVLGFLSTGDQAAKGNYG L/LDQIQALRWLSENIHFGGDP ERITIFGSGAGASCYNLLLSHH SEGLFQKAIQSGT
10261	40629	A	10322	1	4304	MLPVWFTDNLGAAATYVQNQ SEDCLYNLNLYVPTEDEGLTKKR DEATLNPPTDIRDPGKKPVMFL FLHGGSYMEGTGNMFDGSVLA AYGNVIVATLNYRLGVLGRYS QPGLSYHIAFGPVVDGDDVPDD PEILMQQGEFLNYDMLIGVNG EGLKFVEDSAESDGVSAFAFD FTVSNFVDNLYGYPEGKD/DW ADRDNGEMRRKTVLLALFTDH QWVAPAVATAKLHADYQSPV YFYTFYIIHCQAEGRPEWADAA
10262	40630	A	10323	1	2765	MDVGFSRTTVQTLRSRSHCKNIK QKISQWEGRANGISNPEKWCPK DFGVRYNCHQEIIRLKKNPJAER KSKNLDVTSRENVGLDINENTK SHDQSENENKKHEYDDTHFFK NESESNWVCSRVEIESCKEDV LDPETSLPPGNFYTSQILWKKIE ALPPDKLLNLALEHCDSSSEKEL NFRVLDSSYGITKSLENIYSEPE GQECGSPINLPKPRRTFRYLSE SGVTPYKERNCDKKYCENNSC AQSSLASSQEP
10263	40631	A	10324	2	597	RWLIPKVMRIYDTQKKMDREA SQAALQKMLTLLMLPPTFGDLL REEYIGDNGDPQTLQAQFQEM MADSMFVIPALQVAHFQCSRA PVYFYEFGHQPSWLKNIRPPHM KADHVKFTEEEELSRKMMKY WANFARNGNPNGEGLPHWPLF DQEEQYQLNLQPAVGRALKA HRLQLWKKALPKIQELEEPE ERHTEL

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10264	40632	A	10325	2	1766	PGQPLGEQQRVRRQRRTETSEPT MRLHRLRLASAVACGLLLLL VRGQGQDSASPIRTTHTGQVLG SLVHVKGANAGVQTFLGIPFAK PPLGPLRFAPPEPPESWSGVRDG TTHPAMCLQDLTAVESEFLSQF NMTFSDMSMEDCLYLSIYTPA HSHEGSNLPVMVWIHGALVF GMASLYDGSMALAAENVVVI IQYRLGVLGFFSTGDKHATGN WGYLDQVAALRWVQQNIAHF GGNPRVVTIFGESAGGTSVSSL VVSPISQGLFHGAIMESGVALLP GLIASSADVISTVVANLSACDQ VDSEALVGCLRGKSKEILAIN KPFKMIPGVVDGVFLPRHPQEL LASADFPQPVIVGVNNNEFGW LIPKVMRIYDTQKEMDREASQA ALQKMLTLLMLPTTFGDLREE YTGNDGDPQ/TLPKRKF/QKMM ADS/MFVIPALQVAHFQ/CS/RAP VYLPTSSQH/QPSWLKNIRPPH MKADHGDLEFPVRSFFGGNY IKFTEEEELSRKMMKYWANF AR/NGNPNGEGLP/HWP/LFDQE EQYLQLNLQLA VGRALKAHRF /QFWKKALPQKIQ/LEEPPEERH
10265	40633	A	10326	2	435	ILAEFGSLHLEFLHUTELSGNQV FAEKVRNIRKVL RKIEKPFGLYP NFLSPVSGNWVQHHVSVGGGLG DSFYEYLIKSWLMSGKTDMEA KNMYEYEALET/HKLGPEAFWF NSGREAVATQLSESYILRPEV VESYMYLWRQTHNTK
10266	40634	A	10327	3	583	

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10267	40635	A	10328	1	1299	MHLNQLPPILSRLGAVGFFGSM KAHLVSVSRQVRNIRKVLKIE KPFGLYPNFLSPVSGNWVQLPI PGSVAAGEMPASYPYRRAPE VRRVCEALPHHVSVGGLGDSF YEYLKSWLMSGKTDMEAKN MYEALAEIETVLLNVSPGGLT YIAEWRGGILDHMKMGLACFS GGMIALGAEDAKEEKRAHYRE LAVQITKTCYESYAR\SDTKLGP EAFWFNSGREAVATQLSEE/YT YILRPEVVESYMYLWRQTHNP SYREWGWVVLALAEKYCRTE AGFSGDSKTCYSRHPQPTTSR QSFFLAETLNRCLVSACNGPDT GLEARDTAESETVISPAVKGSR GEKAMVRETDKPAKICIGKSK NGKSDLKAASKMDAQFRSLCF EEVTPLWFEKVLNMGPAASPSV SPGGLSLEVWSLVMWHKDARP
10268	40636	C	10329	186	401	
10269	40637	A	10330	194	482	
10270	40638	A	10331	224	495	
10271	40639	B	10332	138	1810	
10272	40640	A	10333	1	1351	MGGVGEGPGREGPAQPGAPLPT FCWEQIRAHDPQGDKWLVIER RVYDISRWAQRHPGGSRLIGHH GAEDATDAFRAFHQDLNFVRK FLQPLLIGELAPEEPSQDGPLNA QLVEDFRALHQAEDMKLFDA SPTFFAFLGHILAMEVLAWLLI YL/LGPVWVPSALAAFILAIQ AQSWCLQHDLGHASIFKKSWW NHVAQKFPVMGQLKGFSAHWW NFRHFQHHAKPNIFHKDPDVT VAPVFLGESSVEYGGKKRRYL PYNQQLHYFFLIGPPLLTVNFE VENLAYMLVCMQWADLLWA ASFYARFLSLSYLPFYGVPGVL LFFVAVRVL\ESHWVWITQM NHIPKEIGHEKHRDWVSSQLAA TCNVEPSLFTNWFSGHLNFQIE HHLFPRMPRHNYSPVAPLV\KS LCAKHGLSYE\VKPFL\TALVDI VRSLLK\SGDIVLDA\YLHQ
10273	40641	A	10334	43	399	

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10274	40642	A	10335	1	2229	FLKVC PQNNAETFGCLGTGEEK GDRGNQQTQKPLHYKSWSLFHR SCPRDFYGSKVGD FQ GKENG R G\GESVYGGFFEDGVS LVKDH\ KEFLLSMANRGKDTNGSQFFIT TKPTPHLDGHHVVFGQVTS GQ EVVREIENQKTDAAASKPFAEVR ILSC\GELIPKSKVKKEKKRHK SSSSSSSSSDSDSRYS\QSSSDS SDSESATEEKSKKRKKKHKRKN RKHKKEKKKKRKS KKSASSES EAEN\LEAQPPVLLFRPEIPLP IPENRFLMRK\SPPKADEKERKN RERERERECNPPNSQPASYQRR LLVTRSGRK\KGRGPRRYRTPS RSRSDLFRRS\ETP\PHWRQEM QRA\QRM RVSSGER\WIKGDKS ELNEIKENQ RSPVRVKERKITD HRNVSESPNRKNEKEKKVKDH KSNSKERDIRNSEKEDKYKNK VKKRAKSKSRKSKEKSKSKER DSK\HNRNEEKRMRFKELKGR DHENVKEKEKQSDSKGKDQER SRSEKSKQLESKSNEHDHKS KEKDRRAQSRSECDITKGKHS YNSRTRE\RSRRRDSSSRVRSRP HDRDRSMK\IEYHRYRDQVYS RRVRSRSRERRTPGRSRSRDR RRRRRDRSSSEREDSQRNNDK YRNQESKSSHRKENSESEKRM YSKSRDHNSNNSREKKADRD QSPFSKIKQSSQDDELKSSMLK
10275	40643	A	10336	3	3366	

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10276	40644	A	10337	3	2431	GCLQELSVLFARGEPRGPHNL LHYMLALIGVPEVFWAFLFHCS I.GLEEEKLAPLKGEEKIVWLRS SFYFQHCLVDKSTLLPSSSVSLG IFHEEKNSGEFPFAKAVRLALV PLRYVKLEDRDNWISVDSVTSE IKLAKLPDFESRYVQNGTYTVK IVAISEDYPRKTITGTVLINVEDI NDNCPTLIEPVQTIHDAEYVN VTAEDLDGHPNSGPFSSVIDKP PGMAEKWKIARQUESTSVLLQQ SEKKLGRSEIQLISDNQGFSCP EKQVLTLTVCECLHGS/GCREA QHDSYVGLGPAALMILAFLL LLLVPLLLLMCHCGKAKGFTF IPGTIELHPWNNEGAPPEDKV VPSFLPVDQGGSLVGRNGVGG MAKEATMKRKVSSAIVKGQH EMSEMDGRWEEHRSLLSGRAT QFTGATGAI/MTTETITARATG ASRDVAGAQAVALNEEFLK NYFTDKAASYTEEDENHTAKD CLLVYSQEETESLNASIGCCSFI EGELDDRFLDDLGLKFKTLAEV CLGQKIDINKEIEQRQKPATETS MNTASHSLCEQTMVNSENTYS SGSSFPVPKSLQEANAELVQEI VTERSVSSRQAQKVA TPLPDP ASRNVIATETSYVTGSTMPTT VILGPSQPQLIVTERVYAPAST LVDQPYANEQTVVTVTERVIQPH GGGNSPLEGTQHLQDVPYVME
10277	40645	A	10338	5	354	RPRLTSQDIKKPDC/DGEDAIGR GFECDLHLEKIVHFALHLEKN VNQSLLEHLKATDKNDPHLC DFIETHYLNEQVKAKELGHDHV TNMHEMGAPDSGVAEYLFDKH TLGSDNES

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10278	40646	A	10339	I	2024	GEALMYHTHFSELLDEFSSQNVL GQLNDPFLSEKSVSMEEVESP TSPAPLIQAEHSYSLCEEPRAS PFTHITTSDFSNDDEVESEK WY LSTDFPSTSIKTEPITDEPPGLV PSVTLTITAISTPLEKEEPPLEIEQ WGLIPRARPLFPKIKLEPHEVDQ FLNFSPKEAKHLHIIFPSWAACT CGSSGNSAIRIILAYSALRVPT ETKKPRDLFGKTGREKGKEETS REKLYVAERERKAPVDHLHLPP TPPSSHGSDSEGLSPNRLHPF SLPQTHSPSRAAPRAPSAISSP LLTAPIHLQSGPLVLTEEEKR TLIAEGYPIPTKLPLSKSEKAL KKIRRKIKNKISAQESRRKKKE YMDLSLEKKVESCSTENLELRKK VEVLENTNRASHGELVIGVLGK GRRWDPLLTSPHAGDQCLGSV QGWAGECTPRQLDGSRTLLISE EDPGSPMGGEALGAIVSYA WRGREALHASRVGAVIQAPIA AGSDICLSDIRESATSSQTNISVT RTLQQLQKLQTLVMGKVSRT CKLAGTQTGTCLMVVVLCAV AFGSFFQGYGYPSPATKMLPS QHSLQEPYASVVRNRLLIYE EHSPPPESSSPGAGELGGWDR GSSLLRVSGLESRPDVLPHFIIS NETSLEKSVLLELQQHLVSAKL
10279	40647	A	10340	I	489	

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10280	40648	A	10341	1	2665	MESTLTLATEQPVKKNTLKKY KIACIVLLALLVIMSLGLGLGLG LRKLEKQGSCKKCFDASFRGL ENCRCDVACKDRGDCCWFED TCVESTRIWMCNKFCGETRLE ASLCSDDCLQKKDCCADYK SVCQGETSWLENCDTAQSSQ CPEGFDLPPVILFSMDGFRAEYL YTWDTLMPNINKLKTGHIHSKY MRAMYPTKTFPNHYTIVTGLYP ESHGIIDNNMYDVNLNKNFSL SKEQNPAAWHGQPMWLTA MYQGLKAATYFWPGSEVAING SFPSIYMPYNGSVPEERISTLL KWLDPKAERPRFYTMFYEEP DSSGHAGGPVSARVIKALQVV DHAFGMLMEGLKQRNLHNCV NIILLADHGMQDQTYCNKMEYM TDYFPRINFFYMYEGPAPRIRA HNPHDFFSFNSEIIVRNLSCKRK PDQHFKPYLTPDLPKRLHYAKN VRIDKVHLFVDDQWLAVRSKS NTNCGGGNHGYNNEFRSMEAI FLAHGSPFKEKTEVEPFENIEVY NLMCDLLRIQAPNNGTHGSLN HLLKVPFYEP SHAEEVSKFSVC GFANPLPTESLDCFCPHLQNST QLEQVNQMLNLTQEEITATVK VNLPPFGRPRVLQKNVDHCLLY HREYVSGFGKAMRMPMWSSY TVPQLGDTSPLPPTVPDCLRAD VRVPSESQKSCFYLAADKNITH
10281	40649	A	10342	590	900	PLYSATVPSAFCSGQ/LVPHIKS FCRLNIFNR*LIELRHLVFFVLLL FRDLQHIMACNMRDAVRFFVC FLVIFFREGLSRSSCQKCSRKSQ NCGLFYNFFDVHVH
10282	40650	A	10343	1	804	
10283	40651	A	10344	207	299	
10284	40652	A	10345	738	1007	EDASCDegSTARAVHSMEPAG ARNRQKPHFPQVRGAEPHPW* RCSHPA VAVDPGIALSGKPLC SWRLGSDLPTVWPLTPDPPVS VS
10285	40653	A	10346	150	509	QLPAGSGEGPYHLEGQLSYCHR GGEKALAAALLSSPTSKTRSPSEP DPEQDEQLRFCKRHLGYQQP RSPVEIRLQHVAIAYQTHHAYD *FVQLYNQHVAQPVLEFPYPGA VVALLSRHL

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10286	40654	A	10347	120	620	SYVKYFPHQPAQKYFQQIHSAL GLHNADHVHKKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSDHRQFL*HQILFDRT PVSVDQSVEKKG*DHPVRPQ*A APGHVHYLTIPERSSQHYHPGA LQE*TSHPDHIQARGSILASVLS GSDRWRRTYRCL
10287	40655	A	10348	599	1185	MCQNLMTHSKSTEWKITKRFL TETEKHIRTFFSLSMKAIHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSACKR DAELANGALGIIELNNDYTSEK SNEAADHFHVPQAKGNVVI TSYMTNRGFFEDKKATFAPSFL MNIKGNKTSVVKNSILEQQGLT
10288	40656	B	10349	1	975	
10289	40657	A	10350	1	1080	
10290	40658	B	10351	58	1128	
10291	40659	B	10352	1	1029	
10292	40660	A	10353	10	108	
10293	40661	B	10354	208	2237	
10294	40662	A	10355	1	1153	
10295	40663	A	10356	1026	1274	LHIEKSNEAADHFHVACHR*R *ACTCHCNPWFPRPLPQDPDCP TSATVEPLYPIRSRRGRTRKPAE GSRAPGCCCCQRPQK
10296	40664	A	10357	434	1128	MCQNLMTHSKSTEWKITKRFL TETEKHIRTFFSLSMKAIHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSACKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLFDTDSRSGKMTIDGI NSNDIYMLGYVSNLTPGYKPL NKTGLVLQMGDPNDVTFITYS HFAVPQAKSNVNVNYGA
10297	40665	A	10358	300	491	SYVKYFPHQPAQKYFQQIHSAL GLHNADHVHKKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSDHHRQFL*HQPAQKY FQQIHSALGLHNADHVHKKHLLG DNRYPIWIMQPSAHHPARQPEH DNHFR
10298	40666	B	10359	1	1226	
10299	40667	A	10360	1369	1548	
10300	40668	A	10361	1	1365	

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10301	40669	A	10362	1560	2384	MCQILMTHSKSTEWITKRFLTE TEKHIRTSSLSMKAIHPA/HNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYVGG GTNFRKESQKLQSAKKRDA ELANGALGIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWLFTDSRGSKMTIDGINSN DIYMLGYVSNLTPGYKPLNKT GLVLQMGDPNDVTFYSHFA VPQAKGNNVVITSYMTTRGFFE DKKATKAPSLMNIKGKNSKV VKNSILEQQLAVN
10302	40670	B	10363	783	881	
10303	40671	A	10364	1	1359	
10304	40672	A	10365	1512	2010	ENFPHPAQKYFQQIHSAGLH NADHVHKHLLGDNRYPIWIMQ PSAHPARQPEHDNHFR*VQQL YDGDShRQFL*HQILFDRTPVS VDQSVEKKG*DHPVRPQ*AAP GHVHYLTIPERSQHYHFGALQ E*TSHPDHIQAK*WHYR/GHYS YARN*RIHHRGWSWR
10305	40673	A	10366	62	368	TGARRVPWPRGARLRGRARA RSDSEGSAGDPPSPFPWWGW RWVTTAASPANLWPSVARSTM VDRAINL/FLLKMKGDALTED KREQAQNEQSAWKFTPGR
10306	40674	A	10367	2	305	CTINNPFS/HGVGFKQHPQA LTEIQKFAMKEMGTPDVRIDTR LIKAVWAKGIRNVPIRVRRLS RKRNEDEDSPNKLYTLVTYVP VTFKNLQTVNVDEEN
10307	40675	A	10368	129	283	HLILFLKHKYCFAREEEEEK*R GVGGEHEEEEEEEEEEEEEIEI FKSIVY
10308	40676	A	10369	777	1755	DIWDQTEHQSSGPWSYGTSTDP EPTSDLAIVIFEKRGGEHEEE KEEEEGRRR/EEEEKEEEE/GRRR EEEEEEEEEEEE/GRRAQEEEE KKEEEEEEEEEWCLGEEESQPG HAEVPSPHKMGALTLRVEGV KEQEAKLLRSSDLMKGDFFSTS QHPPQCSKRTNSNADAKSKK KERPIMTFRQKTFRIRILPLPQ GRIAGSNKLSAKLCTDGRGAG DVGVLTVNMLKRLHFTIDHFLF KIIQMSPSASWNLWSLLDQDSL KCQICLEGYAQGGKPDVQLLPP RLTADWKGHRWGQMMGLDE KLTPSSVMVTSVALFWEVSAQ

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10309 10310	40677 40678	A A	10370 10371	1 1	444 3799	MNRQLSKEDIQMANKEHMKML NITNDQGNANQNHNAIQPYSC KNGHNRRKIDVSMNMVNRHFY TAVHKASDLSFKPTSEKDLDTK LQANFPNLVKAPDKARICFCGK PYQPYVQGSPPVPEIVENESQ LLHFLCVGSSKEIDLGNPKGS QHTGLGHSMGKCNFYFLLPILLV HGWSHLHPCVASMKVAGTQ RTQDQDEAQEKEKRDKRKAEA LVAALQTYKTQNPQGAPANCY KCGKLGHFKKDCCHSSKRKPL
10311	40679	A	10372	1	990	MTQKKNQTEQKEQKNEQKKQ HNERKEHKKKQTEYKTHETNR PRKTERAEHQKRENEGKRR RHKKRT/RERKKTNEETETRKQ REKPEQARQARKEKQKRQGE RQKEEKKRKNRNQENEEEEAN EQDRREQKEETRKRGPRKRRE HKEEEGRREKRRKRKTKEKG RRAQQKERREEEQQRRRRRR GKRKKNESEDEEDKASNKHQR QERERQKRKGAEARARRPAETG RRRRKRKRQKKA\AKQRQERQ GDGVLPAPWTAHPQPSQCW SARAPGGSahrPRRYLLTGQA NGSLAMWDLTTAIGRPRPGPCR WPDGARADGTAGTL
10312	40680	A	10373	99	1365	KEAEGRALARLLGPSEERFAAH EGMRPMRAVFTRQGHIITGTFT RMSQRELGLWDPNNFEPPVAL QEMDTSNGVLLPFYDPDSSIVY LCGKVLTAGQGEQGTGWRGQ GPCPGAPLNRLLIQDSSIRYFEI TDEPPFVHYLNTFSSKEPQGM GFMPKRGLDVSKCEIARFYKLH ERKCEPIIMTVAPRKVRAWDRD LGRRSDAVPRIRQGPEPALEAD EWLSGQGRRNPCFSRLIDGYC CPPTHRLRVTKRNLIDVRPPS GPRRKPSRPATPPCRSSTPLETL LEEIKPLRERVQAQEQRITALEN MLCELVDGPHYPRAPGRASGL PTDPFGGAVRRACVPVPPPLVPL ARAVRTLPLRYASSIAALVERM KAHMWAKGHLTRDATAKRCS PMAQTITTHLHVPCDREDESR WNYICSS

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10313	40681	A	10374	1	361	MINPNPERSDDL VFWGLFRAG GMWSAIIAPVMILLVGILLPLGL FPGDALSYERVLAFQSFGRV FLFLMIVLPLWGLHRMHAM HDLKIHVPAGKWV\FYGLAAIL TVVTLLIGVVTI
10314	40682	B	10375	70	256	
10315	40683	A	10376	224	414	LRWRSLPAFQSGNLSVPAALM NRANARGEAVCVLGRSSRFLA H*LALGRSAAASGSSLKGG
10316	40684	A	10377	439	595	RAISCCPSHLVKRKTTLAPNTQ TASPRALADSLMQLARQVSRLE SGQ*AQRN
10317	40685	A	10378	1	391	FSSGTVPGDRPDEFIGDTLME RRNRRTGRTEKARIWETANTL AITMLMSTVAMPAAAADGVTF VPVTPHTFRHSYAMHMLYAGI PLKGLQSLMGHKCIRSTGRLPQ RFLGLEWGLPGHPGGRLLAMAE
10318	40686	A	10379	278	694	GHRSPALAIAGCPTIQNGAGPQC AAITRVRAARWCGYPGSGIPTI PEDSFMLYPRALTTHQTGFSPA WGKPSVDRLLATLSGPGGEGQ YSCCPSHLVKKKTTLAPNTQTA SPRALADSLMQLARQVSRLESG Q*AQRN
10319	40687	A	10380	2	371	SVQVFIRDKLMERRNRRTGRTE KARIWEVTDRTVRTCDCGGGL PAAAADGVTFECSAPPNIRFR/H SYAMHMLYAR*YPLKGLLSPI G/HKCIRSTGRLPQRFLGLEWG LPGHPGGRLLAMAEV
10320	40688	A	10381	276	508	
10321	40689	A	10382	464	763	
10322	40690	A	10383	1	715	MQHLSHGSRRLISENFRGCQ DQAVSQTLTRPPLVSKEASFF LLPFDLHVLGLPPAFNLSDQT LQFKSLTLVTSVRVPLEVARG LSMLGLLRFMSSLLAVGDMGQ GDQVEFQDTKGNSEGRASSQP MTPLTPTRVRRCPGPTWGAK AEGVGRAEAAADPGSEGDDVV LSRTGLLLAGLLHYFRGRHLE EIMYNENTRRSQLMLFDKFRS VLVVTTHEDPVIAVFQALLP
10323	40691	B	10384	72	195	
10324	40692	A	10385	1	2331	

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10325	40693	A	10386	1	706	MTTSRSDTRSQDDPSAHLASPK LPQRLPKDLSEAQVERLLQAPLI DQPLELRDKAMLEVLVYATGRLR VSELVGLTMSDLSLRQGVVRVI GKGNKERLVLGEEAVHWLET YLEHGRPWLLNGVPINVLFFPSQ RAQQITRQALWRRINHYDELA GIDSEKLSPHVVRHAFATYFAG SGGCIADFCGGSCAGSAAESC LWFAGTGLYLHHAWSGVWS RECSGAAWRDRDVGGGGE
10326	40694	A	10387	39	209	EPGTYVYNETDKSHSPCRPCVL LS**GIYLGSV**R*NGITYGALL AHIPNKFQVDY
10327	40695	A	10388	2	930	AWTHAGILLKHKYSFLVGCASI SDVIAQVVFVAILLHSHLECRE PLLIPNLSLYMGALVRCITLCL GYYKNIHDIIPDRSGPELWGDA TIRKMLSFWWPLALILATQRI RPVNLVFSRHLGGSSAATEAV AHLTATYPVVMHPYGWLTEIR AVYPAFDKNNPSNKLVSNTV TAAHIKKFTFVCMALSLTLCFV MFWDTRV**GKSLIDIHSGSLW PLQELCVVPLWIFSFPPVPTV RAHLTGWMLTLKKTFLAPSS VLRIVLIASLVVLPYLVGHG ATLGVGFLLAGFCGENSTMG
10328	40696	A	10389	1	1389	GDATIRKMLSFWWPLALILATQ RISRPVNLVFSRDLGGSSAATE AVAILTATYPVGHMPYGWLTEI RAVYPAFDKNNPSNKLVSNTV VTAHHIKKFTFVCMALSLTLKD SVQKPDISLTGRLVQTLPTMR HQRGESKDAPLASWLEPSTS SEASQTSSKLTINSQGEKAKQ KLECGTSLIVLRSECKNQERIK AEKRNRSWTTLCGLGAWRPLL FELPVIVQTPDQTNRFQFRYP KTQSGLCSEFFHSFDLLTLEAFV KVWFPGLLILIEYASSKNRKS KMLQNLKLLSADMTLKLFCFVM FWTPNVSEKILIDII.GVDFAE LCVPLRIFSFPPVPTVRAHLT GIFLMTLNYTFVLAPSSVLRIV PHRPASWVLPYLVGHGATLGV GSLLAGFVGESTMVALATCY VYRKQKKMENESATEGEIDS AMTDMPTEEVTDIVEMREEN

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10329	40697	A	10390	57	556	TGRCTCHDRHYWYSPVERIAY NVEAARVVEQRTDLDKLVIE TNGTIDPEEAIRRAATILAEQLE AFVDLRDVRQPEVKKEKPEFDP ILLRPVDDLELTVRSANCLKAE AIHYIGDLVQRIEVELLKTPLN GKKSLETKDVLASRGLSLGMR LENWPPASIADE
10330	40698	A	10391	536	787	GRD*PDYAENAHVMPVVI ED ASDMLLAITQAGRMLMFPVSD LPQLSKGKGNKIINIPSAEARG EDGLAQLYVLPQSTLTIH
10331	40699	B	10392	868	900	
10332	40700	A	10393	1	278	MNPQEANYAYLRG/EVELVRLP DAEGRIAAE/GALPYPPGVLALE EGI/NLLPGFAPELQGVYIEE/HD GSGIIMLPTKLAEVGTI
10333	40701	A	10394	1	811	
10334	40702	A	10395	1	682	
10335	40703	A	10396	442	546	
10336	40704	C	10397	1	1776	
10337	40705	A	10398	2	1354	YFSPAAMKALDLLIKWTRSDQ NLGGCNTGLIRPISPIVLIYKLVI GEQMIDVLGPEKRRRTTQEKI AIVQQSFEPGMTVSLVARQH VAASQLFLWRKQYQEGSLTAV AAGEQVVPASELAAAMKQIKE LQRLLGKKTMENELKEAVEY GRAKKWIAHAPLLPGDGDCTS FSDEPMTGWMAAAVVTLMIR MCFSVYTMLESCQRMVIVGY GRRIPDRQNLMIGGSKP/SIFRQF C/PDFEHLQEPYE/LLWE/MYGN RGYQLVLSFMQKFIDQSIFANT QYDPSRFFPSGKVPPIQLKDLL TAYKFGVKTLYYQNTRDGAED AQDDLVPISIQDDGCEGACILIR RASVASGSGCRMQRERLILATA RICRPDKTRQRRIRHRMRKMP YPALNSQQDTLMAYTTFSQTK NDQLKEPMFFGQPVNVARYDQ QKYDIFEKLEKQLFFLLASGRS
10338	40706	C	10399	1	1269	

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10339	40707	A	10400	1	1909	MGFHHVQAQAGFELLISSDLPAL ASQTARITAREARAPVEENKKA QLERDKQLSEQQQAALAKE KAQVKQLIEMNRITIANGDIGF NFTDGNLIKKIFVDKLTQAQLIN GRLAIARLLVDNNSEGEYAIIPA SVADKIAQRDASSIVLHLSA EEQDEDDPYADFKVPDDLMMWP TVYGRSVDRIRRSRRIRQSCAM PDATLCASYQAYGLRAKHPSFS SQGVPHCVDPVTLKIASEAPSI VGGTLPVPMTSQLPSVTSMQLL LDLDTIPNEPLHYDWEALRESI KTHGLRNSTLSALMPSETSSQIS NATNGIEPPRGYVSIAKSKDGIL RQVVPDYEHLHDAAYELLWEMP GNDGYLQLVGIMQKFIDQISIA NTNYDPSRFPSGKVPMMQQLK DLTLAYKFGVKTLYYQNTDRG AEDAQDDLVPISIQDDG/CESGA CLIRRASVASGSGCRMQRERLI RPTARICRPDKTRQRRIRHRMR RVLPRGATRDRDPSLEAGYQW LPGRGLVIEPQAQVMYQGVQQ DDCTAASRARVVSQSGDDIQTR LGLHSEWRTAVHVIPTLDLNDY HDPHSTEIEEDGSTISDDAVKQR GEIKVGVTGNISQVSLRGSVA WQKGSDDFAQTAGFLSMTVK
10340	40708	B	10401	1	1329	
10341	40709	A	10402	1419	1788	ALTSVLPRPSVHW*SPKPRNVD WHIGRGVAIIMQKSGIPDIDQA NCMIKLESDDGTFFIVHSGGADIG TGLDVTVTKLAAEVLHCPPQD VHVISGDDTHALFDKGAYASS GTCSFGNAARLAAEN
10342	40710	A	10403	73	477	SMFPRIPFGY/WHI/GSRVAIIQ K/SGIPDIDQSNLHDQLESHGTFI VHSG/GFDYGTGLDTV/VLTKL AAEV/LHCPPQDVHVISGDDTH/ ALFDKGAYASSGTCSFG/NAAR LAAVNPRALAYSYGGGGARV CIWGGWGRR

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10343	40711	A	10404	I	756	MSIAYQEIPQNERLRLSDSSITS VVEYLLAVVARSVYTSDDMAIF REHHSYMSLSMAACRKIRPCQ ELPRSHIPMISAMWSQSPDHV VQHEREQQSGFGDGTESHSTSD SNTVEVRQNCSPPIGGVRNHRAL RGHQPAELEPENILKLLLMVAE RKAHKGWYYSGDLCRMDEAG YIKITGRKKDIIVRGGENISSREV EDILLQHPKIPNA\CMGAMSD RLGERSCAYYVLKAPHHSLSL EEVLCWRGC
10344	40712	A	10405	252	1245	GSRLPGASITRSLEFIAGQAVK FNPLLPVSLVKRNTTLAPTHTT ASPRALADSLMQLARQVSRLD SGQRSVVFVRWSRRSIIVDSHA GLITTTQRALGQSDMYRGSLPISE LRHIGPRHLRGVLRVVRCLPFSE PMLVECNPLLPSSLIIEPSLEPT LRFASRIALPDSTVLQIFSGVLP LSSGQAYIQFTYSETPRSTPREA NSAHILSVHQWKCQHIVMAAR VKVGYPQWTPISLSAGLSAVLY KPVERGGRCSHSCSTALSPQGF LSSLLRFISEGVFKSFTDKQMLR DFVTTTRPALIVLLWQPLNVEGT SSTSHCIIMPTCNDHRD
10345	40713	A	10406	269	432	
10346	40714	A	10407	332	933	RVSRGRKVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFRLSE TKEITNPYAMRLYESLCQYRKRP DGSIVSLKIDWIIERYQLPQSY QRMPDFRRRLQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKKRKTTLAPNTQTASPRAL ADSLMQLARQVSRLESQQAQ
10347	40715	A	10408	I	531	MRWKIDLARISKEIIDFYITQGV NRIGFIAGEDEPGKADIREVAFA EYGRLKQVVREEDIWRGGFSSS SGYELAKQILARKDYPKPLFV ASDSIAIGVLRAIHERGLNIPQDI SLISVNDIPTARFSFPLSTVRIH SEMMGSGQVNLVYEKAPDGR ALPLLVFVPSKCLKRGTTTR
10348	40716	A	10409	I	1059	
10349	40717	A	10410	2187	2429	

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10350	40718	A	10411	1	835	MRPFGDYPDGGIDDLKISFSVP AAGVGPHFDQYDVFIHQGTERR RWRVGEKLQMKQHCPHDDL QVDPFEAIIDELEPGDILYPPG FPHEGYALENAMNYSVGFRAP NTRELISGLPDYVLQRELGGNY YSDPDVPPRAHPADVLPQEMD KLREMMML\ELSTHPDPFKQWLG EFISQSRHDLDIAPPDPYPQDE FSDALNQGKVLGALGGLRVL MGDAVYPNGEKMDSPRPALD ALASTIALTAKNFGDALEDPSF LAMLAAALVNSGYWFFEG
10351	40719	A	10412	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQI\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
10352	40720	A	10413	157	413	ALVCS/SSLAIEMQIKTTMRYH LTPVRMAIIKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELIPFDPAIPLL
10353	40721	A	10414	342	528	
10354	40722	B	10415	32	587	
10355	40723	A	10416	1	2141	
10356	40724	A	10417	1	748	
10357	40725	A	10418	321	411	RNRDRYKQWKQDFFHDSYNR QRGCGRWLYRRHHR*CRRYRR QQPHLCRLYES*KKSCFCHLYR SRF/RLRVKYPRDMYSLGTFL RSPVAIRIPLSRNQVQR
10358	40726	A	10419	1	2235	

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10359	40727	A	10420	1	1884	MGKDFMTKTPKAMATKAKID KWDVILKLSFCTAKETTIRVNR INKIDKPLARLIKKEKNQIDT IKNDKGDITDPTIEQTIREYY KHLTYNKLLENLQEMDKFLDTY TLPRLNQEEVETLNRPTGSEIV AIMNSLPTKKSPGPDGFTAEIF QRYKEELMILIPK/PGQDITKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIHHDQGVFIPGMQOG WFNIRKSINVIQHINRAKDKNH MTISIDAEKAFDKIQPFMLKTL NKLGDGTIFYKIIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFINIVLEVLAIRIQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPTVSAQNLLKLISNFSKVSQ YKINVQKSQAFLYTNKRQTESQ IMSELPFTIASKRIKYLGIQLPRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VTYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIASII.SQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNILIFDKPEKNQOWGKDS LFNKWCWENWLAICRKLKLDLP FLPTYTKINSRWIKDLNVRPKTI
10360	40728	A	10421	1	822	
10361	40729	A	10422	2738	2949	
10362	40730	A	10423	1	1134	
10363	40731	A	10424	1	2118	
10364	40732	A	10425	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH**VIFL WSRRIHTASCLPSQRSITGHVH HQ
10365	40733	A	10426	2	1624	
10366	40734	B	10427	1	3690	
10367	40735	A	10428	1	1056	
10368	40736	B	10429	1	2265	
10369	40737	A	10430	1	2037	
10370	40738	A	10431	1	2406	
10371	40739	B	10432	670	2568	
10372	40740	A	10433	3	4072	
10373	40741	A	10434	1	3171	
10374	40742	A	10435	1	1542	
10375	40743	A	10436	1	1008	
10376	40744	A	10437	1	2241	
10377	40745	B	10438	1	2682	

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10378	40746	A	10439	644	949	MRKPTLGRTYSPRPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICAGCCWLP CGTPTS VLT KRWH*P*VIFLWSRRHTASCLP SQRSITGHVHHQ
10379	40747	A	10440	1	1088	MARKDIQVLIIGTYEYLVKGE KVLTLAIKLVKWSGYPGLC LPEYHLGEVEGEDDM EMTAMD GRCLLEVKG SERLQVADQECV GDGSGRLCPDRCECEQRLQLV RPGLCNPRAIALTTKPQSPSPNI KRLVIGE QMIDVLGP EKR RRT TQEKIAIVQSFEPGMTVSLVA RQHGVAAASQEGSLTAVDAGEQ VVPASELAAMKQIKELQRL GKKT MENELLKEAVEYGRAKK WIAHAPLLPGDGERTDDWMDG RRSRHTDDTDVL*SASWRQQV QRQE QPVLRRRQ*DFLLGWL LHHVAGQGRGSSPVQSSAEQL RSFPVWYAVCVSPALRHQSSVL
10380	40748	A	10441	1	2781	MGGKONRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSVMEDEMNMN DGENGTKLENTLQDIIQENFPN LARQANVQIEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTKIYAPNTGAP RFTKQVLSDLQRDL
10381	40749	A	10442	1	2445	
10382	40750	A	10443	1	1428	
10383	40751	A	10444	1	2478	

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10384	40752	A	10445	1	1746	METQKTLQKINESRSWFFFEKIN KIDRPLARLIKKKREKNQIDTIK NDKGDITTDPTIEIQTITIREYYKH LYANKLENLEEMDKFLDITYTL PRLNQEEAESLNKPTGPEIEAII NSLPTKKIPGPDGFTAIFYQRY KEELQHIIKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMIIISDAEKASDKIQPFMLK TLNKLGDGTYLKIIIRAIYDKPT ANIILNGQKLEAFPLKTGTRQG CLLSPLLFNIVLEVLAIRQEK EKKCIRLGKEEVKLSLFADDDMI VYLENPVSAQNLLKLSNFSKV SGYKINVQKSQAFLYTNNRQIE SQIMSELPFTIASKRIQYLGQILT RDVKDLFKENYKPLLEIKEEDT NKWKNIPCSWIGRINIMKAM LPKVIYRFDAIPKLPMTFFTELE KTTLKFIWNQKRARIKASILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPKDNKQWG KDSLFNKWCWEIWLAIGRKRK LDPFLTPYTKINSRWIKDFNIRP KTIKTEESLGIIQDISMGKKFTS
10385	40753	A	10446	2	541	
10386	40754	B	10447	1	1533	
10387	40755	A	10448	753	1468	LVTYSYLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R/WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10388	40756	A	10449	753	1468	LVTYSYLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R/WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR

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10389	40757	A	10450	753	1468	LVTSYSLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSICFLSAHFWLVRVRPK RWCKPVQVSATFTVIADNNLY RQNSFVVSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVRVVKIILLPLL VSITVSLRVKYPMDMYSLGTF LRSPVAIRIPLSRNQVKR
10390	40758	A	10451	753	1468	LVTSYSLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSICFLSAHFWLVRVRPK RWCKPVQVSATFTVIADNNLY RQNSFVVSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVRVVKIILLPLL VSITVSLRVKYPMDMYSLGTF LRSPVAIRIPLSRNQVKR
10391	40759	B	10452	1	2259	
10392	40760	B	10453	1	684	
10393	40761	A	10454	1	1419	
10394	40762	B	10455	1	462	
10395	40763	B	10456	1	915	
10396	40764	B	10457	1	1659	
10397	40765	A	10458	1	1659	
10398	40766	A	10459	1	1224	MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASRKIKYPGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVERINIVKM AHLPKTAKNGPVLPLHSEEKIP FNFH*LFR*TITATKA*QKRR* MCQNLMTHQNRQSRGRSQYF* RRRKNISDRSAVYR*QQLYIRR QPYAERPSHVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFCKESQKLQSSAKKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLF TDSRGSKMTIDGI LPISDPTIKQDFRLLGGQTSVDRL LQLSQGQAVKGNQLLPVSLVK RKTTLPNTQTASPRALADSLM QLARQVSRLESGQ

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10399	40767	A	10460	1	2241	MEDEMNMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRY SRRATPRHIIVRFTK VEMKEKM LRAAREKDRSMRQKV NKTQEQ LNSALHQADLDIYRTLHPKST YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIITNYLSDHSAIKLE LRKLNLTQNRSTTWKLNLLN DYVWHNKMKAIEKMFETNEN KDTTYQNLWDAFKA/EIQITIK EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPIGT AEIVAIINSLPTKSPGPDGFTA EFYQRYKEELVPFLKLFQSIK QGILPNSFYEASTLIPKGRD EKENFRPISLMNIDAKILNKILA KRIOQHKKLIHHDQVGFIPGM QGWFNHKSINVIQHINRAKDK NHMIISIDA EKA FDKIQQRFML KTLNKLGDIGTYFKIIRAIYDKP TANIILNGQKLEAIPLKAGTRQG CPLSPLLFNIVLEVLARVIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPVTAQNLLKLSNFSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIMKMAIL PKVIYRFNAIPKLPMTFFTELE KTKFIWNQKSAHITKGLSQKN
10400	40768	B	10461	1	1254	
10401	40769	A	10462	551	868	SIQHWSRISSLRVYRSKAVAAA LLPMNCSLWSTQAGFLPRFG*R *TRHLSTIEPEDYNLLFRVSLK LSVWLPTWQSKSNGWSQKCL WMHLKFDLSNALLPPTGF
10402	40770	A	10463	1	2985	MEDEMNMKREGKFREKRIKR NEQSLQEIWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRY SRRATPRHIIVRFTK VEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFFTICDDAEDLQSPSTA GPWFGVLYTKGGPYQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPNQCH IGEVLLDGFTA EYFRRYKEELV PFLKLFQSIKEG
10403	40771	B	10464	1	2277	

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10404	40772	A	10465	1	1064	
10405	40773	B	10466	1	1827	
10406	40774	A	10467	1186	1208	ATKMVRLSVAALVQRMKEFCA AKFPAVITCWWSVWAQSA*WR *CWRKTKI
10407	40775	B	10468	1	1992	
10408	40776	A	10469	1488	1920	RVRVTAVITERDCVSRSRWTAV IVRHCTGRSLPAASTVKQYRTS CWERWN/CRFGNDLPSPVVEWL TDN/EFMLPG**NTPVRPDVGLE PT*TRACQESRCN/RLTPGIVL EIIGVWMQQRWSLECRLAIPCIFG WLPRVVGEESGA
10409	40777	A	10470	1	1659	
10410	40778	A	10471	1	987	
10411	40779	A	10472	1	1278	
10412	40780	B	10473	1	1556	
10413	40781	A	10474	1	1905	
10414	40782	A	10475	644	949	MRKPTLGRTPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VFLWSRRIHTASCLP SQRSITGHVVHQ
10415	40783	A	10476	1	1217	
10416	40784	A	10477	83	1134	
10417	40785	A	10478	2450	2607	

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10418	40786	A	10479	1	2604	MPLRAFNPVSSFRWARGMTIV AALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGK QAIHAGMAADALGYVLLAFAT RGWMAFPIMILLASGGIGMPAL QAMLSRQVDDDHQGLQGSL AALTSLSIIGPLIVTAIYAASAS TWNNGRACSSSVTRIVSILSRFI GIITPMNRNPPYTEASVTKQEK TALNMAFRIRSQTLTLEKLNE LDADEQADICESLHDHADELRY SCLARFGDDGNSYDHDYAKLA CLQVEGRGGGTFAHELLAVEY AGWISPAFRLKVNQTFIDYRTG RLQPAIPQSLPEALRLAADLAE QKQRLEQKMLMDAPKVEFAER VATASGVLIGNYAKVGLGLQN YLFTWLRDNGILI/CNR* TQERP QTRIHISWVFH/LLKKP*SIQAM EAG/LSFTTRITGKGQQWLMKR LLDARNRDYKQWKQDFFIDS YNRQSAGHILSQCANLAATTSE YFIHKPHRLIAAETGYSQSTVV RAFREAVNKGILSVEIVGDHRE RRANLYRFTPSFLAFAAQAKNA LIESKLKISSAATKVAVLAKTL ALFNFLSTPPCQNDTPSPCQDD VAJKNKKSQVKKTKRSVSGGA GTTSKKLTSWIAKAKAKADN LRLSKKRTQKHEFKQKVEAAA RKYAYLKNKRSPDIGISNFDN
10419	40787	A	10480	1	2559	

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10420	40788	A	10481	1	1676	MLNGEKLAVKQEALLAAISEK DANIALLELSSSKKKTQEEVAA LKREKDLRVQQLKQVGRGG GTFABELLA VEYAGWISPAFRL KVNQTFIDYRTGRQLQPAIPQSLP EALRLAADLAEQKQRLEQKML MDAPKVEFAERVATASGVIG NYAKVLGLGQNYLFTWLRDN GILIATGERRNVPKQEYISRGYF TLKETVIDTSNGSRISFTTRITGK GQQWLMKRLLDADVVRTTSIV MLAKVTFSLCITMSDFTFSGYE LACFVTHSGLSRSSAGHILSQCA NLAATTSEYFIHKPHRLIAAETG YSQSTVVRAFREAVNKGILSVE IVIGDHRERRANLYRFTPSFLAF AQQAKNALIESKLLKISSAATKV KAVLAKTLALFNFLSTPPCQND TPSPCQDDVAIKNKKSQVKKTK RSVSGGAGTSLKLLTSWIAKA KAKADNLRSLKKRTQKHEFKQ KVEAAARKYAYLKNKRSPDIG GISNFDNLPHCMTVNEALNAVL AKNKDNEQWGAVAGAYADIT DGEDRARHFGLMSSACFGVGM VAGPVAGLLGAISLHAPFLAA AVLNLNLNLLGCFMLQESHKG ERRGELLKIVVLPGDHVVGQEIT AEAIVLKAISDVRSNVKDFE NHLIGGAAIDLQGGGGKPRCVS KSLMLH/CWHSRCLPRWR*QR VQRJRL*VHP*AFFAPAVAFALP
10421	40789	A	10482	1	3213	
10422	40790	A	10483	1089	1373	
10423	40791	A	10484	2720	2968	TTTLVRLPCRSPPKRIKALRSQ RRKSILKPLS*SR*STTK*RNTP CSQVSSLRLSTRYRRRMKHSV NLVWTWVPYSSAP
10424	40792	A	10485	2	2264	
10425	40793	A	10486	1693	1980	
10426	40794	A	10487	1776	2026	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRRSSNRACSS SVTRIVSILSRFIGI
10427	40795	A	10488	1323	2064	
10428	40796	A	10489	53	243	WTVPLGAVPPVRMHEGLGCW CKLNGEVCMSGMCLLCWWD D*RHDLKANLDRMLNVCQDGR KR
10429	40797	A	10490	1	3117	
10430	40798	A	10491	1	1227	

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10431	40799	B	10492	1	2119	
10432	40800	A	10493	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRHTASCLPSQRSITGVHH HQ
10433	40801	A	10494	1	2822	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEIETQ
10434	40802	A	10495	2	163	
10435	40803	A	10496	4051	4355	MRKPTLGRTPSRPPSPAAARG ASKAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVL TKRWH*P*VIFLWSRRHTASCLP SQRSITGVHHHQ
10436	40804	B	10497	1692	1781	
10437	40805	B	10498	1	3477	
10438	40806	A	10499	179	439	KKELVNLTTD*SLENR/WIDVL GPEKRRRTTQEKIAIVQSF/G TGDDGLPRCPATWCSSQPVISL A*AIPGRKSYCCRRRTTGCSCS
10439	40807	A	10500	1	7456	MYQANGKQKKAGVAILVSDKT DFKPTKIKRDKEGHIYIMVKGI QEEELTILNIYAPNTGAPTFIQ VLSDLQRDLDSHTLIIGDFNTPL STSDRSTRQKVNKDTQELNSAL HQADLIDIRTLHPKSTEYTFSS APHHTYSKIDHILGSKALLSKC KRTEIITNYLSDHSAIKLELMIK NLTQNHSTIWKLNLLNDYV VHKEMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRKQERSKIDT
10440	40808	A	10501	2476	2718	WPLRGRGGHRAAPGRHLHLQ RLLLRLHLTACLLQDALDG/GP PRCWRGSCRWCSAGPPRSWA RRPSATRSPSPWPALECS

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10441	40809	A	10502	2	4517	HRLANWIKSQDPSVCYIPETHL TCRDTHRLKIGWRKIYQANG KQKQAGVAIHISDKTDFKPTKI KRDKEGHYIMVKGSIQQEKLTI LNVYAPNTGAPRFIMQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR LTRQKVNKDTQELNSALHQVD LIDIYRTLQPKSTEYTLFSAPHH TYSKIDHILGSKALI.SKCKRTEII TNYLSDHSAIKLELRIKKLTQIR STAWKLNLLNDYWVHNEM KAEIKMFFKNNEN
10442	40810	B	10503	88	501	
10443	40811	A	10504	1	971	MWALFMIRNVKKQRPVNLDLQ TIRFPITAISILHRVSGVITFVA VGILLWLEYRLSYLKGSSKLR DYGQLLTLEIPAALLPIHTGIVN QNINCTETLTASSDNLLRRAFC GDTHLHEVHLNTLFFNHFLCFA VIFDETRNKDICATSGQHAHFV DKKRKRELLSHMIGKGNWQQV LVFTRTKGHANHLAEQLNKDG IRSAAIHGNKSQGARTALADF KSGDIRVLVATDIAA/RGLDIEE LPHVVNYELPNVPEDYVHRIGR TGRAAATGEALSLVRSFFDWC DDCAAAGGMGNRNAQLADGI YHLRCIELYLGDMADFL

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10444	40812	A	10505	1	2201	MSFDSLGLSPDILRAVAEQGYR EPTPIQQQAIPAVLEGRDLMA AQGTGKTAGFTLLQHLITR QPHAKGRRPVRALILTPRELA AQIGENVRDYSKYLNIRSLVVF GGVSINPQMMKLARGVDVLV ATPGRLLDLEHQNAVKLDQVEI LVLDEADRM LDMGIHDIRRVL TKLPAKRQNL LFSATFSDDIKA LAELLLHNPLEIEVARNTASD QVTQHVHFVDKKRRELLSHM IGKGNWQQVLVVFTRTKHGAN HLAEQLNKDGIRRAAKHGKNC KCAYSKFQKPSPHIFTMLIGVC GVNQSAITNVSNVSNMAKISGS GSHRLTKRVIKRDMPINHPV AYSRRRLQTELLFWHARWLN HTRRQFRIKEGDNNGQCFLW TGRFNFNLPSFGRIQHQQRNNA VGFSLGAFVITFIAGRACMPSLF VISTVCLTMVYVFPAYDGV GRFYRASGSSLPVALQYTPNGA SRRYINQWRPSRMLSSLLKKQW RKGMSESLHLTRNGSILEITLDR PKANAIADAKTSFEMGEVFLNFR DDPQLRVAITGAGEKFSGAGW DLKAAAEGEAPDADFPGGGFA GLTEIFNLDPVIAAVNGYAFG GGFELALAADFIVCADNASFAL PEAKLGI VPDSSGGVLR LPKILPP AIVNEMVMTGRRMGAEALR WGIVNRVVSQAELMDNARELA
10445	40813	A	10506	1	168	MCEKNLAYAHKVKAALEKGA SPGDFPREDYETNWEGRFTLA DLNIHGKRALGMDV
10446	40814	C	10507	1	3861	
10447	40815	A	10508	1	7407	
10448	40816	A	10509	290	661	QPLPEGRW/THLWHNDEL DGS RWHK/QQHGLSLPVYVRDNT LRALGNNDQRPDYVWHE/GTA FHLFNLKAARTGNTITAI DASE ANNWTLCLRNQVKNGLQDG SQAESQGLVVKPQGNALITTL
10449	40817	A	10510	3	510	KFHFMSPFPAHSMVQALE*LYA LGGLDKDCRLTEPLGMRIAEFP LNPMPFAKMLLESGNFCSQEIL SIAAMMQIQNIFVVPNHKSHAI RVHRKFAVEEGDHLTMLNIYE AFIKHNKDSKWCQEHFLNYKG LVRAATVREQLKKLLVKFQVP RKSEGD PDLVLRICVS

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10450	40818	A	10511	1	1920	MIWGRAWWLTPVIPALWAAK VAGRVAEERGAVLGHEVG YCI RFDDCCTDQLATRIKRLTESFSLI LSVIMLDEAHERTLYTDIAIGLL KKIQKKRGDLRLIVASATLDAD EEVETVVSMLIEQARALARIG MKRHLRLVPMYAGLPSFEQMK VFERVSRSVRKVIVATNVAETSI TISGIVYVIDCGFVKLRAYNPRT AIECLVVVPVSQASANQRAGR GGRSRSGKCYRLYTEEAFDKLP QSTVPEMQRSNAPVILQLKAL GIDNVLRHFHMSPPPAQSMVQA LELLYALGSLDKDCRLTEPLG MRIAEFPLNPMFAKMLLESGNF GCSQEILSIAAMMQIQNIFVVP NQKSHAIRVHRKFVVEGDHL TMLNIYEAFIKVSTTTARSAAST HHPLEHNKDSKWCQEHLNYK GLVRAATVREQLKLLVKFQV PRKSSEGDPDLVLR CIVSGF FA NAARFHTSGAYRTIRDDHELHI HPASVLYAEKPPRWVIYNEILL QTSKY YMRDVT AIESAWAVGS WLHTFYSTRERTCSLESQKGPR SRDPLRRREPTVYSCRD CWRPLL HAAAPGPRWGELAPAPVECLV ALKWAAACSLVLSRRCPQHLH PCWDPGGLCAWAGILLCCSGQ SGSWLTQHAH
10451	40819	A	10512	3	414	
10452	40820	B	10513	62	1408	

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10453	40821	A	10514	1	1388	MGTSSIFLCVLFLCAGALGLTMS PARGRRLRCYICGF TKPCHPVPT E CRDDEACGISIGTSGCRGIFQVP DQQRDSRSHFPADVTKITWAC GQSPPGFKPLFPSCSSPKTGQM DVLIDLDFGFELRNRGIWGE GA IRDTEEKSADNLEPCSSPPPLEE VICCEGNAGFYEVGCVSTPLEA GYSVLGWNHPGFAGSTGVPPF QNEANAMDVVVFQAIHRLFFH PQDIIYA/LAIGGFTATWAAMS YPDVSAMILDASDDL VPLALK VMPDSWRGLVTRTVRQHLN LN NAEQLCRYQGPVLLIRKTDQD NLTPVPMKDICSNRANCLLVKA LQHRYPGVM AE EGLLVARQW LEASSQLEEASIYSRWEVFED WCLSVLRISYQAEHGADFPW SVGEDMSA/DGR/RQLA/FLAR KHLHNFEATHCTPLPAQNFFRC PWHPGLTQLGLIMEEWGERRH
10454	40822	A	10515	1	1519	MGLFKPLLLASFFPAQASW G VSSPDQVQGVKGSCLLPICFIS PADVEVPDGITAIWYYDYSGQR RVFMGNPEHRVCNLLKDLQP EDSGSYNFRFEISEVNRWSDVK GTLVTVTARSLSPGRHLETLH MAMSWQDHGRILRCQLSVAN HRAQSEIHLQVKYAPRGVKILL SPSGRNILPGEVLVTLTCQVNSSY PAVSSIKWLKDGVR LQTKTGV LHLPQAA WSDAGVYTCQAENG VGSLVSPPISLHIFMAEVQVSPA GPILENQVTLCNTNPNEAPSD LRYSWYKNHVLL EDAHSHTLR LHLATRADTGFYFCEVQNVHG SERSGPVSVVNVHPPKTP TMM VFVEPEGGLRGILDCRV DSEPL ASLTLHLGSRLVASSQPQGAPA EPHIHVLASPNALRVDIEALRPS DQGEYICASNVLGSA STSTYF GVRALHRL/LSVPA AALPGGTA/ VWASCSCCWA WGPATPGGTG YYLTGTYKSGGQTQMLSASLF
10455	40823	A	10516	3	615	
10456	40824	A	10517	373	631	SGGPDTDVVSIPYSCSRMHLCS *LCELLSFSWETLCRAVKENEL PKKE*RAPANQGPTGESSLGL SDSPLQPGGDGVEERRALLF

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10457	40825	A	10518	1	5521	MANRFRSGEDSGGAIWQDCVE EGASELGFLESLLYTQGNDRKQ CSLTNQGRQVFALLMLRKGH HVFVILFGPAGAPPQPLPSVEQ VPLSLVPGPKGVAVSRTPPFFH QVHDCPFQDPKWEEQGSWDKI AALAIAELTLTSPVARDTSDPQ CAQQAFLHGQASWGVSSPQD VQGVKGSCLLIPCIFSFPADVEV PDGITAIWYYDYSGQRQVVS ADPKLVEARFRGRTEFMGNPE HRVCNLLKDLQPEDS
10458	40826	A	10519	1	1149	
10459	40827	A	10520	111	370	SHRRSLGEAARHPSFRPAGTAF E*VSQKVVHPRDLEDRSACVPV GCSLTRESFFRLNNQPHGTRFLP IPSNPESSRRVPSAHLTV
10460	40828	A	10521	1	220	
10461	40829	A	10522	654	967	
10462	40830	A	10523	2	1415	
10463	40831	A	10524	2	293	CGKAFTQHSRLIQH/QRMH KPYEYWEFGEKPRIYLQRKTFM KLDTTTGEQSYQRNQMEPCP YGEKPCCKECKGKSFR/SS ELTRHQAHTGEKP
10464	40832	A	10525	51	378	GDFSPOKPPMAPHGCLTYLAFQ KVKEGKKEKKEKKEKKEKKEK KKEKKEKKEKKEKKEKKEKKEK EVEGKEGRKEGRKEGRKEGRKE KKEISKKEIVAPTSNLNPKCSVL
10465	40833	A	10526	1	235	
10466	40834	A	10527	545	793	NKEMHWPCITGLCSHPWGFK DCSLLE*RLPGQQEQNSIERKK RKKEKKEKKEKKEKKEKKEKKE ERKKERKYHFILLGMPTS
10467	40835	A	10528	127	376	
10468	40836	A	10529	3	710	EPG/NPERLK/GFSYPEFEDLDA LFSTLGLNEESVDSFDDYLP RRGVDSFGDKYQD/RNSDQYH DGCQDRFRDGSQDMGQCGGR D*DDD*GSRDYDRGYDSATGS CRRAFSGYLRDDY/WESSET EQQPPTGSEGVPPVQPS EERPAKKDENKVDGMN/APK VQSGNSGRGPGDGGNKDCW RESRDKDGKKDQVCRSAPES KKPEENPASKFSSASKCAA SVSDGEDEKEG

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10469	40837	A	10530	1	548	MQRSENDILGMDLRPLICIKDE KEEVGEKEEGEKEEEEECEEQEE EGGKEWEEPGNYHLGQSLSHD WQSSETEQPPPTGSEGKVPVPQ PSEERPAKDKENKVDGMN/APK VQSGNSGRGPGDGGNKDCWRE SDRKDGKKDQVCRSAPESSKKP EENPASKFSSASKCAA VSDGE DEKEGADYTK
10470	40838	C	10531	37	289	
10471	40839	A	10532	1	1062	
10472	40840	A	10533	1	1977	
10473	40841	A	10534	1	2050	LPLLHAGFNRRFMENSSIIACYN ELIQIEHGEVRSQFKLRACNSVF TALDHCHAEIETSDDHVIQYV NPAFERMMGYHKGELLGKELA DLPKSDKNRADLLDTINTCIKK GKEWQGVYYARRKSGDSIQQH VKITPVIGQGGKIRHFVSLKKLC CTTDNNKQIHKIHRDSDGNSQT EPHSFRYKNRRKESIDVKSISR GSDAPSLQNRYPSPMARIHSM IEAPITKVINIINAAQENSPVTVA EALDRVLEILRTTELYSPQLGTK DEDPHTSDLVGGLMTDGLRRL SGNEYVFTKNVHQSHSLAMP INHSMDEVPPCISQLLDNEESWD FNIFELEATHKRPLVYLGLKVF SRFGVCEFLNCSETTLRAWFQV IEANYHSSNAYHNSTHAADVL HATAFPLGKERVKGSILDQI.DE VAALIAATVHDVDHPGRTNSF UCNAGSELAVLYNDTAVLES HHTALAFQULTVKDTKCNIFKN ID/RGNHYRTLQAIIDMVLA MTKHFHVNKFNINSINKPMAA EIEGSDCECNPAKGNFENQILI KRMMIKCADVANPCRPLDLICIE WAGRISEYFAQTDEEKRQGLP VVMPVFDNRNCSIPKQISFIDY FITDMFDAWDAFAHLPALMQH LADNYKHWKTLDDLCKCKSLRL PSDRLPKPSHRGGLLTDKGHCS
10474	40842	A	10535	2	445	ERTFNCCYPGCHFTVHGMKD LDRHLRIHTGDKPHKCEFCDKC FSRKDNLTMHMRCHTSVKPHK CHLCDYAAVDSSSLKKHLRIHS DERPYKCQLCPYASRNSSQLTV HLRSHTGPGPADLLEHSRLHQ ADHPEKCCEPSYSCSSAA
10475	40843	A	10536	1	957	

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10476	40844	A	10537	1	1438	MSRRKQAKPQHLNSEEPRPARR ECAEVAPQVAGEPASELDDDDV PKANCLSTESTDTPKAPVITLPS EAREQMATLGERTFNCCYPGC HFKTVHGMDLDRHLRIHTVP FCFSKVYWNGFQLGMISPPKGT MSGDIFDCYNWRRKGSTGCIW TGGGGTPICPGYHLGQIFVAILT KKPLTLTPYVFEGDKPHKCEFC DKCFSRKDNLTMHMRCHTSV KPHKCHLCDYAAVDSSSLKKH LRIHSDEPHYKQ\VCPIASRNS SQLTVHLRSHTA\GDTPPQCWL CSAKFKISSDLKRHMIVHSGEK PFKCEFCDVRCMTKANLKSIIIR IKHTFKCLHCAFQGRDRADLLE HSRA/LHQADHT\EKCEPCSYSC SSAAALRVHSRVHCKDRPFKC DFCSFDTKRPSSLAKHVDKVHR DEAKTENRAPLQKEGLREGSSQ HVAKIVTQRAFRCECTCGASFVR DDSLRCHKKQHSDOSEKQNL
10477	40845	A	10538	1	1427	MIAFDSMSHIQVMLMQEESTAP ATLEHILGHSQLCGSDGLAHAA VWVLAHLHYWFTGLSPGPM VLPLHPAIISSFFHLWRVAFISKA GKPRAAGHLLKRFLRCQFQRA ASSLLFTTVEAMLGTESGTEKV MRGAGTWYHIIENWPSAECV WTEEYQQGRQEDSAEDRKLF VGMNLNQSEDDVRRLEAFG NIEECTILRGPDGNSKGAFAVK YSSHAEEQAALNALHGSQTM GASSSLVVKFADTDKERTMRR MQQMAGQMGMFNPMIPFGA YGAYAQALMQQQAALMASVA QGGYLNPMMAFAAAQMQOMA ALNMNGLAAAPMTPTSGGSTP PGITAPAVPSIPSGVNGFTGLP PQANGQPAEEI\FANGIHPYPA QSPTAADPLQQA YAGVQQYAG PAAYPAA YGQISQA FPQPPMIP QQQREGFVSFDNPASQA TAIQA MNGFQIGMKRLK VQLKRPKDA NRPY

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10478	40846	A	10539	1	547	AAAPMTPTSGGSTPPGITAPAV PSIPSPGVNGFTGLPPQANGQP AAEAVFANGIHPPYPAQSPTAAD PLQQAYAGVQQYAGPAAVPA AYGQISQAFPPPPMIPQQQRE GPEGICNLFIYHLPQEFGDSIEL MQMFLPFGFRE/RFDNPASAQT AIQAMNGFQIGMKRLKVQLKR PKDANRPY
10479	40847	A	10540	96	1080	WFKCYGCNSS/RDWQRSTYLLS WEVRG/RPVDPDSGCKAVVALC SQPAHPSNICKVGGCLTK\HLL LMGAMGIRVACLEVRDGEER GGEEATFTSLAERQVGTAAHRH LHQPALYIQRKVPAALHMCVV QKPSLFQADSRAPLEQGLRQQA SLATARPIVSGANAGPAGLKVP QAAQLQLSPYLHRGVGDEACR YGRSQPTRKAFALCICAAPALP CPALDGSWMVCGLGQETRTSL ANVQSFTQRPQQPLTVWMLN RGRKPAQGTLTVICPIGPHLLT STITESVCVPRRNKYHSRTLPA AQHCQWLVTAVPTALGLVIRA GSKKLC
10480	40848	A	10541	1	392	
10481	40849	A	10542	1	110	FFWSHS*VYYTCFLLNQ*KHLK PGPSGSLSPSISGN
10482	40850	A	10543	1	978	MAAATRGCRPWGSLGLGLV SAAAAWDLASLRCTLGAFCE CDFRPDLPGLECDLAQHLAQ HLAKALVVKALKAFVRDPAPT KPLVLSLHGWTGTGKSYVSSLL AHYLFQGGRLSPRVHHFSPVLH FPHPSHIERYN/DLKSWSVQGN LTACGRSLFL/DEMCK/MPPGL MEVLRPFLGSSWVYGTNYR KAIFISINTGGEQINQVALEAW RSRRDREEILLQLEPVISRAVL DKPAPLPSPNSGHHWKERLLD AVVPFLPLQRHHVRHCVLNEL AQLGPQAKGMRVVQAVLDSTT FFPEDEQLFSSNGCKTVASRIAF

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10483	40851	A	10544	1	560	ATSPHQSQSTVDVQQLHDPQP YPQHAIQVQHIVSEPTASAPSS AQGSSSTQGGQLQQQQQQQQ NSSVQHTYLPASAWNSFRGYSE IQMMTLPPGQFVITDSGVA TPV TTGQVKAVTSGHYVLSESSQSEL EEKQTSALSGGVQVEPPAHSDS LDPQTNKQQQTQYIITTTTNG NGSSEVHITKP
10484	40852	A	10545	3	205	
10485	40853	A	10546	2	348	ADQARGKPTWEAVSATQFOLD FPIT*CYGLL*QRVSRRHIGALQ GKPVPLLVHLLYPITPREGLG DRARLCLKQQQQQQQQQQQQ QLLLLLLLLLLLLLLQQCEGT EGRPPFD
10486	40854	A	10547	1	1146	MVTYKLVLRGCESTWNLENH FSSWQKRA/IRLWTVLDAIDQ MRLPVVRTWCLKEWHYGSLA GLNKAETSAKHGEAQSNISKGC RYADLTEDQLSSGESLKEIVPQI KEGKWVLTAAHGNSLRGIVKH LEGLSEEAIMELNLTGPPIVYE LDKNLKPIKPMQFLGDEVTLCK AMEAVAAQSKAKRRPAGML LSPGTPSLAIPSSAPAPCTCHTD HIWNSPVYSDAILRANPFCVHI SKANYLVNELHTAVNVAGLYI GWRCPHYLWDCFRIGDESRCF CGHLLREHRIISDJSVPCKVSQC RCFMFCFIPSRPEEVGCCCGCFE SNFLCAACDRRWEHETFFDTQ KTRQRGGRPRGADYVFAEMA VLREAILSNSDF
10487	40855	A	10548	2	516	GRLNERHYGGLTGLNIAETA KHGEAQVKIWRRSYDVPPPPKE PDHPFYRNIRMDRRYADLTED QLPSCESLKDITARALPFWNEEI GPQIKGKRVLIATHGNSLRGIV KPWEGLSEEAIMELNLTGPPIV YELDKNLKPIKPMQFLGIDEET VRKAMEAVAAQGKAKK
10488	40856	B	10549	123	237	

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10489	40857	A	10550	1	952	PAA PQVAGRLGLGCPLHLHVF AVVSAMLLRLCVPRVLGSSV AGLRAAAPSPFRQLLQAPRL CTRPFGLLSVRAGSERRPGLLRP RGPCACGCGCGSLHTDGDCAF VDFLSDEIKEERKIQKHKTLPK MSGGWLELNGTEAKLVLRKVA GEKIPVPFNNNSIPPFTYGEKD PSQSQKVVEDREPELTSLPKFVV EVIKNDGGRKALVLDCHYPED EVGQDEDAESDIFSTRREVVSFQS TGESEWKDTNYLTNLTSLDWA LYDHLMDFLADRGVDNTFADE LVELSTALEHQEYITFLEDLQEV LSRAHRADRC
10490	40858	A	10551	1	879	AAGCRKENSLDLRSQFPRGRDS EDFNVKEEANA AAEIRYTHIL NRVLPPDIRILA WAPVEPSFSAR FSCLERTYRYFFPRADLDIVTM DYAAQKYVGTDFRNLCKMD VANGVINFORTILSAQVQLVGQ SPGEGRWQEPQLCQFEVGTGQ AFLYHQVRCMMAILFLIGQGM EKPEIIDEVLLNIEKNPQKPQYSM ACFEPLVL\YACKFENVKWIYD QELRSSNITHLQQLWANHAVK THMLYSMLQGLDTPVPCGMG PKMDGMTWGNVVKPSVIKQTQ CLCRRSEDAHI
10491	40859	A	10552	231	358	
10492	40860	A	10553	2	319	
10493	40861	A	10554	573	1660	MAAPTARPVLTLLVALFGM GSWA AVNGI WVLPVVVKELP EGWSLPSYVSVLVALGNLGLL VVTLWRRLAPGKDEQVPIRVV QVLGMVGTALLASLWHHVAP VAGQLHSVAFLALAFVLALAC CASNVTFPLFSLHPPRFLRSFF LGQGLSALLPCVLALVQGVG RLECPAPINGTPGPPLDFLERF PASTFFWALTALLVASAAAFQG LLLLLPPPPSVPTGELGSLQVG APGAEEEEVEESSPLQEPQSAA GTTGPDPKAYQLLSARSACLL GLLAATNALTNGLVLPVQSFSC LPYGRALALPPGLWCWAVLPI WACFLGHGCCAGPWQGWGG LLSAGRVLWGLPDGRWQS

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10494	40862	A	10555	154	850	QFFRVITCLPFKGPDYRLYKSEP ELTTVAEVDENGEKSEPVSEI ETSVVKGSHFPVGVVPPRAKSP TPESSTIASYVTLRKTKKMMDL RTERPRSAVEQLCLAESTRPRM TVEEQMERIRRHQQACLREKK KGLKCFSVLSDQSPLOQSPNLR DNPFRITQTTRRDDKELDTAIR ENDVKPDHETPATEIVQLKETE PQNVDFSIRGLLDPCPSVILPGR SIKRAKNQNS
10495	40863	C	10556	39	436	
10496	40864	A	10557	2	959	
10497	40865	A	10558	34	1044	QGCAGAGPLHPARLPCCVHGC PVRMHALSCHVRCHFVTFR LMYLDWLPTVIEPCGVGSNKV PVVQHPHHVHPLTLITYSNEH FTPGNPPPHLPADVDPKT/GMC SCGTGRCAVARTCRIRSCVPCE ALSPCDARGAHSAGIPRPPHPPD ISPYYPPLSPGTQGPVYPITGG FRHPYPTALTNASMSRKHQD SKKEEEKKKPHIKKPLNAFMLY MKEMRAKVVAECTLKESAAIN QILGRRLGYNARAFGLKRGWR LDKYRGFVWMEMAVVWSLPPA FSFQGGKKKKRKRDKQPGETND KPESSLGASSLMVVGNWYTRN QEKHIPTLELDHTVSV
10498	40866	A	10559	2	398	
10499	40867	A	10560	174	362	
10500	40868	A	10561	14	266	
10501	40869	B	10562	67	474	

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10502	40870	A	10563	1938	3291	ERRKRFGMLDATDGGPTEDAA LRMEVDRSPGLPMSDLKTHNV HVEIEQRWHQVETTPLRREEKQV PIAPVHLSSDGGDRLSTHELTS LLEKELEQSQKEASDLLEQNRL LQDQLRVALGREQSAREGYVL QATCERGF AAMEETHQKKIED LQRQHORELEKLREEKDRLLAE ETAATISAIEMKNAHREMER ELEKSQRQISSVNSDVEALRG QYLEELQSVHRELEVLSQYQS AKCLENLAQALEAERQALR QCQRENQELNAHNQELNNRLA AEITRLRLTLTGDDGGGATGSP LAQGGDAH*LKGLMVRVKESEI QYLKQEISSLKDELQTALRDK KYASDKYKDIYELSIKAKA\A DCDISRLKEQLKAA TEALGEKS PDSATVSGYDI\MSKSNP\DFL KKDRSCVTRQLRNIRSKSLKEG LTVQERLKLFE SRDLKKD
10503	40871	B	10564	58	4405	
10504	40872	A	10565	3	156	NSSHHCHHHHHHHHHHHQH QHNCVHQHHHHYHHYDYHH DDNY YHHHHHHH
10505	40873	A	10566	10	445	HRSTITRQCPSGLETRIALLP VFPSPGSRTPPSTPGSSSPQPR/P PLTRGPGPPRTHALASGTRGPA RGEEKVADTPHHGEGGCPNSE KEPFLHPTAPPRLPTSPESGP VPHTLQAPPLRRHLGGTPAGA PASPQSSEWGG
10506	40874	A	10567	1	288	
10507	40875	A	10568	50	542	TLSPERLSPELRLPYMITLGDA VHNFADGLAVGAFA\SWKT GLATSLAVFCHPELPHGLR LAAPGAVPCAKELLLNLASALT AFAGLYVALAVGVSESEAW\A LAVATALLFLYVAICDMLPAML KVRDPRPWLLFLHNVGGLLG WTVPADAVPVRG
10508	40876	A	10569	1	690	
10509	40877	B	10570	34	465	
10510	40878	A	10571	1	624	
10511	40879	A	10572	3	933	

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10512	40880	A	10573	1	1481	RRFPAGAVAVIERGVRGGSQR CRTMADQLYLENIDEFVTDQN KIVTYKWLSTLGVHVNQAKQ MLYDYVERKRENSGAQLHVT YLVSGSLIQNGHSCHKVAVLRE DKLEAVKSKLAVTASIHVYSIQ KAMLKDSGPLFNTDYDILKSNL QNCSKFSAIQCAAAVPRAPAES SSSSKKFEQSHLHMSSETQANN ELTTNGHGPPASKQVSQPKGI MGMFASKAAAKTQETNKETKT EAEVNTASAGNKA PGKGN MMSNFFGKAAMNKKFVNLDS EQAVKEEKIVEQPTVSVTEPKL ATPAGLKKSSKKAEPVKVLQK EKKIRGKRVALSDDDETKETENM RKKRRTIKLPESDNSEYEVFPD SSGAYEAESPSPPPSPPLEPVP KTEPEPPSVKSSSGENKRRKR VLKSKTYLDGEGCIVTEK VYES ESCTDSEELNMKTSSVHRPPA MTVKKEPREERKGPKKGTAAAL GKANRQVSITGFFQRK
10513	40881	A	10574	1	100	

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10514	40882	A	10575	2	2271	PELLTEGVKEPIMDSQERDSGD PLVDESLKRQGFQENYDARLSR IDIANLTRREQVQDLFNKKYGEA LGKYPVQVPYKRIKSNPGSVII EGLPPGIPFRKPCTFGSQNLRIJL AVADKIKFTATNPFQGLIPKPD EDDANRLGEKVILREQIKELF NEKLR*GPWGLNRPVLVPYKL IRDSPDAVEVPGLPDDIPRNP TYDIHRLKILKAREHVRMAIIS QLQLLQQQQHHISEGRPFAEIC NDAKVPGESEARKPPFCVGT LFLKKREPEVSMNKDRYPQE APRNLQSLRTLLDILDDPRGGC VHLRQSQSRWRGADTRELPRG MLEGLRQLLSAIGCPRDPTCAP AQPGDQPLQRLAFTLANEPQTV LEKPPPRFRRRGAARSPEQLYTP RRGGVLPAPERTQSASADAGS LACRALVDSGCPTGPPCPKGS RRLTITSGVDCGLLKQMKLEQ EKVVLQGLEMMAGSRLQRLQ PVQDRQCRLLGQSRASADFPA GSPHPLGRLLPKVQEVARCVGE LLAAAGASRALPTSSSGPLCPA LTFTSFPGWQQQTILMLKEQNR RLTQEVTEKSGRVMQLEKQSA LIMKQLFEAQALSQQDGEASGL HLHLARLGWAEPQGSSTVQPF GGRPVSPNVSGWRPAAQAVP EWAPSCPTCHPGFPGPPAPGR TEPLTRFWLLVLTWAGALLSLH
10515	40883	A	10576	346	3136	ALRTRRLWPGGHCRAEAPQWP P/ASPLAPATAAAHSRHLSL SDKGSMSDCGPGTSGELGLR PKIEPEVLIIQVTPDALPTSE EMTDSMPGHLPSEDSGYGMET LTDKKWTDGAKAIGISEPIKV LYSKFLMHPEELFVGLPEGISL RRPNCFGIAKLWKILEASNSIQF VIKSGEEIRWDRELFRCRACSM GGSLQIAKSYTTGLESKSCDP AVESKASAGQDEMOPHARPKL LTEGVKEPIVD
10516	40884	A	10577	60	352	
10517	40885	B	10578	1	720	
10518	40886	B	10579	1	1478	
10519	40887	B	10580	1	1895	
10520	40888	A	10581	2	413	

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10521	40889	A	10582	2	969	WGSWAPQSRGCPYPQPGAAQGR ALAPQHRGSCSPPTWTTGGKE/Y LMRAHFGLPSVEAEDKEGKPP SVKFEIPYFTTSGIQVRLAPGSL YGRKRSSLGKSHPSLLQVDGQ YSQQQAGAGHPRTGKRGSQTPG ARQRVEPGKCWPVVCVPHVPC PPTSTALRKHLRPQRAIYTSRLA PGALGGHSCVLLPGLAGLAC GAFPGPAWVTRCCHSARSVL HQGAPPGPDITVPARLPEPEVE VSCRGRPALNAQQSPPLPPP PPSAAAEASCSSHHVQRRLRAG PEGQGFYLFHNRNKHSLKLA PREPFCVVTDSRIQFGPH
10522	40890	A	10583	50	1083	NPRAIFKSVRTCPVPTQPCRNV KARSCGVGATGTSFTLSVWPH RYITQEGHKLETGAPRAPGTVT NAVWCVRSEGIRKNEVFLDVI ESVNLVSAINGNVLRSEIVGSI KMRVFLSGMPELRLGLNDKVL FDNTGRGKSKSVLEEDVKFHQ CVRLSRFENDRTISFIPPDGFE LMSYRLNTHVKPLIWIESVIEK HSHSRIEYMIKAKSQFKRSTA NNVGDPHFPLPNDCLRNPSFKIT TVGERLSWVPENSEIVWSIKSFP GGKEYLMRAHFGLPSVEAEDK EGKPPDSVFKFEIPYFLTSGIQ VRYLKIIIEKSGYQALPWVRYIT QNGDYQLRTQ
10523	40891	C	10584	175	454	
10524	40892	A	10585	1	193	LLPRPGSGDLFLSPVLPS/HSAS WACPLPRSPMPSSCC*R*RKE MASGFSKGPTLGCCPTCP
10525	40893	A	10586	2780	2965	SPSQGESIPT*WRPTGPSPTSSP GPA*SSLSRPSRSSASASPMCMC VRPSMWAASLLKSL
10526	40894	A	10587	1	1502	
10527	40895	A	10588	1256	1990	RCAPMTTCAWASCCSPWPTPF GTGPSTSVSTSWPQFWGWWG WL*VGAAPAGGRQHPSPPALPR RSSGRSKLSRPSLCQLVPGIL*T RLLSPQKESLPWRGWSWREFPL PQLNLTATEADPGVSSLSAQ RHLHSYKIKVLSRQESLAPAPA SGYPESTALPQNGRGPWAVGF GQIPFLCIHNVGRSLGAGPGSG KPLPCVFRSTFSSSHQYCRLLGR KHNFHTFKGLRCCGCGPDGR

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10528	40896	A	10589	375	678	RCCCTTRPARKCRTTMGIRHS TWPAPTATRTTHSGSRSPGSTA ASPRGLCRPALTDPCPGHLSG LPVASV*AGSCPHVPGDQTTRK SGTVFPTQCTRP
10529	40897	B	10590	1	2452	
10530	40898	B	10591	1	1140	
10531	40899	A	10592	1	1617	
10532	40900	A	10593	1	1448	RERSCLHLVCIRCSDVVEMGS VLGLCSMASWIPCLCGSAPCLL CRCCPSGNNSTVTRLIYALFL VGVCVACVMLIPGMEEQLNKIP GFCENEKGVPCNILVGYKAV YRLCFLGLAMFYLLLSLLMIKVK SSSDPRAAVHNGFWFFKFAAAI AIIIGAFFIPEGFTTVWFYVGM AGAFCFILQLVLLIDFAHSWNE SWVEKMEEGNSRCWYAALLS ATALNYLLSLVAIVLFFVYYTH PASCSENKAFISVNMLLCVGAS VMSILPKIQESQPRSGLLQSSVIT VYTMYLTRS/CMTNEPETNCNP SLLSIIGYNTTSTVPKEGQS/VQ WWHAQGNIGLILFLLCVFYSSIR TSNNGQVNKLTLT/SGESTLIGR WVGAR/SDGITGRDGGTDVSPE AVRINGK/RDGCSLYSYSFFHF MLCLASLYIM/MTLSWYRYE PSAWMESQWTA VL/WVKISSS WIGIVLYVWTLVAPLVLTNRDF
10533	40901	A	10594	3	343	GVLLCRL*QGQNYW/NFLQTK VTGNMRDKRTTPMPEFLHASW PNTELRYWKENCPEQKGP*PM MALMS*GCPLPWPAPNVTSSSKG WSPGQLWMYRFGRPLRISSETG WSLWLT

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10534	40902	A	10595	1	2500	MEDAWGIRKETGRVKEEAKEV TGWGNNWRNVEKSSMSRKVK AARPGFKLPMSTDIIPKCTIKD LLPKEKSSTEAVFHTVVLERHE SPDIEDFSFKEPQKNVHDFECQ WRDDTGNYKGVLMQAQKEGKR DQDRRDDIENKLMNNQLGVSF HSHLPELQLFQEGEKMYECNQ VEKSTNNGSSVSLQYIPSSVQT HRSKKYHELNHFSLLTQRKA NSCGKPYKCNECGKAFTQNSN LTSHRRIHSGEKPYKCCECGKT FTVRSNLTIHQVIHTGEKPYKC HECGKVFRHNSYLATHRRHHTG EKPYKCNECGKAFRGHSNLT HQLIHTGEKPFKCNECGKLFTQ NSHLISHWRIHTGEKPYKCNEC GKAFSVRSSLAIHQTIHTGEKPY KCNECGKVFRYNSYLGRRHRV HTGEKPYKCNECGKAFSMHSN LATHQVIHTGTSPKFCNECSQ VFTQNSQLANHRRHHTGEKPYK CNECGKAFSVRSSLTTHQAIHS GEKPYKCIECGKSFTQKSHLRS HRGIHSGEKPYKCNECGKVFA QTSQALRHWRVHTGEKPYKCN DCGRAFSRSSLTFHQAIHTGE KPYKCECGKVFRHNSYLA TH RRIHTGEKPYKCNECGKAFSM HSNLTTHKVIHTGEKPYKCNQC GKVFIQNSHLANHQRTHTGEK PYRCNECGKAFSVRSSLTTHQA
10535	40903	A	10596	330	432	
10536	40904	A	10597	1	147	
10537	40905	A	10598	1	380	RTRGRGQRGMELVQVLKRGL QQITGHGGLRGVYLRVFFRTNDA KVGTLVGEDKYGNKYEDNK QFFWHRWLHSMDDPPTTKPL TARKFIWTNHKFNVTGTPQY VPYSTTRKKIQEWIPSTPYK
10538	40906	A	10599	9	536	VLKRGLQQITGHGGLFRGYLR VFFRTNDAKVGTLVGEDKYGN KYEDNKKQFFGDERLQASGLA LTLCEQTEEGSCLWSQSKLGK SQSMNFKNKSTRSFQRTVSAGK TKYYHPVAVGRQQQARA TCD HVDPRTEHGPAA WPHYWPRL GLKHALLTFTVALQYRAQPLFR LPNLPL
10539	40907	A	10600	239	263	
10540	40908	A	10601	1	600	

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10541	40909	A	10602	1	1178	
10542	40910	A	10603	1	1038	MHLEVNSSPEPLDENLDNTVTS ALSGHEQRIQTSPLVLLTTKTEI LARFSQLQFPEEQSSFAYPANC VKSKGMNTKLLPLRLKVCREL TIDSDRDILYRTLFMGDSGMGK VQFEFGEEVHIVIKSTGFGPFSS YATLEPFVAVQLWGGGQHYQ GQQPPMGMMGQVNGNHMM GQRQIPPPYRPPQGGPPQQYSGQ EDYYGDQYSHGGQGPPEGMN QQYYPDGHNDYGYQQPSDEPQ GYDRPYEDSSQHYYEGGNSQY GQQHDA YQGPPPPQQGYPPQQQ QYPGQQGYPKQQQGYGPGSQ GPGPQYPNYPQGGGQYGGYI PTQPGPPQPPQRPYQYDQGQY
10543	40911	A	10604	130	213	LKVST*AMPLPR*TPSRRCQP*R TGTS
10544	40912	A	10605	124	208	LKVST*AMPLPR*TPSRRCQP*R TGTS
10545	40913	B	10606	140	589	
10546	40914	A	10607	1	302	
10547	40915	A	10608	2	98	
10548	40916	A	10609	2	190	
10549	40917	B	10610	1	856	
10550	40918	A	10611	123	1287	AFSLGK\MSEKLLFGPNGERMP FSKVKALCAGLQATVAAPKNA EENKAIQDVAKDTAFLGITDEA TEGQFMYLTGGRLTYSNWKKD EPNDHSGSDECVILLNGLWN GISCTSSFIAIFQWAHYQYRQAE NYPKGELHTLRVKLCGPSWPT NAIHFRSRLLMPLGPTVLLMTM AVFQLSQAVAMCSWCCGLVLP PAGCLQDKASKPRETQAQPL CVRGNFRIPSRQDFAAALARAL SGLDLWASLVVPFADFLGSSLS VPWFYSLENDDEDLTRLRLN GERTFLES PGKKRIGAGTPPMS QEAVMLAVMERDPGQCRGEE GPTECRAMWPGWGRHSLPGH PAMLCFLGSDLEIRGSNGWE PPFIPGLQPELARGIQSGRGAE
10551	40919	A	10612	292	445	LSICLQSAVCTPGMD/PAAPCSL GILDWGTLPSTAEPGREGPADA WVDPGVR
10552	40920	A	10613	363	575	HLLPTQGCALCPAEGWPAPWQG YTPTCDCAEDTTQLERAGQLPP VF*SCHRRGGVSSQ*GSPGVPQL LHQPE

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10553	40921	A	10614	3	638	SSKLSGLTINNVVDIILAHHFGQE ELQANLDI.IQTYRMHIAQDINQ DNLQLFLNSYNRRDLIERPIL GQNDNKSSTLKGSTLLVVGDN SPA VEAVVECNRLNPINTTLAL KMA DCGGLPPG*FSPGKLT EAF KYFLQGMGYIPLVLCYSTSGS MTSVARSRI THSTSSSLGSGESP FSRSVTSNQSDGTQESICESPDV LDRQQTMEVSC
10554	40922	A	10615	3	1152	KSCFNAFFNFEDMQEITQHFAV CHVDAPGQEQEAP/SPFPTGYQ YPTMDELAEMLPVLTLSLKS IIGIGVGAGAYILSRFALNHPEL VERPLCSLMVDPC/ALKGWIDW AASKLSGLTTNVV\EIILAHHFG QEELQANLDLIQTYRMHIAQDI NQDNLQLFLNSYNRRDLIER PILGQNDNKSSTLKCSTLLVVG DN SPAVEAVMADCGGLPQVVQ PGKLT EAFKYFLQGMGYIPVCA AQSPHVRVSTASMTLRARSRT HSTSSSLGSGESPFSRSVTSNQ DGTQESCESPDVLD RHQTMEIS LDDVLLSALLRNGKSAQKKKI SAKPKLEFLCPRPGTCDHGSRE KQGHSRGPGQFPGRWPGRAVA ETRGAIDHRL
10555	40923	A	10616	169	270	GICPFLQLSFYHLLD* DTRYLQI LRLQLKPHSFH

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10556	40924	A	10617	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSLGADAI AKQRKTSVSAAASVSATIPIRR VQGPTVVGSWARGVSAASGP RGITGPKGKARSEKGC SLSHGPGQ TNKPLVVQKGQKMEQANHVP GLVISVVYKDILKKIVQRETSH LIHVRYAEAITGRRRTAPEDKGS LGRDMLAKAGAIHYMNMGNKL PIWCHLLEEGLVLEWALEGQF GRAKNACPQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILG VQKP NGQWSLVQDLRLISEAVIPLY VVPNPYTLTSLQIPEEA EWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPGQFR DSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLATSSAASCQQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYLGILARGTRTLGK ERIQPILAYPHKTLKQLWGFL QIT/GFCQLWIPR*SKI
10557	40925	A	10618	1	1022	MKPSVWALIQNLSPYEKGILG LTKRHQGRCLTDGROGIQPLPP SQAHTGIPLHPYSIQVDCAIDR GKLCFCCIGECNYSDDQGPQT VAGSWARGISAAVSVSATILISR VQGPLHVLGQEVFLLRRQTNL AGSERTENGAGQSPGGACYQC GLQGHFTKDCPMRNKLP RPSCP LYQGNHWKDGEPHEDCQIIIV QTSAAREDLLEVPLANPDNL Y TDGSSFVENG E VAKA VIAQFPT TVGVSCLDGRLRVLEVLARIR /LGEGNKGY SIRKRGSIQIVPCR *HDCISRKPHHLSPKSP*ADKQL QQSLRIQNQCAKITSILIHQ*QT
10558	40926	A	10619	1	2091	
10559	40927	B	10620	1	2269	
10560	40928	A	10621	1	1776	

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10561	40929	A	10622	112	1465	LLKGARCLIQRPFA/LQQETHR AHTLLLEWEPQAEATAFTTLKQA LLQAAALTLPTQRNFSLYVTDR AEIALGVLIQTGTTQPVAVLT IEKGKERGEQHHKQLAEAAER KERKRQEVREKEKEKTERQSK KEREEETKMESEKRETEKEVS TLAALEEFSPQPSGLAEAGA GSLFSWGGVEGEVRGGGRAAH SAHRLVQVPGQVRVQVFENP LLKAIKSDLPRSSLWSGRKTSV SAAALKEIRKEISKGTQIPLGYR LCPLQAVGGGEFGPTKIHVPFS LSDLKQIKADLKGKFSDDPDYR DVLQGLGKTFDLTWRDVMLLL DQTLAFNEKNAALAAASEFGGI WYLSQVNDRMTEERDQFPPTG QQAIPMDPHWDLDSHDGWS HKHLLTCVLEGLRGIRKKPMN YSMMSTIIQKKEENPSAFLQQL WKSRLRYTPPSSKSL
10562	40930	C	10623	52	690	
10563	40931	C	10624	199	285	
10564	40932	A	10625	59	411	SWPSDKQTLVVQRGQKMEQA NHPDPTDHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSSAEASCQ QATLALLNFLANQGYK/LSRSK AQLCLQQVKYLCL
10565	40933	A	10626	280	571	DIYVPIRII*KLPAAYAD/PAVPP CTSGRIWL*IHAGAWSSFWLVS Y*LLPQFQILLVYSEIQILPGLV LGECMCQGICPFLLDFLVYLRR GVCSIL
10566	40934	A	10627	60	148	WGRGEPLCLAQGL*THQSAPC QNRPLGSL
10567	40935	B	10628	1	397	
10568	40936	A	10629	55	219	LGKHHLLGSIDPRGSWVTGEYI FLRPPIAA*GRQ*DFLPPELWW TSLNNSWAFS
10569	40937	A	10630	3	494	
10570	40938	A	10631	2	689	
10571	40939	A	10632	157	277	DV*SNNSMTSLQVRCRTSMYLS GSSENFPRSTWICDAVAETPLA QEPATVPGP
10572	40940	A	10633	230	543	PSDRQTLVVQRGQKIEQANHL VGLVTSVVWKDCLKKIVHGMMA FSMLISC/PRQLSSRSITIQGILGR AVTRYFSHLLSCNWTLLQIDQ GHQATDGLTNGTPNELN
10573	40941	B	10634	1	669	

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10574	40942	A	10635	119	409	GDICHHLGLTPVGSHLLSCSR* QVA*VGAVTAATIGTGILLQQL AFLVCNWLLSGSSENFPRSAI CFKSEREKGTICIQVGNPPPTA CKGHN
10575	40943	A	10636	3	482	LSSYSGGDLEKLYV*LRDCKYT NQHSVSSSRFVNIPISTLCLTQG L*MHPMDTLYLATLGGDLENL CVHTLYLANLVGMWRTFVSSS GIVNAPISTLSKQTT*LSVKWTN QQDVGGARQENKSRLPEPAVT TPLGSPPTPWKLCSFALCNKSC YCPK KKK
10576	40944	A	10637	1	2331	
10577	40945	A	10638	879	1353	SNNRTEGARGKRQLMSSP/STE PRVRLTIEGQETDFLLDTGAAFS VLISCLGRLSSRSVTIR*ILGQPV TRYFS/QPLSCNWETLLFSHAFL IMPESSTPLLGRDILAKAGAIHYI NMGKNLPICCPLLVEGINPEV WALEGQFGRAKNARPLQIRLK
10578	40946	A	10639	345	1996	
10579	40947	B	10640	97	1110	
10580	40948	A	10641	728	5171	
10581	40949	C	10642	1	2049	

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10582	40950	A	10643	1	2019	MNAHPEFRMAMKDGEIVWD SVHPCYTVFHEQTETFSWLSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGFENMFV SANPWV SFTSFDLNVANMDNFFAPVFTM GKYVTQGDKVLMLAIQVHHA VCDGFHVGRMLNELQQYCDE WQGGAQYPLRPEAHKGIQDIV KYLKAQGLGRKCSPCNTPLG VQKLNGQWRLVQDLRLIN/EGF F*SSKLQAMQAMFAENSMSSV YSPTQEA EYWLPHGILQPADCF FEAASTRSMWPRE/DWLSTT/S LTTWNMDFADFGTTIKQDFRLL GQTSVDRLLQLSQQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGH LDHGSHSYRRSDNSLDPRSHSC CRSDIGLGRSHLYCRSDYQRE TTIPSPVKGNAQAPCMKSNN LIVLGTVTLDVIGLVMVPVLP GLLRDIVHSDIASHYGVLLAL YALMQFLCAPVLGALSDRFRGR RPVLLASLLGATIDYEIMATTPS WEDEEPIEHSQQIIVQTYATR DDLLEVPLANPDNLNLYADGSSF VENGIRRAGYAI VSDVTVLENS LAAVTLQNRQGLDLTLAEKGG LCTFSGKECCFYTNQSGISSPLE DITTAGPFLHPIQQEVARAIIQ FPTAFGVSCLEGRLRGEASWTS
10583	40951	A	10644	803	1171	
10584	40952	A	10645	1	2148	
10585	40953	A	10646	1094	3886	SNDRTEDDCGKHPFMSSPP*TEP WVCLIEGQEIDFLDITGTTFSV LIPCLGRSSRSVTIQGILGQPV RYFSLHSCNWETLLFSHAFV MPESPTLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSPCNTPLG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYLLSQVPEAEW FTVLDLKD
10586	40954	A	10647	762	1298	

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10587	40955	A	10648	893	2165	GPRGTGPKGKARSEKGRSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVYVYKDKLKVQRETS HPLIHVRYAEAITGRRRTAPEDK GSLGRDMLAKAGAIHMMNMG KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQROYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPI LGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAEWFP VLDLDAFFCIPLHYDSDHSQF LFAFEDPTDHTSQLIWTVLPGQ FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSSSEASQ QATDLLNLANQGYKASRSK AQLCLQQVKYLGILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIARPLYT
10588	40956	A	10649	2	403	
10589	40957	B	10650	51	1038	
10590	40958	A	10651	581	1128	SPCRAQRHSCMWGLWQQSPCS PGSWQDSSPAQSGPPR*PFSVP SSPWCLPSTWPLSPSPLPASWR RKTSAPSLLSLATAGPP*AGVC E/AKTPKKKYSDDDEEESEEN SRDSESDFSDDFSDFFVETR RRRNQKRQINYNKEDSESDGSQ KSLRRGKEIRRVHKKRLSSSESE GYFFIKS
10591	40959	B	10652	1	4296	
10592	40960	A	10653	2	447	KEKKRNKKKKTIGSPKRIQSL NNKLLNSPAKTLPG/AC/GSPQK LIDGFLKHEGPPAEKPLEELAS TSGVPGLSLQSDPAGCVRPPV VKYCTDLIEEKDLEKDLVIKY MKRLMQQSVEVWNMAFDFIL DNNQVVLQQTGYSTLKV
10593	40961	C	10654	286	336	
10594	40962	A	10655	421	638	

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10595	40963	A	10657	1	888	MMNEKNLEKGLGVDSVDKDA MNAAIQQAIIKAQPSMSPKKAPP APAKEARNVVAVGTGGRGTHD RDPSEKPPRLQWFEQQA KLA KQQEEDSEEEEDLDGDVLEIG KSKIKVLAESVSDWEDIDSDEE LECEDTEAMDDVVEQDAEEEE AEEGPPLGAIPITDCLFCSHHSS LMKNVAHMTKDHSSFFPDIEYL SDIKGLIKYLGTHSSSNVCKGL WDLEKRPSIDLK/CRT*YSTKRH /CTRTLSASSHFILCQWFSVLS/P VHASTDQEIQEMHDDQSNPQN AVVREHCVGWGWGV
10596	40964	A	10658	1	1545	MATYTCITCRVAFRADMQRA HYKTDWHRYNLRKQVSMAP VTAEGFQERVRA/HGPSRRRRA RARP/LYCTVCSKKFASFNA YE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDA MNAAIQQAIIKAQPSMSPK KAPPAPAKEARNVVAVGTGGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQQEEDSEEEEDLDGD VLEIGKSKIKVLAESVSDWEDI DSDEELECEDTEAMDDVVEQD AEEEEAEEGPPLGAIPITDCLFC SHHSSSLMKNVAHMTKDHSSFF PDIEYLS DIKGLIKYLGKVGVG KICLWCNEKGKSFYSTEAVQA HMNDKSHCKLFTDGDAALEFA DFYDFSWRLAVGGHDWVERLT ASHYFYGYYPGARVGHRS LMR YYKQRFGLSRAVAVAKNRKAV GRVLQQYRALGTGSGAAL MRERDMQYVQRMKSKWMLK TGMKN NATKQMHFRVQGSQK EIQIFHSSEIDGIATAVEDDFASP TPTKDAKN
10597	40965	A	10659	3	943	

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10598	40966	A	10660	1	2427	MATYTCITCRVAFRDADMQRA HYKTDWHRYNLRKRVASMAP VTAEGFQERVRA\HGFSRRRRA RARP/LYCTVCSKKFASFNAYE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDAMNAAIQQAIIKAQPSMSPK KAPPAPAKEARNVVAVGTGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQKEEDSEEEEEEDLDGD DWEDIDSDEELECEDTEAMDD VVEQDAEEEEAEGLPLGAIPIT DCLFCSHHSSLMKNVAHMTK DHSFFIPDIEYLSDIKGLIKYLGE KVGVGKICLWCNEKGKSFYST EAVQAHMNDKSHCKLFTDGD AALEFADFYDFSRLAVGGHD WVEVEGRIRGCGSREDNECLL VCNFSVIGVAIQTRKGRTPIRA EELPSEKNLEYDDETMELILPSG ARVGHRSMLMRYYKQRFGLSRA VAVAKNRKAVGRVLQYQYAL GWTGSTGAALMRERDMQYVQ RMKSKWMLKTGMKNNAATKQ MHFRVQMDCRGIAVLVFKAPS FYLIMAPKHKSGDAGDSNMPK GSRKVLPLSEKVKVLKEKKLY AEVAKIHGVKLQTFGVSVTAH KGSVDPKSEQQDILLQRVKEQ SFHSVEADPAEAGAGSGLSQLR KGI.PQCSSRLNGSSSATAKVGAG AEEAPRASEGCEGCQHA VTSQ
10599	40967	A	10661	3	658	GTKGWAFPIITDCLFCSHHSSSL MKNVAHMTKDHSFFIPDIEYLS DIKGLIKYLGKVGVGKICLWC NEKGKSFYSTEA VQAHMNDKS HCKLLIQDGAALAEFADFYDFR SSYPDHKEGEDPNKAEELPSEK NLEYDDETMELILPSGARVGH RSLMRYYKQAIWLKKNLWQLP KIRKAVGRVLQYQYRSPGIGLS TGAALMRERDMQYVQRMKSK MGC
10600	40968	A	10662	1	221	MNPLANSTLTDVHPHFIFKQMA ELDRDMDEAGNHHSQQITNTRT ENQTPHVLTHKWELNNENTRT QGREHHTSEEFIAIQPEYYQKE KNSNDINLEGTSYWTEHNCSGI YKVINCLESEIHSEEN*CN*IFL SDNIQVELR*IFLMCDVPCPVSV CSHCSTPTYE

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10601	40969	A	10663	1	1815	MHEAGNHHCQQSNTKRNQTP DVLTHK WEGFDQLRLEGLLCD VTLMPGDDDAFPVHRVMMMA SASDYFKAMFTGGMKEQDLM CIKLHGVSQVGLRKIIDFIYTAK LSLNMNDNLQDITLEAASFLLQILP VLDCKVFLISGVTLDNCEVEVG RIANTYNLTVEVDKYVNSFVLKN FPALLSTGEFLKLPFERLAFVLS SNSLKHCTELELFKATCRWLRL EEPRMDFAAKLMKNIRFPLMTP QELINYVQTVDFMRDNTCNV LLEASNYQMMPPYMQVMQS DRTAIRSDTHLVTLLGGVLRQQ LVVSKELRMYDEKAHEWKSALA PMDAPRYQHGIIVIGNFLYVV GGQSNYDTKGKTAVDTVFRFD PRYNKWMQVASLNEKRTFFHL SALKGYLYAVGGRNAAGELPT VECYNPRNTNEWTVYVAKMSEPH YGHAGTVYGGVMIYSGGITHD TFQKELMCFDPTDKWQKAP MTTVRGLHMCCTVGERLYVIG GNHFRGTSDDVLSCEYYSPH LDQWTPIAAMLRRQSDVGVA FENKIYVVGYSWNNRCMVEI VQKYDPDKDEWHKVFDEL GGIRACTLTVFPPEETTPSPRES
10602	40970	A	10664	1	1226	MNEIEFLERTPVDESDDIEQH DEIPTGKCIAPFDKRLKHFRVT EGSPVTFCTKIVGIPVKVYWF KDGKQISKREHCKMRREGDG TCSLHISTTSDDDGNYTIMAA NPQGRISCSGHLMVQSLPIRSRL TSAGQSHRGRSRVQERDKPLQ ERFFRPHFLQAPGDMVAHEGR LCRLDCKVSLPPPDMTWLLN GQPVLDPASHKMLVRETGVHS LLIDPLTQRDAGTYKCIATNKT GQNSFSLELSVVAKEVKKAPVI LEKLQNCQVPEGHPVRLCRVI GMPPPVFYWKDNETIPTCTRER ISMHQDITGTYACLLIQPAKSD AGWYTL SAKNEAGIVSCTARL DIYAQWHHQIPPPMSVRPSGSR YGSLSKGLDIFSAFSSMESTM VYSCSSRSVVESEDEL
10603	40971	C	10665	166	229	
10604	40972	B	10666	251	371	

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10605	40973	A	10667	79	1391	PWEGSAPATSPLEGDSAWGSA DGSESWSCRELLQPGDVLGESC GLTPPALPAHCIEGCLPPLTQE LRCCQPPRMGRWALDVAFWL KAELTLGLELLYYCFFIGINFY NKWLTKSF/HIFPLFMTMLHLA VIFLFSALSRAVQCSSHRAV VLSWADYLRRVAPTAALREVA SLFRKPSAEMLCPPARQGEA RELSQNPRIIRAGEGRLQGHRRV ATVICAPAPFSVMGLSPELQQCI VGNFASRYTMTKSSAVLFIIFS LIFKLEELRAALVLVVLLIAGGL FMFTYKSTQFNVEGFA/WCWG PRSSVAFAGPSPRCSCRRLNSAS RIPSTPCSTCSHSCS/WGLFPLFA VFEGVTGLLLRVLGSLFLGGILA FGLGFSEFL/VSSRTSSLTSLIA GIFKEVCTLLAAHLLGDQISLL NWLGFASASREYPTSLPS
10606	40974	A	10668	1	1129	MGRWALDVAFWLKAVLTLGL VLLYYCFSIGITFYNKWLTKSF HFPLFMTMLHLAVIFLFSALSRA ALVQCSSHRAVVLVSWADYLR RVAPTALATALDVGLSNWSFL YVTVSLYTMTKSSAVLFIIFS FKLEELRAALVLVVLLIAGGLF MFTYKSTQFNVEGFA/WCWGP RSSVAFAGPSPRCSCRRLNSASR IPSTPCSTCSHSCS/WGLFPLFAV FEGHLSTSEKIFRFQDTGLLR RVLG/SLFLGGILAFGLGFSEFL VSRTSSLTSLIAGIFKEVCTLL AAHLLGDQISLLNWLGFASAS REYPTSLPSKPCIPEVTQSPFQK PLVSVLLPVTLSDSDAGSVPGG SAAVPTPLGRCCGHLQSGWVGP
10607	40975	A	10669	566	1026	PVMPKLIYVIRTGKQLKISLGH VDFQTVPSFLQQLNV/WQTAKA SEHPDRNDCAVLRQKRLSGS VENTSGKRKCWGGQSGFTTSE LEETEEDSLSDYGDVDRK DALAEPFCMLIGEIFELRGKPY QLEIHWQVPTGPDHLEEEANEK

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10608	40976	A	10670	1717	2340	GIDVQGGKNSFSLSSFLERLPRD FFSHQEETEEDSDLSYGGDDV DGRKDALAEPFCFMLEIFEFLR GMFKWVRRTLIALVQVTFGRIT NKQIRDTVSWIFSEQMLVYYINI FRDAFWPNGKLAPPTIRSKQE SQETKQRAQQKLEENIPDMLQS LVGQQNARHGII/NKYSNALQE TRANKHLLYALMELLLEI/CPE LRVHLDQL
10609	40977	A	10671	181	399	NRVIVPISQIMKRKRKVSIVLN VTGY*/RGM/RKPGLLNLASGFL LSTSPTSSENSRCRLGWQIDPW EEGETYV
10610	40978	A	10672	66	535	CWWQDPLQRTQKSVTATSTK IDISNVKIPKHPADAYFKKQQL WKPRNRKLAGKLSIPAARDAP RARPPHEAPPPPPPELRYRVP RPAPSSWRHPSGKGRRGPPGIG GRIVGERQLRTEYGNDRPREG DPAPGCCGGARTLSLYGEIKLR VKF
10611	40979	A	10673	67	585	SAAKSEMAGEKVEKPDTEKKK PEAKKVDAGGKVKGNLAKK KPKKGKPHCSRNPVLVRGIGRY SRAMYSRKAMYKIRKYSAAK SKVEKKKKEKVLATVTKPVGG DKVGGTRGVKLRK/MPRIYPT EDVPRKLLSHGKPFQHVRLK RASITPGTILILTGRHRGKRVVF
10612	40980	A	10674	2	282	CIALYCHLLNICSVKVKAEMQNL GREFIVPGMDSATSLIWATK/DL MNAVIEAPEKKPLLKREKQDES QSEIKWASQKKHLNPVQALSEF KAMDSI
10613	40981	A	10675	2	2798	
10614	40982	A	10676	14	2858	PDWRETKRPSASGLWNLALA QLAAEMTAVHAGNINFKWDPK SLEIRTLAVERLLEPLVTQVTTL VNTNSKGPSNKKRGRSKAHV LAASVEQATENFLEKGDKIAKE SQFL*E*LLAAVEYVRKQGD MKTAAGEFADDPCCSSVEQGNM VQAA*TLASVTCLLILA/DMG NVYTLILQLKVVEDDILKLRNA GNEQDLGI*YKALKPEVNK/VNI MAVKRQQLKDVGHRRDQMAA ARGILQKNVLIIFYTASRA
10615	40983	A	10677	1	4545	

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10616	40984	A	10678	1	1921	MAGLGMGEEGIPGGERWEHKK RAHIVSNHRITRTGTHPYTHSPY PHKDNVHTARREHKTQDLGTI RSVGHSSSEHTQHTTPTDTPVPLV VIVCRVCYRPPHGETRAEYTRH RGQNNRRTKFWVGIKEENLAQ QERTEEQLANIARGGYVLKDC AGQPELIFIATGSEVELAVALAAYE KLTAEGVKARVVSMPSTDAFD KQDAAYRESVLPKAVTARVAV EAGIADYWKYVGLNGAIVGM TTFGESAPAELEEFEGFTVDNP LASRAVRLRLPFNNDQVEAAV GWKLAVRHNGPTALILSRQN LAQVERTPDQVKEIARGGYVL KDSGGKPDII.IATGSEMEITLQ AAEKLAGEGRNVRVSLPSTDI FDAQDEEYRESVLPNSVAARV AVEAGIADYWKYVGLKGAIV GMTGYGESAPADKLPFFGFSTA ENIVAKAHKVLGVKAGSHIPRK KYDVPGKKSFPVKYSTIGSPSP ERPVSITITPNSFVIITANRVLHC NADTPEEMHHWITLLQRSKGD TRVEGQEFIVVEKLIRGLAMED SRNMFAL/S*IQRPQRQSH*KSN RRS*CLSQV*KRASW*AFTNI* WPDRLHGLRKYSF/WSPGNIHHL RHCRML*VVRLRLRLNAVYE
10617	40985	A	10679	1	2940	
10618	40986	A	10680	2	404	
10619	40987	A	10681	2	546	WCPHRWRPHTLTPTAAPAVTK SPEATLHYGQVSWNSQNLHLE GQLQASASLQGSFMLK**GDPLD F/VMSPPRPLFERLKARISQSTK TFTPCERLEKRRSTFLEGLTLLRS FRTGSVVQRQVEEEQMLDMWI KEEVSSARASIIDKWRKFGGMN QEAMAKYMALIKEWPGYGST LFDVEGTDIT
10620	40988	A	10682	1	555	
10621	40989	A	10683	1	627	

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10622	40990	A	10684	1	7232	MPEPPTHSMGSCAAGASLTSTA PCSTAPSPIDHLRAKECERTAQ DWQAAPPAALVRDPLAALVRT WRTFMSSSRIVNTPIGTLCLAQ GFQWFSVLSQVHASTDQEIQE MHDEQANPQNAVGTLDVGLID SVCASDSPDRPNSFVIITANRVL HCNADTPEEMHHWITLLQRSK GDRTRVEGQEFIVRGWLHKEVK NSPKMSSLKLLKKRWFVLTHIPG LLQEFREDALNWGPDEKIFKET ELVNDMDKINGRIERAE
10623	40991	A	10685	1	2146	IDSVCASDSPDRPNSFVIITANR VLHCNADTPEEMHHWITLLQR SKGDRTRVEGQEFIVRGWLHKE VKNSPKMSSLKLLKKRWFVLTH NSLDYYKSSEKNALKGLTVL NSLCSVVPDEKIFKETGYWNV TVYGRKHCRYLYTKLLNEATR WSSAIQNVTDTKAPIDTPTQQLI QDIKENCLNSDVVEQIYKRNPI RYTHHPLHSPLPLPYGDINLN LLKDKGYTTLDQEAIKFNSLQ QLESMSDPIIIGILQTGHDLRP LRDELYCQILKQTNKVPHPGSV GNLYSWQILTCLSCFTLPSRGIL KYLKFLKKRIREQFPGTEMEKY ALFTYESLKKTKCREFVLSRDEI EALIHQRQDMTSTVYCHGGGSC KITINSHTTAGAVEVEKLIRGLA MEDSRNMFALFEYNGHVDKAI ESRTVADVLAKEFLAATSEV GDLPWKFYFKLYCFLDNDVP KDSVEFAFMFEQAHEAVIHGH HPAPEENLQVLAHAHATSSIMQG DYTLHA/AIPLAEEVYSLQRLK ARISQSTKTFTPCERLEKRTSF LEGTLRRSFRTGSVVRQKVVEE QMLDMWIKEEVSSARASIIDK WRKFQGMNQEQAMAKYMALI KEWPGYGSTLFDVEVRTGCHV LGWAGCWHLRTWITAKFMWR EDKMEHFALSTSFRAPKIVPLT PPFSSQFLFSCVNVNASVILGMN

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10624	40992	A	10686	28	561	MDIVQDATFVYATLQTAHYHR DAGLPVYLYEFEHHARGIIVKP RTDGDADHGDEMYFLFGGPFAT GAKVPPDPTTGCPVSHLWMQT HPSIGWPQGAHQFLICYALPNE SLLLRRKQKQKE*GGRNPNDG NLPWPRYNKDEKYLQDFTT RVGMKLEKKMAFWMSLYQS QRPEKQRQF
10625	40993	A	10687	148	444	
10626	40994	A	10688	1	1531	PLPGARRCLHEFWGQLASMYV STRERYKWLRFNEDCLYLNYY APARAPGDPQLPVMVWFPGGA FIVGAASSYEGSDLAAREKEGL VFLQHRLGIFSFLSTDDSHARG NWGLLDQMAALRWVQENIAA FRGRPREILTLFGQSAGAMSISG LMMSPLASGLFHRAISQSGTAL FRLFITRNPCLKVAKKVAHLGAC NHNSTQILVNCLRALIRAKVM RVSNKMRFLQLNFQRDPEEIIW SMSPVVDGVVIPDDPLVLLTQG KVSSVPYLLGVNNLEFNWLLP YIMKFPLNRQAMRKETITKML WSTRTLAKNSWGAEHGSKSL VGPPLAQLAPRPQNITKEQVPL VVEEYLDNVNEHDWKMLRNR MMDIVQDATFVYATLQTAHYH RDAGLPVYLYEFEHHARGIIVK PRTDGDADHGDEMYFLFGGPFA TGLSMGKEKALSQMMKYWA NFARTGNPNDGNLPCWPRYNK DEKYLQDFTTRVGMKLEKK MAFWMSLYQSQRPEKQRQF

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10627	40995	A	10689	138	1898	ICKYIMNDQWARQNCLHSPTY GPSENVLSSAESKPEIQLSPSCPL IFSSQQALSQHVWLSHLSQLFSS LWAGNPLHLGKHYPEDQKQQ QDPFCFSGKAEWIQEGEDSRLL FGRVSKNGTSKALSSPPEEQP AQSKEDNTVVDIGSSPERRADL EETDKVLHGLEVSGFGEIKYEE FGPGFIKESNLSLQKTQTGETP YMYTEWGDSEGSMSVLKNPR THSGGKPYVCRECGRGFTWKS NLITHQRTSHGKPPYCKDCGR GFTWKSNIETHQRTSHGLKPY VCKECCGQSFSLKSNLITHQRAH TGEKPYVCRECGRGFRQHSHL VRHKRTHSGKPPYICRECEQGF SQKSHLIRHLRTHTEGKPPVCT ECGRHFSWKSNLKTHQRTSHG VKPYVCLCECGQCFSLKSNLNK HQRSHTGEKPPVCTECGRGFT RKSTLITHQRTSHGKPPVCAE CGRGFNDKSTLISHQRTSHGK PFMCRECGRRFRQKPNLFRHKR AHSGAFVCRECGQGFCAKLT KHQRAHAGGKPHVCRECGQGF SRQSHLIRHQRTHSGKPPYICRK CGRGFSRKSNIHQRTHSG
10628	40996	C	10690	160	294	
10629	40997	A	10691	3	82	SWACAIHPTGYLIEQAGG*WVT ARRD

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10630	40998	A	10692	1	1399	MLRRYRPDITSCHGSTAESKGG VVL DVSGRARPLRRTRNSPST SLTSSKMSGLDGGNKLPLAQTG GLAAPDHASGDPDRDQCQGLR EETEATQVMANTGGGSLETVA EGGASQDPVDCGPALRVPVAG SRGGAATKAGQEDAPPSTKGL EAASAAEAADSSQKNGCQLGE PRGPAGQKALEACGAGGLGSQ MIPGKKAKEVTTKKRAISAAVE KEGEAGAAEKKV VQKEK VAGGVKEETRPAPKINNCMD SLEAIDQELSNVNAQADRAFLQ LERKFGMRRLHMQRISFIQNI PGFWVTAFRNHPQLSPMISQGD EDMLRYMINLEVEELKHPRAG CKFKFIFQGNPYFRNEGLVKEY ERRSSGRVVPFSTPTLRWHRGQ DPQAHHRNREGNTIPSFNWF DHSLEFDRIAEIKGELWPNPL QYYLMGEGPRRGIRGPPRPVE SARSFRFQSG
10631	40999	A	10693	3	441	
10632	41000	A	10694	190	2716	
10633	41001	A	10695	1	793	MARQKKMGQSVLRVFFLVLG LLGHSHGGFPNTISIGKRKRASR RSRLSLTRDHCPGKAFAVAFRA ERSTGGEQEAAGMLQGGEESRLF GSLWTLWPWRACSSWKLQSGD ADCLAAPGRITRARGAQSVVSG CRETGWGLFMRNTVQEHSFR FAVQLYNTNQNTTEKPFHLNY HETSPIPLKSPVVFCCALVVHS TLHRPCLCSVSSLAHRSHIPSPH CHCKNCCCTPLQPTNVLDVYA LFARSREKANVTLLKLPLEVIPF
10634	41002	A	10696	2	2744	
10635	41003	A	10697	2	2740	
10636	41004	B	10698	47	7237	

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10637	41005	A	10699	426	2118	GFGHTVHAAEGGDFGGSWQGD DSVLLCSTVDPGSWAASRGKG SPCRGPLCGCCPGRSS/QPSKVE VAVSCSCGALLGMCMPVVL LEGCPRGVAAGKKGSPQAQTV RRSPSADQSLEDSPSKVPKWS FGDRSRARQAFRIKGAASRQNS EEASLPGEDIVDDKSCPCFEVTE DLTPGLKVSIRAVCMRFLVSK RKFKESLRPYDVMVIEQYSAG HLDMLSRJKSLQSRQEPRLPVQ QGTRTGIDMIVGPPPTSPRHKK YPTKGPTAPPRESQYSPRVQDI VGRGPAITDKDRTKGPAEALP EDPSMMGRLGKVEKQVLSMEK KLDFLVNIYMQRMGIPPTETEA YFGAKEPEPAPPYHSPEDSREH VDRHGCIVKIVRSSSTGQKNFS APPAAPPVQCPPTSWQPQSH RQGHGTSVPVGDHGLVRIPPPP AHERSL SAYGGGNRASMEFLR QEDTPGCRPEGTLRDSDTSISI P SVDHEELERSFSGFSISQSKENL DALNSCYAAVAPCAKVRPYIA EGESDITDSDLCTPCGPPPSAT GEGPFGDVGWAGPRK
10638	41006	A	10700	1	774	
10639	41007	A	10701	124	815	HPGTAMDALNSMQNFLRGRPK TFKSLNAIEWSVKSGQIRNLES ARVSMVGQVKQCEGITSPEGSK SIVEGIIIEEEDEEGSESISKRK KEDDMETKKDHPYTWRJELAK TEKYWDGWFRGLSNFLSCPIP KLLLLAGVDRDLKDLTIGQM Q GKFQMQLPQCGHAVHE/DAP DKVAEAVATFLIRHFAEPIGG FQCVFPGLLVTCCPPLLQHRAL LVNTFAPEAHC
10640	41008	A	10702	69	370	
10641	41009	A	10703	1	224	MCNTPAYCDLGKAAKDVFNK GYGFGMVKIDLKTCSGVEFS TSGHAYTDTGKASGNLETKYK VCNYGLTFTQK*NTPAYCDLG KAAKDVFNKGYGFGMVKIDLK TKSCSGVEFSTSGHAYTDTGKA SGNLETKYKVCNYGLTFTQK
10642	41010	A	10704	2	171	

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10643	41011	A	10705	1	740	MCNTPTYCDLGKAAEDVFNKG YGFGMGKIDLKTSCSAVEFST SGHAYTDTGKASGNLEPECKV CNYGLTFTQKRNTDNTLGTEIS LENKLA KGLKLSLDITLVPNTG KKSSELKASYKWDFSVGSNV DLDFSGPTIYGWAVLVFEGWL AGYQMSFDTAKSKLSQNNFAL GYEAAADFQLHHTVTDTGTEFGG SIYQKVNGIEMSLNLA WTA/GSN NTHFGIATKYKLD CRTSLSAKA VVLGTRV GSC
10644	41012	B	10706	1	318	
10645	41013	A	10707	2	100	
10646	41014	A	10708	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSPV VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSSSTEYVTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAI PVGYFYPGFSFTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHSSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLI VPTPAELFDYTSALQ FFDMLRDL LKNVDLKGFE PDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMLV LKNVRETDEVG KARLTWIGTINVCAADVLI V PTPAELFDYTSALQFFDMLRDL LKNVDLKGFE PDVRILLTKYSN SNGSQSPWMEEQIRDAWGSMLV LKNVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSSSTEYVTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
10647	41015	A	10709	284	969	RVSGRKWF FIALKRMPAMKK AMNLFGLSNVRTVHPGFTV YISTHISFSLSGYRTGLRSFGLV KQKKSPIRMPCVYTNP CVSIHP LWLRLRSPSARWLCGSPSLG WTRTEPAPSPRGRTEKARIW EVTDRTVRTWIGEAV/AHAA DGVTFSPVTPHTFRHSYAMH MLYAGIPLKVLQSLMGHKSSIS TEVYTKVFALDVAARHRVQFA MPESDAVAMLKQLS

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10648	41016	A	10710	2817	3297	AGCVRHRLSENRLDHRALPAA SKLPAYA*LPPPLPAGRL*RIPH RQFL*HQI/RL/PTERRCLLTRRT EKARIWEVTDRTVRTWIGAV ARLAADGVTFSPVPTPHTRHS YAMHMLYAGIPLKVLQSLMGH KSISSTEYTKVFALDVAARHR VQIFAMPES
10649	41017	B	10711	1	963	
10650	41018	A	10712	1	1296	
10651	41019	A	10713	1	1167	
10652	41020	A	10714	349	3195	
10653	41021	A	10715	163	864	
10654	41022	A	10716	576	754	
10655	41023	A	10717	1	1449	
10656	41024	A	10718	1422	1600	
10657	41025	A	10719	489	726	ISCCSFFSPRPPHTRFHSYAMH MLYAGIPLKVLQSLMGHKSIS TEYTKVFALDVAARHRVQFA MPESDAVAMLKQLS
10658	41026	A	10720	1	1596	
10659	41027	A	10721	1	1572	
10660	41028	A	10722	2	100	
10661	41029	A	10723	561	804	TLRQTKPDNSADPPHTFRHSY AMHMLYAGIPLKVLQSLMGHK SISSTEYTKVFALDVAARHRV QFAMPESDAVAMLKQLS
10662	41030	A	10724	1	867	
10663	41031	B	10725	1	825	
10664	41032	A	10726	1	942	
10665	41033	A	10727	2	100	
10666	41034	A	10728	39	359	RILGKGAGQTRAESLVWGRGV PARCC*PGGPFLVPGPPP*VR/H LSYARPMML*PGIPLKVLQSLMG HKSISSPEVYRKVFALNVAARH RVQFAMPEFDAVAMLKQLS
10667	41035	B	10729	41	724	
10668	41036	A	10730	1	1023	
10669	41037	A	10731	1	1314	
10670	41038	A	10732	1	1128	
10671	41039	A	10733	892	1611	
10672	41040	B	10734	78	1099	
10673	41041	A	10735	1	936	
10674	41042	A	10736	766	1056	
10675	41043	A	10737	1	1422	
10676	41044	A	10738	1214	1721	

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10677	41045	A	10739	2592	3233	RWGRWRTGGSSRSEPTMELRA PAWPRGRPGQGARGPAGSEL GNATAPSPAELCRNLCRMEE PNTDGRPETGSGNKRKGADK WWKIKTGMRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKVISSTDFYTKVFALDVA ARHRVQFAMPESDAVAMLKQL
10678	41046	A	10740	6323	7130	
10679	41047	A	10741	319	522	RNTRYWVINSISVIPSSALISK SPRLMAKKTAFHFLGISRTSVAE FTFTRSGISRDHCYKAGAADR RPNAPPRAEFQSGWFLIMECFA R*VGDPQL/TA/HFDAV/RRE/IM PL/PREG/KTL/QTEVREMPKRC AVFLAINLGDRFDIKADEGGIT DIEFITQYLVLRVAHEKPKLTR WSDNVRILELLAQNDIMEEQEA MALTRAYTTLRDELHHLALQE LPGHVSDECFATERELVRASW QKWLVEE
10680	41048	A	10742	2	640	
10681	41049	C	10743	1	2358	
10682	41050	A	10744	1264	1894	RGDKPQHIVTVHRADVVKAAQL FKQARARHYHAFNMFFGAFEL FNWRHARENFPPAGKQLCQMV VERADIFGNRHIFVVENHQHIR TDIARVIHRFKRHACGNRAIAN DTDGAAIAFAFTAILYGIQFSCAS FYL FVVYEHGSLKT VGCPLQEV /WRTALESCKPAHIQLSGVLAIS SIVMQSVNAMPSSWSGYSSSQA ASAARWLLARSLGIC

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10683	41051	A	10745	872	3111	VLKPNHLTERKGC/GFACGRYG KLGAWELDYSPDLDIHFLNDCP MNA MTAGERKIDGRQFYRLRA QRIMHLFSTRTSSGILYEVDARL RPSGAAGMLVTSAEAFADYQK NEAWTWEHQALVRARVVYGD PQLTAHFDAVRREIMTLPREGK TLQTEVREMREKMRHLGNKH RDRFDIKADEGGITNIEFITQYL VLYAHEKPKLTGWSDNVRIL ELLAQNDIMEEQEAMALTRAY TTLREPRFSRFLFWGCSPLGLF DYLDLDFKIDNSHGGFRKTVLL TFLPPALLYLFPNGFIYGIGGA GLCATIWA VIIPAVLAIAKARKKF PNQMFTVWGGNLIPAIVILFVLP WFYFIPPGICTSLVYRASPPIS MPAKAVAYCVLRISGGDGSCD VICRGKVADRSKFVNPWNSKT HTEPTQSQATSNRTSATTAE QRSDEKEGNNRTRHEEQRSQN ATQHKRRERATTTQKTCSETVT PTTMNMCNEPLRRHARVLPP VLYVQRRYDESHLRISISACNV CRTERHAVHTDEIHTSTVADDC KERVAVMRLRLPLCAACRHIG DVIVYSAVYCEHRCMRLLATR RHYVVTLTTHLRRRLFLTEVNA RYVCIYDDEHSRSTVTHAHP DHQSAHYDTYVYDGTVS YMR LNTSVRLIRRAHTCTSRALMD SHSKDGRPMDYASAVVVTHTPL
10684	41052	A	10746	1577	1668	TINPPELAFVKTVH*SPRICLGF HIFLLN
10685	41053	A	10747	486	674	HWWKNWRCWIPVIWH*RRSR TIWRCKCKWITASTLLSRSSPSK LPCCMSGQPVVAGRKR
10686	41054	A	10748	254	396	ADDQIPHSKTHLKLSEVEENQ Q*EI*RPLLQ*GGMVPRCVHG RSG
10687	41055	A	10749	3	674	ISAEINRPF AIRGDLG/VVWERQ KQETGWRSWVP/WPHVHAEDII LGNPPDI/PEVTMVHLPRVEATL /APLALLTKTVWLPWIKLES PRI RFQFSHHVRRAVLCEDAYYKL TLAQVEKLKNGGKVIASDELML TKFRIPNTLEFCAPVMADAPAI ALLRLSLACDLAQAMMPAFH KPISSSFVNDYAGTSFACAASD MDERRMLNAPLSRLTLVEKL RRCWIPVIRH

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10688	41056	A	10750	1	1755	
10689	41057	A	10751	1	1662	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTVRTWV ALYEKHGEKGLPKPGVSADP ELRIKVVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNAISVDPE KAASALELSKDRRIEDLERQAL SKPDKYADVKKRISEIYHENRG RYGYRRVTLSLHREGQINHK AVQRLMGTLSLKAAIKVKRYR SYRGEISSTKLFLTAFRMIVVA IILIAITFDWNRKPTINQKVS AELNRPF AIRDGLGVVWERQKQE TGWRSVWPWPHVHAEDILGN PPDIPEVTMVHLPRVEATLAPL ALLTKTVWLPWIKLEKPDARLI RLSEKNNNWTFLANDD/NKD ANANRRHGRFGWIIFFSIKGG SPLMTNDIHGSLVYTTGKPRPKL EGDVESRQLRLADLGPLIGVDS GKGAEKSKRSEQKKGEKSVQP AGKVL PYDRFETDKWDVMDA DVRFKGRRIEHGSSLPISDLSTH IILKNADLRLQPLKFGMAGGSIA ANIHLEGDKKPMQGRADIQAR RLKLKELMPDVN
10690	41058	A	10752	1	477	SELGHAGLNGDILVWNPVLED AFELSSMGIRVDAADTLKHQLA VGDEDRLELEWHQALLRGEMP QTIGGGIGQSRLTMLLQLAHI GQVQCGVWAAAVRESVPSLPL QLFHFTRHVVRQPLSKIRNHQ RIGIKFPALQAFHNGAKTTGKI GADTKLLA
10691	41059	A	10753	414	794	RPSPLPTGLGDTGLGLPRFIEM EKLPLFDVAEAEQELQEGPLPEY SGPGLALAKWGLG/LKQVVM ASLFVALFLPFGRAQELSLACL LTSLVVTLKKNNSMTAGILVC LVTVVSPLIKVLIYDQ
10692	41060	A	10754	88	227	
10693	41061	A	10755	26	261	
10694	41062	A	10756	164	361	
10695	41063	A	10757	1347	1656	RVGRPGHRASASGGNPQNHR RLGEPVSARHPAYLSTGSGDAA AARYRRSA*SLRR*SRASSHPPE RAGTPVAPGTIDIFRWRTAARQ HRPRLYRRLPHSAA

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10696	41064	A	10758	2096	2248	RLIGLHGQNSRSVPQLPMESAS VA*RCTAALDGGVSSTSTRWLF ASCTRL
10697	41065	A	10759	1	2240	
10698	41066	A	10760	1	1082	MEHERYVGISNLMKPELYLA VGISGQIQHMYGANASQTIFA! NKDKNAPIFYADYGIVGDAG ALMSEIDFDAIIVGAGLAGSVA ALVLAREGAQVLVIERGNSAG AKNVTGGRLYAHSLEHIIPGFA DSAPVERLITHEKLAFTMEKSA MTMDYCNCGDETSPSQRSYSVL RSKFDWLMEQAEAEAGAQLIT GIRVDNLVQRDGKVVGV EADG NRVMKKILTTPIKAEDLQDIRV GDVIYL*RHRSLSVG*RAESGG* RSGRIVKRTG
10699	41067	A	10761	987	1191	
10700	41068	B	10762	1	1506	
10701	41069	A	10763	204	527	GPDRQCIGPLAE*NTGNSHKAA LRQQRAGEGRWWQKPHGEWRA ATADGRTYAISAQATAPQSPA GQSTMPRPRLWSTPALPVMIPA VTVDQRITPASVSTTKQAISA
10702	41070	A	10764	1041	3024	
10703	41071	B	10765	1	763	
10704	41072	A	10766	729	989	HLTRQGIPTDLQLRVLSVRRKT NKQKGHPHRKRICTSPSSKTKS R*NHKDGEKTEQKNWKL*NAE HLSSSKGTQFLTNGPKLDGE

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10705	41073	A	10767	89	1755	LSEGLTNRKDIHTKTPSVRRHH HQRPKCWKFPGHSGRRRK*R /CIQVGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMTELPFTTASRKRIYGLQLTR DVKDLFKENYKPLLNEIKEDTN KWKNPSCSVWGRINIVKMAILP KVIYRFNAIPIKLPMTFFIELEKT TLKFIWNQKRARIASLSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYNYLIFDKPEKNQWGWKDS LFNIWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRSKTIK TLEENLGNTIQDIGMGDFMSK TPKAMATKAKIDKWLILKLSF CTAKETTISVNRQPTWEKIFAI YSSDKGLISRIYNELKQIYKKKT NNPIKKVWKDTNRHFSKEDIYA AKRHMTKCSSSLAVREMQIKT TMRVHLTPVEEVVRAGEMAKTR RCQNVKGASEGIRALALFLIN LTVHMEGNHIDGDIEIQTNRSP LQAPGEICESFTALMAMQLLSKL FWS
10706	41074	A	10768	533	760	
10707	41075	A	10769	1067	1225	
10708	41076	A	10770	1080	1250	SSGLHSWDARLVQYTOINKYN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10709	41077	C	10771	55	1842	
10710	41078	A	10772	1575	1745	SSGLHPWDARLVQYTOINKCN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10711	41079	A	10773	2798	2871	
10712	41080	A	10774	601	876	
10713	41081	A	10775	1194	1421	

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10714	41082	A	10776	587	1683	GWKFWPGQSGRRRK*/R/CIQLG KEKVKLSLFADDDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVGRISIVKMAILPKVIYRF NAIPKLPMTFFTELEKTTLLKFI WNQKRARIASILSQKNKAGGI TLPDFKLYYKATVTKTAWCWY QNRDIDQWNGTEPSEIMPHIYN YLIFDKPEKNKQWGKDSL FNK WCWENWLAICRKLKLDPLFLP YTKINSRWIKDLNVRPKTIKLTLE ENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLSFCT AKETTVRVNRQPTTW
10715	41083	A	10777	1260	2176	SSGLHPWDARLVQYMQINQCN PAYKQNRQKQPHDYLNRCKRG L*QNSTTLHAKNS/AIN*CWKF WPGQLGRRRK*/R/CIQLGKEEV KLSLFADDDMIVYLENPIIASQNL KLKLSNFSKVSQYKINVQKSQA FLYTNNRQTESQIMSELPFTIAS KRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWKNI PCSWI GRINIVKMAILPKVIYRFNAIPK LPMTFFTELEKTTLLKFIWNQKR ARITKSILSQKNKAGGITLPDLK LYYKAIVTQNSMVLPLKQRYR PMEQNRALRNNAAYLQLSDL
10716	41084	A	10778	3813	3983	SSGLHPWDARLVQYQTQKN CN PAYKQSQRQKPHDYLNRCKRS L*QNSTTLHAKNSQ
10717	41085	A	10779	1312	3348	
10718	41086	A	10780	1636	1815	
10719	41087	A	10781	67	403	KFLCRPPIIRPPKTFNTLIVLARR CIQCFRFFDIACFN RVGKGFGV GHQLRGFRHDIRGFAQWTHLP DGCAFRDRCYAAGAQCENVPA LTACGDNNQRIGACWYPQGEV
10720	41088	A	10782	506	915	WASVKSPVPCWNCWISHRRRV TCRHVRFAPGFNLAKA/VQGAA LVITGKGRIDSQTAGGKAPLGV ASVANQFNVPVIGIAGVLGDGV EVVPQYGIDAVFSILPR LAPAE VLASGETNLFNSARNIACAIG QGIGK
10721	41089	A	10783	1	906	

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10722	41090	A	10784	2	597	SILKLVACDNDNPLVGARGAAA VFGPQKGATPEMVEELEGQLQ NYARVLHQQPEINVCQMAGA GAAGGMGIAAPVFFNGDIKPGI EIVLNAVNLAAQVQGAALVITG EGRIUSQTAGGKAPLGVASVA KQFNVPDDLGLLAYVGDGVEV VHQYVGIDAGFNILPFLAPLAEV LASGETNLFNSARNIACAIGQG
10723	41091	A	10785	1	1140	
10724	41092	A	10786	13	628	LLIPARPPGINPYWKVSEANLI RYFQQVGDSTVLPMVLYNFA LTGQDLTPALVKTLADSRNIIIG IKDTIDSVAHLRSMIHTVKGAH PIHTVLCGYHDHLENTLLGGD GAISASGNFAPQVSVNLLKAW RDGDVAKAAGYHQTLQIPQM YQLDTPFVNVVKEAIVLCGRPV STHVLPPASPLDEPRKAQLKTL LQQLKLW
10725	41093	A	10787	3	1185	EQSGRGARDGGARDGVREGG\ SWTQQHGLPLTKVELATVAEY PVCLWQRLTLSPQYGSIP/RGD QSDGWKVDYNGPFSWKGQH FVINGIDTCSGCKFAIPVCSASA KLLPMSSQNVYHRDILHRIDSE QGTFRVKEVQQWALGRGPFY WSYYISHHPEAAGLVEQCNGIL KTPSQFQMGRNTLQGWGKVL SLEGCAFSSSKSNLCSVVLKV VPKEGMVPPGDTTMIILNCKLR LPPMPLNLLASKEVTVD/YQG EIGQLLHNRGKEECVWNTGDC LTYLLILPSSVIKVEKPQPHPG RTINGPDPGSMKTWVTPPAGA VFLIGSWLRYDYGQYTWRAAS SQMLDRKGMNLASNLFHIGILG IFVGHFFGMLTPHWMYEAAMY GSCDTDNANV
10726	41094	A	10788	396	504	WKLRLERRAIQGDSPVHKNARA GELDE*AATRAIPG
10727	41095	A	10789	24	611	EILPVPGPVVIAW/AIFRRIAGES WSAIVISGLSIARHAQQRJITFT ASLAARLEIALKIVRNADGTES ASEQLYQVVAGACKMPWQSE AMKDVLCIDKRRMLMRTTGGTE TSKYPEEKKSTEIPVAAASERGG AQSLNQCATEAVVLTRVDSHL KVGDSLSTHTSFLKKFAARFGG QLEKALGLGSMQAFSDIRGL
10728	41096	A	10790	212	578	

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10729 10730	41097 41098	A A	10791 10792	1 3	1707 313	NAE/TVKMFTTSSKEDATFGLG WRVNGNATMTPTFGT/LASPT YGHTGSPPLPPICPVRPPGYLRR LSPRFRLFGISLPQRPPGILERS LQRRRNPSGWRRRNQ
10731	41099	A	10793	1	1992	MDVQSAADDTGMLPLVVRGPF NVVWQRLPAALEKVGKMTVD STRSQGNMAVTVKPLSDSDWQ ELGASDPGLASGDYKLVQVDL DNRSSLQFIDPKGHTLTQSQND ALENAILAVIRHEICLSDVVRIR ASRRFDKTSCTDRQKILKGY LLPAGWLADVDPRLVGMNV WTLVPAALFFGAGMLFPLAT SGAMEPPFLAGTAGALVGG QNIQSGVLASLSAMLPTGQPG VVDLNGIVDRAVLAAGDAD VASGAARLSARHSIVISSMGE RCCFIRSRITRIGFLAAGVGLD QLAPDFATPVIRELLALLCLFS GGGLAMYGYLRWLRNEKAMRL KEDLPYTNLSLILMVVAVI VMGLWIPPTCIVDDRMAYIPG LADSPNDTIKGNTRLRISDLLH HSGGFPADPQYPNKAVALGALY SQDKGQTLEMIKRTPLEYQPGS KHIYSDVDYMLLGFIVESVTGQ PLDRYVEESIYRPLGLTIITVFN LLKGFKPQQAATELNGNTRDG VIHFPNIRTSVLWGQVHDEKAF YSMGGVSGHAGLFSNTGDIALF NAETVKMFTTSSKEDATFGLG WRVNGNATMTPTFGTLASPT YGHTGWTGTVIDPVNHMTI VMLSNNKPHSPVADPQKNPTMF
10732	41100	A	10794	2	137	NCLSPVSN*WPAKTGRPLPS ATVTASTRNVLSKHWRIVVST VC
10733	41101	A	10795	271	553	ATQRQDLHFVRSPGDVAVYQTIT PEAADA VVARNPDTAQHLHC/ VYP/HTSNAALAQKYLHIAASP EVMVPLSAFHAASYSMFFMEF NLJAMWANFS

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10734	41102	A	10796	1	747	MLLGLHSLAFLQRESFGSKQS WGCQLAALLQRRITKMTTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQAQVLDLIS NVAGDRVTYRITKGEDLREQG YMGLHTVGRGERSPVLLALD YNPTGDKAPVYACLLGDIITY RNGKKVEVMNTDAEGRVL
10735	41103	A	10797	444	548	
10736	41104	A	10798	951	1648	TTGRFPSPVQDSFVNNESSRMGL PDEFTLQREFERARQQALAQ W/IAAFEGGFTGIVATLDTGRPG PVMAFRVMDALDLSEEQDVS HRPYRDGFASCNAGMMHACG HDGHTAIGLGLAHTLKQFESGL HGVIKLIFQPAEEGTRGARAMV DAGVDDVDYFTAVHIGTGVP AGTVVCGSDNFMTATKFDHF TGTAAHAGAKPEDGHNALLAA /AQATLALHAIPHSEGASRV
10737	41105	A	10799	1495	2282	FDRHVGEFFLNQLETTNSLAKL HALIGVARRIFKGAHRRTVVGE GYQETFMVELFFDAVKAVTFPPT EHVFLVQFHVVKGDFTAAIHTQ TELFKFGHFDARFAHINKPFGV DRFVRRSPVARHHHDVRGVGA AGNKTLLTIKINLTISTGISRFQA THVGARARFGDR*VRTDSTTV GHRDCHITGGHR/HKSFQPGHEA PQAVPLPGRFH*PSHDHCR* LVSLAGAAVRSQDPVPVMPIS PGLDWVRQIVCCVMASDAD
10738	41106	B	10800	1	3618	
10739	41107	A	10801	3	490	TGIVATLDT/GRPGPVMAFRVD MDALD/LSEEQDVSHRPYRDGF /ASCNAGMMHACGHDGHTAIG LGLAHTLKQFESGL/HGVIKLIF QLHRYAAHAGAKPEDGHNALL /AAAQATLALHAIPHSE/GASR VNVGVMQAGSGR/NVVPASAL L/RQPTRSALNTTQQLNAR

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10740	41108	A	10802	1	513	MGIESLQAFLRSAGALGVWVY TFLERLIPTGLHHFIYQQFISGP AAVEGGQIMYWAQHLQEFSL AEPLKSLFPEGGFALHGNKIFG AVGIYLA MYFAAAPENRVKVA RLLIPTPLAAMLVVIPEPLAEFTF LFISPILYAVHAVLTASMSPPVM YLPGVVGNMGEGKID
10741	41109	A	10803	1	4941	
10742	41110	A	10804	1	1083	
10743	41111	A	10805	1	1363	MPVRKNMIMNEGNITPTNGC RIRASCGVPMICINQLKDGKCK PSPLTAARMKQKAILFLIRTVR TDTHVVEDTGRKGSRKANSRE RFPDAFPEFHGFADFRVLRQAM IQIWLVSVMVQHVNVCCTDAC RIVQTRIVVTAGFQLSNASLVA MRRWVYRVRRIQYRRTQTAV FHSTHGNRYREGQPVGTLDIDRY KANENVELVHYAQPLLNEADS LAKVMPSPDIPKQRRWLGLQM LEGDIYSRAYAGEASQHLDAAL ARLRNEMDDPALHIADARYQCI AAICDVVSNLTAEPSRFTTAV DKIVLNRFLGLPIFLVFMVLMF LLAINIGGALQPLFDVGSVALF VHGIQWIGYTLHFPDWLTIFLA QGLGGGINTVLPVPQIMMY\ CFSSFLKTPALACREIFVPLMRL RVNLRWYPPVL*RISSWWTNSRI PTTFSTRGSACWRATPAK
10744	41112	A	10806	199	1083	RLFEHPRLGVAAVENGALGKR SAVVLPFGDAVNHKTRFIEFVK SAIEGNRLTVRAIGPQFTTQTPV IVFNQGVSGAQNIAGRAVVLLQ TNSFGTGEIHKETLNILHLRPAPA VD*LVVITDDHHFAGVARQQA DPRVLNVVGILEFVHQDIGKTF AVVLQDMRLVKPQLVSAQQQL GEVHQARAVTRFLIRLIHLLPGL LHRITVALNMMRTQAFIFLAVD VPHCLPRRPLLVEVHGFQDTQ KVAAWRGHRFALFVIAKEVQ RNVHWHRRVKIGWAEKRNAL RQKAGNFQMRQ
10745	41113	A	10807	49	273	DFLGRGAFNVINIGAWASRPVQ GSTVDLSHGLHLVLHLKNNL*F YGFDSHFLKSFYKGTSSISIQVE VGISQGNL
10746	41114	B	10808	91	2183	

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10747	41115	A	10809	8	219	FSLWPL/KKFSNRFLKKKPMEF GSWTTRELIASFAGVRAITLA GVLSIPLLLPDGNVPARYELVF LAAY
10748	41116	A	10810	84	509	
10749	41117	A	10811	3	163	ENTTWLYAD*NAGRDADFGHA KRKWTWLTWLAIAAVATAMAN RQPAGLFAFLT
10750	41118	A	10812	1	707	MGWRMGIWLRVFTVAKHLQR AESDQIGFRLKEHCWKRYAVR HPVKDVSFGSPVLTVMNRAQ/ SN/PARTVGVWLRMFRLRKR/ RKPRPLPLSPLHMDV/HAGNLV HSASGLKLIDW/EYAGDGDIAL ELAAVW/VENTEQHRQLVNDY ATR/AKIQPAQLWRQVRRWLP/ WLLMLKAGWFEYRWQ/TGD RQFIRLADDSWRQLHRSNKES RELVARLRVFAQSSGGAVDQE GGRVQCFREGL
10751	41119	A	10813	1	227	SFINVERYRAEPQTADAAPLKR GAFGSWLPPEPDHYAED/DHQQ YLHKNPYG YCGGIGGVCQAY KIVQIQYIARTA
10752	41120	A	10814	1	283	
10753	41121	A	10815	315	569	
10754	41122	A	10816	65	580	SDRS*IPVRPTHDRSGNRHDGSS GYCRCYG*HG*HRGIRYRCWPE KSQTRSGLLPLTVNYQERTYA AGRIPGSFFRREGRPSEGETLIA RLIDRPIRPLFPEGFVNEVQVIA TVVSVNPQVNPDIAMIGASAA LSLSGIPFNGPIGAARVGYNDQ YVLNPTQDELKESK
10755	41123	A	10817	235	1236	TDHDGRNDTQRIGSGERNRPF NANTAHHQCRFAGFALFCGEIF TTNQRRQPHQRRDNTNTHGSD GHHGINTLSNANQHEGIGHFVN RTAHIERQHQTHDHRQHNNAA NSGTEVSQ*AR*HAAY*RYVAE REIHSGDRCGKRNSAHKIMPG WWCALPDTAPSLSKVVFVKGC PHLCPWCANPESISGKIQTVRRE AKCLHCAKCLRDADECPGSAF ERIGRDISDALEREVMKDDIFF RTSGGGVTLYRGEDPAEDARY AHTNQPRQNKAVVDDEATDV GGAGTVKLNRCQIARISQDVI TVASRCEHGFCPCDTVHRHD GDHTGTEDFVF
10756	41124	A	10818	1	400	

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10757	41125	A	10819	783	1116	SVLHLYEQNTEVHDTGRGYP KTLDIVPAFEASHLLWQSYENS WEQIFSAVGASWQKHGYGTDV LTQLGYGQRHWNIDIDAGATL RWEKRPYDGDREHNLVVEFD MTFRF
10758	41126	A	10820	3	474	TCGEAASIVDRIRGFFEPSSILV STLVLTLPRTGLPLVTDLSLPM RLLPTEIMAGSPIRS/RDISLGDD PGINGQRAQGTWERWTVRADE PQAFHIEGVMFQIRNVNGAMPF PEDRGWKDTVWVDGQVELLV YFGQPSSWAHFQFYFNSQTHKV GPRAVA
10759	41127	B	10821	93	786	
10760	41128	A	10822	191	748	GPATPRQPFKVLASLGRVLVQHG GRWDAQHLHNAVHLVDLIGAT EEQLSGVHLHKDAAQGPHVNG QVVGCAQEHLR*AVEAALDIL VDPLAKLAGAAEVHNLGGAAL GVAQQDVFGLGAVNDAAEQ AWPERAVPCRAAAPASGSGSA RRRGSCCAGGORTGCRTAAQIP STSGFRNMKCRFRCTI
10761	41129	B	10823	1	2724	
10762	41130	B	10824	116	2458	
10763	41131	A	10825	1	1317	

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10764	41132	A	10826	99	2052	NPADGRTGFTLCATGEALSSAT IAAAERRQALQEGCDDILS/HG DADMVSMAR/PFLADAELLSK AQSGRA/DEINTCIGCNQACLD Q/IFVGKVTSCLVNPRACH/ETK MPILPAVQKKNLA/VVGAGPAG LAFA/FNIAKQIPKKEEFYD/L/ RYYRMIIEVTGVTLKL/NHTVT ADQLQAFDETILAVG/IVPRTPPI DGDHP/KVLSYPDVLRLDKAPV/ SN/KVAIIGCGGIGFDTAM/YLS QPGESTSQNIAGFC/NEWGIDSS LQQADCDAPAKASKPGQGLGK TTGW/HRITL/LSRGVKMIPGV S/YQKIDDDGLHVINGANQGS DMLRLQGE LDSASRIGRRSAAP KLGLSLNDGRFCFINCHILDRLPY KGLVPACSWNGGSLDPLEGRP DEPHVEVLGIPPAAMLDAQPRL ASTLNGCLGVA GPYEDERTQE GLPGPRDTAAEEVLGVQTTGA GSRGRVVRGPQADLPSASGPGA ACWSMSPPPDQPPCVLAHGFFR RTPSTQQRPAEQCFHSPAPLEL PLSSTSSILSFAEYGNAMAWLY RGKILPSGTPDDDLKAQSANDGN PDPTMEKAFIQLIHDGIRSIAMS NPILSCRRYGRYQEWCLTIPAV FISAPYVRRYVRFHEHQEGGGV RQEATVREIPLAIAVIPNSRTPC
10765	41133	A	10827	1	525	DAMVSSWNRAAPNTIPTAAKA GGNYLSLLVGSEARRHGYQE GIALDVNGYISEGAGENLFEVK DGVLFPT/PGFTSSALPGITDAI IKLAKELGIEVREQVL.SR/EKS LYLADEVFMSGTAGEITPRRS NGYSGLAKRCGPVTKRIQH ALQGVYSWVTPGYFESVRCTA
10766	41134	A	10828	8	573	REPAGENGPPVCDGAMLDLKA/ WGSECHQQLTGRDNQIQRSIY LLPERAKLAELRLVIPGQVDY LQHIEELAAFIKGLGDVPLRLN AFHAHGVYGEAQSWASATPED VEPLADALKVRGTCTRPDKTRQ ASHQALCANCRMRRERLIRPTV RHKPVGMIRDRKRIRHYAPTA GCGVNALSGLRFGTDL

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10767	41135	A	10829	1	479	SNATNGIEPPRGVYSIKASKDGI LRQVVPDYEHLDHAYELLGEM PGNDGYLQLVGIMQKFIDQSS ANTNYDPSRFPSGKVPMMQQL KDLLTAYKFGVKTLYYQNTR/G RR*RRTRRS GAVNPGTMGCESG ACKNPGYLRMPGCRKRTPLIPA LPGFGFW
10768	41136	A	10830	1	443	MDSLMDMLASTQGRMDQDQR VTVSSLPGFQFVGSKAYKPSRR PDKAFTPHPASQYQILHAPLVA AIVSGLTAARVVFVRLQQPSLG VLSNTSGCDATNVVGRQLQDNA SVSPGIVHTDSVIWRSCQVRRS AVHTLRQKTRLFDAVDA
10769	41137	A	10831	1	323	MDLVTGSRKVIAMEHCAKDG SAKILARRCTMPLTAQHAGHML VTELAVVRSFDGKMWLTEIAD GPTSQAQPAATYRIPLSNSRV RRYRHYRYRYNLSIRKKRHRPL
10770	41138	A	10832	526	975	TPYPAYVQHVTGRIJRRGKRI RQCLPVLESFHNQKSRGETE GASGFSLQHLHGDSRAA PGPY RVSTAAADSGGRAGSSAPSAV PRGC*GPSLAPAGRSQR*HRGG GQLSPAAPTANKAAGLGPPA RLNFFIRAQCDSRINDITR
10771	41139	A	10833	1906	2049	PLSIIEADFRIWANAG*RMVAGI KPSIARVPLVLQVSALEVPEQC YRH
10772	41140	A	10834	1	808	MPKPNTRWSAWGLRRLKRW SVARGSNLNRSVQYEFTGRGD RIGWVKGIDDNWHLTLFIENGR ILDYPARPLKTGLLEIAKIHKGD FRITANQNLIAGVPESEKAKIE KIAKESGLMNAVSPQRENSMA CVSFPTCLAMAEAEERFLPSFID NIDNLMAKHGVSDHIVMRVT GCPNGCGRAMLAEEVLVGKAP GRYNLHLGGNRIGTRIPQITRRI EHRANDARTHRKVAEAFTRFA LFRPAPYQFIKRRQDFRLVMFSI YMPVPS

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10773	41141	A	10835	248	830	HHYRKMNIQQSKWLIIVTVCDG KLNWLLSGSKVCCTWMLCVQ/ SEPELAKAWIFANLLAAFLIDDI IQPSLDFPPRRAEITIAADGTISA LNPGDPANTVAPVGRLLKLVKA TGSEVQRGDDGIFRLSAETQAT RGPVLQADPTLRVMSGVLEGS NVNAVAAMSDMIASARRFEMQ MKVISSVDDNAGRANQLLSMS
10774	41142	B	10836	328	481	
10775	41143	A	10837	14	675	FRKLQVCWLPRPHLRPWWTCK PRWFGSCLRVFL/LEIVI/GDV/ WGLRLWSALGVAFFG/WAFITS LQAKRGWMRIVPIILLAAALVS VRPLQDWAFGATHTAQTQTHL NFTQIQTVDELNQALVEAQGKP VMLDLYADWCVACKEFEKYTF SDPQVQKALADTVLLQANVTA NDAQDVALLKHLNVGLPTILF FDGQGGQEHQARVTGFMDAET FSAHLRDRQP
10776	41144	A	10838	1	1413	GMALTYTALGLVVAAGLQFQ AALQHPYVLIGLAIVFTLLAMS MFGLFTLQLPSSLQTRLTLMNS RQGGGSPG/GAILLYIAQSGNM WLGGGTLYLALGMGLPLMLI TVFGRNLLPKSGPWMEQVKTA FGFVILALPVNIAPGSLDKALNQ YAAHSGFTLSVDASLTRGKQSN GLHGDYDVESGLQQLDGSGL QVKPLGNNSWTLEPAPAPKED ALTVVGDWLGDAENDVFEH AGARDVIRREDFAKTGATTMR EVLNRIPGVSAPENNGTGSHDL AMNFGIRGLNPRLASRSTVLM GIPRPLRPLRSAAFTGSRFARQ HGCHCTWYAVVVRVTDTS VGGVVNFVTRAIPQDFGIEAGIL MSDLKHGSLVGACLGRLPGPA VLYLAVAVLGVRRGVVLC PLGGTGLGYSCGGAFQFAAS CFLGRYGVVQGVHVCFGPRSV FLDDCLRFDLPLVWLSCLR

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10777	41145	A	10839	1	908	LLKPFHVIAIATGRSLAVFCMG RLRTICSHA TPPASAI/LLYI/AQS GTWGGGGTLYLYALGMGLPL MLITVFGTRLLPKSGPWMEQV KTAFGYVILALPVFLLEVRIGD VWGLRLWSALGVAFGGWAFIT SLQAKRGWMRIVQJILLAAALV SVRPLQDWAFGATHGTQTQTH LNFTQIKTVDELNQALVEAKGK PVMLDLYADWCVACKEFEKYT FSDPQVQKALADTVLLQANVT ANDAQDVPTSAFFISPPNALVAI IVQLRFGDFYNRVSKGSRPTVF GRTLKARRITLSEKSLKAKIH
10778	41146	A	10840	3	808	SSGGHGRRAGRLQHPLLRVH VPVVDTSVPCSRQLQWHHLPL CPGQLQHGHFHGPWCFFPSG*G *GQGGRLPGSAVQERGCARYP GPHEVVCHVPLLPAAALLPLQR L*QLCRGL*PPLPLGQ/PTASGV ETIATSSCSCCHSVHTWWASWP SAWSTC*TTLRGWEPTPPSRIL GSCGPHCRGDVDRGHVHPGE* AFQSLVPCQGT PKGPMAPP*VG RGVSP/PGTRVEAALSCESPFA RQSMCFNLHTHSIDPKQSRRPY SDNVGKE
10779	41147	A	10841	2	646	CSWQPAVPTQPQAPGSAAPRQ LPGHSRGAQPALVSPHKGLTPV PGTPA/PASTPPAPAGGGLPSP AAGAPPAHCPG/HPPAPATAAP VPGLCGPCSLPACQTR/PPTH VNTKKRV/PG/VRPAARRPWPP GCTWRGARTVTFHLQNLPGVN CQMLTVGRSGIRPTCTIASCSV NKLHPQMHPATQPHHRMALSP SHSEGPSHCWGLSLGDISPIR
10780	41148	A	10842	3	550	

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10781	41149	A	10843	2	1132	LCLVMILYTRRRWCKRRRVQP PQKSASAEAAAEIHYPVSLIGG HGRESLRNARVQGHNSGTL RETPILDGYEYDITDLRHHLQR ECMNGGEDFASQVTRTLDSLQ GCNEKSGMDLTPGGDGRKARL MNKYKDNIIATSPVDSNIIQQAT LLSHTSSSQKRINNKARGMHV *H*GEGDSTGEAENDPQLTFYT DPSRSRRSRGRNDRGGRNKTT LTLISITSCVIGLVCSHVNCPLV VKITLHVPEHLIADGEPVLLRM GSQLDASDWLNPAQVVLFSQQ NSSGPWAMDLCARRLLDPCEH QCDPETGRREHRAAGNCQRDH ARAHSVWLGSPPYHDTSLRWS PMYTTMESAPHAFFPSVTADAE
10782	41150	A	10844	3	3935	HASGPGGLKMLAGLCALLACC WGPAAVLATAAGDVDPKSELE CKLKSITVSALPFLRENDLSIMH SPSASEPKLLFSVRNDFPGEMV VVDDLENTLPYFVLEISGNTE DIPLVRWRQQLWLENTLLFHHI HQDGAQSLPGQDPTTEEPQHESA EEELRILHISVMGGMIALLLSIL CLVMILYTRRRWCKRRRVQP QKSASAEAAAEIHYPVSLIGGH GRESLRNARVQGHNSGTL SIR ETPILDGYEYDIT
10783	41151	A	10845	184	357	ALQGWSKNLHPEDIQLGKTPP P*QVAQEGGWSRRVSGDWTWIL EEQPGSTTRRVSVGM
10784	41152	A	10846	226	609	VILSSFDLIKHGILLEISDSIQFRG CKRSRIPELGGLEELW*PGDCR QPRPWRAGRHLQPGSLGSLVS KHQLRGSRKTL/YSAFRKCHLL SVWEGKPLKI*RGDQVADSSQK KQLAADAHTPYRGGDI

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10785	41153	A	10847	20	1317	SSHQKQMLAPCFLGSLQNQWH HTAGKGK/WVLGTCAFGEQLA ASGHMKETRADRSKKLFRHYT VGSYDSFDTSRGGVRKPYAGF FPDLQDICDEQPRPLHSTLRPAC GGIQPGKQQMPFAKTDTCASD KHVEKKLERLIHQAVSDAPEPS RVVKGIFIGLPCARLWVVPYL MGHVQEVMTAEGYERASQATF REQMQEVPCCQORSTGSSMKT GNKIRRVTDNVLTRSGPLINDIL SVAVDSSSVSLIWMHLFSSHPL GIVRYWCGMGISCKLLLTRVC YLITPLDLERFPFNTQVTFPE RRVSVFLLPLSWCLDTRLPREP GCRSRDSFTHRVPFYSVTPTSG DVPGSHPFCDKPVRRGDDPYIR NDRGTLYSTLQFISTCVQVVG YGHLPGFKSDAAQAVPRLLSQ KRDQNHKEEITDGDERP
10786	41154	A	10848	1930	5781	RAKSPANIHMTGNSHITLTLN VNLGNSPIKRLRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTLNMYAPNTGAP RFIKQVLSDLQRLDLSHTLIMG DFNTPLSTLDRSTQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIHTNLYSDHSAIKL ELRIKNLTQSR
10787	41155	A	10849	1	3654	
10788	41156	A	10850	1	5127	
10789	41157	A	10851	209	3816	QGRPTFRFRKYREHHKDPREE QLQDT*SSDSPKLK*KKCK*GQ PERKVKLPTKGSPD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTETIQTIREYYKHLANK LENLEEMDKFLDYTLPRLNQE EVESVNRNPTGSEIEAITNSLPTK KSPGPDGFTAEPYORYKEELVP FLKLQFQPIKEGILPNSFYEASII LIPKPGRDTTKKGNFRISPLMNI DAKIL
10790	41158	A	10852	1	3663	

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10791	41159	A	10853	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYWVHNEMKAIEKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRRQERSKIDTLTSQ LELEKQEQTHSKASRRQEITKIR AELKEIETQ
10792	41160	A	10854	1	3354	
10793	41161	A	10855	1	5073	
10794	41162	A	10856	1	3235	
10795	41163	B	10857	1	3300	
10796	41164	A	10858	1	2563	MKAIEKMFFETNENKDDTTNQ LWDAFKAEVEVSLNRPITGA GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPLLLKLFQSIKEE LPNSFYEASIIIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKLIHQDQVGFPGMQG WPNIRKSINVIQHINRAKDKNH MIISDAEKAADFQIQPFMLKTL NKLIGDGTIFYKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNILLEVLRAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS GYNKINQVKSQAFLYTSNRQTES QIMSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDQPEKNKQWGDSD LFNKWCWENWLAIRWKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITQDIGMGKDFMS RTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKHKMKCSSSLAIREMQI KITMRYHLTPVRMAIIKSGNN
10797	41165	B	10859	1	3420	
10798	41166	B	10860	1	4019	

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10799	41167	A	10861	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFSSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTONHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYHNLWDTFKA VCRGK FIPLNAHKRRKQERSKIDLTSL KELEKQEQTTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLRLARLIKKKREKNQI DAIKNDKGDITDPTEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPIGTAE IVAIINSLPTKSGPGDGFATKF YQRYKEELVPFLKLQFSIEKE GILPNSFYEAHILIPKGRDOTT KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISDAEAFDKIQPFMLK TLNKLGIKYLGIHLTRDVKDI.F KENYKPLLKEIKEDRNKWNKIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGO
10800	41168	A	10862	1	4449	
10801	41169	A	10863	824	3693	AWKGTDDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNLLLL NDYWVHNEMNAEIKMFFETNE NKDDTTYQNLWDFAKAVCRGK FIPLNAHKRRKQERSKIDLTSL KELEKQEQTTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
10802	41170	A	10864	1	3297	
10803	41171	A	10865	1	4791	
10804	41172	A	10866	3	3316	
10805	41173	B	10867	1	3415	
10806	41174	B	10868	1	4753	
10807	41175	B	10869	1	3384	
10808	41176	A	10870	1	3345	
10809	41177	B	10871	1	3772	
10810	41178	A	10872	1	3720	
10811	41179	A	10873	1	3894	

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10812	41180	A	10874	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVVHNEMKAEIKMFF ETNENKDDTTYQNLWDAPKAVC RGKFIALNVYKRKQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQ
10813	41181	A	10875	1	3780	
10814	41182	A	10876	1	3852	
10815	41183	A	10877	1	3345	
10816	41184	A	10878	965	4362	TWKGTTSRCKIMPYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEYTFSSAPHHTYSKI DHIVGSKALLSKCERTEITNYL SDHSAMKLELRINKLTQNCSTT WKLNNLLNDYVVHNEMKAE IKMFFETNENKDDTTYQNLWDA FKAVCRGKFIALNAHKRQERS KIDTLTSQKLEKQEQTHSKA SRRQEITKIRAEKKEIETQKTLQ KINESRSWFFERINKIDRPLRLI KKKREKNQIDT
10817	41185	A	10879	1	3921	
10818	41186	A	10880	1	3988	MTGSNSHITILTNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWKRIYQAN GKQKKAGVAILVSKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDYRTLHPKSTEYTFSSAPIHI TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRINKLTQS RSTTWKLNLL
10819	41187	A	10881	2	462	YFTDRLRLARAGTPL/IMFGTIA RSGVRIVSREPLNRRAILIALSL AVGLGVSQQPLIQFAPEWLKN LLSSGIAAGGITAIVFSLAGHPA LATNAQPMFAFLHQTTFFQNL IRVKEAICSDQFNNTMFRGLQG NSACTKCNPRCLNELTPTE
10820	41188	B	10882	16	163	

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10821	41189	A	10883	2	1509	RDEVNGCIRLVYDMYSTFGFEK IVVKLSTRPEKRIGSDMWDRA EADLAVALEENNIPFEYQLGEG AFYGPKEFTLYDCLDRAWQC GTVQLDFSLPSRLSASYVGEDN ERKVPVMIHRAILGSMERFNGIL SEEFAGFFPTWLAPVQVVMNI TDSQSEYVNELTQKLSNAGIRV KADLRNEKIGFKNRSGELSHLP PINQSKPRNFPSAALPQVPQPTH LSQRPRASPKPPPPDPERVELSL EEHREMLEGFYEEISKGRKPTLI LRTQLSVRVNAILASLESVKPL YTMALGLLVKYPDSALGQLRIE STVDGSRLYITGNGVLFQHVKF HAFLLYLGYPQAAREVRIMQF CHTLREFALEYRTCRERVLQQQ QKQATYRERNKTRGRMITETE KFSGVAGEAPSNPSVPVAVSSG PGRGDADSHASKSLTTSRPED TTHNRRSRDRHGPRGCQVCSA QPSLLRAVPVADMRALMTGKD CPPCPGKRLRGAELGPL
10822	41190	A	10884	296	757	ISRRRRALSPKAESSLSILPRE KRSPSRTWILTPRRLFSLAISSKS AGNTLSSRIFK*KA*ACK*RG VSTRCRIFLALFIVTIKHLMMR STASNRQYSISIWTILPCWSARC FSIKIAGIPAEPPRYLLISPGLTG LKINFFTTVSFW
10823	41191	A	10885	1	519	MGLPWQVGMGAIFWGAIGLLL LTIFRVRYWMIANIPVSLRVGIT SGIGLFI GMMGLKNAGVIVANP ETLVSIGNLTSHSVLLGILGFFII AIIASRNHAAVLVSI VVTLLG WMLGDVHYNGIVSAPPSVMTV VGHVDLAGPIGNSLV/GCYPFAI LRRFSDGSGGLGRNQI
10824	41192	B	10886	1	3489	
10825	41193	A	10887	817	1528	WGSRDNRDEIRNTLVLDTLRLQ RVCAQRAFLVLVFLGKVTFEEL NFTFILVIQNVRGDTVEPTVVR DNHRTARELQQGVFQRAQGF IQVVGWVFEQQHVAANLSRCR LVNTPTQQVRFSTATFRVIWV TPTAGKLSGGFLFKMYGLPAA AIAIGTLLNQKTARKWAVL*SP PALTSFLTGITEPIEFSFMFVAPI LYIHAILAALFMWKFVPEKTR KTLLEEALSNRIAAE
10826	41194	C	10888	1	573	

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10827	41195	A	10889	2321	2554	WRKRCVKVRNLSPLCLPDRKL TLPCCSIAIRNCIAKL PVS* LWV ALWGWVTGRLRLNLIFLTRK RQKLSSSQGSRW
10828	41196	A	10890	1	4350	KULELRSKREAGMLERSSSRMV TCSQWAATRNPPVVALPIYGFI RCLVPFGLLHIWNVFQM QIGE YTNAAGQV FHGDI PRY MAGDP TAGKLSGGFLFKMYGLPASAIA IWHFVKPETRAKVGIMIFAAL TSFLTGITIEPIESFMFVAPILYII HAILAGIWHQSQVFFWGCVTVR RSRTV
10829	41197	A	10891	137	686	
10830	41198	A	10892	3	3831	SIGMMGLKNAGVIVANPETLVS IGNLTSHSVLLGILGFFIIAIL/AS RNIHAAVLVSIVVTLLGWML GDVHNGIVFAAPSVMTVVGH VDLAGSFNLGLAGVIFSMLVN LFDSSGTLIGVTDKAGLADEK GKFP RMKQALYVDSISSVTGSI GTFSVTAYIESSGSVSVGGRTG LTAVVVGLLFLVLFSPLAGM VPGYAAAGALIYVGLMTSSL ARVNWQDLTESVPAFITAVMM PFSFSITEGIAL
10831	41199	A	10893	6	146	MCSEK VAMCCDDDDDDDDDD DDDDDDDDDYSCSHGFWD FSY TWNTSPQGHGLMGSPHGLVE IRDKLGDRTQRVYIQRITGNGL EFENPCKQFRGLTRMYIRRLTR LSVQWYMALE RPPVLQKYRY RGSKAHETSHSMSTVTSNEKQ DNTRIDTQGTNR/VATLRHRE TVLANEVAPYAATDNVLAAS DVGDVSWKLPVAQCFS PCFAV GTPHLTWQ/SGLLQECQEHQQ VTDTPYHCPKPNVTPSLK
10832	41200	C	10894	1	1197	
10833	41201	A	10895	1	763	
10834	41202	A	10896	2	412	LFEFTLDVKVRESPI LFRDESM RTACSPDGLCSNGFGLKCPF TSRDFMFKRLGGFEAIKSAYMA QVQYSMWVTGKDAWFFANYD PRMKREGIHHVVVERDPQYMS DFNEMVPEFIEKMDALAEIGL TVRELGI

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10835	41203	A	10897	3	663	ARGKKPPRRGKEDFWDSIATR VSVNPIKFPVEA*PFLKPLQV SVGPLGGRLPLPIGNLLQVAD GTLSTGTDLLEMVMARVALV QPHEPGATTVPARKFFDICRGL PEGAEIAVQLEGERMLVRSGRS RFSLSLTPAADFPNLDDWQSEV EFTLPQATMKRLIEATQFSMAH QDVRYYLNGMLFETEGEELRT VATDGHRLAVCSMPIGQSLPSH
10836	41204	A	10898	377	1077	WRGQRCLASVFFPRHPGAEGRG RPVFAETIFL**SRRGLAR/TGR RKLPVKLKAADFPNLDDWQSE VEFTLPQATMKRLIEATQFSMA HQDVRYYLNGMLFETEGEELR TVATDGHRLAVCSMPIGQSLPS HSVIVPRKGVIELMRMLDGGD NPLRVQIGSNIRAHVGDFFITS KLVDGRFPDYRRVLPKNPDKH LEAGCDLLKQAFARAAIILSNEK FRGVRLYVSESQLKSRQ
10837	41205	A	10899	591	871	VRGFPSGAEQLYG*SVSLILLP NLSNSG/RTGFPVAPLPYSKSPS DFMSLLISTVPGSQL*QPIQRAE LVCTTCSPIVSAPTQAPTQGA SH
10838	41206	B	10900	1	1765	
10839	41207	A	10901	1	1177	MKSLIIVNPADICGRTCEVAC VVAHPSEQELNADVFLPRLKV QRLDSIKRFWEQMMRIVTAAV MASTLAVSSLSHAAEVGSGDN WHPGEELTQRSTQSHMFDGSL TEHQRRQMRDLMMQARHEQPP VNVSELETMHFPGMLFETEGEE LRTVATDGHRLAVCSMPIGQSL PSHSVIVPRKGVIELMRMLDGG DNPLRVQIGSNIRAHVGDFFIT SKLVDGRFPDYRRVLPKNPDK HLEAGCDLLKQAFARAAIILS EKFRGVRLYVSENQLKITANNP DQEEAEIILDVPYSGAEMEIGF NVSYVMDVLNALKCENVRMM LTDSSVSVQIEDAASQSIAAYV GMPMRLEGSPLGNPEFQKISSP CALYIALCSKARHHTGRYLGLC
10840	41208	A	10902	527	925	

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10841	41209	A	10903	1	1514	MAFGLFWLIWILMSTITRIGID MSLALFTEMTPPPNTGGGLAN ALAGSGLLILWATVFGTPLGIM AGIYLA EYGRKSWLA EIVRFIN DILLSAPSIVVGLFVYTIVVAQM EHFSGWAGVIALALLQVPVIRT TENMLKLVPSYSLREAAAYALGT PKWKMISAITLKSAVVGNMTRI L/LRMAPIVVKTAPLLFTALSNO FWSTDMMQPIANLPVTIFKFAM SPFAEWQQLAWAGVRNLFYY GKFHALKNINLDIAKNQVCVC YNQCTESLVNGLYANAAHLVS VGQRSTGNSSVIKARQSSIRP MIVKYSALCLCRMRSERFIRRT KHKRFDRLQCTCRPDKRSASG NLAFVISLRPVLVAVVFALFA AFPMFSDVSIQLRHIFANFLPA TGDVIQRYIEQFVANSNKMTAV GACGLIVTALLMYSIDSALNTI WRSKRARPKIYSAFVYWMILTL GPLLAGASLAISSYLLSKQWAI DIDSVNRLGAILITALITGDT
10842	41210	A	10904	900	1250	WYACDQCQTCLPDHAPECAVA *AKTCCTA IETGT YRQSGRERK QSAMVL*RVRVLL**RRETACH VRAGLL*S*GTALGGHYRRLQQ *NSTGRHAGSGGTPLQRSSVV SSGVADG
10843	41211	A	10905	626	850	LRFLVFNILSRYSLISTVQKFS AMLNGTLPLENIIH*LRNITAIM NLVIFHGLSA*SVCIYIPGRGSV MSDRV
10844	41212	A	10906	307	858	
10845	41213	A	10907	698	1115	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTA AKNLA EAFEHYNEWHPHSGTRRRAR FSVRATYAAGRLATIPGYRGGP LGLMCGQPNRKPTDGANERLT MIRAATAMSE
10846	41214	B	10908	1	721	
10847	41215	A	10909	1	2615	
10848	41216	B	10910	1	1164	
10849	41217	B	10911	1	1930	
10850	41218	A	10912	689	1033	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTA AKNLA EAFEHYNEWHPHDGPESVFM PSR*APMTR*KIYSPPPYRSSQR AHRHA

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10851	41219	A	10913	393	686	NPSQLWEAAPQWKW IQGAGK VSCQLSRAADQLGRQHHISDPC FSIVPLIL*FAAYFPINPAVLKLA PVALYADAIRYNARTPLQGSLL PLTRLVWA
10852	41220	A	10914	1313	2370	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHRANPDANVV SEDLVRESVSGSVVNLHGVDRD MAAIRQLKATHDTSVSSEQVD NVRMLLAMVDDFRCVVIKLA ERIAHLREVKDA PEDERVLA AK ECTNIYAPLANRLGIGQLKWEL EDYCFRYLHPTEYKRIAKLLHE RRLDREHYIEEFVGH LRAEMK AEGVKA EYGRPKHIYSIWRK MQKKNLAFDELFDVRAVRIVA ERLQDCYAALGIVHTHYRHLP DEFDDYVANPKPNGYQSIHTV VLGPGGKTVEIQRITKQMHEDA ELGVA AHWEI
10853	41221	B	10915	1	1556	
10854	41222	A	10916	1566	1947	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPH/ECAGLSLAT GISAAAGL*WARRSFIQRDSRD PRYRAPIRIHPLPGANHLRQ
10855	41223	B	10917	1	1571	
10856	41224	A	10918	2024	2589	QDMQNLVLVRETSVKPFY PGL KVPEAFR/RIQGRKGEGEGAY VYRSAFSVFQKPRFSCALGGAJ AASWAGGGAPSPCGRAELPW GPGVGVAGTVCPERPRRERRL RGEREEEAADKVMARRWRKSR RRKRKEMEERMSPEETEGTNF DFAGEAVGQAERKGFAPSAAE ESFHEEEKRRRKEQSDLTF
10857	41225	B	10919	690	2724	
10858	41226	A	10920	3892	4338	

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10859	41227	A	10921	2573	3473	ANGARLALPPLGTFQGRQLRRR RPRWRRRRPGEASGPVMRLRG PRPGASAPWDGGGQVAR*WC PFPSQGWDDGSGGGQGDGAR FRTHRAKVQDGDGR*DEADG VHRHAPLQGLVVLVQVGVADE REDDAGNEGLQHLQQPGYGGH IASDLAGPGPGPHFGGVSHTR DAGEEGGGDGVVPRTAVGQEL DIGGGVDDGGREAEERGRIAGEG DGEVAPRQGEAGLEPAQLHDE DDQGHGEAEAPGEHGPVAHGP RPGAHASHQREGHAGRHLQQLQ AKETQGLCQGPGRPHDHGGPQ
10860	41228	A	10922	819	1274	NPLPRLQLRRLQLHLPVVRNCCQ TRRCGR*HRQLRQ*ARRKLVR SVYFGSCLRQLLREEWK*Y*RV *VLGWYSAVSTSSLPFDYCLP NSDGYRRVVDPGSLSGHPFLYQ RYGQWHDHVDHQPDLGLGPPGS LHPDPAFCRCVLRNCGNLLA
10861	41229	A	10923	720	3546	RDGRKPLQFDAARNCGGSSQSQ RSGSRKRRGDRRI/TLSMLKTRK ANRWA*SFRKMAAISTP/RTDI ACAKYRYETLHADRVLYYIDS RQHQLMQAWAIVRKAGYVP ESVPLEHHMFMMMLGKDGKPF KTRAGGTVKLADLLDEALERA RRLVAERTRYSAKSWKTVFRL VIGEOMIDVLGPEKRRRRITQE KIAIVQSSFEPMVTSLVARQH GVAASQLFLWRKQYQEGSLTA VAAGEQVVPASELAAMKQ
10862	41230	A	10924	764	1227	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHNPTEWFLS HCHIHKYPKSTLIHQGEKAET LYYIGKGSVAVLKDEEGKEMI LSYLNQGDITGDLGLFEEGQER SAW
10863	41231	A	10925	2467	2653	WLPFGLSHHNSPHPTSWGANG GFCQLLSMSVLMHSGTLGAH WDFSPVIGLEANRGVGDGS

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10864	41232	A	10926	1	860	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEPFY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RLFARLSLDSALPDRTTIMNFR HLLAQHQLARQLFKTINRWLAL GVMMTQGTLDATIEAPSSTK NKEQQRDPPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNLQGNLLHGEKQF VSAMPATKEPQRELAEDVDV LLIAERPQKVKTLK/TESAQ'G' KRPSTST*KPASVPGWSTRA SSSGSSAS
10865	41233	B	10927	754	910	
10866	41234	A	10928	2395	3454	
10867	41235	A	10929	1	1377	MSCMTPASDGTGISIDDEEAKQ FRESVVEWLMTNHPHDCPVCE EGGNCHLQDMVTMTGHSFRRY RFTKRTHRNQDLGPFISHEMNR CIACYRCVRYKYADGTDLG VYGAHDNVYFGRFPEDGTLESE FSGNLVEICPTGVFTDKTHER YNRKWDMQFAPSCQCCSIGCN ISPGERYGELRRRIENRYNGTVN HYFLCDRGRFGYGVNLDKDRP RQPVQRRGDDFITLNAEQAMQ GAADILRQSKKVIIGISPRASVE SNFALRELVGEEFYTGIAHGE QERLQALQKVLREGGIYTPALR EIESYDAVLVLGEDVTQTGARV ALAVRQA VKGKAREMAAAQK VADWQIAAILNIGQ/HPLFVT/N VDDTRLDDIAAWTYRAPVEDQ ARLGFAIAHALDNSAPAVDGIE PELQSKIDVIVQALAVFRLVIGE QMIDVLGPEKRRRTTQEKIAN
10868	41236	A	10930	19	586	IAALLKDKHPAMLLLAATKRG KALAAARLSVQLNAALVNDATA VDIVDGHICAEHRMYGGFAQE KINSPLAIIITLAPGVQPECTSDTS HQCPTEVVPYV/APRHEILCRER RAIKAASSVDLSKAKRVVGVG RGLAAQDDLMVHELAAVLN AEVGCSPRIAEGENWMERHAQ HKSWNPLSWAPLGSQAHP

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10869	41237	A	10931	1	1364	MLRILCALCSLLTGTRADPGA LLRLGMDIMNREVQSAMDESH ILEKMAAEAGKKQPGMKPIKGI TNLKVKDVQLPVITLNFVPGVG IFQCVSTGMTVTGKSFMGGMN EHVALNITANRLLRDEETGLP VFKSEGCIVLVNVKTNLPSNM LPKMVNKFLDSTLHKVLPGLM CPAIDAVLVVYNNRWTNLSDP MPVGMGTVKYVVLMSAPATT ASVIQLDFSPVQQQKGKTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVN QDTMIGELPPQTTKTLARFIPEV AVAYPKSKPLTTQIKIKKPPKV AMKTGKSLHLHSTLEMFAR WRRKAPMSFLLEEHNKGG HSLHENQLQMATSLDRLLSLR KSSSIGNFNERELTGFTSYLEE AYIPVVNDVLQVGLPLPDFLAM NYNLAELDIVEGGIMEPADI
10870	41238	A	10932	111	415	VSALSLLHRAPCRRLPPLQ DAGLHGWEHGVQGRGPAAH RDPV*EGWHHSGHLAQGHSEG *PCGDSETPAGREGKTAGHRTG RCGCRQEQTGAQQD
10871	41239	A	10933	2	219	FLGGEGVIFPRGWGGAAMRFV STGSRHTTP*GSEKSAGPHTQW HQNSK*ATSETRLHSCASEGIVP AGCRPY

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10875	41243	A	10937	76	614	PDRRWSSLDTMNHTGQTFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHRISETSVPD HV/VLVPVQHPLEHPCCLGFIA FAYSVKSRDRKMVGDTVGAQ/ ALCLHRQVPEHLGPDSDGHPHD HSAHRHPSADLPGLWIDQEASL RPGALPMTICIPRTPTSI RPA PR GQELCP
10876	41244	B	10938	695	1011	
10877	41245	A	10939	410	5501	EAKTHKSVVMTDPLLDSPASS TGEMDGLCPPELLIPPLSNRGI LGPVQSPCPSRDPAPIPEPGCL LVEATATEEGPGNMEIIVETVA GTLTPGAPGETPAKLPGEREP SQEAGTPLPGQETAEEENVEKE EKSDTKQDSQKAVDKGQGAQR LEGDVVSGTESLFKTHMCPECK RCFKKRTHLVEHLHLHFPDPSL QCPNCQKFFTSKSLKTHLLRE LGEKAHHCLCHYSAVERNAL NRHMASHMEDIS
10878	41246	A	10940	446	1704	GGPDM DARAPAVGGSCHQHOP SGAPGP/CIGRMES/EVGVRDHA IPEGARCNRFRKETT EGPLHCSR CGLLCPSASLRGHTRKQHPRL ECGACQEAFFSRLALDEHRRQQ HFSHRCQLCDFARERVLVK HYLEQHEETSAAVAASDGDGD AGQPPLHCFPCDFTCRHQLVLD HHVKGHGGTRLYKCTDCAYST KNRQKITWHSRIHTGEKPYHCH LCPYACADPSRLKYHMRHKEE RKYLCPCEGKYCKWVNQLKY HMTKHTGLKPYQCPECEYCTN PIADALRVHQETRHREARAFMC EQCGKAFKTRFLLRTHLRKHSE AKPYVCNVCHRAFRWAAGLR HHALTHTDHPFFCRLCNKYA KQKFQVVKHVRHHHPDQADPN QGVGKDPPTPTVHLHDVQLED PSPAPAAPHTGPEG

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10879	41247	A	10941	1	944	MSILLTSIARQSRDKRTRLGHK QRILAGLSNHPIRNLQGLRR FALVDRQLVVQNVVTRWCRM VYQSAANVFIQHRPISHDERVQ QRGTAITMMVQQAQWAERGK SGLSGVAIGPAVDTSALQAQLR ETLPPHMPVPPVLLQLPLSA NGKLDRLKALPLPELKAQAPGR APKAGSETHIAAAFSSLLGCDVQ DADADFFALGGHSLAMKLA QLSRQVARQVTPGQVMVASTV AKLATIIDAEEDSTRRM/WRNH SAVA*R*WPDVLPFPCVRFCL AVQRALALSRTMVDYRHSVT APQWPHADGGKPG
10880	41248	A	10942	1	939	MRTILTIDIQLRYPRRPGAFGTH TFLKCAFSNKQRRFTVKRFAFL AARYPASQEMPPVRHGHAVAA AIPCGNVNPANGNTPARYKQGQC GLCSSTLQDALRDFIQVAHTCEI PLMPACFGLADDKLWRWLNE KLPCSLMLLPTLPPSVGLRLQN QLQRKIVLFGGVWMPGDEVKK VTCKNGVVNEIWTRNHADIPLR PRFAVLASGSFFSGGLVAERN IREPILGLDVLQTATRGEWYKG DFFAPQPWQQFGVTTDETLP QAGQTIENTLFAICSMGGFDPI AQGGGGVCVSAALHAAQQIA QRAGGQQ
10881	41249	A	10943	25	479	
10882	41250	A	10944	2	453	APSRTSGSSVGLQGSYVLVDVG REFGCERVKG*FLVHRAGHL/L TLWLFSSQINKMEWWSRLVSS DPEINTKKINPENSKVSPGWL ELQQEGEGPRCFQSFTDSCHCL PS/LSDLDSETRSMVEKMMYDQ RQKSMGLPTSDEQKKQEILKK

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10883	41251	A	10945	3	1110	RDPQERRERGRTRVQSSGTWIGA GAMGGEQEEERFDGMLLAMA HQHEGGVQELVNTFFSLRRKT DFFIGGEEGMAEKLITQTFSHH NQLAQKTRREKJARQEAERREK AERAARLAKEAKSETSGPQIKE LTDEKAELQLEIDQKKDAENP EAQLKNGSLDSPGKQDTEEDDE EDEKDKGKLPNLGNGADLAQ *RLNPDPCRELDLA VPF.CVNFR LKGGDMVVDI/RRQHLGVGL KGQPAIIDGELYNEVKVEESISW LIEDGKVVTVHLEKINKMEW WSRLVSSDPEINTKK\INPENS LSDLSETR\SMVEKMMYDQ\ RQKSMGLPTSDEQKK\QEILK\K FMDQHPMGFFPKAKFPTNPC
10884	41252	A	10946	50	426	
10885	41253	A	10947	1	942	QVWKQCNCFKHYSNETDNSTTQ LVGLQTLQVVVPSLILCEHCMN FSSPHVWCCLVQAVPGQGQT MQVPVSGTQGLQQVSN*KY*A VYQRRGFKE\IITTYQTQIIQQ PQTAVTAGQTQVIPLALSHRSK TDLEESDN*VRYFPVNADGTIL QQGKCTHKLP*DFLGQLFCPLD N*HLSSSGQGTVTVTLPVAGNV VNSGGMVVMVRKICIFQLCL*NF LEHAT*CLLKFEPLYVNAKQYH RILKRRQARAKLEAEGKIPKER RVCITLGR*ERRIAGFYF*NYLL YPKEKDSPHMQVGRHIHIFILLFI TLY
10886	41254	A	10948	24	378	
10887	41255	A	10949	15	658	QRPNAAQTQPSRGQLSAPARA GRFHQPQSCRPSRVGCKGHVCIP GDRSLALWPRLGCGE*TSSAL DSQGILVSNFPHEGS/PTPQSG LKTGRILLNHGRRLKVSQSEG RFLEVGWKQRGPTAHRTHSNR TRRRHALSTGGDTGRARNARS GGGRSPSSLPAASSTPGVCWS PRMSQARQPPSCRRGVPRRPEM LRLSLSPSCQICVCVRFH

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10888	41256	A	10950	1171	1639	PMALWADGRARHKVGTECEC GMHPGLKCSGR TLGSQTM LAT TPCDSPT*1/SNKNGLRSV/SYR* CLINALWLFSPHILVRCGTESS *LLPSLVPSWLP*LVRVRPLPT GWC*IPSCCLKPPTWSSHSPQ RLP*NPATLVCLQNGTARSHSS TPV
10889	41257	A	10951	2	357	HERLLNPGRETWDATCYSETAS CSVA*ATVQ*HDHGLS*PQTPG LKWFHFLPSWDYRHHVPPCP ETGCPVTDQGVQWSYHGSL*P QTPRLKQSYHVS LPSWDYRW EHPVAGKQA
10890	41258	A	10952	15	578	IQITPKGRRTKPCRQKRTIVTP RQSTPRSNRGKDTRSKQRDETT E*TTTRAQDTNKEGATQDR TETA RRTQSNMEKEKFNQHNKRKRD RDSRKDKGHERETKNTERNRT KRREKRKDNKNHNEAKSQRQTR KKKETKETATRKREEPSNSCSM HPFQISWLHSVGDNGRRDQLLC QGPHLYLMCFQ
10891	41259	A	10953	2	369	DIDPTGLQSQSGPKGQDPPLMF SEDYQKSLLEQYHLGLDQKLR KYVVGELIWNFADFMTNQCP KTTSPVILFLPSCEEPQANKATL VCLMNN/FYPGILMVTWKADG TLITQSVEKTTPSKQS
10892	41260	A	10954	1	417	FGTGPSASPRTSFRHQCGH*PH WTA VTVDSQGAGQPKTTSPVIL FLPSCEEPQANKATLVCLMNNF IPGILMVTWKADGTLITQSVEK TT/PSKQSNKNKYVASSYLSLTPE ISWRSRRSYSCQVMQEGSTVEK SVAPAECS
10893	41261	A	10955	113	767	GPMRPGTGQGGLEAPGEPGPN LRQRWPLLLGLAVVTHGLLR PTAASQSRALGPGAPGSSRSS LRSRWGRFLLQRGSWTGPRCW PRGFQSKHNSVTHVFGSGTQLT VLSQPQ/ALTPSVILFLPSCEEP QANKATLVCLMNDYFPGILTV TWKADGTPITH/GVEKTTPSKQ SNKNKYVASS/YTSLTPEQWRS RRSYSCQVMQEGSTVEKSVAP

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10894	41262	A	10956	1	344	GSAAGQVQQQQRRHQQGVK TVKYDRKELRRRLVLEEWE VIVE QLGQLYGCEEEEMPEVEIDIDD LLDADSDEERASKLQEA LVDC YKPTTEFIKELLSRIRGMREN*A PPPKKSV
10895	41263	A	10957	3	349	TMNNMRGQILLFLLIWLWNR YGQLVGSSEKHKIASQLELIQS QFHYCVTLDKLLNFSEPVHV K QEQLLSVCSEKEVTEVKVLALV NHVGSKCCFLFCSGPSP*PKFSV SQVFS
10896	41264	A	10958	998	1383	
10897	41265	A	10959	39	402	TDHIMREYKLVVLGSGGVGKS ALTQVQVQGFVEKYDPTIEDS YRKQVEVDQCCMLEILD TAG TEQFTAMRDLYMKNQGQFALV YSITGQSTFNDLQDLREQILRG* RTREDVPMILVGN
10898	41266	A	10960	25	739	YKKNFIDISLSVKCETCTHMLT SSSL*C*NLCISFLIDFNL*AG FVI*VGFTAQSTFNDLQDLREQI LRVKDTEDEVISFLCKMLCHLS VAK*KSACFQNLARQWCNCAF LESSAKSKINNVETYNCAWAA QTS AFLVCFKLTA RLLALSITNV SSCTGWGVQRSHQDQGS KHA ASSVWKVGFIVRLGTGTCLSS LERGYMCMEKEMFDPYTPSRV LKPRSEALELFGPLKSLT
10899	41267	A	10961	946	1424	YFRFLCVIFCSFLLRCLVSRVLL YPMLIAEIPRVQGRGGPSWPL GGRLKELSRLLTFLKVRKLSIL SGWREVP LGQPSL TEPP/PPAPP HPGPGSWLASASAPHL SQPPAA GPAGQPPSPGSPVPGGCSLALP VTSVLCLEPPALKPAAASAPVV AVH
10900	41268	A	10962	1	148	TALQEFGTRSGIPALGCP PPDP* PPPGSCPPPEQLLSVG EPSRCS CSP
10901	41269	A	10963	10	233	LGAARRAQLLESWPRA/PPPAR LHACHLQ/LPRTPKVHTS*PTQ QQGGFSLCKKKNVPVSVEMIC SSARLKLTE
10902	41270	A	10964	1	331	RPLLSLTLCWELRAALSYWRA GRAPPPPARLHAGPASGFWVLT PSGGEGERP THLWGGGGRG GGRRKKD*GGQGRGAGGFATF SPPANAPRLHTSLTNSSARWIFL CV

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10903	41271	A	10965	4	1023	FPRAGEKPYTCESGRAFNQS* TLTTHMTIHAG*KPYKCEECGK AFYRFSYLTKHMIHTGETFYK CEECGRGFNWSSTLTKNRIHT GEKPYKCEQCGKALNESSNLT AHKIIHTGEKPYKCEECGKAFN RSPKLTAKHVIHSGEKPYKCEE CGKAFSQSSILTTKRIHTGEKP YKCEECGKAFNRSSNLT.KHKII HTGEKSYKCEECGICRTPKMAV FSQCHQVLKITNIHYPSSIAITVH GDRAQSHVDICTLGDKASGAIH GTAFTYTQCEQRAYNETAVSR YTISRPPSHHGGDSEITTEFPAI GRCNGVHKSWGNSRCSDRWRS
10904	41272	A	10966	1	290	
10905	41273	A	10967	1	1508	MSWAARPPFLQRHAAGQC GVGRKEMHCGVASRWRRRR WLDPAAAAAA VAGGEQQT EPEPEAGRDGMGDSGRGEC SRRAGEPVTALSA T P P P P P P V I S SSMGSPGLPPAPPFGSPVSSP QVRGCDQLTA W P L S F S C F C P N P V L G V R G L H C P P P P G P G A G K R L C A I C G D R S S G M W L R G * T E R E S L G H V S S P V G * D L T Y S C R D N K D C T V D K R Q R N R C Q Y C R Y Q K C L A T G M K R E G K D P P C P G V L D H M P F S L I P L R P P E E M P V D R I L E A E L A V E Q K S D Q G V E G P G G T G G S G S S V S V G V N P L S F V M G V G G G S L G L W A K R I P H F S S L P L D D Q V I L L R A G Q * P W I P L T S * H L T P L * L P D L F L A T G L H V H R N S A H S A G V G A I F D R S V A L G * A G M * I E G V G L * A G P C L R A I I L F N P G K R R I T F V S Q G Q G N L G A S S S P M E T Y C K Q K Y P E Q Q R * D G A G G H * G S L G G G E C Y E D V F L F F F K L I G D T P I D T F L M E M L E A P H Q L
10906	41274	A	10968	945	1131	MICTVAISYVLFVDVYISLLSAT CSPKQGS AVFQHD*VSPGI*NG SERCCSRDRHRQFLW
10907	41275	A	10969	37	332	AEGIRTIQGTENIFCKVWGRQ VLSQTNTLEGQSNHDGCLRL KRTFTISTTAHYSRFFLQRF/VFP YTGFEKQCS TAW*KPRYLLSHS VKGKRN LHPA
10908	41276	A	10970	137	283	
10909	41277	B	10971	1	624	

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10910	41278	A	10972	3	618	KTQDPAKAPNTPDILEIEFKKG VPVKVTNVKDGTTTHQTSLELF MYLNEVAAQHGVGRIIDLGDN RFIGMKGRGIYYTPTGTILYHA HLHIEAFIMDREVRTIIQGLGLK FAELVYTGFWHSPELCLRHCI AKSQERVEGKVQVSVLKGQVY ILGRESPLSLYNEELVSMNVQG DYEPTDATGFININSLRLKEYHR LQSKVTAK
10911	41279	B	10973	1	1102	
10912	41280	A	10974	748	1396	LYLQRPFFQIRSSLQVLGHRQIF PQSPRCLHLAPPLMRHSHRSPT WY*FSPRRTQSRPVSAQPLGS CGGIQPAAPPVTPQSQLSPPRGS R*LGSDGAGTQPRHVQNPCLT CVHM*SPPPCLNLQARCPQSL RAKVVPAAVEQARARVGHVESPG SHCWLEREPEVGSGPQQGQRPL PAGAAD*CLGAFWQTHLDLGD SLISCSDHLQGWQLSQA
10913	41281	A	10975	1	846	
10914	41282	A	10976	2	851	WNSAELGRGGPGAGGAVIGM MRTQCLLGLRTFVAFAAKLWS FFIYLLRRQIRTVIQYQTVRYDI LPLSPVSRNRLAQVKRKLVLVD LDETLIHHHDGVL RPTVRPGT PPDFILKVVIDKHPVRFFVHKR PHVDFLEVV SQWYELVVF TAS MEIYGSAVADKLDNSRSILKR RYRQHQCTLELG/SYIKD/LSLV VHSDLS/GIVIL/DNSPGA/YRSH PGYGGRI/DNAIP/KSWSVTPSI DTALLNLLPMLDALRFTADVRS V/LSRNLHQHRLWYTA CFPLPP
10915	41283	A	10977	25	153	
10916	41284	A	10978	1	741	MMSFDSMSHIQVMLLQEVPS YPASKKNEA/PQTSGGGPGT KGLGE/PAVVPMSPAVGT/PALT QCHGPHAEDDLEELTTDPVA RDCPLDLLMDGKTGAIISSLLHS NCLPAPFCQCSHAVKWLKTV HSCCPLGEVQPORRCVIA TAKE KGIGVKHHCNIHSDNVNSIITAT VAAHQQQQLPQNGNNSGIKNN QNSSENTVTNNSKNISNHIICRN SSKNSKSSSSSSSSNNKNSSNTI NSNNKAR

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10917	41285	A	10979	1	669	MMSFDSMSHIQVMLLQEVPS YPASKKNEA/PQTSGGGPGT KGLGE/PAVVPMSPAVGT/PALT QCHGPHDEDDLEPILTTDPVA RDLTMPTAASQHLKQCLEHH HYFHSYNINSDIIVSRNNISSHIT TPVHHCHISDNVNSHITATVAA HQQQQLPQNGNNSGIKNQNS SENTVTNNSKNINHHICRNSSK NSKSSSSSSNNKNSSNTINSN NKAR
10918	41286	A	10980	3	980	IESPGFPFGLQRPVPHRGEFL RCTSSEALPCFYSWTVTFSPWT VAAAQGGPRPGASRTLLLATQ SEIAAAELGPGSWGPPSCPSE QSSHGPPASS*AAPLQTRRLRS RAS*RSAGPSVAALPAPLSRQPE RHPSVSASRSGHPGCPSPPPP AARPVQPSPCRAPPGSAAGRAR APHA*AAPGSWLSAGAAARR WPFQTAKGSGS*DRPGRPGPDA PAAPGWHRAPPSSSSGAGTG RHPQPFGRPRRTAPYAAPCA FVATLVFS*LLIFGGAFSPALS HCPTSA*LKRLLEPAPIAFPPG LHPGTLLSRAE
10919	41287	A	10981	1	5229	
10920	41288	A	10982	1	7044	
10921	41289	A	10983	1	3228	
10922	41290	A	10984	10	209	TLSGGEPQRLAERRARLQDEE RRRQQLE*MRKREEDRARQ EEERRRQEERTKRDAAEKVM
10923	41291	A	10985	293	363	
10924	41292	A	10986	3	434	
10925	41293	A	10987	3	1536	
10926	41294	A	10988	315	993	VPVAPIHFHSHFSPAPTFTQSR QDSMQCILRQHCHLILSRSSSL VPAGLRGAMAFALAIRDTASY ARQMMFTTLLICPELLALLLS LSHSRSLLLHGYHGPS*YALFFS LSFSLVTWVGAKPGRYQSLIFV VVVGCTFQNGEPLREEDSDFIL TEGDLTLTYGDSTVTANGSSSS HTASTSLEGSRRTKSSSEEVLER DLGMGQKQVSSRGTRLVFPLE
10927	41295	A	10989	3	320	

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10928	41296	A	10990	3	582	GPPTPRRPRPLPSSLPSRRSRDPP RIPLCA*FPQTRKQIARSEPD*T WASQSSSTIPRIWRVFHA*KFST APL.TATPPPGKMCAGCRETVK TT*PPLRGGPAPFLLPSRAVARG TRPGFRSALSFRRPGNRSRGVN LIKLGRLSPPPYPGGGSYTPE NSQPLPSLLHLEKCALRDAE RQLKPPDHHLMAVWLPDVWN GEGEPSPSHTRHSLRASSNYV LRAPEGNLLARRLPRETAINLQ PKACYKTLSPESFSHFYNQFC PRRHQWLPAPPPGHFFLG
10929	41297	A	10991	3	338	NSPSRPRSSQRGVAGRREAGP VAVP*GGPKKGRGC*GNRWG QRPRWMLRASGSGESTTPACSA ENRHAS*RKKRRRPGQVSWE TEETRSGHSGPRGHAEP LHRP QRR
10930	41298	A	10992	3	226	TILSS*SSSSSSPSPSPSPSPSP SPSPSPSPSPSPSPSPSSFFLRWS PALFPRSLSFLFPGTGTFPSCP
10931	41299	A	10993	24	489	KEYLVRTK*QKQKGENPLVKIT FRPPPGRLRTYPSAPWSARSTYG RAAAVWRPHSPSAPRRGTHPW PAGHRGQRASGEGVGTHTHAH MSSVCACSTHTCWSRNCCKDPR EDRGRGLTVLLEAAVCNSCLLL VLKTPRNPQLPILYTDSDTKSST GNP
10932	41300	A	10994	1	1491	
10933	41301	A	10995	140	308	RNVIKLKGWSRPSKQQDNPTLR PGPPSPAGGFGQLLMRMRPLA GGGKSWGIAHFYKPLQRERRA GAECGLARQVRAEVTKWIGVN RRPRKRRKMEKEEVFEKLLPD QLGLLLEHLLQKTLSPRTLQS LQRTYHLQDQDAEVRHRWCEL IVKHKFTKAYKSVRFLLQEDQA MGVYLYGELMVSEDARQQQL ARRCFERTKEQMDRSSAQVVA EMLF*RGQDRFSLKKCDKVKG MVKTQQATGQPDSPPRALTG RRVPATADADEKAFGGWRKIL GYRTFL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *~Stop codon, /~possible nucleotide deletion, ~possible nucleotide insertion)
10934	41302	A	10996	219	688	RRMHAYVSLDPLRPPFFFLF FFFFFFLRRSFALVAQAGVHW RDLGSPQPPPRFK*FSCLSLPSS WNYRHHAPRPANFVFLVETGL QLPTSGDLPASASQSVGITGVS HCAWPGNWLLKETRCSSVGR QITGPITDAWVDPGIPDRYLQ
10935	41303	A	10997	3	298	FFFFFLRQSFALVAQAGVQWRD LCSPQPPPPPRFK*FSCLSLPSSW NYRHHGPPHPANF*FLVEMEFH HVGQACLKLLPSGDPALASQS AGITGVSHRA
10936	41304	A	10998	2	438	APSVRSGNERDLARDEEAQETQ VRGCHASGGCTPAATAGASPP AWAGRRGTGQRLRSQPRQTGR QPPRVQPLAPPGAPAPLPNPQ NCRKTRSHPRFWAGTLAPGPC PGLWCLPGLVQVDVLAAGRCD HLSCLPPLCPQAFLL
10937	41305	A	10999	2856	3044	GAATGEGGCCRLPGHPALAST A*AIPCRGPRVQETSPPPVLGW DPGSRAMSRLVFAVVGAG
10938	41306	A	11000	1	908	GLGDPGVPLRSGGLGPPADLK GDQAVAE*LHEASGVTEHHPS AQPGPGGEAAEPAHLIV*EPEG GSPGHPGGGPGHPG*SEGPAAG KPGPAGGSAQGCRRSSEPSGT *SGRSPR*GPHGHPDCRTHPAR EGAQVHSRSLPGGAPVRRGCS QGPEQLRQEDFLRVQQLSAA GPLRPQLYPQVWLCPEHQLLLE QYPRSYFSEIDVFKPCGVQQG CPVLDRASSKISPEDAAGSVVR LRSLWAASGLQQGASGLATFL QLLTCGVLPWDEELVHLLDE VVASAAALRCPDPVPMPTCG

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10939	41307	A	11001	218	990	VLQLLKAMRLEFLPPGGFMV LLASGVKLQTFATQVPSWLHP VDPSGLELPAASPVQCAHTP QPLGGRWDVWPWSRQGRSSG RLGPHGSPWRRWEAQAWQPA GPKPCPVGS*GPVNRNGQRRW AGTAGDPVHPPQLAQVLSPL PGADRAGQLLRVQGPSPCPPG TPAGPQGRCAAPVPTGVSPSTP PCKLREQAPALASPERGSHSAA VG*RAPQVLPKW*PELMFRWV RSFFLLVGSWLTSGVKLHPFVV SVTALKGDASGVIPSSRWVHGL AGLRCEAADLRDSGAQLASPS GSLTRTGGGAACQSRVCPHSS AFGWSMGLGAMEQGAALIGEA RASREPMEEVGGSGMAACRSQ ALPRGQLRPSEKSRAPVGWH CWGPSTPSAATGPGAKPLIARG RQGRPAQAQSGAPAKPMPTRNSS WPAKAVRSPGSHWRLSLHTSL QAERAGSGLGQPRKGLPQCSSG LKGSSSAAKVVAQEEAQRAS EGCEDYLARCHLSIRKMRNRN
10940	41308	A	11002	3	644	EPPGPTGPPSPQSPWHPLGR WSSTHVVFTHLHLAAGPWSCD HRWMGKQLPVSLASGVQGV RFRSQDMYQSSRNKFPSGAAH VPQEWAVPWKNQGNTHQSSRP SESGCCAQAEGSNQCHQREAE AGPSRLSLPDGGRRLTPRHNP GPWYWNNSPQRLN*WRRGDPS WPEPQGKPHTTGARVPACQRR EICLSFPRGPRRRQKENIYEYL
10941	41309	A	11003	202	438	FHGHAPAGEMRGWPRVTKRSP AQSGKTHFPPGSPGPDSTESI FRRAWKAPGPGRGRTADPET ARCGAWDEIVEPV
10942	41310	A	11004	520	1094	GPLSQCPPLRLLPPLGVYSKGR APHADTHSPGHRRTAHAQPA AAAATATR*QRRRLPPRRTPF RRPAARPDRRVPAHSSAVLPRP GKPGAFQALRKMDSVDVSGGP GEPGGKLGFARLRRAPPDRLPG CPSSHSFQTQSLSFMAHNVDPE LESATSLGLLRRSWFCFTWQK QTVYWSVTGRIRHSGEK
10943	41311	A	11005	1	138	SISLMNDVKILNKILANQIQQH RKLHHDD*VGFIPCLRILVYI

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10944	41312	A	11006	65	297	NQRLPQFLPTTTPPATRAT*D EEKSPYPGPGSDKKCP TLQ.LPSP PTPSAGGFPLGESGSPGGLVK AQIMEGISM
10945	41313	B	11007	322	6900	
10946	41314	A	11008	3	215	
10947	41315	A	11009	1	234	
10948	41316	A	11010	149	300	
10949	41317	B	11011	28	162	
10950	41318	A	11012	700	861	RRKCIPGRNRSKHKGPDGAGRP *VCREQEQEGQCAWTGYPGAQG PDOPYCGKGPYS
10951	41319	A	11013	291	744	LKKRTKCDQLLKTSFLDLGRGPI LKWLCTSKWGHQIIIRA*GTE YKTTSTFFFFETASRLCHPGWE CSGAISAHS*FLLPGSCHSPASA S*VAVTTDTREHAQLIFF*HFSTR DGFHVVARWLDLLTCDLPLSL QVLGYRNYIIIVRQLPSR
10952	41320	A	11014	139	414	SPKTAPPGFFFSF*LHLMLMKFT PGAIKLVFLQFLLGISFFFLGKP PSSWFRNESC SVFRKESQSWQ GRAHVWG*SDPWSSGRSRAH L
10953	41321	A	11015	5	565	VHTTEATCTTTGAKPCPWPSKL ATRQDHSVLSTSNPRGPTPHKS GSPETAGALSSGDAGSRGEGPR TVSSERSSPGKGGSTLLGTTA*G PGPAHFASAVLGPSSKSLQAAS *EVDSPSSLLKTAVSVLASTVR LSVSFMPFFITVSVTSSVISASS PSELASMATLPGASG*AAAVN FELDEE
10954	41322	A	11016	188	515	SQTVSIVGELPIPRKRCEIGIWD AQKR/CPRLTGPWATISVPTISK KATGN/PQHPNHPRARYQINAE *WKVHIF*TNDRPSHECPCTLV VHRTLQDLRHKSSTSGGKTHG
10955	41323	A	11017	80	397	SVQRSVDHL*DHP*TSVDWELY LDGSSFANPCKVTLKTTTSPAS VTPEADWSMHQSQRNLSRDS FSLKFGLIIHDFLPTFNPLENP CGFLTRCCVPNQISS
10956	41324	A	11018	104	392	PSQFHLKLLHMLALLYPVGTG QVKDSSLQKSTSVPPDSPQTG HSLKLGPNPGRFR*RPQCQPGV LPDVELSCHSWNVLWTTAA KTPIFCY

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10957	41325	A	11019	125	1404	NLALGMAMWN\RPCQRLPQQP LVAEPTAEGEPLPTGRELTEA NRFAYAAALCGISLSQLFPEPEHS SFCTEFMAGLVKWLSEAVLP TMTAFASGLGGEGTDVSVQTL LKDDPILKDDPTVITQDLSFSLK DGHYDARARVLVCHMTSLQLQV PLEELDVL EEMFLESLEKEEEE SEMAEASRKKKENRRKWKRYL LIGLATVGGGTVIGVTGGLAAP LVAAGAATIIGSAGAAALGSAA GIAIMTSLFGAAGAGLTGYKM KKRVGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYRTFSAPWA ALAIHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGIVAALTWPASLLSVAN VIDNPWGVCLHRS AEVGKHLA HILLSRQQGRRPVTLIGFSLGAR VIYFCLQEMAQEK
10958	41326	A	11020	3	1693	CQRLPQQPLVAEPTAEGEPLP TGRELTEANRFAYAAALCGISLS QLFPEPEHR*VLLSCPLGTPVGL HSDAHYGGRLAVAVHVEGTLF FTSSTFAAASVFQKARPWQHPG EQMAFSGKPLVAAVTSAGGS GAPSVGCTELISTSVLGYHTAL EMAGLVQWLELSEAVLPTMTA FASGLGGEGADV FVQILLKDDP LKDDPTVITQVHPTPGVKDGKL IF*ARVLVCHMTSLQLQVPLEEL DVL EEMFLESLEKEIEESE*ES PATKTEGGGEDKDRKHPLMGD KMTESKTDLWIYEMGNAGVLL FRRYLWLQPKKKENRRKWK YLLIGLATVGGGTVIGESS*RCA PLVAAGAATIIGSAGAAALGSA AGIAIMTSLFGAAGAGLTGKVQ KE*VGAI EEF TFLPLTEGRQLHI TIAVTGWLASGKYREDQEDQA ALAHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGKCPHLPWPASLLSVAN VIDNPWGVCLHRS AEVGKHLA HILLSRQQVPGNGCVIGFSLGA RVYIFCLQEMAQEKGEHLL
10959	41327	A	11021	208	324	VSLLKAADNWL VNSYPFCNSV SSEFFFR*IRDFFLFWIH
10960	41328	A	11022	1265	1459	
10961	41329	C	11023	188	730	

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10962	41330	A	11024	64	228	QHLLRRWGRSGLLNDR*VSN EIKMEINKFIELNNNSDTIYQTL WDTANTVLKFM
10963	41331	A	11025	1	648	
10964	41332	A	11026	26	613	VGAGGRGWRFAAAVRRRAAGG GLRPGPAPGPRAGGGGPRGAH LALLRRAGALRAGKEYGKADA RWVYFDPTIVSVEILAVALDVS LALFLIYAIVKEKYYRHFLQITL CVCEL.YGCWMTFLPEWAHPEA PNLQQPATGWLYWLGFLLFF* RCVGLIPRNWLLWAVHGPRTS RKWHQKGNQFQWKEVFSGT
10965	41333	A	11027	2	252	ARGRAGVAGGPR*AAELPGL RDPFPASRPLRRSDCLGLIRHK PPDPGAGARVEGEALPSWSPGG ALEEGVT*PGRGPPWE
10966	41334	A	11028	3	637	RQVRRGGGGEPAHQCPRRRL GEGPGAPNRLGGPARDPRCSPW PRADSPRPNRLSSQPLRPAYL GPACFP*PSWGVSRSLPSLAPW RPHRLPDSQRFPPNGGSRSRATS GSWTWKSKECREWRPSGSRGT RGSSGSGAGSSGSSAGVGRRAG HGRWHLR*GPLFAAPASATCP LWHGWKGASLDLGLQPWATF YPRVTGARGGRTLGP
10967	41335	A	11029	158	462	
10968	41336	A	11030	339	866	QICHSPPGNKAHSHLLPYQTPV PSSQYPPSPSRTLQLPFPTWNP CQWPSRGSCGPAVGTGPPFPT GIPSV*APSARG*HHSSACGCH PGCAGPQPARSPHGPAPASGCH TVSGCCCHALLQSCLAAGRPSA GTWPHPPGGLPSAPGTETPCTA FEGFQPPCWLSQLPLSPCL
10969	41337	A	11031	621	944	TPOGGTAPSGGRHPWASAPIR LPPL*CSARGCH/SSRMSPGT RPSGPLQDCHPPRPQTPHAGS HHTSAPQAPAGTF**RQRVAPG SSCWHLPQSWSCSAWLGGC
10970	41338	A	11032	3	257	AGRASKGG*NPSKAVQGSVPG AEGSPPEGCGQGPAGLGLPGA RQDCSRA*QHPPGPGGQVEY LDISLAPGSTGIQGLEAKHL
10971	41339	A	11033	94	227	SSYVFKSILAFGMTWMRLTII LSEVTQG*KTKHQMFSLICGS

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10972	41340	A	11034	404	894	FVYFFRGELCKISSTLGFKGTGQ GLQPSKVS**VPSRPAGNRP YPETSQPPGPSGG*HWLAGW Q*GGPEPGWTCIWP*GS*GTEIG SPSQGPPEPAGVPSRDAGSAA TGCHTLAGLVVWPPRLCHRRV TDGRKSMKRCLSRSYCTSSVRA SGGGAGRIT
10973	41341	A	11035	1	408	
10974	41342	A	11036	68	204	SFLWHPGLHFFHTHH**NYKS SSK*MVRIRVTFSKFIFVRNNYC
10975	41343	A	11037	5	188	PQCRHLRLRQGLALSPKLECSAI TAHCSLELPGSSNPPSASRF*GS RSVAQAGVQQCYHSSLQPTP GVKQSSSLFPFLRLQPKVSSATL PVRLQE
10976	41344	A	11038	1	263	
10977	41345	A	11039	2	283	
10978	41346	A	11040	1	1965	MAAENEASQESALGAYSPVDY MSITSFPRLEPEPAPAAPLRGR KDEDAFLGDPDTGEAR*PRPCP ALGSPRSSFFCVKHGPGPLRETR KDPFSAAAAECSCRDGLTVIV TACLTFATGVTVALVMQIYFG DPQVRGTNGEGEETGEWVG* CLRNCCKGSSVDAAVAAALCL GIVAPHSSGLGG*GAVEVGVPQ AYFLPPGL*ASCAARALREETL QRSWETKVGTLVRRESSGESLF IALLLTQALIC*VLAQDGFNVT HDLGQWGLGIWERHEVDGEG* NL*DLEPPPLPGSLLRPDLAEV LDVLGTSGPAAFYAGGNLTLE MVAEVSARVVRVGACPKVPIA GHPRPHFGVYRGDLSPGSQGP PSGEASQSMATSFWPNLTSLV SREQUALHWVAEVRRLRLFPFGF KDIRSGEIGYCHRADDMLRWV LGRTWGLQRQRVWVGKGQEK SSYELDGAPTAQVLIMGPDF IVAMVRYASSDSEPGTRDPLNQ EGVGAG*RFSPNRTANHSAPS LVGFASLLSWG*GL*VGGAM AWLPLCGTYLALGANGAARGL SGLTQVRFTPWLAFFSREPSG LDCRCLS*QSNLLQVDSECAE TSWGGHRDR*RKSSQGCPCWV HGSRRITNNFIIVKDRSPDAA

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10979	41347	A	11041	1	363	SSMTTVHATTATQKTVGETLA* LLQNIIPVSTSVAEAMGKVIPEP DKRLTGMAFCVPTHNMLVVVAL ICHLQKAAKYDGMRRFCNATT GITFNHGFVRLLSWDEFGSSNR VVDLMVHTASKE
10980	41348	A	11042	162	303	CLLLKSCSQEAAAALALPALGL VFDVFL*IVFVRTKYLRVGFNRN FF
10981	41349	C	11043	56	118	
10982	41350	C	11044	345	410	
10983	41351	C	11045	7	439	
10984	41352	A	11046	2	80	
10985	41353	B	11047	205	5326	
10986	41354	A	11048	1	813	
10987	41355	A	11049	1	1454	
10988	41356	A	11050	2	1624	
10989	41357	A	11051	1	1185	
10990	41358	A	11052	1	2149	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTTRPVLK ELLKEALNMERNWYQPLQKH AKNMPNSIILIPKGRDRTTKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGMQGW NIHKSINVIQHINRTIDKNHMIIS IDA EKAADFQIQLFMLKTLNKL GIDGTYLKIRIKYLGJQLTREV DLFKENYKPLLNEIKEDTNKW KNIPSCWVGRINIMKMAILPKVI YRFNAISNKLPMFTFTELEKTT NFIWNQKRARIKSIKSNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWKGDSLF NKWCWENWLAVCRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPLAIREMQIKT TMRYLTPVRMAIKKSGNNR QTESQIMSELPITIASKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCS WIGRINIVKIM AILPKPTNVHVTNLAAQDTTAL EAAQISLEGHPQEKEISVTAMPL
10991	41359	A	11053	1	2031	

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10992	41360	A	11054	1	1188	
10993	41361	C	11055	1	353	
10994	41362	B	11056	151	1608	
10995	41363	A	11057	1	373	
10996	41364	B	11058	1	488	
10997	41365	A	11059	1	1257	
10998	41366	A	11060	2	3527	
10999	41367	A	11061	1	2373	
11000	41368	A	11062	1	1755	
11001	41369	A	11063	1	1599	
11002	41370	B	11064	220	1286	
11003	41371	A	11065	1	1826	
11004	41372	A	11066	1	1645	MDFKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAIFYQLISNFSKVSQGYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINILKMAILPKNW KKTTLKFIWNHAKACIAKSILS QRNKAGGITLPDFELYKATVT KTAWYWYQNRDIDQWNRTEP SEITPHIYNHMFIDKPKDNKKW GNDSLFDKWCWENWLAICRKL KLPDPLTPYTKINSRWIKDLNV RPKTIKTEESLGNITQDIGIK DFMSKTSKAMTTKAKIDKWDL IKLKSFCATKETTIRVNRQPT WENIFAIYSSDKGLISRIYKELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKHKMKCSSSLAI REMQUIKTMYHLTPVRMAIJK KSGNNRRTRENYFKIHESKKSQ NSQGNRKEQSWRRHATRLQ TIVQGYTVAKTACYWYKNRPT DQSNRTENQEIRLHTYHNLI FKPDKNGETTPYSINGARITG
11005	41373	A	11067	1961	2588	KLAQDRDALSPPLLFNIVLEVL ARAIQKEIKIGLQKEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSQYKINVQKSQAF YTNNRQTESQTMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVNRYRFAIP IKLPMTVFTELEKNYFKVHMGT KKEPASPSQS
11006	41374	A	11068	2	278	
11007	41375	A	11069	3	274	

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11008	41376	A	11070	261	1382	LELSFPAGQRGVLSGDPQNLCTCPSGSWHVPRCWAVEQRPNLPRTVTQLVAEDGSRVYVVGTAHFSDDSKRDVVKVSAAATHIIPDTGWCKLLPGSRDGLVRFPTYRVSMCLKMDESTLLREAEQLSLEKLQQA VRQVRSRGQSGSGSGSKPPHITEQLGMAPGGEFREAFKEVGTG*GRGWPGCGSQAVTFKRAIAALSFQKVR LAWGLCFLSDPIR*GCPDPGRPAGWSVGMAEMIGEPDLHRTIVSERDVIYLYMLRQAARLELPRASDGDGRPQAWDL*G*GPRGHVPGIEKNWSTDLNIQEIM*VPAPCKPHPTSPQVAFFGLLGYSLYWMGRRTASLVLSLPAAYCQCLQR
11009	41377	A	11071	3	506	KDCQF*VGPEQKKALYKVHAPIQAALQLGPYE*ADQKRTCVRFRGHTCETAFTFWKSLGLDKVTKPRSSSSQLLALAIRSSPGSTTDACLLDSFSGKSRISSWFGS
11010	41378	A	11072	2	374	IRRESTHLQALGTTTPQDR LTC TGHS AQPPACASPLPPGPP*SSAWPLPPSTRLARQKQAAATAQP*PLTTQTTLGPWSSASTWTSAHKQPGAAAQEWSTAGSRQLLAGASGSSPSSCSVWTN
11011	41379	A	11073	3	553	
11012	41380	A	11074	239	547	GHHFQMNNVCRCSVWMLSLEPHVPGQIHSC**ERAKLCGKEFRMHNLMMGHMLHSDSKPFKCLYCPSKFTLKGNLTRHMKVKHGVMERGLHSQVSRPSLEA
11013	41381	A	11075	1	267	MAISMVTTKSTTIRITTAAGCHYENDMAHNHSDRGGGLPKVVLVLT PFLTPPGKGGGAAGALERRTEEGDRDAGGAAQEGGLTPTSVP PSS*HTLWLR TVDPEASTSPSTRHPYPNRRGGGGRALPHPRR*V*AGCHYENDMAHNHSDRGGGLPKVVLVLT PFLTPPGKGGGAAGALERRTEEGDRDAGGAAQEGGLTPTSVPSS
11014	41382	A	11076	1	1707	
11015	41383	A	11077	1	1407	

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11016	41384	A	11078	1	1275	MVKGSIQQEELTLKIYAPNTG APRFIKQVLSDLQRDLDSHTIM TGDFTNPLSTSDRSTRQKVNKD IQELNSALHQADLIDYRTLHPK STEYTFFSAPHRTYSIIDLIGGSK ALLSKCKRIEITTNCLSDHSAIK LELRICKKLTONRSTTWQLNNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTIQKISESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDQGDITTLERVVLEEDP TLHLNNTYTPRKVLYRWNRQSS TSVIETNKTSVELSLPFDEYDIIIE IKPFSDDGGDSSSEQIRIPKIS/NK KTK*PNPWRQK*G**LAVADA YARGSGASTSNACLTSAISTI
11017	41385	A	11079	1	426	MLHTKQHLSMGTEDMDDKLH FSDCSAASLVSLSTTTGGHVL NMSADIARYLPVLYRWNRQSS TSVIETNKTSVELSLPFDEYDIIIE IKPFSDDGGDSSSEQIRIPKISNA *ARGSGASTPNACALSAISRIMI SLTARSSL
11018	41386	A	11080	3	620	DRTLAEPHTAPARSGHRGWC PRPHRRRRNRGRQLLAPGRGA DPGAGEAATVQWRLLRGQPAA ALHVQQGAGDAANAGLQRGA HADSHDRAPAGHAPGPVAAA GRGHDGQVPAALG*AGGPVGL RRPEPPLQTRGKGR LAPATQQV GQARRLPTRGQQLLRPPQFAA HHGPRPRLGGRGRGGSHKSPPH GIWPRLAGWRATLE
11019	41387	A	11081	335	640	PLGVLWSLVKSLVHSDAGAGE L*EVITGSTWPNP*QCCLVPNV DDEEEGEEQDDDDDEEEGL*D IDEEGDEDEGEEEDDDVVEEG EEDEGEDDWKFAKE
11020	41388	A	11082	2	204	

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11021	41389	A	11083	3	1471	SKDTKRDVDSKSPGMPLFEAE GVLSRTQIFPTTIKVIDPEFLEEP PALAFLYKDLYEAVGEKKKE EETASEGDSVNSEASFPSRNSDT DDGTGIYFEKYILKDDILHDTSL TQKDDQGGLEEKRVGKDDSYQ PIAAEGEIGWKGFTICREKSL PKGVYGEGRISRPCGDRW* AEESHHIRGRQSGYPENKLCGF LLKTPHHVLERADEAGSHGNE VGNASPEVNLNVPVQVSFP FASGATHVQETSLEEPKILVPPE PSEERLRNSPVQDEYEFTESLH NEVVPQDILSEELSSESTPEDVL SQGKSEFEHISENEFASAEQST PAEQKELGSEKKEEDQLSSEVV TEKAQKELKKSQIDTYCYTCKC PISATDKVFGTHKDHEVSTLDT AISAVKTVIRDSOKTKSGEGAY GREMKSPHKFPEGKIHNDKEH DRIVQEFLAETGPKVTRFNEQC RFRPRIVYYENNQTQIMVEEPQ
11022	41390	B	11084	148	235	
11023	41391	A	11085	30	420	VSGTRGPSPCLGTSWASGAWR PPLGGLPPSAGANGPRVRSAA GCSLVAGCKVLGSWVSFAGR SHVACAGSSGESVVRARCPGTA* AAGGPGPQAFQAA*QGSRMH RAPPRPNRQVQTWWEAGAGTG
11024	41392	A	11086	2	73	ERLRMPGVAKGRPR*GNPRRG RG
11025	41393	B	11087	1	1412	
11026	41394	A	11088	39	427	PPYWGHHFSSAAASAALKGKD GGSSRSLVPPAQ*HSHSPSKTHC VHTPSRSCAQLTHLTQSPPSL KIAQSPSFDARAHARLRWQIPS APRVPPLSALSPTRTAGSVRFE SQSTKTSRSHRFLPRT
11027	41395	B	11089	1	813	
11028	41396	A	11090	3	365	RTPSSKGCGRPPRGMGAQGS GCGRRRSPRRSQARRWSHPC* PPSPPPWPRPARSPPGCSHRAAL SSPSPSSFLARHSARPLALAL GPPPWCSGSCASSAPFDLQHPE QSQNQDARG
11029	41397	C	11091	295	412	
11030	41398	A	11092	21	164	GAVTENDFYDLVRTIGGDLVE KVDLIDKFVHPK*VKSFLILPLT SV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
11031	41399	A	11093	1	1373	GISTMVGSALRRGAHAYVYLV SKASHISRGHQHQA WGSRPAA ECATQAPGSSVVELLGKSYPD DHSNLRKVLTRVGRNLHNQQ HHPLWLIKERVKEHFYKQYVG RFGTPLFSVYDNLSPVTTWQN FDSLLIPADHPSRKKGDNYLYN RTHMLRAHTSAHQWDLHAG LDAFLVVGDVYRRDQIDSQHY PIFHQLEAVRLF SKHELFA GIKD GESLQLFEQSSRSAHKQETHMT EAVKLVEFDLKQTLRLMAHL FGDELEIRWVDCYFPFTHPSFE MEINFHGE\WLEVLGCQVMEQ QLVNSAGAQDRIGWAFGLGLE RLAMILYDIPDIRLFWCED\ERF LKQFCVSNINQKV KFP LSKYP AVINDISFWLPSENYA\NDF*Y LVRTIGSDLVERVDLIDKFVLPK THKTSHSYRIMYR\HMEPTLSQ\ REVRHI/HIQAQEEAAVQLLGV
11032	41400	A	11094	8	119	
11033	41401	A	11095	2	475	QAGPSGGIPEGIAITGDDSSMHA IAPEDLPVGGQDVEAEDSDTGDL DPVLTVFRRGVEREFFSNWYKT AWSFSKLAQKGLSS*PSSLSS SSSSDKAVTAGTELFASSLSSSS DPRRSISSSSLLFVAPLPVVSSTL AGPYLPTAFFTPGRLAFFSFS
11034	41402	B	11096	677	696	
11035	41403	A	11097	1	357	STMIEAHVDVRTTDGYFFLLFC VGFTKKHNNLIPKTSYA*HQY ICLPHQDDRVTHQNPSLPDGSIA RVL SIYYLISRRMNSIISQGL QKVHIHIVPGSLMNQELDDLI TVFFKA
11036	41404	B	11098	1	541	
11037	41405	A	11099	14	671	PAPWRLGKNKRLTKGGKKGA\ KKKGVNPFSSKEWYD\VKAPA MFNIRNIGKTLVTRTQGTKIAS DGLK/GVRVFEVSLADLQNDV AFRKVKLIT\EDVQGNCLTN\F HGMDLY/TRDKMCSMVKK\WQ TMIEAHVDVKTTDGYLLRFLC VGFTKKRNQIRKTSYA\QHQQ \VRQIREGRWMEIMDPRRWQD QMDLEEVGHELIAGSIWKHRH KGLPIYLSSP

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11038	41406	A	11100	1	217	RQGLTLSFRLECPGVISAHCSLN LPGSSKPPASAPQVAGTTGVYH HAS*FFIFFVEMGFHHVAQPL CNFVF
11039	41407	A	11101	2	442	LDVQIQEAQRTPGKFIKRYSP RHFVIRLSKLTKERILRAVRQ KHQVTYKGGPIRLAADFSTETL QARRDRGPISLLKQNNYQPRI LYPEKLSIIYEGKIQSFSDKQML REFAIRKPPQLLELKGSLNLETN PGNT*KQNFFKA
11040	41408	A	11102	2	545	EPRPGKTAHVYGPDCLCGSCV QLSFGSAFFSTRWVSYEQANCK GEQFVFEKGEYAHWDWWTSS QRT/DLSSLRPIKVDSEHKILY ENPNFTGKKMEIIDDVPSFHA HGVQKEKVSSVWLRSGTWVGY *YPGYRGLQYLLEKGDYKDSS DFGARHPQVQSVRCIHD MQGH QCGAFHPSK
11041	41409	A	11103	2	389	EIIDDVPSFHAHGYQEKVSSV WVRSGM*VHCQPWLTLPQELR LWGPRSGETLALTAPVSKTCD FGARHPQVQSVRCIHD MQGHQ CGAFHPLGTQEEEEAGQKEQM EQVPFWLARGDICELSGKKS
11042	41410	A	11104	1	446	MEEEELEFVEELEAVLQLTPEV QLAIEQVFPSPDPLDRAFNVA EYINTLFPTEQLPMPSAHGGVSS CGNAGGPVSFATRENARCGIW GSGGVCDGVFGA/GAAGWGGV *GGGALGWMLSGRRIVLRS AIF TSPVSRAGSPERGWS CDC
11043	41411	A	11105	1	210	SSDGRHLAFDQGS PG*VLGHVG KQRAVDVQPSVAVRVRQPLLL LSTIMSGLLGWEQGIDILNSIEI CSI
11044	41412	A	11106	2	287	AAESPGRSTRTDGAGLTRSLPR GSR CAGAWVAAGGLSWARGG GRQEAGWRNDG*GGTGARGG AGSRAAAHARGAAGHRASVSK PGPSRSSRFQCC
11045	41413	A	11107	150	389	GEEIAWLGAA RPKPTPSRIPL* PSLFPWRPHKFPERSVFAQSOP ASQSPPLRPPPSHPEGSCLSGR LPPPGYLLPLR
11046	41414	C	11108	43	213	
11047	41415	A	11109	3	246	SSFPAPAREGALAPCRCLAGISV TLQGNP*GRCHHHHHHHHHHH HRCYDSQESGKLPRPGPKAELE GPPAWLLVGP GAHP

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11048	41416	A	11113	1	726	
11049	41417	A	11114	2	251	LSCGRSLHQGSVTSCKTINALT LTVDITWRGCAW*GCACTFHCR SATNMIRAYVVFSTISVLSLQEI RLSLRAILADLRSLICF
11050	41418	A	11115	1	1041	
11051	41419	A	11116	1	398	MGPNSTLENLLKGATSVFYNR DQEEAQKKERKLGRGTKALAA ALQ/SWQSPGAPRCIH*LLSVW QARVF*RGMPRQQDEATSLSI QWQKPVETELSPDMEVTGFRA SLTDERVHLEPVLPEQYTEQRR QGHL
11052	41420	A	11117	5	137	
11053	41421	A	11118	5	272	
11054	41422	A	11119	2	211	WNQPRCPSTVNWIMKIWIYT MEHYAAIKRNMIMSFATWME LEAIFLSKMPQ*QKNKYCVFLH ACLES
11055	41423	B	11120	1	1560	
11056	41424	A	11121	1	588	
11057	41425	A	11122	80	574	EPAAQGNVLVDLLC*MKNRNR WLPNELSQLVHTQSQFSKTG MSAKHTAFAMRMSPAQMIDIV VGLSTGQSPFMVLMQGGHSA MQETRIASLPVTAIPAGMKIPCV TAGSACMVGPSVRVNEWFSAY GMAGMAYSRVSTFVRGLSPRY LTTREAPGCGSSAGH
11058	41426	A	11123	48	131	
11059	41427	A	11124	1	1195	
11060	41428	A	11125	2	1028	
11061	41429	A	11126	1	1008	NMMEQVLDIPSL*VISKDNANV TIDAVCFIQVIDAPRAAYEVSNL ELAIINLTMTNIRTVLGSMELDE MLSQRDSINSRLRIVDEATNPL ALKIAARMIEDGELDKRIAQRY SGWNSLGGQILKGQMSLADL AKYAQEHHLSPVHHQVAEWM RARNGQLFRLRSNHLTLLEQN NFIYARGAKIYPDIHIDRSLLKCP SDLFAANARCGICQSDERCLR YQPRRERGLYRIDITYPGKSYTT TALPSRFVWFVTGKAQSTQAS ALSYSIDSLLYHHLDLVYQRLGH LDDGTDSDWNHVPTLNGQCTLV LIHEYVDTRGPEIKTILVISWWN ILVFH

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11062	41430	A	11127	3	333	DIQIGEEENRKRWLRTGKCSFLP KEREWMDRLMSWGLVDTFRH ANPQTADRFSWFDYRSKGFD NRGLRIDLLASQPLAECCV*T GIDYEIRSMKPSDHAPVWATF RR
11063	41431	A	11128	2	136	YCKLACLQVDSRGSQVFALDV AARHR*QFAMPESDAVAMKHL LS
11064	41432	A	11129	3	431	GVFGRVSEKQRPAAAPAGERPL PRPRPLPCGAAARTGPFAAQAA *RAAAAAPRSERRHHGAEEGH QRCIYRHAADRALGEAARRTG YALRPAGEPELAAAARRR*RAP DPGPRVPRHLGLLATRACPPGG AHCSPERGAISW
11065	41433	A	11130	64	2436	RRQGLEGWWAIGLEGLTGKAL AWLFTVPGVRGLQWSPRFFLTR LRTLCKVLGVLFVAGGKKG PTCILQILKGQRREQA*CISGWA ERVWASGQA*WEVWLHWAKS RNWLFWKQHVHALRVRLDTT LFSLEEGSSFWNQGLTWKVVR RTFSFSINHTPRITLGVPSVHSF QLPGLLNFGFEKVCVLSPRIFN LTHENFLSSEGPEIGLLGATFN CLNKRLAKYMRNRNVHPKPLV RYLHSLRPPEAAP*AWCGPR HLSCROMSSSSQIGNDSFQLQV TPVHLLPLSHITRKNPEMYDLP LLFFNPQESAILQLFHQDGECLH CSPVIGDWCHLGHSGACPSFSV PSGLFVPSLLCGAAFGRLVANV LKRYSVCVRVCAHVHVCAVRV VYACVWVRMTISLTVLIESTN EITYGLPIMVTLMVSTLPPGPCQ AQGHVVRPTGPIFRSLEWETE EMDK*GHDFAHVLVSECISSEA *GMLFCGPGDRSLFSTFRAVW SLSRLLDSVIAAGKQ*A*RT*SV GYSLLCPDLKGDPSAVSILRTT VHHAFFPVVTENRGNEKEFMKG NQLISNNIKFKVKTA*EERQV RDKRSRLTRLSELELRNMCDE HIASEEPAEKEDLLQQMLERR* EPGGAPTARRATQRWGEPLAQ MFPLTFHGLILRSQVLTVLLVRG VCYSESQSVSLSEAEISQARPDE
11066	41434	A	11133	3	80	

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11067	41435	A	11134	2	958	LKCELSVDQGLAPAIQTVRLTHE SLTALEIPNALLQTIQDLILDLR VRCVMATLQHTAEIEIKRLAEK EDWIVDNEGLTSLPCQFEQIV CSLQSLKGVLECKPGEASVFQQ PKTQEEVCQLSINITQVFIYCLE QLSTKPDADIDITTHLSGDVSSP DLFGSIHEDFSLTSEQRLILVLS NCCYLERHTFLNIAEHFEKHNF QGIE*ITQVSMASLKELDQRLFE NYIELKADPIVGSLEP*YAGYF DCKDCLPPTGVRYNKLKEALVNI IAVHAEVFTISKELVPRVLSKGI EAVSERAQSTDAVCFILOQKWS
11068	41436	A	11135	52	1053	MDEEERVYRACYLICISLLSSPG NPGHLSPMLDLNDNTRPSVLG HLSLFLIQKYNHSLFFSPLAWR YKTPHRVAFVEKLTKLVLSQLP YF*IISNMFYFVFLIFKTAESNP INHI*TRLCLFLVF*KMIQEVMMH SLVKLTRGALLPLSIRDGEAKQ YGGWEVALRSHSAHFCLDVVF RRLTHESLTALEIPNDLLQTIQD LIFRPGSQL*PVSRIFFSAGTFRF KNHLHDFTGFHTCLTGAPRGPV GGCASDDGQAAADTSQWLS*I VLYL*LFLASMFSLSDVDVFL AP*R*FSKHLFCF*EQRLILVLSN CCYLERHTFLNISHGSP
11069	41437	A	11136	50	426	
11070	41438	A	11137	2	949	QQVWKQNCFKHYSNETDNSTT QLVGVQTLQVVVPSLILCEHCM NFSSPHVWCCMVQAVPGGQGO TIMQVPVSGTQGLQQVSN*KY *AVYQRRGFKE*ITTGQTQIII QQPQTAVTAGQTQVIPLASHR SKTDLEESDN*VRYQPVNADGT ILQQGKCTHKLP*DGLGQLFCPL DN*HTTSSGGQGTVTVTLVAGN VVNSGGMVMVRKCFQLCL*N FLEHAT*CLLKEPLYVNAKQY HRILKRRQARAKLEAEGKIPKE RRVCITLGR*ERRIAGFYF*NY LFSPKEKDSPHMQVGRHIFILL FITLY
11071	41439	B	11138	26	80	

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11072	41440	A	11139	203	797	HRHARHLFRTTPT*LSWQGS *TPRWKGVRAVVTQPRKERRA ESEQFQATKPRSQL*LQPPTPSL VSSCQLKTTAASRPLT*PSKSVY PSAPFHPWLPC/SKPERSVSPES NDSISEELNHFKPIVCSPTPPK RLPDGRVLSPLIJKSTP/QPKQK PAEADFL*GQSTDPQKVGTDLS GAADQKDPFKSHSYLSGS
11073	41441	A	11140	33	379	EATSNFKQPPSLPFWCLKSRSTL KPRQSKVCSSFPVI*GKTGNEL ALQIP*FKSSCGPRFPD***PAGR /SAPSLGPPSPQSAHQ*EHWWQ VCIKHGITNAEPPAEHLKVLVR E
11074	41442	A	11141	248	622	SESSGRFWLCGLGPGTSPILLSL KFPHELLPASGRSPSPRPVR GKATQVVAWGYRCVDEDP RCLGTPGRTD/PHCGQGLLCPL GKSCSTSQPLSQDGRGTSWDR SHACSPGGHPHRCIGCM
11075	41443	C	11142	1	1311	
11076	41444	A	11143	452	1286	
11077	41445	A	11144	2	299	GLPLAHGLGRFGMDRIYEGQ VEMTGD*CDVESIDGQPGAFTC YLDVGLARTITGNKVFGALKG AVDKGCSVPHSTR*FPACDSAE FALGIPYFVQPN1
11078	41446	B	11145	49	832	
11079	41447	A	11146	1	1074	
11080	41448	A	11147	1	360	
11081	41449	A	11148	1	1155	
11082	41450	A	11149	75	266	
11083	41451	A	11150	2	222	
11084	41452	A	11151	1	549	
11085	41453	C	11152	453	665	
11086	41454	A	11153	1	1962	
11087	41455	A	11154	1	295	ASTAGVSYVVAQAGLKLGLS LSKCRDPRCEPPCE*MSLYKV MAMARKAMSL/YIYFFLDEFM YFAGTWKLETIILSKLSQGQK TKHRMFSLVGGN
11088	41456	A	11155	1	363	
11089	41457	B	11156	1	375	
11090	41458	A	11157	1	197	
11091	41459	C	11158	1	270	
11092	41460	C	11159	1	146	
11093	41461	C	11160	1	268	
11094	41462	C	11161	1	301	
11095	41463	A	11162	1	289	
11096	41464	B	11163	19	240	

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11097	41465	A	11164	2	253	
11098	41466	B	11165	1	978	
11099	41467	B	11166	1	316	
11100	41468	A	11167	191	319	
11101	41469	A	11168	608	763	
11102	41470	A	11169	274	437	
11103	41471	A	11170	1	417	
11104	41472	C	11171	1	792	
11105	41473	A	11172	3	449	IYLTKEIKDLYKEKCKTLLKEIT DDTNKWKHIPSSWMGRINIVK MTTLPKAIYKFNAIPRIPPSFFT ALEDITLKFIWNQKR/CPHSQCK IKQKEQIWRHHTT*FQAIL*GHS HQNS/IGTWMKLENIILSKLLQG QKTKHCFSLIGGN
11106	41474	A	11173	1	441	
11107	41475	B	11174	1	597	
11108	41476	A	11175	5	265	
11109	41477	A	11176	3	280	SIYPNTCTRMFIVALLTIAKTWN QAICPTMIDWIKKMWHIYSME YYAAIKNDEFMSFVGWTWMKLE TIIFSKLSQGQK\TKHRMFSLIGG ELEQ
11110	41478	A	11177	590	747	KAYQPEKAQDQVDSQPNSRTRG TWMKLETHLSKLTQEQQTKHCF IFSLISGS
11111	41479	A	11178	3	274	FYYKDTCTHMFIVALTIAKTW NQPKCPSVIDW/IMKNMWHIYT MEYYAAIKNDEFMSFSGTWMK LETHLSKLTQEQQTKHCFSLI SGS
11112	41480	A	11179	1940	2061	
11113	41481	A	11180	493	743	KATRSVNC/WWDHL*RPFWGS PH
11114	41482	B	11181	1	1248	
11115	41483	B	11182	50	8445	
11116	41484	A	11183	40	125	
11117	41485	B	11184	1	1896	
11118	41486	A	11185	1	624	
11119	41487	A	11186	1	357	
11120	41488	A	11187	1	304	
11121	41489	A	11188	681	834	
11122	41490	A	11189	3	2128	
11123	41491	A	11190	175	402	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
11124	41492	A	11191	46	790	NPGAVKMPAYHSSIMDPDTKLI GNM/AHLLPIRSQFKGPAPRET/ KDT\DIVDEAIFLPSGPNVFFKN YEIKNE\ADRTLIYITLYISECLK KLQK/CQFPKAQGGGKEMFYA GESTNFSHFLGEPGFPTLTAILC PNPANK/QEDE\VMRALFTNQP KGRRLGLRLCEKSFSDP\QNG* T PAKWVWDLAFVKRQFMNKSLS GPWTVESPGQPTVSRGPAAAF FQQDVTQSFCLYLKFKYRDERR ACLYLKNS
11125	41493	A	11192	1	828	
11126	41494	A	11193	1	525	
11127	41495	A	11194	43	1826	THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLPLPAAGRVVVRRL AVVRSGRSLSLTADMTKGLVL GIYSKEKEDDVP/QFTSAGENFD KSLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLESSEVDPGCG DAQAAAEAGVGLGYEYDDLK QKKKMAVSAKLYGSGDQEA W QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSNPANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICSIAVS AAKLNLPIIIGLAPLCENMPSG KANKPGDVVRKNGKTIQVDN TDA\EGRLILADALCYAHTFNP KVILNAA\TLTGAMDVALGSGA TGVFTNSSWLWNKLFASIEGT DRVWRMPLFEHYTRQVVDQCL AD\VNIGKYRSAGACTAAAF KEFVTHPKWAHLDIAGVMTNK DEV PQSTGKA*LGRPTRTLNEF L/LRFSQDNCLVQILKNVHFSVL NWTVELKKVFE
11128	41496	A	11195	1	273	

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11129	41497	A	11196	2996	8256	LPTRRSWAVFFKGGESGAHTLR RKARKKKKKQVKGGSPKKGEE AKKVEAPRLPKLAAPGGGAGA KGGAGGTSMDRLWSWVLHLG LLSALGCGLAERPRRARRDP AGRPPPAAGPATCATRGPRPP RLAAAAAAGRAWEAVRVP RRQQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAF TLQVWLRAGGQQRSPAVITGL YDKCSYISDRGWVVGIIITSD QDNKDPRIYFFSLKTDARQV
11130	41498	A	11197	75	266	
11131	41499	B	11198	1	363	
11132	41500	A	11199	1	649	PRIRHEVIEEVRIMMLEIINSLT NSLHHNPNLVYALLYKRDLE QFRTHPSQDIMQNDLVISFSS SRLLQAGAEISVERVLEISQGV ALRCPKDRLKEISQKLKFKYVE EEQPRGVF*SPYVWSLVQLQ SALYWEFHRTQLFHPWDSRLR GRDASSPGTPSSQGRPFQSSFIS GVTEVGGTGYLVYLLKEDCT SVFSSHTLIWRIGC
11133	41501	A	11200	108	210	
11134	41502	A	11201	53	259	
11135	41503	A	11202	1	2679	
11136	41504	A	11203	1	675	
11137	41505	A	11204	834	1077	KGLWTVPPSFGDTVSGPPVPTG GSAGHTVPPPPR*CRRQPPPSPP WRLFLPQLRSRSSQPPAGPAR HLPPPAARPECFCA
11138	41506	A	11205	1	681	
11139	41507	A	11206	1777	1940	VPILPQPLLLHPHLLS*VPILPQP/ PAPPYPNPFITSPPHTWGLQFH SVTSPPPAQOFTLKRVAEAKGI VK
11140	41508	A	11207	3	547	
11141	41509	A	11208	1	578	
11142	41510	A	11209	194	379	
11143	41511	A	11210	1	927	
11144	41512	B	11211	1	916	
11145	41513	A	11212	1	441	RRKLQKQALGPEQNLETLNL ATSVFYNRDQEEQVQKEKRDQ RKAALVMAIRQTNLGGERT EHEAGQSPGKACYQCGLLGHF KKDCPMRNKLPPR/RVSTMLRQ SLEGALPQRMKVPWVRSPOPD DPTTLGRVPGASASSCHHPH
11146	41514	A	11213	164	359	
11147	41515	C	11214	157	189	

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11148	41516	A	11215	13	399	VEAFPTGSEKATAVISSLLSDIIP QSRLEPTISIPSDNRRAFISQISQAV FQALSIIP*NLIPYIPGPSSRKH/T LTKLSHLKDDWTILLPLSLRLI QACPRNATGYSFVKVLYRHSFL LRPSLIPDTRPT
11149	41517	A	11216	2	152	WYGEIMGDVQSQCIFER*WAMF LRAASSGIRGGVGT*SGRH*AE GRFYGDFRGNRAASVFSR
11150	41518	A	11217	1	1143	
11151	41519	A	11218	28	453	
11152	41520	A	11219	275	1128	DISTPSLATDHMPITIPNLIT/TY PTQRQYPIPPHALKGLKPVTDDL LQHRLLKPINSPYNSPILPVQKP DKSYRLVQDLRLTNQIVLPIHP VVPNLYTLLSSIPSTTHYSVLH LKDAFFITPLHPSSQPLFAVTWT DPDTQQSQQLTWAVLPQGFRD SPHYFSQALSHDLSFHPASHL IQYIDDLCSFESSQDDTL LLQHLFSKGYSQDDRPFTSQI TQAVSQALGIQWNLHIPHPQS SGKVEWTNGLKLLLLLLTANI DDTSYLQIPHKGLO
11153	41521	A	11220	1	606	
11154	41522	A	11221	713	835	LSQWRSDNGPAFISQITQAVSQ APGIQ*NLIPYIPHPQSSGK
11155	41523	A	11222	1	1133	AEALPQFYFHLSDIRGMLLHE PDLQKGKAVSQEDPQWSYQA DSPGIARRDYMVSRLVEGLKK AAYKAVNYDKLKKTTQVTIVP GPDFNLASHIIPDTPDPHDCYL SDTPGIHSISHISFAIPHPDHTW FIDGSSTTPNRHTPAKAGYAIVP STSIIEAALPPSATSRQAKLIAL TRTLTLAKELCVNIYDSKYAF HILHHHAVIWAERGFLTKQGW SNINASLIKTLKATLLPKEAGV IHCKGKHQKASDPIAQGNTYAD KIAKEAASGPTSVPHGQFFSFL VTPTYSPTKTSTYPSLLTQGKW FLDQGGYLLPASKAHSLPSFH NLFHVGKPLAHLLEYLSFLS WKSILKEITSQ*SICYSTTPQG
11156	41524	B	11223	1	1156	
11157	41525	A	11224	1	4991	
11158	41526	A	11225	3	590	
11159	41527	A	11226	203	1772	
11160	41528	A	11227	1	1669	
11161	41529	A	11228	1473	1604	
11162	41530	A	11229	82	159	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 95/40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11163	41531	A	11230	1	1323	
11164	41532	A	11231	377	631	LLKGKLTNRKDIHTKTPSVRRH HRRPKPGRDITTKIILNQYPW* TSMQKSSIKYWQTESSTSKLS TMIKLASSLGCKNWKKL
11165	41533	C	11232	1	1677	
11166	41534	A	11233	753	966	FVFLWSLMMVTYRWGFGVDV LSVC*FSFQSQSEPQLQVCWSLL EVHS*PCLPGYQQRNCSWPRG SCDVVIT
11167	41535	A	11234	1253	1459	LSDSPKLK*RKKC*GQPERKVG LPTKGSPSD*QQISWQKCKPKE ESGGQYSTFLKKRIENPEFHIQ
11168	41536	B	11235	1	924	
11169	41537	A	11236	299	436	
11170	41538	A	11237	259	536	FQKEWYQLLVPLV/EIWL*IH VLDF*LVNY*LLPQFQSMMLV SSEIQLLPGLVLGECMCQGIYPF LLDFLWSLMMVTYRWGFGVD VLCVC
11171	41539	B	11238	79	1587	
11172	41540	A	11239	1608	1763	
11173	41541	A	11240	1	2001	
11174	41542	B	11241	1	741	
11175	41543	B	11242	1	1368	
11176	41544	C	11243	1	3924	
11177	41545	A	11244	470	619	KVTRGWGSPHQDAG*SPCQSH QDQTP*GILKEHQEKARRK*RQ LCVLQL
11178	41546	B	11245	1	3546	
11179	41547	A	11246	363	476	
11180	41548	A	11247	1	759	
11181	41549	C	11248	376	986	
11182	41550	A	11249	556	821	MSIRSTWRRAEFNSWVSFLTR LVDLSLVFDDGDVQVGFWCGC PSCLLVFL/ISQDPQLQVCWSL QEVHSRPCSPGYQQRLQYSEY
11183	41551	A	11250	119	340	
11184	41552	B	11251	1	942	
11185	41553	A	11252	436	732	LHIWPFLLPCKAQNVHCSKFC PLGRFPFMAVLQGCPRKGL*CC SCPLGGIWIWISCRICAFRTYLRP IMYIPLPFADGMLLCTAHSMAR CFGYCSLVV
11186	41554	C	11253	1	1878	
11187	41555	A	11254	720	1535	ILPEVQGGAGTI*LSLFLIE*PLF LSPA*LPWPELPTLC*IGVVRDG TPVLQCFSGKMLPVFAHSV

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11188	41556	A	11255	2	1059	WLLAASPLWLCRIRP/LILAAFM GWQSRSA LGTQSQESGKGSPD QVLVPQDCGPWLGSVELVSPV GSQAGEEPILSENKGRVTQMKI PEERSGSNICCSAIFAVLQPPLLI PRQTRSGVDLQQNPDTLQRLVL TVRRKTNKEKGHPHQNPCTCTSP ASKTKGALRFIKQVLRDLERAL DSHTIMGDFNTPLSTLDRSTRQ KVNKDIQELNSALHQVDLIDY RTLHPKSTEYTVFSAPHHTYSKI DHTVSGKALLSKCKRIEILTNCI SDHSAIKLELRICKLTQNHSTTL KLNLLNDYVWHKETKAEIK MVFEIDENKDTIYQNLWDTFK AVCRGKFIALKAHKRKKQERV
11189	41557	A	11256	82	159	
11190	41558	A	11257	820	1358	HTDGLVWMPFLFVSFSPNSQD RQLQVCWRLLLEVHSRCPFGY QQRWLQNNRY/SVNRKCCCLIV PLEVLSQRSTHQHVGEWLCLL GRKFPAAGMEACTAMLCSSSVL EAATLSFSVQHRCTGGS*KPQ QGRVYPSEGREHNGAAAFGPF CSSECPASCPDPTQPCAPGTYI PFFSCQT
11191	41559	A	11258	2435	3261	QVRGYRCRFVTWVNCMSLRFG VQRIPSPSLTGTQPPVGD*HLT RPGTPLR*NFORNDQAVTFVAVH VHIFVQPLLLIPMQTSGGVDLR QTPTDLQLRVLTVRRKTNKQK GHPHRNPICMSPSSKTKARQAN IQJQEIQRTPQRYSSRAATPRHII VRFTKVEMKEKKLRAAREKGR VTHKGKPIRLTVDLAETLQAR REWGPFIENILKEKNFQPRISYPA KLNFISEEEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNQ YQPLQNHAKL

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11192	41560	A	11260	1439	2544	VSSTTKEKALSVPPRWICILQKK NPPNHQPVSLPEVFLPQILKFSG PPHWRRIEYDKVMRLNIGDM KTKKKMLEKYEQLEIRHQQKS RT*KAVCCIT*LSRHILLGQAPL VQQSM*QPESHQVNPPTS YGIHQTPKLS*IGIK*RPWIM/MSEV KGYKVGNNFFAKAPNRAPPLL KPRQTGSGVDLQQTAPDLQLR VLTVRRNTNKQKGHPHNPICIT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPMME DQNMENKQEEKFREKRMKRN EQSLQEIRDYVKRPNRLIGVPE SDGENGTKELENTLQDIHQENPPS LARQANIQIEIQRMFPQR
11193	41561	A	11261	2772	3111	QSGPSAAGLLEFAGGFLQTLFA WVSAAEVGGCKGSGSSLS*PK KGVMDGTWIKGSLPPEYCAFPPT G*KNGAP/LRLYPTPGSEGPPTT ESP*/FASTAVGDQATARQQRGW GRGARH
11194	41562	A	11262	248	597	DRCPAAWDRHPAGIQSSRREPS KATWTLRSKLSVQDGRDSSL RLNCKVAARLGAGHPMLRLG LRC*YPGKQGLEWTSKLLQQTIC H*GS*LLKGKLTNRKDIHSKTPS VRHYHQR
11195	41563	B	11263	1	2250	
11196	41564	A	11264	1298	1681	GVSVPLLWGASQLGYLGVMDDP LAEAVCPFSDQLHSGRTSTVF KAALGQSGAHCPERCVAQS* AD*RALREHKQ*FGSTLCGPVM VVAMELGSSTMVELVSSPANS VKVFLFLHIFSTCCFLTFS
11197	41565	A	11265	1272	1497	SGLLPIKVAFTKQFLFILLRIWL *RGYVFCWSKVVTTPREQPQCIT DGYQIFIMQKTLSCLSILGKRT MSLMQ
11198	41566	A	11266	1	1071	
11199	41567	A	11267	788	1286	
11200	41568	A	11268	3	455	
11201	41569	A	11269	1	711	
11202	41570	A	11270	225	525	GGGENFSYPWYLLVGCGWFSS SPIVPDVPFSLLLPAQKKKPAP PKVPEPKPKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK

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11203	41571	A	11271	914	1261	TAKPKTNWCCRAPTSLASTFA TMPFKKAECVGDAPATVKDE PQRISARLSAKPAPPKPEPKK KAPAKKGEKVPKGGKKADVA GKEG\NNPAEN\GDAKTDQAQK A\EGA\GDAK
11204	41572	A	11272	3	359	
11205	41573	A	11273	440	642	WKAEREIEIPR/PKKAPAKKGE KVPKGGKKGAEGQDGDNPTE NGDAKTDQGGKAEGAGDAKR TVSHQN
11206	41574	A	11274	499	723	
11207	41575	A	11275	147	459	STVYVLPSPSPMPKRKAEGHA MGDKAKVKDEPQRRFARLSA KPAPPKPEPKKAPAKKGEKV PKGGKKGAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK
11208	41576	B	11276	179	400	
11209	41577	A	11277	24	601	
11210	41578	A	11278	266	441	
11211	41579	A	11279	17	570	HQPKKDLTGFVKWPYIRLQR QRAILYKRLKVHLAINQFTQAL ARQATATQLLKLHAKYRPETKQ EKKQRLARAEEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIADVGPIELVVFLLPA LCRKMGPVYQCIKKGARLGR LVHRKTCTTCRFTQ\VNS\EDK GALAK\LV\AIRTNYNDRYDEI R\RHWWG\NVLPKPSVARIJAK\A EKAKAKELAH*TTGGSYQDQLQ
11212	41580	A	11280	175	289	RPCVKESGKPHLKSSTMWTTL KLLRI*PRRTTCSPLS
11213	41581	A	11281	205	361	
11214	41582	A	11282	144	396	CLEVLHKILFFEMESHVSVTQAG VQWRDLGSLQPLPPG\SSNSPTS ASQVAGIRSMRQKGRANFFVFL VEMGFHHVGGADLELL.TL
11215	41583	A	11283	241	550	
11216	41584	A	11284	2	106	
11217	41585	A	11285	2	447	PPLSRLLCPRHPHSGWPEGYSPE HLRCGLRSGTLRSRQALHCQVS SNP*PPSLWF*GCGNV*ELCLF VLVPSVNLVQVLLSEIWEFHRT

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11218	41586	A	11286	1	2172	PAGRCRTAWAVAAQQLMLSA ALRTLKHVLYYSRQCLMVSRN LGSVGYDPNEKTFDKILVANRG EIAACRVIRTCKMGIKTVAHSD VDASSVHVKMADEAVCVGPAP TSKSYLNMDAIMEAIKKTRAQ AVHPGYGFLSENKEFARCLAAE DVVFIGPDTHAIQAMGDKIESK LLAKKAEVNTIPGFDGVVKDA EEAVRIAREIGYPVMIKASAGG GGKGMRIAWDEETRDGFRLS SQEAASSFGDRLLIEKFIDNPR HIEIQVLGDKKHGALWLNRECE SIQRRNQKVVEEAPSIFLDAETR RAMGEQAVALARAVKYSSAGT VEFLVDSKKNFYFLEMNTRLQ VEHPVTECITGLDLVQEMIRVA KGYPLRHKQADIRINGWAVEC RVYAEDPYKSFGLPISIGRLSQY QEPLHLPGVVRVDSGIQPGSDISI YYDPMISKLITYGSDRTEALKR MADALDNYVIRGVTHNIALLR EVIINSRFGKRNLT*FLUSKGF PEAFKGHLLTKSEKTQFLAIA SLFVAFQLRAQHFGQNSRMPVI KPDIANWELSVKLDHKVHTVV ASNNGSVFSVEVDGSKLNVST WNLVASPLLSVSVDEHSEGLFQ CLSREAGGNMSIQFLGTVYKV NILTRLAAELNKFMLEKVTEDT SSVLRSPMPGVVVAVSVKPGD AVAEGQEICVIEAMKMQNSMT
11219	41587	A	11287	62	2600	
11220	41588	C	11288	277	508	
11221	41589	B	11289	94	1440	
11222	41590	A	11290	57	237	FLHAENKAHRPGISLCGLRAQP RQPASRHAW*SMRSEQRPLWT ASGRSSGQTRSSRLG

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11223	41591	A	11291	3	1968	EFDYSEDKSSWDNQENPPPTK KIGKKPVAKMPLRRPKMKKTP EKLNDTPASPPRSPAEPNDIPIA KGTYTFDIDKWDDPNFNPFSST SKMQESPPLPQQSYNFDPDTCDD ESVDPFKTSSKTPSSPSKSPASFE IPASAMEANGVDGGLNKPAPK KKKTPLKTDTRVKKSPKRSPL SDPPSQDPTPAATPETPPVISA VHATDEEKLAVTNQKWTCTMT VDLEADKQDYPPQSDLTSTFVNE TKFSSPTEELDYRNSYEIEYME KIGSSLPQDDAPKKQALYLMF DTSQESPVKSSPVRMSPTPCS GSIFFETEALVNTAAKNQHPV PRGLAPNQESHQVPEKSSQKE LEAMGLGTPSEAIETAPEGSFA SADALLSRLAHPVSLCGALDY LEPDLAEKNPPLFAQKLQREAI VHPTDVSTSKTALYSRITTEVE KPAGLLFQQPDLDSALQIARAE IITKEREYSEWKDYEEESIRE VMEMRKIVAEYEKTIAMIEDE QREKSVSHQTVQQLVLEKEQA LADLNSVEKSLADLFRRYEKM KEVLEGFRKNEEVLKRCQAEY LSRVKKEEQRYQALKVHAEK LDRANAIEIAQVRGKAQQEQAA HQASLRKEQLRVDALERTLEQ KNKEIEELTKICDELIAKMGKS
11224	41592	A	11292	63	2203	
11225	41593	A	11293	27	586	
11226	41594	A	11294	89	288	
11227	41595	A	11295	1	522	HERFETTYFKKFP*GYVYTGDD CQRDQDGYWITGRIDDMNLN SGHLLSTAEEVSALVEH*RLQ EAAVVGHPHPCEGVNASYCFV TLCDGHTFSPKLTEELKKAIVM RKRLAPFATPDYIQNAPGLPKT RSGKIMRRVLRKIAQNDDHDLG DMSTVADPSVISHLFSHRCLTI
11228	41596	A	11296	2	569	
11229	41597	B	11297	1	990	
11230	41598	A	11298	1	252	
11231	41599	A	11299	39	174	RHIISSNEVH*KEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEIPLSSL

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11232	41600	A	11300	16	379	ILDTSMPMRWTQKNFSMILAQPE QQCKTLSQNKNDRIKKKEE KKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKKKEKE EEKKK/QEEEEEEEEEEEEEE EEEEEEEEEEERRR
11233	41601	A	11301	1	249	
11234	41602	A	11302	1	353	
11235	41603	A	11303	1	847	
11236	41604	A	11304	3	224	QEKRRRKEKKKVKEEEEEEE EEEEEEEEEEKKKKKKKKKK KKKKKKKKKKKKKKKKKK KKKKKKKKKKGRKTDLAVDPV
11237	41605	A	11305	1	417	
11238	41606	A	11306	1	1314	
11239	41607	B	11307	1	133	
11240	41608	A	11308	45	266	
11241	41609	A	11309	35	313	FLQMEDTYIVTKLLLLRFAWL YLDLVFVLI*YRKKRRKKRRKK KEKEKEKEKKKKKKKKKK KKKKKKKKKKKKKKKEMALQS CSLWYLYA
11242	41610	C	11310	240	391	
11243	41611	A	11311	1	579	
11244	41612	A	11312	141	410	PEPILTMESKGMWQLFELTL/H NSKVNTLSKELHSEFSEVMNEI WASDQIRSAVLISSKPGCFIAGA DINMLAACKDPSRSNTAITRKH RE
11245	41613	A	11313	1	358	KWFTPMFEIKGGYA*SKNWR LSVRCGGWPLRRLMEEGSLPNP SRIYYRNKLRLKSQNNSSVDPC MRNLDECEVCRDGLWELFCCDT CSRVFHDDCHIPPVESEKMKES AGSQCCQES
11246	41614	A	11314	1	921	
11247	41615	A	11315	108	2765	

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11248	41616	A	11316	98	2418	AKLMAQQGQQGQMASGDSNL NFRMVAEIQNVFGQNLQEQVC PEPIFRFRFRENKVEIASITRPF FLMGLRDRSFISEQMYEHFOEA FRNLVPVTRVMYCVLSELEKTF GWSHLEALFSRNLMAYPDLNE IYRSFQNVCYEHSPLQMNNVN DLEDRPRLPYGKQENSACH MDDIAPVQEALSSSARCEPGFS SESCEQLALPKAGGDAEDAPS LLPVSKCLAIQIDEGESEMPKL LPYDTEETFDLKTPQVTNEGE EKGCLLPGEGEESDDCSEMC DGEERQEAASSLARRGSVSSEL ENHPMNEEGEELASSLLYDN VPGAEQSAYENEKCSVMCFS EEVPGSPPEARTESDQACGMDT VDIANNSTLGKPKRKRKRKRG HGWSRMRMRQKNSQQNDNS KADGQVVSSEKCANVNLKDL KIRGRKRKGKPTRFTQSDRAAQ KRVRSRASKKHKDETVDFAKAP LLPVTCGGVKGILHKKKLQGGI LVKCIQTEDGKWFTPTFEIKG GHASKNWLRSVRCGGWPLR WLMENGFLDPPRIRYRKKKRI LKSQNNSSVDCMRNLDECEV CRDGGELFCCDTCRVSFHEDCH IPPVEAERTPWNCIFCRMKESPG SQCCQCESEVLERQMCPEEQLK CEFLLLK VYCCSESSFFAKIPYY YYIREACQGLKEPWLWDKIKK
11249	41617	A	11317	1	1210	
11250	41618	A	11318	1	743	MRYKKEQPLFLPKYDLGADA ILQPQEEDCGSTQVRGGHHRK TEETGLLVTSLNQGKIPHDVST KLLSPQRSSVFLLLITSGVHTD SSKAVLESRRSLGYEASFLEYF QSFYKLPVDRLYAWHCSHDH NTTVAINTDRPGLLLTLTLVTI GQGSKKAPSGFHSHPAPTVMKQ QPILCDDRDFSPSFPSTNTPSQF ATNEVLTTGPPPGAG/CCQYSTI TRKTGPNCAQAGCGGARPAK
11251	41619	A	11319	314	486	
11252	41620	A	11320	3	122	
11253	41621	A	11321	1	289	
11254	41622	A	11322	1	399	
11255	41623	A	11323	3	259	

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11270	41638	A	11338	1	503	MKHQHFAALLVPEKFLIAQSTAS RVDRRQIWRDVSERGEISQCL KVGTSLSNSTDVS AVEAVRATV LGSGLTPTVLRNAGPYTRIST VPACLLGQEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEERKKS
11271	41639	A	11339	1	651	MNIDANIPNKILENRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTKDKNCMIISDAEK AFDKIQQCFMLETNLKLGIGG I YLKIIIRAIYDKPTANIILNGQKL EAFPLKTGTQGCPLSPLLFNIV LEVLAIRQEKEIKGVQLGKE EVKLSLFADDMIVYLENPIVSA QHLLKLISFSK VSGYKINVQK SQAFLYTNNRQTENQIMSELPF TIASKRIKYRGQLTRDLKDLFK ENDKPLLKEIKED/DKEMEEHS MLMGRKNQYRENSHAAQELE KNYFKVHMEPKKSPHYQVNP PKEQSGRRHVT*LQTILQGYSN QNSMVLVPKQTYRSMEQNRSL RNNATYLQLSDL*QTQEKQAM GKGFPPI**MVLGKLASHM*KPE TGLSPYTLKYKNQFKVD*RLKR* T*NHKNQRRKPRHYHSGHRHG QGLHV*NTKINGNKNQN*QMG SN*TKELLHSHKRNRYRQSDQATY KMGENFHNLLIRQRANIQNVQ* TQTNLQEKKNQPHQKVGEHGE QTLKRRHLCSQKTHEK/NSPSL AIREMQIKTTMRYHLTPVRMAI IKKSGNSRKHQKKEEEEEEEEA EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEKCSLKHTEAPCVKGIEITFW NKFSLCDITKSYLSGVQKLEER AHKVKLALKFKKEIKMALHGG
11272	41640	A	11340	1	2184	
11273	41641	A	11341	1	870	GSTISCARCAELRGSASRFRPLP AAAMKWMFKEDHSLHRCVE SAKIRAKYPDRVPLTMGQLYE KEKDEDGFLCVAYSGENTFGF
11274	41642	A	11342	2	259	

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11275	41643	A	11343	1	461	GCRRCRRRCCCARCAELRGS ASRFRPLPAAMKWMFKEDR WLEHRCVESAKIRAKYPDRVP VIVEK/VSQGSQIVDIDKRKYAL VPSDITVAQFMWIIRKRIQLPSE KAIFLFVDKTPVQSSLTMGQLY EKEK\DEGFLYVA\YSGRGLTF
11276	41644	A	11344	1	966	
11277	41645	A	11345	1	1037	RPPFPVPGVQKCLPTRGGLHIG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSVASGREM VVLSPVAEVTIVLLD\EGTTTP IAFVKG/DILFPYIERKMLKIEYL QTHW\EEEEFQ/QDVSLEFENK A\EEADHLDGAVPIPGKHLGIG VDDLLQMM\QAVVDNVCWQM SLDRKTTALK/QLQGH/MWRAA FTAGRMKA\EFFADVPA/VR/K WREAGMKVVIYSSGSVEAQKL LFGHSTEGDILELVDGHFDTKI GHKRRRVKVKTRKVIADSI/GCST NKHFVFWTDVTSRRASAGLRE AGCCTLAVVVRPGNAGINR*L RKTYYSLITSFQWNYLPSST
11278	41646	A	11346	346	858	
11279	41647	A	11347	1	234	
11280	41648	A	11348	1	1696	
11281	41649	A	11349	1	234	
11282	41650	A	11350	1	1696	
11283	41651	A	11351	1	211	
11284	41652	A	11352	1	417	
11285	41653	A	11353	1	1458	
11286	41654	A	11354	219	329	
11287	41655	A	11355	132	451	
11288	41656	A	11356	1	996	
11289	41657	A	11357	1	867	MARLWGAISLWPLWAAPVWG GAAAVGVRACSSAAPDGVGE PALRRSYWRHLRRLVLGPPPEP FSHVQVQDGPVLRGVAAPVER AQLGGPELQRLTQRLVQVMRR RRCVGLSAPQLGVPRQVLAL PEALCRECPPRQALRQMEPPF LRVFNPSRLVLDRLVTTFPEG CESVAGFLACVPRFQAVQISGL DPNGEQVWQASGWAARIQIH EMDHLQGLFLDKMDSRTFTN VYWMKVND*SFATGAEDSGY QDANTFTLSWANLTHWQLGW LAYDRKLDCCQGMAD
11290	41658	A	11358	3	226	
11291	41659	A	11359	1	756	

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11292	41660	A	11360	35	142	
11293	41661	C	11361	151	484	
11294	41662	A	11362	1	1245	
11295	41663	A	11363	2	1464	CQAKFIMNRLKK/NERQKVQDI KEVKQNIHLIRASFAGKGKQLE EKMQPLEPEAIMLSELMQEQT KCRMFLSLISGKHGVHMDSKTG ATDSGAYLRVEEIQTTIREYYK HLYANKLENLEEMDKFLDKYT LPRLNQEEVESLNRPIGAEILAI ISSLP TKKSPGPDGFTAIFYLRY KEELVPFLKLSQSIEREGILPNS FYEASIIIPKGRDIT/KKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNL RKSINVQIHINRAKDKNHMII HEEKAFDKIQPFMLKTLNKL IDGTYLKIIRAIYDKPTANIILNG QKLEAFPLKTGRQCPLSPLL FNIVLEVLARAIHQEIKGIHL GKEEVTLSLFADDMIVYLENPI VSAQNLLKLISNFSK VSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASRRIKYLGQLTRDMKD LFKENYKPLLSEIVTVF
11296	41664	A	11364	41	559	
11297	41665	C	11365	63	370	
11298	41666	A	11366	3	211	
11299	41667	A	11367	47	358	PDMGLEDEQKMLTESGDPEEE EEEEELVIGLRLSVHTGNLGRP GM*NFPLLSIQN*MGDPHSAIS GGQCGSASWPSARIPLQQVREQ CRASWKKCVKARERLEL/CDE R/*SSRSHTEDCTEELFDF/LH A/RDHCVAHKLL*QLAFCTDPP TTSERAMPSQLEEMCKRPGSG
11300	41668	A	11368	1	2082	

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11301	41669	A	11369	1	2013	MKHLKRWWWSAGGGLLHLTL LSLAGLRVDLDLYLLPPPTLI QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLREVRLGVFPVPTSV DAWLVSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGGCASEE NGVLREKHEAVDHSSQHEENE ERVSQKENSLOQNDDEENKI AEKPDWEAEKTTESRNEGISLG DIPLPGSISDGMNSSAHYHVNF QAIQDQVNLHEAILCPNNTFR RDPTARTSQSQEPFLQLNSHTT NPEQTLPGTNLTGFLSPVDNHM RNLTSQLLDLYLDINIFDEINLM SLATEDNFDPIDVSHLFDEPDS DSGLTLDSSHNTSDIKSNSSHS VCDEGAIGYCTDHESSSHDDL EGAVGGYYPEPSKLCHLDQSDS DFHGDLTFOHVFNHTYHLQP TAP*ESTSIEFPWP*GGRSQEG RE*DTLKDTRNLSRDEQRAK ALHIPFSVDEIVGMPVDSFNMS LSRYYLTDLQVSLIRDIRRGK NKVAAQNCRRKLDIILNEDD VCNLQAKKETLKREQAQCNKA INIMKQKLHDLYHDFSRRLRDD QGRPVNPNHYALQCTHDGSILI VPKELVASGHKKETQKGRK
11302	41670	A	11370	3	255	
11303	41671	A	11371	1	1611	
11304	41672	A	11372	109	207	MLCLQRFYMFVDFQSRPQF*L KSCQHHSCHQ
11305	41673	A	11373	1	666	
11306	41674	A	11374	1	1254	

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11307	41675	A	11375	33	1458	KLPLKAKMGKEKTHINIVVIGH VDSGKSTTTGHLIYKCGGIDKR TIEKFEKEAAEMGKGSFYAW VLDKLKAERERGITIDISLWKFE TSKYYYVTIIDAPGHRDFIKNMIT GTSQADCAVLIVAAAGVGEFEA GISKNGQTREHALLAYTLGVK QLIVGVNKMDSPEPPYSQKRYE EIVKEVSTYIKKIGYNPDIVAFV PISGWNGDNMLEPSANMPWFK GWKVTRKDGNASGTTLEALD CILPPTRPDKPLRLPLQDVYKI GGIGTVPVGRVETGVLKPGMIV VTFAPDNVTTEV*SVEMHHEA LSEALPGDN/VGAFNVKNVSVK DVRRGNVAGDSKNDPPMEAA GFTAQVILNHPQISAGYAPV LDCHTAHIACKFAELKKKI ¹ DR RF ¹ GKKLED ¹ GPK ¹ FWKSGDAI VDMVP/GKP ¹ MCVESFSDY ¹ PPL GPFAVHDMRQT/VAGGAHQKQ VDKKAAGA/GKVTK ¹ SAQKAQ
11308	41676	A	11376	1	880	
11309	41677	A	11377	1304	2340	KETEQRKRLRNEPEEQEIRT RKTRSPQTPDQQT ¹ YKKGRNER LCGISQPTKEPTRGGFCFRNPP SNRIFACWGKPAWTACCNLSR ARRMLMERNARAAGSRKRMG RMDCWARVLDINLAAEAKSEP EKKAGVKRICKRRCTGSSFDL ¹ DY ¹ *LFNGDY ¹ DRMYSP ¹ ARVP PPPIARA ¹ VVP ¹ SKRQ ¹ RVSGNTS RRGKSGFNSKSGQ ¹ RGSSKSGKL KGDDLAQAIKE ¹ ELT ¹ QIKRKS ¹ GF LFLGKTW ¹ EKIEQSKQA ¹ VE KK ¹ *SQKEEQSSQLR ¹ *KKDET ¹ *C *RLEVLKGA ¹ EDSA ¹ EGDLLD DDDNE ¹ DRGDDQLELIK ¹ DDKE ¹ E AEEEEDDR ¹ DSANGR ¹ DDSLST

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11310	41678	A	11378	80	1141	ETQNRISSPSPCEIFLIFSIFRL CEKPYHQTRSASNVTKTDPRS MNSRVFIGNLTLVVKSDVE AIFSKYGKIVGCSVHKGFALSF SMLMKRNARAAGVAGEDGRMI AGQVLDINLAAEPKVNKGAG VKRSAAEMYG/SQ*QNTLLRPL YFSSFDLDYDFQRDYVDRMY SYPARVPPPPPIARAVVPSKRQR VSGNTRRGKISGFNSKEWNSG VSSKFWKR*KGDDLQAIKEEL TQIKQKVDLSLENLEKIEKEQS KQAVEMKNDKSEEE\QSSSS\K KDETNLKMESEGGCRLTLPEE GDP\LD**YDE**RSGGNDPAGS *SKDDEKVEAEE\GEDDRD\SAN GVEDDS
11311	41679	A	11379	1	1134	
11312	41680	A	11380	1	642	
11313	41681	A	11381	397	898	
11314	41682	A	11382	1	663	
11315	41683	A	11383	44	398	ATMLGLNIIRKWFYKSSEKSL GLRGGGLGRPLAFTLYSLQAAL LCVNAIAVLHE/ERRISSKNICA GGTRTIGIGWIWEKEPGIKSQL MNLIRSVRTEMRVPLIIVNSIAI VLLLLFG
11316	41684	A	11384	3	754	GLYYRKCQLISKEDVTHDTRLF CLMLPPSTHLQVPI/GEHVYLKL PITGTEIVKPYTPVSGSLSEFKE PVLNNKIYIFLIKIYPTGLFTPE LDRLQIGDFVSVSSEPNFKISK FQEEEDLFLAAGTGFTPMVKI LNYALTDIPSLRKVKLMFFNKT EDDIIWRSQLEKLAFKDKRLDV EFVLSAPISEWNGKQGHISPA SEFWKRNLDKSKVLVCICGPVP FTEQGVRLLDHLDNFSKNEIHSFT
11317	41685	A	11385	1	1785	
11318	41686	A	11386	95	369	
11319	41687	A	11387	511	728	
11320	41688	A	11388	1	100	
11321	41689	A	11389	1	777	

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11322	41690	A	11390	2	707	PNPKCR*VFPVFLFYRP1*FPSS PA/SLIARPS*VPILPQPPL/TPY NPPTTSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEIGVNAHV FSLDLSQISQHLGSFSSDPTKYI QEFRYLTLSYNLTWSDNLNVL T STLSPDERERVFPVSQSH/V**P/ SGFMSQTSRKALEQFPERIPQW NYQANS PGKNFKN*NLALKPH NRN*STLPSCTIHERKQPDGNA FLSYNYLPP
11323	41691	A	11391	2	339	LLLFRSLPAKLNQAPILWPPL/PP PPYNPSITSPVHTWFLSQFHSET SPPPPAQQFPLRAVAGTEGIVR MNGKEFFLQPNLTLITAGFKSQ TSRKALEQFPERIPNGTIRIQIPQ
11324	41692	A	11392	1	993	
11325	41693	A	11393	3	1127	TKETRFHIGPKTPAPVTDWEGS LPLVFNHCRDASLIHSRFGKGV PHRDTCLGSPPLAASPAFLGKG QAAHCQAE LSPNSSASTPPPY NPSITSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEIGV RVHVP FSLDLSQISQCLGSFSSDPTKY TQEFQCLTLSYNLTWSDNLNVL TSTLSPDEWERVSSLAQSHADN VPGFTSQTSRKALEQFPE/TDPQ WNHQANSPIARRDYMVSCLV EGLKKAA YKAVNYDKLKTETQ GEDENPAQVVARLAATLRFT ALDPEGPEGRILNMHFITQSAP DITKKLQKLESGPQTQQELINL TFKVHNNGEETDAARSPWKPP GPSRTPSFRACFPCPHNFCGY
11326	41694	A	11394	1	312	
11327	41695	A	11395	1	244	MFADR*LFSTTHQSIVPLYL/LF GA*AGVLATALSLIRAE LGQP GNLLGNDHIYNVIVTAHAFVIF FIVPIIIGFGN*LVPLIIGAPDM AFPRINNISF*LLPSSL LLLASVA IVEAGAGTRLNKSYPPLAGNY SHPWKPPVDLTIFSLHLAGVSSI LGAINFITIINIKPPAITQYQTPL FV*STTHQSHRTTPIYSAHELA SSPQPLSLIRAE LGQPGNLLGN DHIYNVIVTAHAFVIFFIPIIIG GFGN
11328	41696	A	11396	1	1287	
11329	41697	A	11397	3	583	

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11330	41698	A	11398	3	419	ILSISKLRSLTSLAGEGSDVTPKAS GVTRHIKGPVAAEMSAFILPL PG*VSPGWEEAASAVNLGLRT TLALRRGVCLIRSRPGTLGLD GASPRTESLHTGTACKGAVDGS SEVDEKLKRIALDFLGLHGDD PRSSWH
11331	41699	B	11399	1	1242	
11332	41700	C	11400	504	755	
11333	41701	A	11401	155	710	ETETTGEREGSLSNHSPNPTAA GLSLDTMKSCHPCNHSSLLSTAA SPPKLWRCFKEEHVELAVLGAP PKPLLPPTSHRDPTASVYLKAP THVWWSLFKHPLS*TPCCMGFI AFAIVSVKSRDRKIGCERDPGI AYASTAK\CLNIWALILGLLHD HSGSSSPVLI\VPGLWDRSGGIT GGQELCP
11334	41702	A	11402	1	1158	
11335	41703	A	11403	80	996	LKGFSLMSGALDVLQMKEE DVLKFLAA\GTHLGGTNLDHF MEQYIYKRKSDGIYIILMRTW EKLULLAARAIVAIENPADVSAI SSRNTGQRAVLKFAAATGATPI AGRFTPGFTTNHQAAREPRIL LVVTDPRADHQPLTEASYVNLPL TIALCNTDSPRLRYVDIAIPCNNK GAHSVGLMWWMLAREVLRM RGTISRHPWEVMPDLYFYRDP EEIEKEEQAAAEKAVTKEEFGQ EWTAPAPEFTATQPEVADWSE GVQVPSVPIQQFTEDWSAQPA TEDWSAAPTAAQATEWVGATTD WS
11336	41704	A	11404	1	819	
11337	41705	A	11405	1	1032	
11338	41706	B	11406	63	344	
11339	41707	A	11407	49	281	FFKSTVCSFQKQFQTLVPVIGGS IMY*DISDHRGQR**NVGPCGH
11340	41708	A	11408	985	1213	TQCVTINY*GMKWGSFGYVVFH KDGICALIDKRHFTFCVSFKGSQ IQSSAAFLIPDVQVHQRLQKDF QGLMVPIVGS
11341	41709	A	11409	1	774	
11342	41710	A	11410	3	249	
11343	41711	A	11411	3	619	
11344	41712	A	11412	3	493	

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11345	41713	A	11413	3	292	DALPRWPSPSGDGGAVREAGQ QGTRLERPAAVLIRAADPGRRRT QALA/GLPRG*PHPRMDPPESFQ ATGGTQQMTSTAPSWLTM*LR SVSGW*ELKD
11346	41714	B	11414	190	315	
11347	41715	A	11415	227	545	
11348	41716	A	11416	1	1896	
11349	41717	B	11417	52	1822	
11350	41718	A	11418	1	458	
11351	41719	C	11419	196	327	
11352	41720	A	11420	258	375	TRALSKFGSSRVEQS*AGYSGP GTP*EGGSGLGETVC
11353	41721	A	11421	3	854	
11354	41722	A	11422	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGHTGTFVSDGFKG GLIEIPDSIGKDKKACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
11355	41723	A	11423	1	642	
11356	41724	A	11424	260	534	
11357	41725	A	11425	1	438	
11358	41726	C	11426	391	750	
11359	41727	A	11427	786	926	AQQRQETIQGGRSLRSTLYL* GRSGTSLSQKLAQLSSLTGDST
11360	41728	A	11428	488	649	VLQLLKVAHPFLFIPPGGFVFSL TSGVKLHT*ALQLLKVAPELL IPPGSWSH
11361	41729	A	11429	1	2028	
11362	41730	A	11430	1022	1417	SLMGTSTSSALGMHVPRAITRD VLSAPVIVSGNTAKFCTMLGHF LKKTRTERRDIQAP*SFISLPKS TWEKLSAAMVSTLR*GASDQ K/C*LLGGNDRVSLIVIQVEG/PL QDPGTLGRLLQSLTVKRISV
11363	41731	A	11431	1	535	
11364	41732	A	11432	3	1186	
11365	41733	A	11433	201	458	QVDGCIPELKV*F*KKRGRGRGR RGRRRRRRGRRRREEGGGGGGG SFWRTHHTKPKDQHKDDTMG HFRSCAFQEGFVVHVPLSSEK
11366	41734	A	11434	1392	1532	AQQRQETIQGGRSLRSTLYL* GRSGTSLSQKLAQLSSLTGDST
11367	41735	A	11435	1253	2820	
11368	41736	A	11436	1504	1718	VIGIWALALGILARPQGFHV HLQDVGGA*AAKGLLRNVV R**VDQVQVSGAQGIAGVVVT VGGEEDF
11369	41737	B	11437	1	1383	

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11370	41738	A	11438	3	310	VHGRASSLGVG/TPIPKGHGQIK P/DRLKPPVYGACKLLDMELEM AFFVGPGRNLGEP/IPISKAHEPI FGMVLMAWSARHIQKWEYV PLGPFLGKSFGTPVKSS
11371	41739	A	11439	1	1337	MSFIPVAEDSDFFPIHNLPGVVS TRGDPRPRIGVAIGDQILDLSIHK HLFTGPVLSKHQDVFNQPTLNS FMGLGQAAWKEARVFLQNLLS VSQARLRDDTELRRKCAFISQAS ATMHLPATIGDYTFYSSRQHA TNVGIMFRDKENALMPNWLHL PVGYHGRASSVVSGTPIRRP GQMKPDDSKPPVYGACKLLDM ELEM AFFVGPGRNLGEP/IPISKA HEHIFGMVLMNDWSARDIQKW EYVPLGPFLGEEFWGHCLLPW VVPMDALMPFAVVPNPKQGRG PCRYLCHDEPYTFDINLSVNLK GEGMSQAATICKVQILKYMY WTMLQQAHSPTLSNGCNLRP GDLLGFLGPISGPGAQKNFGS MLELSWKGTKPIDLGNGQTVR KFLLDIGDEVITAMATRDFFW YS/QGQDGYRIGFGQ/CAGKVLP ALLPIMRFFLLF
11372	41740	B	11440	100	383	
11373	41741	A	11441	1	263	MEYYAAIKKDEFMSFVRIWMK LETHLSKLSQGQKTKHRRFSLI DG/IHHRSTRTENSSQRTGRKC WN**PTCGLARSWFGKTWSGN
11374	41742	A	11442	2	160	
11375	41743	A	11443	150	308	CLHR*GRGSPRPGPGGSGTGA GPGAGPSLAPPLPAQNAEGLGG RRRGNKYL
11376	41744	A	11444	1	372	
11377	41745	A	11445	49	177	SQQGLYAKPTSSQAL*GDGQAS AEMGRILSYE*EHAVFGFSSL
11378	41746	B	11446	1	420	
11379	41747	C	11447	1	334	
11380	41748	C	11448	1	268	
11381	41749	C	11449	1	564	
11382	41750	A	11450	1	264	
11383	41751	A	11451	33	194	
11384	41752	C	11452	1	309	
11385	41753	A	11453	1	738	
11386	41754	A	11454	1	2028	

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11387	41755	A	11455	3	1008	LKDAVFSIRISPESQKLFQFQWE DPESGVTTQYTWLTQQTGFENS PTIFGEALARDLQKFPKDLGCI LLLYMDDLLGHSTAVRCAKG MDALLQHLEDCGYKVSKKKA QICRQVTKWGDWERFEWEPL QQQAFCKLKEKFMSAPALGLP DLTKPFTLYVSEREKTA VGVLI QTVGPWPTPVAYLSKQLDGVS KGWPPCLRALAATALLAQEAD KLTIVQNLNIKAPHAVGTSQA KPELIALTRALELSEGTWMKLE THLSKLSQGGK/DQTLHLVLTGIS RST*ACSCLASLQVGLTGSQSL SLENPLRVGIQRRRCFTCAVDG EGFLLGVMPA
11388	41756	A	11456	677	879	KRRNHQILIRSHLQSVEDNLK SGLGSTASL*MSWTQPRNGAE VGFLILGYIKETPRNAETPSMV
11389	41757	A	11457	1	624	
11390	41758	A	11458	3	130	VEEEQGHFSRNR*IIISW*RNEN GLDRMDCSCRNGERDKGHG
11391	41759	A	11459	1	1477	MADPPWSSVQVKNKYDSGLSS VSAEPLASSASSHPGMSDNAPA SLESGSSSTPTNCSTSSAIPQPGA ATKPWRSKSLSVKHSATVSM SVKPPGPEAPRPTPEAMKPA NQKSMLEKLLFNSKGGSKAG EGPGSRDTSCERLETLPSEFESE ELEAASRMLTTVGPASSSPKIAL KGIAQRTFSRALTNKKSSSLKGN EKEKEKQQREKDKEKSKDLAK RASVTERLDLKEEPKEDPSGAA VPMPKKSSKIASFIPKGGKLN AKKEPMAPSHSGIPKPGMKSM GKSPAPAPSKEGERSRSGKLSS GLPQQKQQLDGRHSSSSSLASS EGKGGPGGTTNLNHSISSTVSGS VGTITQTGNTSVVQLPQPQQQ YNHPNTATVAPF*EGFHL*HA *VITF*TANYASSDNDLNVGYT H*LTASEFFQSRLLSLEAVGLH AHTC*A*LGSNIPFSVRLRPVPA ASAEDLRGHQGLIKDRAQVS
11392	41760	A	11460	1	327	LLLMLGLKHNVKLPRGPMVTL RESVWETLNLFLK*SFV*LNMLIF KKSS*RLQ*VRFHFLCPRVLIVQ LPFMSENMRCLVFCSCVSLLRM MVSSFIHVPPFKVLSFFALG
11393	41761	B	11461	119	203	
11394	41762	B	11462	1	677	

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11395	41763	A	11463	2	74	
11396	41764	A	11464	1	1256	MSASQDSRSRDNGPDGMEPEC VIESNWNEIVDSFDDMNLSESL LRDIYAYGFKEKPSAIQQAILPC IRGVNVIAQARSQTKMATFAI SILQQIELDLKATQALVLAPTRE LAQQIQKVVMALVDYMGASC HACVVRGTNMRAEVQKLQMEA PHIIVGTPSRVDFDMLYRIRYLAP KSIRMLVLNEADEMLSRGFKG QIYDISKRLNSTTKVVLLSAT MPFDVLEVTKKFMRGPH/IRIL VKKEELPLEGIRHFYINVEPEEF NLDTLCDWYEP*PITQAVIFHQ PPGGKVDW/LSPEKMHARDST VPPMHGDMTKKERD/VIMREF RSGS*PEF*ITPLTPGQPLMC QPGFL*SFKMLTLPPTRGKLLI HRNRSRVDRFGKGVAINMVT EEDAKRTLARDIETFYNTSIEEMP
11397	41765	A	11465	1	402	KSRGRGLPYTMDAFMLGGMG LKYPNFVAT*ARGYPGFAPSYG YQFPGFPAAYGPVAAAAVAA ARGSGSNPARPGFPGANSPPG VADLYGPASQDSGVGNYSAA PQPGSGFR/HTGIAGPLIATAFT NGYH
11398	41766	A	11466	226	486	
11399	41767	A	11467	2	432	
11400	41768	A	11468	1	834	
11401	41769	A	11469	205	570	
11402	41770	B	11470	61	939	
11403	41771	A	11471	96	269	
11404	41772	A	11472	123	593	VAVLEARLLSPVRASKMTKKR RNNGRAKKGRGHVQPIRCTNC ARCVPKDKA\KKFVIRNIVEAA A\VRDISEASV\DAYVLPKL\YV KLHYCVSCAHSNVVMESISVK ARKDARTPPFRPPGGCWPHVP PPKPNVRELEFFKDLKDRLISS WEEK
11405	41773	A	11473	1	228	
11406	41774	C	11474	187	423	
11407	41775	A	11475	1	546	
11408	41776	A	11476	1	1254	
11409	41777	A	11477	1	1386	

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11410	41778	A	11478	1	1445	HLKAKMGKEKTHINIVVIGHVD SGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVL DKLKAERERGITIDISLWKFETS KYYVTIIDAPGHRDFIKNMITGT SQADCAVLIVAAGVGEFEAGIS KNGQTRHALLAYTLGVKQLI VGVNKMDSTEPPYSQKRYEEIV KEVSTYIKKIGYNPDTVAFVPIS GWNGDNMLEPSANMPWFKGW KVTRKDGNASGITLLEALDCIL PPTRPTDKPLAALPLQGVHKLKLG GIGTVSSAPMETGFSNPGMVV TFAPSPR*QRKVKSVEVMHHEA LINEALSGEQGLSMSKKVSVK ECFVRGNVAG*PAKNDPTQWE ASWLSLLQVILEPSQAQISAGL CPLYWDCVHTGSHLHAKFAELK EKIDRRSGKKV\EDGPKIL/RS LGDAAIVDMV\PG/RPMCIVESFS DYPPLGRFAVRDMRQTVAVGV IKAVDKKAAGAGKVTKSAQK
11411	41779	A	11479	1	996	

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11412	41780	A	11480	1	1875	MPSDLAKKKAACKKEAAKAR QRPKKGHEENGDVVTEPQVAE KNEANGRETTEVDLLTKELEDF EMKKAARAVTGV LASHPNST DVHIINLSLTFHGQELLSDTKLE LNSGRRYGLIGLNGIGKSMLLS AIGKREVPPEHIDIYHLTREMPP PSDKTPLHCVMFVDTERAMLE KEAERLAHEDAEEKLMELYE RLEELDADKAEMRASRIHLGLG FTPAMQRKKLKDFSGGWRMR VALARALFIRPFMLLLDEPTNH LDLDACVWLEELKTFKRILVL VSHSQDFLNGVCTNIHMHNNKK LKYYTGNYDQYVKTRLELEEN QMKRFHWEQDQIAHMKNYIAR FGHGSAKLARQAQSKEKTLQK MMASGLTERVVS DKTLSFYFPP CGKIPPPVIMVQNVVSFKYTKDG PCIYNNLEFGDLDTRVALVGP NGAGKSTLLKLLTGELLPTDG MIRKSHSVKIGRYHQHLEQEL DLDSLPLEYMMMKCYPEIKEKEE MRKIIGRYGLTGKQVSPINRL SDGQKCRVCLAWLA WQNPHM LFLDEPTNHLDIETIDALADAIN EFEGGMMLVSHDFRLIQQVAQ EIWVCEKQTITK WPGDILAYK EHLKSKLVD/EEPQLTKELPTTC
11413	41781	A	11481	194	418	YGLASVSPTQISSSSCNPWME GGTLVGGDWIGSHDSEGVLTR SGCLISVWHFSCAVSPATL*RRCL LLLLRLPP
11414	41782	A	11482	1	675	
11415	41783	A	11483	1	1125	
11416	41784	A	11484	1	711	
11417	41785	A	11485	673	796	
11418	41786	A	11486	3	570	RLQEFGRNRHLPVNSPKLTNT KGKRRGTRYMF/SRPFKKGHV VPLATYMRIYKKGDIVDIKGM GTVQKGMPHKCYHGKTRGVY N\VTQHA/VMGIVVYKQA*GQR FLPKRI*CCVIEH\KHS/KSRDSF \LKRVKENDQKKKEAKEKGT WVQL\NRQLAPPREAHFVRTN GKEPGACWNPIPEYFHHNR
11419	41787	A	11487	1	2091	
11420	41788	A	11488	1	2208	
11421	41789	A	11489	430	1032	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hud	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
11422	41790	A	11490	3	1158	EDQIDRLDFIRNQMNLLTL.DVK KKIKVETEEVANKVSCAMTDEI CRLSVLVDFECSEFHPNPDVLKI YKSELNKHIEDGMGRNLADRC TDEVNALVLQTQQEIIENLKPLL PAGIQDKLHTLIPCKKFDLSYNL NYHKLCSDQEDIVFRFSLGWS SLVHRFLGPRNAQRVLLGLSEPI FQLPRSLASTPTAPTTPATPDNA SQEELMITLVTLASVTSRTISM GIIIVGGVIWKTIGWKLLSVSLT MYGALYLYERLSWTHAKERA FKQQFVNYATEKLRMIVSSTSA NCSHQVKQIATTFARLCQVQ DITQKQLEEEIARLPKEIDQLEKI QNNSKLLRNKAVQLENELENF TKQFLPSSNEGSVTIEIALVTLLG GNNRL
11423	41791	A	11491	132	381	SKAESVFPPTLPRQRPAAAAGP HWGAG*GQDEAGLHPGPEDRG FLRETPADPGLQAGLGQVHPPR SRADPPAPYQVPPRMGT
11424	41792	B	11492	129	470	

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11425	41793	A	11493	1	1955	FVSCQAPWSHPPAQLSPVGADA MTLTLVSLICGLSVGPRTCVQ AGTLPKPTLWAEPA SVIARGKP VTLWCQGPLETEEYRLDKGLP WARKRQNPLEPGAKAKFHIPST VYDSAGRYRCY YETPAGWSEP SDPLELVATGFY AEP TLLALPSP VVASGGNVTLQCDTLDGLLTF VLVEEEQKLPRTLYSQKLPKGP SQALFPVGPVTPSCRWRFRYY YYRKNPQVWSNPSDLEILVPG VSRKPSLLIPQGSVVARGSLTL QCRSDVGYDIFVLYKEGEHDL VQSGGQPPQAGLSQANFTLGP VSRSHGGQYRCYGAHNLSPRW SAPSDPLDILIAGLIPDIPALSVQ PGPKVASGENVTLLCQSWHQID TFFLTKEGAHPPCLCKSKYQS YRHQAEFSMSPVTS AQGGTYR CYSAIRSYPYLLSSPYQELVV SGPSGDPSLSTGSTPTPGPEDQ PLTPTGLDPQSGLGRHLGVVVG VSVAFVLLLFLLFLLLRRHQ SKHRTSAHFYRPAGAAGPEPKD QGLQKRASPVADIQEILNAAV KDTQPKDGVEMDARAAASEAP IQDVTY AQLHSLTLRREATEPPP SQEREPPAEP SIYAPLAIHLAHG GPRSHTQQKETQRLQKARELPP VDTNEPQPAWDP

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11426	41794	A	11494	22	1991	GLIPLQSAQSPEGDAMTPALTA LLCLGLSLGPRTRVQAGFPKPK TLWAEPGSVISWGSPTIWCQG SLEAEQYQLDKEGSPEPLDRNN PLEPKNKARFSIPSMTHHAGR YRCHYSSAGWSEPSDLELV MTGAYSKPTLSALPSPVVASGG NMTLRCGSQKRYVHFVLMKEG EHQLPRTLDSQQLHSGGFQALF PVGPNPSHRWRFTCYYYMN TPRVWSHPSDLEILPSGVSRKP SLLTLQGPVLAPGQSLTLQCGS DVGYDRFVLYKEGERDFLQRP GQQPQAGLSQANFTLGPVSPSN GGQYRCYGAHNLSSEWSAPSD PLNILMAGQIYDTVSLSAQPGP TVASGENVTLLCQSWWQFDTF LLTKEGAHPPLRLRSMYGAH KYQAEFPMSPV TSAHAGTYRC YGRSSNPVLLSHPSPELLEVV GHS GGSSLPPTGPPSTPGLGRYL EVLIGVSVAFVLLFLLLFLLR RQRHSHKIRTSGLRLCPSSPRPE K'AD FQRPAGAAETEPKDRGLL RRSSPAADVQEENLYAAVKDT QSEDGVEIYTRQSPHDEDPQAV TYAEVKHSRPRREMA SPSPLS GEFLDTKDRQAEDRQMDTEA AASEAPQDVTYAQLHSLTLRRE ATEPPSPQEGSPAVPSIYATLAI
11427	41795	A	11495	1	1818	
11428	41796	A	11496	3	574	IRCSSVDPRVRPRVRGASGAAA YCCRHVSI PRDHTTHNQSRKW HRNGIKKPRSQRYESLKGVDPK FLRNNRFAKKHNTKGLKKMQ ANNIAKAMSARAEAIKALVKP KEVKPKIPKGGQPINLIRLAYIA HPKLGKRARARIKGLKLCRP KAKAKAKAKADQTKAQAA APASVPAQAPKRTQAPTKASE
11429	41797	B	11497	45	331	
11430	41798	A	11498	1	1779	
11431	41799	A	11499	1	837	

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11432	41800	A	11500	3	557	ERGYSFTTTAERDIVRDIKEKLC YVALDFEQEMATAASSSLEES YELPDGQVITIGNERFRCPEAL FQPSFLGMESCGIHETTFSIM KICDVIDIRKDLYANTVLSGGTT MYPGFADRMQKEITALAPSTM KIKIAPPKYSVWIGGSILAS LSTFQQMWISKQEYDIESGPSI VHRKCF
11433	41801	A	11501	1	1188	
11434	41802	A	11502	1	684	
11435	41803	A	11503	1	1398	
11436	41804	A	11504	22	1239	
11437	41805	A	11505	837	971	
11438	41806	C	11506	1	3018	
11439	41807	A	11507	23	368	
11440	41808	A	11508	1	816	
11441	41809	A	11509	1	441	
11442	41810	A	11510	195	293	IKVSPSGRDPVRDN*ITW*FLPY CSSTTGSLH
11443	41811	A	11511	56	372	MELPASPALFARTPQPLGGRW DWAPWSRGWRSSRRLLGPHRSP RRGSEAQA WRAAGPEPCPAGR QLRPVNIWLFALILTHFTGTFQ VLA*TSQALI*NPRVLYPD
11444	41812	B	11512	108	326	
11445	41813	A	11513	3	326	GSKKKFH*HSRILERSRWRTS YQGRPQPSWLHPVDPHRGCR WSCLPVPCRAPSTPQPLGGRWD WAPWSRGRRLSGRLGPHRSPR NRGRLRHGGLQVPSRASQEGS
11446	41814	A	11514	3	619	VRDIHGSPTHHRPGGLRGKNGF VGEARDPRYSGHCFRECRTO ALVAFT*C*SCGFTVEKN*GLSC LPAGQGSGPAARHV*ASHPLHG LPCGSLP/NRAPPTPRPVPT TQGLRNASARRGTGRQLHLQP WCGIH*VKPAGLLSLLHGQAC GDPATPSRERLSQPAVPTALGS RRRLLGAGSPGSSLPSPRQP GGRRRPP
11447	41815	B	11515	1	1524	
11448	41816	A	11516	1	1365	
11449	41817	B	11517	1	654	
11450	41818	B	11518	1	795	

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11451	41819	A	11519	486	929	QKQEEWPEPTYPRALAAFR GRARDLQPAPEPPITLSMGS APEPPRGAPPAPRRRIPSTTQG LRSSGAGRRTCRQLHLQPRCRI HWVKPAGLLSLWLFQMHSASC WWNYHSGAWRMVALFSWLH* ECPSGESGAPILHFFPALP
11452	41820	A	11520	35	473	VLQLLRHHVWSCSFPPGVVVS LALAVKLQTFVTQEPSWLHPVD PAPGLQVELPASPLQCTRSTQPL GGRWDWAPWSRGRSSGRLGP HRSPWRG*EAQAWRAAGPEP/ WPRGKA/C*GPARNRAKRRFP CTF*EEVTVCSPPKRGDD
11453	41821	A	11521	23	229	RSWNPTLFVGMYNATAAWK PI*QFLKKNMKNLP*DPGREPLN QTG*KGKRGQEAFLKGISSR MSQ
11454	41822	B	11522	152	901	
11455	41823	A	11523	1	3063	
11456	41824	A	11524	242	263	VLQLIKAVWTQRTQEPSWLHP VDPALGLQVELPASPACTP QPLGVLPLPGLPLWRHLRSPSVH HCTVGAPFWAGQGRSPLPQR CALFLAGP
11457	41825	A	11525	1584	2082	QRAGSPHSRSLSPVPLPGLPLW RHLRSPSAHRCTMGAPFWAGQ GHSRLPQLAGRRGGGASGNR CCVQRLQASWSSRWAWAWRA PHSEQPAGPAGPQQ*GTWHPG QRLQRMYYWVLQCCRLTGAVL DFSPGLSCLPAGQGSPPAARHA *AFHPLHGLLCGRSLPD
11458	41826	A	11526	1293	1558	CIQHCHHCCCYRCRASAAGAA SLQGSTHYRIQHCTPCPVLLTP SVRLRDVCTRSIWPLVVTGLPS AMNVSSWCSTSSPAFGVLVLWI
11459	41827	B	11527	179	1031	
11460	41828	A	11529	1	342	
11461	41829	A	11530	1	3081	
11462	41830	A	11531	1	371	
11463	41831	A	11532	1	501	
11464	41832	A	11533	1	836	
11465	41833	A	11534	88	573	
11466	41834	A	11535	1	675	
11467	41835	A	11536	1239	1556	FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFLRWSFAVVAQAV/ VQWHNLSLPGFKQFSCLSLP SSWDYRCPPPRANFCIFTRDG VSPCCPGWSRTSLDLR

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11468	41836	A	11537	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTIDPVEKALRDA KLDKSIQHIDIVLVGGSTRIPKIQ KLLQDFYEAAYGA AVQAAIL SGDKSIENVQDLLSDVTPFP LGIE TAGGVMTVPH
11469	41837	A	11538	2	295	NRMGNHFAEFKRKHKKDISEN KRAVRRLRTACERAKRTL/SSST QASIEIDSLYEGIDFYTSITRAPF EELNAWGISWWWLPPVPGAS SGPTIEEDV
11470	41838	A	11539	1	1659	
11471	41839	A	11540	1	810	AGKPHCGGEFCTPNVHHFFR*F *ANPKRTII/ENKEALTPPTV/C* RAKPTLSSAPRAVI/EIDSS*E/GI GLYTSITPPRFEELNADLFLAPL TPVEKALRNAKLDKSIQHIDIVL VGGSTRIPKIQSFLQDFFNGKE LNKSINPDEAVAYGA AVQAAIL SGDKSIENVQDLLSDVTPSLG IETAGGVMTVLIKRNTTPTKQT QTFTTYSIDNQPGVLIQVYEGER AMTKDNNLLGKFELTGMPPGG MPGGFPGGAPPSGGASSGPTI EEVD
11472	41840	B	11541	848	2399	
11473	41841	A	11542	1	876	
11474	41842	A	11543	16	1203	SIPHEPWPVSLLLFQEQVPGKK ELRKGLALLEAIISICGSLDKVL KEKRKLFHSMGEGTINGLLDE LLQTRVLNQEMEKKVRENAT VMDKTRALIDSVIPKGAQACQI CITYICEEDSYLAETLGLSADQT SGNYLNMQDSQGVLSFPAPQ AVQDNPA MPTSSGSEGNVKLC SLEEAAQRIWEQKSAEIVPIMDK SSRTRVALIICNEEFDSIPRTG AEVDITGMTMLLQNLGYSVDV KKNL TASDMITTELEAFHRPE HKTS DSTFLVFM SHGIREGICG KKHSEQVPDILQLNAIFNMLNT KNCPSLKD KPKV IIIQACRGDSP GVVWFKDSVGVSONLSLPTTE EFEDDAIKKAHIEKDFIACSSST PDNVSWRHPTMGSVFGRGLIEH
11475	41843	A	11544	2	654	
11476	41844	A	11545	3	291	LIPPLLRPLVQSGGIPEMGKFMK PGKVVLVLAGRYSGRKA VIVIR YSVDIPLDKTVVNKDVFRDPAL KRKARREAKVKFEERYKTGKN KWFFQKLRF

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11477	41845	A	11546	157	386	
11478	41846	A	11547	2	531	FWQESASGHLWLSGFLSGPFSLSAEMGKFMKPGKVVLVLAGRYSGRKAVIVKNIDDGTSRPPYS HALVAGIDRYPRKVTAAMGKK KIAKRSKIKSFVKVYNNHLMPTRYSDIPLDKTVVKNKGFTDPALKRNARMEAKVKFEERYK TGKNKWWFFQKLRVLDAFVLII KNYKE
11479	41847	A	11548	1	414	LGGKGTWGETKPAMAAAEEDGGPEGNRERGGAGATKTLITYGNHLFSPQWLETRPERQECPVCKAGISREKVVGEKSLTFSLHFLRLKTPQICRLPV*LFLPP*GFQPFQDGGFHFSFGVGAFFPGFFNPSY
11480	41848	A	11549	1	654	
11481	41849	A	11550	3	663	RQGEVVSGLLGRVYVYLGGKGTWGETKPAMASAEESGAPNVPNRERGGAGRPKTPFECNICLETAREAVSVCGHLYCWPCLEH QWLETRPERQECVPCKAGISREKVVPLYGRGS/QRSPQDPRIKNSPRPPGGRGPAPE/SRGGSQPF GDTGGFHFSFGVGAFFPGFFTT VFNAHEPFRRGTGVDLG/QGHPSLQLGKEFLPGFSAIFFLFWL
11482	41850	A	11551	3	369	
11483	41851	A	11552	375	851	
11484	41852	A	11553	1	927	
11485	41853	A	11554	104	845	

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11486	41854	A	11555	200	1496	ETIQAVVFMSLHFLYYCSEPTL DVKIAFCQGFQDKQVDVSYIAKH YNMSKSKVDNQFYSEVGDST FTVLKRYQNLKPIGSGAQGIVC AAYDAVLDNRNVAIKKLSRPFQ NQTHAKRAYRELVLKMCVNH KNIISLLNVFTPQKTLLEFQDQVY LVMELMDANLCQVIQMELEH RMSYLLYQMLCGIKHLHSAGII HRDLKPSNIVVKSCTLKILDF GLARTAGTSFMMTPYVVTYY RAPEVILGMGYKENVDIWSVG CIMGEMVRHKILFGRDYIDQW NKVIEQLGTPCEFMKKLQPTV RNYVENRPKYAGLTFPKLFPS LFPADSEHNKLSAQARDLLSK MLVIDPAKRISVDDALQHPYIN VWYDPAEVEAPPQYDKQLD EREHTIEEWKELIYKEVMDSVEE KT*KWC*LKGQSPSAQVQQ
11487	41855	B	11556	56	1564	
11488	41856	A	11557	1	970	
11489	41857	A	11558	1	903	
11490	41858	A	11559	237	479	PVGTNTECEIPFQPMETGHSSR VDASGYK*PCLLCVSVSRGKTA GECTLF*VHHFLSSLCPVNLGA NNQLHYIPWFSTDG
11491	41859	A	11560	1	477	
11492	41860	A	11561	125	1133	
11493	41861	A	11562	1	837	
11494	41862	A	11563	2	708	CQHYKFRYHQGGEGQEEPPLN PHGAARAAYVLRKCTFDMFNF LASQHRVLPEGATCDEEEDVQ LRSTRATSLELPMAMRFRHLK KTSKEAVGVYRSIAHGRGLFCK RNIDAGEMVIEYSGVIRSVLTD MRKKFYDGKIGICYMFSMDD FDVVDATMHGNAARFINHSCE PNCFSGVIPGGGPNKIVIFGLR RILGGEEVNLRTKKFPIEDAKIN KLPCNCGAKRCRRFLN
11495	41863	A	11564	2	136	
11496	41864	A	11565	1	551	AILYAKRASVFKLQKPNAAIR DCDRAIEINPDSAQPYKWRGKA H/RAQKIAEHRKRYERKREEREI KERIERVKKAREEHERAQREEE ARRQSGAQYGSFPGGFPGGMP GNFPGGIPMGGGMPGMAGM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNANMSKYQSNPK VMNLISKLSAKK

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11497	41865	A	11566	1	804	
11498	41866	A	11567	64	1215	PPSFAIHLPTMDPRKVNELRAF VKMCKQDPSVLYTEEMRFLRE WVESIGGKVPPATQKAISEENT KEEKPDSSKVEEDLKADEPSSE ESDLEIDKEGVIEPDTDAPQEM GDENAEITEEMMDQANDKKVA AIEALNDGELQKAIDLFTDAIKL NPRLAILYAKRASVFKLQKPN AAIRDCDRAIEINPDSAQPYKW RGKAHRL/LGHWEAAHDLAL ACKLDYDESDASAMLKEVQFRA QKIAEHRKRYERKREEREIKERI ERVKKAREEHERAQRE/EEARR QSGAQQYGSFPGGFLGGMPGN FPIGGMPGMGGGMPGMG/GM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPAINMSKYQSNP KVMNLIJSKLSAKFGGQA
11499	41867	A	11568	1	265	VKAKIQDKEGIPPDQQRILFAG KQLEDGRTLSDYNIQKESTLHL VLRLRGGIIEPSLRQLAQKYN DKMICR/KCCGHTNNLRPKKK
11500	41868	A	11569	3	318	
11501	41869	A	11570	7	57	RFFNFLGGIP/P*SGPKGMTL/DQ TQGSKSKQIQWPALTFFKLVER NIPSSVTAVEFLVDKQLDLTE DSAFQPYQVRNFRLLFKIKG*L NFIDIQTFFKQYSLNISSNF*LC EKPNECSQLILLIG*TVY*FFNFL GGIPLNLGQKE
11502	41870	A	11571	1	2109	
11503	41871	A	11572	50	251	
11504	41872	A	11573	1	1922	
11505	41873	A	11574	2	479	
11506	41874	A	11575	1	909	LILTSVLLFQRHGYCTLGEAFN RLDFSSAIQDIRTFNYVVKLLQL IAKSQLTSLSGVAQKNFYNILD KIVQKVLDDHNPRLIKDLLQD LSSTLCILIRGVGKSVLVGNINI WICRLETILAWQQQLQDLQMT KQVNNGLTSLPLHMLTNILY RFSGDGWDIITLGQVTP/TLYML SEDRQLWKKLCQYHFAEKQFC RHILSEKGHIEWEVGCNFATF RKHYPAKEQYGRQHCIFCRHCS ILFWKDSGHP/CTAADPDSCFTP VSSQQFIALFQVLRAPCHPY WRFVNPAPVACGLIVSVL
11507	41875	A	11576	1	1035	

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11508	41876	A	11577	63	606	FAKNERTQRGKRRG\TRYMFSSR PFRR\HGVPV\PGPHICRIYRK DIVDTQGGVLFKKGMPHKCY PWPKEGVQLLPQHA\VAIVV NQPVLGQSFFPRE*IVRIEHIKH SKSPR*ASLK/RVLKENDSEKER SPNEKGTWGSNLKRHLAPPQK KHTL*RTNGKEPEL\LEPIPYEFH GHNRC
11509	41877	A	11578	1	490	
11510	41878	A	11579	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLA L*G*DLTHHII\FPFFFL**PAPP REAHFVRTNGKEPELL
11511	41879	A	11580	336	476	GMGTVQKGMPHKCYHGKTGR VYNVTQHAGIVVNKQVK*VV LCG
11512	41880	A	11581	1	626	WAFRPEPPSSSKFAQNDGPQRG KRRGTRYMFSSRP*ENHGVPV LAHFMRVYKKGDI\VRHPRGM GYCSKKGMPPTSCYPWQKLGR VYNVTPAMLFIVCKQTKLKG NDSLPRG/ILMWRI*AHLRHF*G ARD/RASLKTGRENGSRKKER KPKGGKVTWGFQLKRRHLGFP PQEEATFLLEPIGGREP*ACLE PYFPYWISWGINRC
11513	41881	A	11582	499	723	
11514	41882	A	11583	96	411	PAPTSRRCRRRAPLPPKKKAEGD AKGNKAKVKDEPQRRSARLSA KPAPPKPEPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGAGDAK
11515	41883	A	11584	3	493	
11516	41884	A	11585	588	759	GEGCGWAEVGRCRPGPPDPAG PAGAAGP/GAARGGLFRGVLS SSRCGGGSSSSRSGR
11517	41885	A	11586	213	626	
11518	41886	A	11587	1	645	
11519	41887	A	11588	1	739	
11520	41888	A	11589	327	676	NPNPSWNLAHVWMDRK*EQ RGIV/V**SNINKS*KEKMSMQC LEMPRNPDI*GRIDVSFQNLMR LTR*SQMGYLPWDLKQELTF KLS*KQVMLS\VVVTFVRNMLQ LRFLTSFSG
11521	41889	A	11590	11	328	

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11522	41890	A	11591	1	378	LFIVTVCPAFLRFSSAICDSFLIC PQVGCGVRRVLVTVGVLLSIS LDMAATGVSLGSSWSLFLGIW LMIRFQVS*WYPNWLILSWRN ISITSTPSYYFTYFPTFCYQISPPN QLFCFLCSWFL
11523	41891	A	11592	1	780	
11524	41892	A	11593	1	1461	MVTLMGHAALCLHYVMQLGT TGGAWYFPRASSQAREMPQCP TLESQEGENSEEEKGDSSKEDPK ETVALAFVRENPGAQNGLQNA QQQGGKKRKKKRJIISGKVLED FLALAMHFADEETGQKRCSLN QTIQLLITPDGTGSIWHQAFSSIV RRAAQQYGFREGGEDDDWTL YWTDYSVSLERVMEMKSYQKI NHFPGMSEICRDLARNMSR MLKMFPKDFRFFPTWCLPADP AQLDLWSQTFWPRPTAPDGT GADGLGLRLGSLGK/VSFWFPA CHGLG*PEASYYTAS/MACGSLP/ WKLSTFSAYLEDHSYVNEQIW RDIEDVVIKTLISAHPIRHNHYHT CFPNHTLNSACFEILGF DILLDH KLKPWLLTEKMQTAGALFISP ALPSYSNFPLOVARREFQTSVV SRDIDTAAKFIGAGAATVGVAG SRAGIGTVFGSLIIGYARNPSLK QQLFSYAILGFALSEAMGLFCL MVAFLILFAM
11525	41893	A	11594	1	2301	
11526	41894	A	11595	3	381	
11527	41895	A	11596	1	729	
11528	41896	A	11597	1	1006	MVKVKARVNEFGYTGCGLVTRA AFNSGKVDIVAINDPFDLNYLA YMLQYDSTHGKFGHTIKAENG KL VINGNPITIQE*DPTKIKWG DAGTEYVVESTSIFTAMEKVGA HLQRGAKRVMIFAPSTEAIMFM MKVNYEKYDNSLKIISNASCTT NCLAPLAKVIHDSNGIVERLMI TVHVITTTQKTVDGPCRKLRPD GHRALQNIIPASTSTAKAMVKV IPELNKKLTGMASHVPTAKVLV VDPTCHL/EKPAKYVDIKMM KQASEDPKIGILGYTEHQIVSSD FNSDTQSTFDAGAGITLNDHF VKLISWYDNEFGYSNRVVDLM AHMASKE
11529	41897	A	11598	3	508	
11530	41898	B	11599	1	5068	

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11531	41899	A	11600	58	659	PVATTCECIFIHLGEADVWIGN AA/WELYLYLEQSIQHDSMPMSD KTTG*GDN*FYASS/GAGKFVS RAVFINLEPIVTDEVCTGTYHQ LFHPEQLITDKEDAAHNYAWG HHDIGKIIGCYSTNKTCTIQQV DWCFTSLKVGINCQLPTVVPAG NLANIKRAACMLSNITIAIAEAW VCLGHKSDLSYANCSFVHQFFN KSIH
11532	41900	A	11601	511	1173	
11533	41901	A	11602	3	497	WCDGPQNRYALICQQC/YSHNG MALKEEFYIAFRCA YCFFLNP ARKTRPQAPRLPEFSFEKRQVV EGSSSVGPLPSGVLSSDNQFNE ESLEHDVLDNDTEQTDKIPAT EQTNQVIEKASDSEEPKQET ENEEASVIETNSTVPGADSI PDP ELSGESLTAE
11534	41902	A	11603	2	764	
11535	41903	A	11604	1	444	
11536	41904	B	11605	44	1748	
11537	41905	B	11606	1	1134	
11538	41906	A	11607	1	549	
11539	41907	A	11608	212	548	
11540	41908	A	11609	1	905	ESVAAAAARFPPTAPKELERQQ RRRFRFHHLFLFSLRTPCRVSV SLQPWLWKATEVMAMFEQMR ANVGKLLKGIDRYNPENLATLE R/YVETQAKENAYDLEPNLAV LKLYQFNPAFFQTITVTAQILLK ALTNLPHTDFTLCKMIDQATI QERNGPIDQIFVPSGTLLEDPA HFPGFWQTPGNGRACQKAWD ENHWLFGKVLTFG*RLLVVRK FIC/HVVGYHLP SHIDR/WLLAE MLGD/SDKPAKRCWMSKIRLR EDDRRQGFUCS/QE*EHLNPRN/ IVEKIDFDSVSSIMASSQ
11541	41909	A	11610	186	209	QLWPN*LLSRNKEATLRYSQLP TCHSICY*MPAF*HTISDLSFNK NINCKSYHLRVFYKYV*IVCHF *VPKYVWTKYYQTSCT*WR* SGVE*PPISSSSACCLLRRLPT EGTCPEIFWNPRLGISAECRDSC GPTSF
11542	41910	A	11611	2	2948	
11543	41911	B	11612	1	999	
11544	41912	A	11613	1	657	
11545	41913	A	11614	1	707	
11546	41914	A	11615	1	297	

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11547	41915	A	11616	1	1287	
11548	41916	A	11617	242	540	LTNEKKVQDQMDSQPNSTRGT RRSLYPFLLLKLFQLEKEGILPNS FYEASIIIPKPGRDITTTKKEF* TNIPDEHRCKNPQ*NTSKPNPA AHPKAYPP
11549	41917	A	11618	193	916	
11550	41918	A	11619	1	2169	
11551	41919	A	11620	1	615	
11552	41920	A	11621	39	568	NSAWARRPLVLPMLSLVSPWK SSQHIFRVLPNPNLDGRRKNNSP LPITCHLRVWARRYAHVVLRLK ADVIDLT/RAGEL/TEDEVERVI TILQINPRQYKIPD/WFLNRQKD VKDGKYSQVLANGLDNKLRED LIERLKEDSAPIEGLRHFWGLR/ VRGQHTQDQLGRRGRHRGAS GARR
11553	41921	A	11622	1	378	
11554	41922	A	11623	1	222	
11555	41923	A	11624	2	367	
11556	41924	A	11625	2	376	QTYSLRRATPRHIVGFTKVM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFDTKQML KDFVTTTRPALQELLKEALNME RNNQYQPLQKHAKW
11557	41925	A	11626	1	633	
11558	41926	A	11627	164	714	IGVNRHLIQESPSWNLGAPLE QIFQRKEQAAIFAILQPLLVISRQ TGSGVDPQQTPADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTHINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
11559	41927	A	11628	504	936	TESSSININKDDHAKTP/PKDH NSSPAREQNKTEFDELTEIGC RRWVITNSSSELKEHVVTQCKEA KNLEKMLQELLTRITSLEKNIN DLMELKNTAQELREAYTHINSQ TDQAERISEIEDQLNEIKGEDN IREKTVKRIE

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11560	41928	A	11629	1949	3232	PGKQDLEWTSKKLQQTCTRRGT LLVEGKLTNRKE*HQHQKQLR PHGNLIQRDHNCSAPAREQNWMM ENEFDKLTVGFRRWITITNSSK LKERVLTQCKEATNLAKRLEK LLTRITSLKNNKNDLMELKNATA QELREAYTSISGRINQAEQRTSE IEDQLNEIKRRGVSVCPQPS EDT PRSTARVPKGMVPPRPRVPLVT PPREKKEAPWLACLRTRALRLI DPSPQVWDIVSCDAENETKLEN TLQDIIQENFPNLAQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREK\GQVT HKAKPIRLTADLSAENLQAR/R TEWGPPIFNILKEKNFQPRISYPA K\LSFISEGEIKYFTDKQMLRDF VTTRPALK\ELLKEALN\MERD N\RYQPLQNHAKFVKTIAREE TCINLMCQITS
11561	41929	A	11630	1	421	
11562	41930	A	11631	2	415	
11563	41931	A	11632	59	492	GHIGVRPSLHPVTSTTSGNVSP LARAMASISELACVYLALILHD DEVIIIEVNTILIKAAASVNV/ PFWPGFLFGKALANVIGSLICN VGAGGPALAAAGAAPAGGPAPSI AAASAEKKMEAKKEESEED DDMGFLGFTKPVL
11564	41932	A	11633	100	527	PPRTGQRQPLHSARRHGSPVS/E LACIYVSA LISARTDEVTVTEDK INALIKSSPL*MLSPFWPWLCLQ RPLANVNVIGSLICNVVGPVPEA ASQPGA\GPARKVLAPSTAAAP S*RRRKLEAKRRKNPKEVLNDE HGLLVFLN
11565	41933	A	11634	1	675	
11566	41934	A	11635	1	1032	

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11567	41935	A	11636	3	976	HEAKHQMADDAGGS/AGGPEG PGGPWDGK\TLLSGEVFGIVIR GRGSRP/RGRGRGR\GRGARGG KGPRIK/WIGMPVHVQGAALVK DH*RSKFPWKEIYLFSLP\KGIK DS*FSFLAGPLSKDEGFEGCLPV QKQTRAGQAQVSRPFVAIGG LQMAHVGSGVLSAPKEVATG HPVGAILAKLSIRPRAQKGIWG TKYWQSPNTVP\CKV\TGRCGF VVVRLIPAPRGSGIVSAPVA\K KLLMMAIDDCTYSAPGCTAT LGNFAKGHPLIAIFK\TYKLP*P PDLWKETVFTKV\PYQ\FTDH LVKDHPPESSVQRDLRLQLVAT
11568	41936	C	11637	279	322	
11569	41937	A	11638	1	107	
11570	41938	C	11639	69	134	
11571	41939	B	11640	223	950	
11572	41940	B	11641	1	684	
11573	41941	A	11642	1	564	EFGTRDNRVLLPLVNPTVFDDI AVD/GVYPLGRVSFELFADKVP KTAENFRALSTGEKGFG\YKGS\ CFHRLFP\GFMCQGW*L*SHHN GTGGKSHLWGRNLKDENFIIL KHTGPGILSMANAG\PNNTNGSP VFLTCTA\KTE\WLDGKH\AGL GKVKEGMNIVEAMER\FGSRN GKTSKKIISIA\DCGTTN
11574	41942	A	11643	1	877	MSGALDVLMQKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVS\VISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIAAFREPRLLVVTDPR DHQPLTESSVYNLPTIALCNTDS PLRYVD\ICNNKGAHSVGLMW WMLAREVLRMRGTISRGHWPWE VMPDLYFYRDPEEIEKEEQAAA EKA\VTKEEFQGEWTAPAPEFTA TQPEVADLSEGVQVSPVPIQQF PTDDWSTQPATENWSAAPTAQ ATEWVGATTDWS
11575	41943	A	11644	1	1674	

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11576	41944	A	11645	1	1121	MLEAVLEESPREEA AFSWVMK GNLAAAGKTIQAQDRDAVGLSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQMKEDVL KFLAA\GTHLGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWEKLL \LAA\RAIVA\ENPADVS\VISSRN TGPEGLCLKF\AA\ATGATPIAG\ RFTPGVFTTNQ\IAAFREATGF LVVTWTPGLD\HQPLTEA\SYV YLPTIA\LCNTDS\PL\RYVDIAIP CNNKGAHSVGLMW\WMLARE VLRMRGVTISREHPWEVMPDL YFYRDPREEIEKEEQAAAEKAVT KEEFQGEWTAPAPEFTAQPEV ADWSEGVQVPSVPIQQPFTED WSAQPATDWSAAPTQAQATE WVGATTDWS
11577	41945	A	11648	1	396	
11578	41946	A	11649	1	567	
11579	41947	A	11650	1	226	
11580	41948	A	11651	3	377	
11581	41949	A	11652	19	450	PDRRWSSLDTMNHTGQTFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHIRSTSVDP HVVWSLFTLFMNPCLGLFIAP AYSVKSRDKMVGVDVTAQA YASTAKALNIWALILGILMTIL LIVIPGLIFQAYG
11582	41950	A	11653	210	2206	
11583	41951	A	11654	450	644	SLRLWV\TERTAV\TNLPSSRGV GDKPPVGS\PHLFLSLV\AFNPL QSTRNPASASQPQ\PCSAEQPAR RG*\AEPALRTV\PIHAEMWLPR LHEFEHRLVHRCFTLTFVDET DHCAVLPRGAGSGQGQGFERIL SQSPGSLWESC*\PGLWLNLSNP PPCPLPAPLGR\TAQ
11584	41952	A	11655	66	157	RGTWSIIA*\KSQGISWDRFEET LCREPFT
11585	41953	A	11656	1	2538	
11586	41954	B	11657	68	1602	
11587	41955	B	11658	1	1464	
11588	41956	A	11659	587	1081	ILSWLTLWSILRLYIVTLTGKIC SLTSEASEATSPPRGNTNNSRVA LA\VVTLVWRVCSFIDSKAFIL AFAFFFSHWFSILFPFPHQATL WYFWGDFECRSRGRNIHTDDR ARLVPMTERGGPPQGGEPART RSRQGGRGGMEGGE*\YPCPPH LGGQERKPG

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11589	41957	A	11660	180	583	YTEVLKGPDGAENHGTRTT** MHKPH*PIRSTGRKADKQLQQS LRINKINVQKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQL TMDVKDLFKENYKPLLKEIRG YKQMGHESMLMGRKNQYSEN GHATAQ
11590	41958	A	11661	82	159	
11591	41959	A	11662	2	1008	NAAPLQQRNKAGCR/YDLDEL REEGFRRSNFFKLKAEVRTQCK ETKNLEKTLDKWLTRKTSVEK SLNDLMELKTMVQGLRDKCTN FSNGFDQLEERVSVIEEQMNEM KQEKKYREKKDRSMTQKVNK DIQELDSALHQEELIDYRTVHP KSTEYTFFSAPHRITYFKIDHIVG SKALLSKCKRTEIITNCLSDHSA IKLELRIRKKLTQNRSTTWKLN LLLNDYVWHNEMKAEIKMFFE TNENKDTTYENLWDTFKAVCR GKFRALNVHKKRQERSKIDTLI SQLKELERQELTHSKASRMQEI TKIRAEQKEKETEKNIQKNQRI QELFLKDKQON
11592	41960	B	11663	1	1529	
11593	41961	B	11664	111	1350	
11594	41962	C	11665	1	2127	
11595	41963	B	11666	1	1350	
11596	41964	A	11667	1	1506	

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11597	41965	A	11668	1	1855	MIHVPLYSSLGDRVKSCEKKRE RERERRKKERKKERKKERKK RKKASSKEREGRKKERKKKL RKKEEKERKKRKKRKEGRKE RKKEKERKEGKKERKNIPGKR RESTDPLKEMDHRCLLPEMLK GTWWTTPARASGPAVPLLCE RQWTVDTTSVVPSTHMPGQM TQPIPADSHNMDEAGGHYPK QTNTRPENQILHVFTDKWELNT EYKDPKKRTTDRAYLRVEAT LAADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRGRMTPHM AGYSSETKLPEERSGSSICGSPIS AVLQPPLLIPRQTGSGVDLQQT PTDLQLRVLMERSSSPATEQSW MENDFDEMDEGFRRSNYSEL KEEVQTYCKEVCGRGKFKALNA HKKRQETSKIDTLTSQLEKELEK QEETHSKASRRQEITKIRAELEK IETQKTLQKINERSWFFKEKINK IHRPLARLIKKKTEKNQINAIKN DKWDITNNLTIQATIREYYKH LYANKLENLEEMDKFLDTYTL PRL*/N/CRQSLIAYYQIKVQDQ MDSQSNSTRGTRRSWYHSF
11598	41966	A	11669	2678	2897	PDGAKKHGKRTRDERTSFSEF NQLEERVSVIENQMNMKREE KFREKRVKRNEQSLQEIWDIM* KDQMRSTS
11599	41967	A	11670	843	2004	NNQCREVLKGVGDGAESQGSRT REERRSLSRCDQLEERVSVIED QNMNMKREGKFRKRIKRNEQ SLQEIWDYVYKRPNRLIGVPES DGENGTKLENTLQDIQENFPN LTRQANIQIEIQRTPQRYSSRR ATPRHVVRFKTVEMKEKMLR AAREKGRVTHKGKPIRLTADLS AGTLQARREWGPINFILKEKNF PPRISYPAKLSFISEGEIKYFTDK QMLTIVHLKTLDIYMYNIRRPK GGEKKADQEVNSEPRNNIVLET KGDGRGPQAPSPGGPPRRVRR SASGSRAGITFHPVHYL TRRPFA HRFHYQSHGYGVGSVQSALR HKTNSAARAALRDGGVDCRGR ERGSACQKRSDDEAGGLVLS LPRVMGSGWEVRR
11600	41968	B	11671	1	3221	

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11601	41969	A	11672	82	160	
11602	41970	A	11673	1	551	AAAMADSGTAGGAALAAPAP GPGSGGPGPRVYFQSPPGAAGE GPGGADDEGFPVRRQKGVTVS YDRKELRKRL\NL\EDWIL*Q\LN GAFYDCQ\EEEEPELEIDVDELL D\MESDDARAA\RVKELLVDC YKPTEAFISGLLDKIRGMQKLS TPPEEVRVPDPGRITVAPTQGSL PPDLVATAITGGT
11603	41971	A	11674	362	650	
11604	41972	A	11675	1	651	
11605	41973	A	11676	1	3101	
11606	41974	B	11677	1	2838	
11607	41975	A	11678	1326	1980	TSEASRQSERVDSAAALSLSLS RSSKCRPWGTARVARAGGCLT PLLSRRFLETRPFTGPWDPGLG VTCWCCPPKRLKSTPRPKFSV CVLGDQQHCDEAKAVDATFEV CLGDQVLSNANGFLSLSAKKY DAFLASESLIKQPRILGPGLNK AGKFPSSLREEGQAICYSTNLT *SSLPSQVLC\LA\AVGHVKMT DDELVYNH\LA\VNFLVSLLK
11608	41976	A	11679	11	720	EAMSSKVS\RD\TYE\AVREV\H GTQRKRRKF\UETVELQISLKNY DPQ\KDKR\FSGTVRLKSHSPAL SFSVCV\LGDRQH\CD\EAKA\V DIPPHGPSEAAEKTSTKNKKLV QKSWPKKV*MPFLA\SESSDQA RFPRIPRAPGLNKA\G\FP\SLLT HNGKHGGPKV\DEVKVPQSRFQ MKKVLCLAV\AVGHVKMT\DE LVFNH\LA\VNFLV\SLLK\KNW QKCSGALYYQEAPMGQSPKRL
11609	41977	A	11680	34	507	
11610	41978	A	11681	407	806	LRVGM\LRQSKANGPDDHLLG ASCTCGPSTGSPSRLPSLPQRP QKGLLHQ\RATRMKPGNIAKGL WKRLSKGTVMKLWLLTAVPRL SGLLVCP\LVHQL\LA\FAFKLRF PIFLWFRANRRHARFSILFKLS RP
11611	41979	A	11682	1	1551	

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11612	41980	A	11683	1	751	MAGYSSETKLPEERSDSSIRGSR KSTVLQTLILLIPRQTGIKKLTQN RSTTWKLNLLNDYVWHNE MKAIEIKMFFETNENKDTTYQN LWD/YIQSSV*REIYSTKCPQEK AGKIQN\DLTSQLKELEKEQEQ THSKASRRQEI\TKIRAEPEKIQT QKTLQKINESRSLFFKRINKIDR PLARLIKKKREKNQIDAINKVEK GISPPIPQNYKLPSENTNTSMQ IN*KI*KKWINSWTHTPSQE*TR KKLNL
11613	41981	A	11684	49	551	VRATYFHHAPANCTEFVPRQL VSRAENLPQATSLPTEKASRAF RVLLIPRQTRSGVDLQQTPTDL QLRVLI\RRKTNKQKGHPHQN PICTSP\RRSNFFELKEEV\THG KDAKNLEKRLDKWLTRISSVE KSLNDLMELRTMA*ELCDECTS FSS*FNQLEERSVSI
11614	41982	A	11685	1	1566	MNSLLTGQIPESQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRSQS SICGSPISAVLQPPLLIPRQTGS VDLQQTPTDLKRLVLT\VRKRS NKQKGHPHQPICTSP\SKTKD RSTRQKVNDIQDLNSALHQA DLIDIYRTLHPKSTEYTF\FSAPH HTCSKIDHIVGSKALL/EQM*KN RNYQKLSLRPQCNC\LELRICKL TQNHSTTWKLNLLNDYWM QKRPLKIQCCFMLKTLNKLID GTYLKIIRAIYDKPTANIILNGQ KLEAFLLKTGTRQGCPLSPLLL NVVLEVLARAI\QEKEIKGIQL GKEEVKLSLFA\DDMIVYLENPI VSAQNLPKLISNFSKVSGYKIN VQKSQTFLYTNNRQTESQIMSE LPFTIASRKIKYLGQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRACIAKSILSQKNKAG GITLPEFRLYTRLQ
11615	41983	A	11686	1	4962	
11616	41984	B	11687	101	3772	
11617	41985	B	11688	1	1047	
11618	41986	A	11689	21	287	

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11619	41987	A	11690	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSAEDEINEMKRE EKFREKRVKRNEQSLQEWDYL KRPNRLIGVPESDGENGTLE NTLQDIHQENFPNLRQANIQIQ EIQRMPQRYSLRRATPRHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRR WGPIFNILKEKNFQPRISYPACK
11620	41988	A	11691	1	1257	
11621	41989	A	11692	1	759	
11622	41990	B	11693	107	511	
11623	41991	A	11694	170	726	LLEGKLTNRKDIHTETPSVCHH HQRPKDIIHQENFPNLRQANIQIQ QEIQRTQRYSSRRATPRHIIVR FTK/VEMKEKMLRAAREKGRV THKVKPIRLTADLLAETLQARR EWGLIFNILKEKNFQPRISYPACK LSFISEGEIKYFTDKQMLRDFVT TRPALKELLKETLNVERNRYQ PLQKHAKL
11624	41992	A	11695	1	569	MAGYSSETKLPEERSGSNICCSP ISAVLQPLLIPIRQTGSGVDLW QTPTDLQLRVLTVRRKINKQKG HPHQNPICSTSPSSKTKGQIRAE KEIETQKALQKINESRNWVFEK INKIDRPPARLIKKKREKNQIDA IKNDRGDIITDPTIEQTTIREYYK HLYANKLENLEERDKFLNTYTL PRLNQEEVESLNRPI TGSEIAII NSLPTKSPGPDGFTDAFYQRY KEDLVFLLKLFQSIEKDRILSN SFYEASIFLIPKLRDRTTKKEN* QTERSTTPKPHLYITIEDQRPD QSRTEGNRDTKSPSKNQ*IQEL/ WFLKRSTKLIASTKTNKEEKRE ESNRCKK**RGYHHRSHRNT NYHQIRL*TPICK*TRKSGRKG* IPQHIIHSPKTKPGRS
11625	41993	A	11696	3	1039	
11626	41994	C	11697	1	1251	
11627	41995	A	11698	1	807	

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11628	41996	A	11699	1	713	MNSLLTGQIPESQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRKRS NKQKGHPHQPKICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFSSAPH HTCSKIDHIVGSKALL/QQM*K NRNYQKLSLRPQCNCQTRTQD*E THSKPLNYMETEQPAPE
11629	41997	A	11700	1	1768	MNLSRHLNEVKGELLWSLEWR DPDGGSSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFLGLQKKMDLKGFKSCFKI YCSSKHLKLTGFISEAVLCYGE GGEGDTVLTMKERWPHCEICVLI QCNKGRLLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQPKICMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQEELTILNIYAPNTEAPR FIKQVLSDLQRDLDSHIIIMGDF NTPISTLDRSMRQKVNKDIQEL KSALQQAADLIDIYRTLHPKSTE YTFSSAPHHTYSKIDHIVGSKAL LSKCKRMEIITNCLSDHSAIKLE LRICKLTQNRSTTWKLNNVLLN DYVWHNMKAIEKMFETNG NKDDTYQNLWDYIQRSV*REI YSTKCPQEKAGRJ*N*HPNIQL KELEKQEQTSHKVSRRQEITKIR AELKEIETQKTLQKINESRSWFF EKFNKIDRRRLARLIKKEKNQ IDAIKNDK/GISPLIPQYKLPSE NTINTSTQIN*KI*KKWINSSTHT
11630	41998	A	11701	535	666	KGRNIQLNGLVIGTLSN*LKCL KMFFTMLPGYINGGSSDFFLH
11631	41999	A	11702	20	262	
11632	42000	B	11703	1	1254	
11633	42001	A	11704	1	1032	
11634	42002	A	11705	481	1491	
11635	42003	A	11706	2	717	

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11636	42004	A	11707	348	1976	SRVRPVVHLRRAPMVCQGHHT PPVCGSLAGPDCVHYSVPAG YSSETKLPEERSGSNCCSPISAV LQPQLLIPRRTGSGVDLQQTPT DLQLRVLTVRRKTNKQKGHPH QKPCMSPPSKTKGSNSHITLTL NVNGLNAPIKRHRLANWIKSQ DPSVCCIQETHLTRCDTHRIKIK GWREIQANGKQKKAGVAILV SDKTDFKPTKIKRDKEGHYMM VKGSIQEEELTLNYPNTGAP RFIKQVLRDLQRDLDSHTLMIG DFNTPLSTLDRSTRQKVNKDIQ DLNSALHQVDLIDIRTLHPKS TEYTFFSALHHIYSKIDHIVGSK ALLSKYKTEIITNCLSDHSAIK LELRKKLTQNRSTTWKLNLL LNDYVWHNKMKAINTLFETN ENKDDTTYQNLWD/YIQSSV*REI HSTKCPQEKAGKIN*HPNIQL KELEKQEQTSHKASRRQETKIR AKLKEIETQKILQKINESRSWFF EKINKIDRPLARPIKKKREKNQI DAIKNEKGISPLIPQKYKLPSN TINTSMQIN*KI*KKWINSSTHT PSQD*TRKKLNL*INTSMQIN
11637	42005	A	11708	1124	1717	LLEGKLTNRKDIHTKNPSVRHH HQRPKVDKTTKMGKQSRKTG NSKNQASAPPPKERSSPATEQN WTENDFDELREEGFRRSNYSEL KEEVRTNAKEVKNFEKLDLW ITRITNAEKSLLDLMEKTTAR ELRDECTSPSSQCNQLEERISAM EDKMNMKREEKFREKRIKRR EQSLQEIWDYVVRPNLCLIGVP
11638	42006	A	11709	1	3549	
11639	42007	B	11710	209	403	
11640	42008	A	11711	3	248	
11641	42009	A	11712	61	594	IQPLVSVLDEKPSNGVLVHVMK LLIKTFLDGIFFDLMEENVLNT DEIHLIGKCLKFVVSNAENLVD DITETAQTAGKIFREHLWNSKK QLSSVHGSEHEDKALTCHWVG HPGFPEKLKERKKFCGIMVVGL FGFTTDSGKAGADIHGRFLQGN FCNDAVTKAHVEKDFIAFKSST

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11642	42010	A	11713	1	430	FSAVREDGGCYLWQIYPIKERM DRIRLVLIIENKFDHLPFRNGA DFAIMEMKKLLEDLGYSVVDVE ENLTAR/HNVSQGETGKGLPIF ITQLIACFQRYSWRCHLAEVFW KVQQAFFESPEATVQMPTIERVS MTRYFYLFPGN
11643	42011	A	11714	3	1195	
11644	42012	A	11715	35	1288	
11645	42013	A	11716	1	1641	
11646	42014	A	11717	1	2933	MVCSAAPLLLLATTLPLLGSPV AQASQPLWPMAGKQTMWAQT STLTLTEELGQSQAGGESGG QLLDQENGAGESALVSVYVHL DFPDKTWPPELSRTLPLAASA SSSPRPLLTGLRLTTECNVNHK GNFYCACLSGYQWNTSICLHYP PCQSLHNHQPCGCLVFSHPEPG YCQLLPPVPGILNLSQLQMPG DTLSLTLHLSQEATNLSWFLRH PGSPILLQPGTQVSVTSSHGQ AALSVSNMSHHWAGE
11647	42015	A	11718	1	357	
11648	42016	A	11719	73	1494	KSSHCIKMGPIFHKTSELFLPA TSCPSCPDQNEEDVSQTQYKEC CGGGWCSHSIFAVWHFI*RPDA T*FG*SSAYGFVADQCP*GSS* LYHLWYSYSGSENKQCG*RAA LGAGFSDKTPAHTVTMACISAN QAMTTGVGLIASGQCDVIVAG GVELMSDVPIRHSRKMRLML DLNKAAXMGQRLSLISKFRNF LAPELPAVSEFSTSETMGHSAD RLAAAFVSRLEQDEYALRSHS LAKKAQDEGLLSDVVPFKVP KDTVTKDNIGRPSSEQMAKLLK PAFIKPYGTVTAANSS/LLTDG ASAMLIMAEKALAMGYKPKA YL/RRDFMYVSQDPKD/HLLG PTYATPKVLEKAGLATMNDIDA FEFHEAFSGQILANFKAMDSD WFAE/NYMG*KKPRFGLPPLWR RFNNWG/GSLSGHPFGATGCR LVMTAAANRLREEGRASMA*V AVACAAGGQGHAMIV/EAYPK
11649	42017	A	11720	1	642	

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11650	42018	A	11721	17	960	KSGARSLQPQLRAPEDGGPLS LPNAAMARGPKKHLNRVAAIP KHWM LDKLTGGCA/PRHSPVP HKL/RECLPLIIFLRNRLKYALT GDEVKKICMQRFKIDGKVVRT *YNPTPAGFHGMSA/FDKTGEE NFPS*SIDTKGSAFA/VHPYLTTL EEGQSTSLVPKVKKRSFVGHKK GIPSSWVTS*WPATIR*PRSPSSK VN*YHFRDLETWQRLLDFIKF \DTGNL\CMGDWGGANLGRN WVLITN\RERHPSFDPWFHVVK DANGN\SFATRLSNIFVIGKGNK PWISLPRGKGIRLTIAERDKRL AAKQSSG
11651	42019	A	11722	1	460	
11652	42020	A	11723	1	243	
11653	42021	A	11724	94	311	
11654	42022	A	11725	400	792	
11655	42023	B	11726	473	596	
11656	42024	A	11727	1	1707	
11657	42025	A	11728	3	484	
11658	42026	A	11729	122	253	
11659	42027	A	11730	1	803	RGGRGGAGAAGELAGPLPSP APFESPGFTPPGPWGSICPAFA HALHSGTVPARSGRTMARGAA LALLLFGLLGVLVAAPDGGFDL SDALPDNENKKPTAIPKPSAG DDFDLGDVVDGENDDPFPN PPKMPNPNPNHPSSSGSFS\DA DLADGVSGGEGKGGSDGGGSH RKEGEEADAPGVIPGIVGAVV VAVAGAISFIA/YQKK\KLCFK\ ENAEQGEVDMESHRAQRQK PAVQRTLLKIEDCEPKQPAF GSRVRTAA
11660	42028	A	11731	335	476	
11661	42029	A	11732	2	169	
11662	42030	A	11733	49	289	VPVVQVPAAPGPLPGPATGSCS ASAAPRPDPPPGHPEGHGHS P/GVLGFVEVGIFSYCEQPKQCV TIKIFESPPIRRRL
11663	42031	A	11734	22	412	ARVGFLLGQEGKAGARASGPA DDVC/GKGASAIRSHMRASRSP PSPRRCHHHHEATGTASGSAAG GPGAGCVWLCRLALTPSAQDG RNSTFQTYKKEVCLPRHSHPCW MHAAGTTAGGSVAMSACCPSS SR

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11664	42032	A	11735	250	571	KGPRVTQGATVPKRQAPSAGL D/GSPISQFPWSY/DV*AIAILCG QGV T*PLPVSPGGPAPPESSVAL AEWVCSGSRRLPLNSGIARRPIG VIQPLDFLQNWPKPVLRC
11665	42033	B	11736	1	1593	
11666	42034	A	11737	2	1175	
11667	42035	B	11738	206	354	
11668	42036	B	11739	850	1461	
11669	42037	A	11740	2	663	VLLDERSAALDGA KR DGT LAL AAGALCREARAAQVFFLKGGY EAFSASCPCLCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSINKAGGRV FVHCQAGISRSATICLAYLMRT NRVKLEAFAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFV SIPDHSTNSALSYLSLITSSHC
11670	42038	A	11741	1	474	
11671	42039	A	11742	3	1354	WAVCATRVGGAVGGTAKKPR SPEPRVTLTSSQSGFWFGAER PGGLAFFPRKAPPCWPREQTKS TAGPITLGALRPAMVMEVGTL DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIA GSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAALD GAKRDGT LALAAGALCREARA AQVFFLKGGYEAFSASCPCLCS KQSTPMGLSLPLSTSVPD SAES GCSSCSTPLYDQGGPVEILPFLY LGSAYHASKDMLDALGITALI NVSANCPNHFEGHYQYKSIPVE DNHKADISSWFNEAIDFIDSINK AGGRV FVHCQAGISRSATICLA YLMRTNRVKLEAFAFEFVKQRR SIISPNFSFMGQLLQF*VPQD/VL VPHCSAEGWEAPDMAVLDRG TSTTTVFNFVFIPIVHSTNSAL SLPRFGPINGPFPAG
11672	42040	A	11743	196	1260	
11673	42041	A	11744	5	447	
11674	42042	A	11745	1	328	
11675	42043	A	11746	3	364	
11676	42044	A	11747	1	816	
11677	42045	A	11748	1	1377	

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11678	42046	A	11749	1	989	EGRTVLGGGLGSAAAMASRL LNGAKMPILGLGTWKSPPGQ VTEAVKVAIDVGYRHIDCAHV YQNEVEVGVAIQEKLREQVVK REELFIVSKLVCTYHEKGLVKG ACQKTLSDLKLDYLDLYLIHWP TGFKPGKEFFPLDESGNVVPSD TNILDTWAAMEELVDEGLVKA IGISNFNHLQVEMILNKPGLKY KPAVNQIECHPYLTQEKLQYC QSKGIVVTAAYSPGSPDRPWAK PEDPSLLEDPRKAIKAKHNKT TAQVLIRFPMQRNLVVIKSVT PERIAENFKVDFELSSQDMTT LLSYNNRNRVRCALLSCTSHKD
11679	42047	A	11750	1	855	
11680	42048	A	11751	2	367	
11681	42049	A	11752	2	376	QTYSLRRATPRHIIVGFTKVM KEKVLRAA/NKPIRLTVDSLAE LQARKEGGPIFNILKEKNFPQRI SYPAKLSFISEGEIKSFDTKQML KDFVTRPALQELLKEALNME RNNQYQPLQKHAKW
11682	42050	A	11753	1	1536	
11683	42051	A	11754	1	2541	
11684	42052	A	11755	1	1788	
11685	42053	B	11756	1	1014	
11686	42054	A	11757	1	777	
11687	42055	A	11758	1	1029	
11688	42056	A	11759	1	2052	
11689	42057	A	11760	1	1392	
11690	42058	A	11761	1	993	
11691	42059	A	11762	1	1240	PTDPAEGLCLDAKTNKRKGP STPILPFCSPFIRGPKVDSTHGA WGQKQHR*TGIF*RSRAPSPPA KEHGSSPATEQSWMENDFDEL REEGFRRIWYSELKEEARTHGK EVINLEKK\LDEWITRITNAEKC LKVELMELETNAELREECRS LRSRRNQLEERVSAMEDEMNE MK\QEEKFREKKKKK*TKAL KELWDYVVKP/NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANWQIRGNYRERQRLPPRG RATPRTHIIVRFTKVGNGREKM FKGQPGGKGRVTLKGKPIITLT ADLSAETSTSQTKEWGPINFIL GKEFSNPEISYLSQT*AFISGREE LNSFYRTSQMLRDFCHHQASRL P*KSTRPALKELLKEALKHKG GNNPVPSHLQKFIA

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11692	42060	A	11763	1	1917	
11693	42061	A	11764	268	307	AHHTHLCLLTSPPEGR*VCWG CGLGWGVVLSLVCPP
11694	42062	A	11765	2	349	
11695	42063	B	11766	1	1734	
11696	42064	A	11767	1	603	
11697	42065	A	11768	1	420	
11698	42066	A	11769	115	796	EWSSVRRSLVEKRALRRPHQC LCFRMKTILSNQTVDIPENVDI TLKGRTVIVKGP/REGTLRRDFQ SPSMENFTFLERKKRLRVDK W/WGNRKE/LATVRTICSHVQN MIKGVTLGFRYKMRSVYAHFP HQPLL SRGNGSLV/E/RNFFG*K NISARVRMRP/GVA/CSV/SQAQ KGEF/ISLEGNDNELVSN/ALI QQATT/VVKNKDIFKLDGIYVFE KGTVQQADE
11699	42067	A	11770	1	295	ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCP*MSLYKY MAMARKAMSL/YIYFFLDEFM YFAGTW/MKLETILSKSQGQK TKHRMFSLVGGN
11700	42068	A	11771	3	342	
11701	42069	A	11772	1	182	
11702	42070	A	11773	1	439	
11703	42071	A	11774	1	325	
11704	42072	A	11775	2	91	
11705	42073	A	11776	167	861	IWAILADPRMAQGKLRMEIGTK LRCLIWTVHKGVHVWTFWWV ERSQTGNLEVRRLWGLLTHL HSGVNSLFTRARIWNPSMIDW/I KKMWHIYTMEEYAAIKKNQF MSFAGTWMKLSAPAAPTVLFL ASFTNHYNLRASLLVESCLAPS YTSVEPRFSIPQSLTPARGSSDG HTCFSHQSHDLSL/CADSTHFW LSAHIWQANAPPVPRAPSEL KTR/LKCSQ/LNLRPP
11706	42074	A	11777	1	660	
11707	42075	B	11778	1	2633	
11708	42076	A	11779	1	2985	
11709	42077	A	11780	398	605	
11710	42078	A	11781	204	585	VTMCDRKAVIKNADMSEEMH QDSVECATQALEKYNIEKDIAA HIKKEFDKKYNPTW/HCI/VGEG TFGSLC*HIETKH/HLTSYLGA WAISFCFKFWFKRHGTVAHPV IPFQKQGI/ALNFQLPED
11711	42079	A	11782	1	810	
11712	42080	A	11783	188	534	

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11713	42081	A	11784	1	1188	
11714	42082	A	11785	1	1137	
11715	42083	A	11786	19	428	ERRNSGNMALRVERSVRAVLC SLHVVLAPAAPCLSRPWQLGM GAVWVYCNLPEVGTGLNKQDE FGALERVKAASELYSPLSGEVT EINEALAEENPGLVNKSRVEDG WLJKMTLSNPS*LDELMSSEEAY EKYKISIEE
11716	42084	A	11787	66	631	RRDPRTPANMALRVVRSVRAL LCTLRVPLPAAPCPRPWQLG VGAVRTLRTGPAALLSVRKFT KHIEWVTTEGIGTVGNSFAQA EALGDVVYCSLPEVGTGKI*TKP SWSLVLESVKAASELYSPLSG AEVTEINAEALAEENPGTCKTNFC YEDGWLIKMTLSNPSE/LDELMS SEEAYEKYKISIEE
11717	42085	B	11788	46	743	
11718	42086	A	11789	209	401	MKPPVRSLSLTPPRSIIHGSSATEI EELNTTFKYLTGEQTEKMWQ RLKGMEIKLKN*G
11719	42087	A	11790	135	313	
11720	42088	A	11791	1	624	
11721	42089	C	11792	81	299	
11722	42090	A	11793	5	166	SPVMMSSFFLVCLLTT*RSPPSS SSSSSSSSSSSSSSSSSPSSSFS GSVV
11723	42091	A	11794	3	173	
11724	42092	A	11795	169	291	SCNSSLSFLSLSLVADPQIATYR /S*CSRLGHKGTLPGS
11725	42093	C	11796	1	429	
11726	42094	A	11797	1	279	
11727	42095	A	11798	3	376	
11728	42096	B	11799	1	736	
11729	42097	A	11800	753	2455	
11730	42098	A	11801	1	312	
11731	42099	A	11802	48	397	
11732	42100	A	11803	51	286	
11733	42101	A	11804	1	420	
11734	42102	A	11805	11	537	PDRPTRPCRQCARSFRRLKAA VGVEGSLSSGELGTRVPAAPS PTTRPRAMAFCLPSFACIY/SALI LHDDEVTVTEDKINALIKSSR V*MLSPFWPLGFAKALANVN MGSILCNVAGAGGCCPASWVL QPAGRSLLPPLAASSLREKKV EAKKEGFRGSFD*LTWGFGSF
11735	42103	A	11806	114	399	

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11736	42104	A	11807	3	599	AIRRLRISAREEERENQPRLLPL SLGAGGGVGGFVQWPRFKAR DLRGKKKEELVKQLVDLKVVE LVPSARRQKQGGAAASKLSKI RIVVRKSLAPCSPLFTQTQKEN LRKFYKGGKKYKPLADLRPKKTR AMRRRLNKHENLRITKKQQR KERLYPLRKYAVKALGGALSIIK HKENLTKKQQRKERLYPLRK YAVKA
11737	42105	A	11808	226	370	AGSP*FPQFSEA*RRGALGSGA DQDLSHPRITETLTSCSLQTSS PR
11738	42106	A	11809	3	7964	RSGSSSKFEPRSRSASVLPASAL GPPNTSPRQLVAHCALPATRMP VTEKDLAEDAPWKKIQQNTFT RWCNEHLKCVNKRIGNLQTDL SDGLRLIALLEVLSQKRMRYKY HQRPTFRQMQLENVSVALEFL DRESIKLVSDSKAIVDGNLKKLI LGLVWTLILHYSISMPVWEDEG DDDAKKQTPKQRLGWQNKI PYLPITNFQNWQDGKALGAL VDSCAPGLCPDWESWDPQKPV DNAREAMQQADDWLGVP
11739	42107	A	11810	1	636	
11740	42108	A	11811	3	261	OKKPLKQPKQA*EMDEVRA AEALAGAGALGRPELNTCLCS PEDKAFKQKQKEEQKKLEIK AKAAGKGPLATGGIKKSGKK
11741	42109	A	11812	1	621	
11742	42110	A	11813	1	1024	
11743	42111	A	11814	174	332	SHCLANAPGDVKVRNDPESPRE L*HL*R*RYNTRWKRSI*EEWC QGHSWRG
11744	42112	A	11815	1	1323	
11745	42113	A	11816	1	2322	
11746	42114	A	11817	1	336	
11747	42115	A	11818	22	391	PPPPAAKTRRKKVLATKVLGTV KWFNVNRNGYGFNRNDTKEDV FVHQTAIKKNNPRK\YLRVSGD GETVEFDV\VEGEKGAEAA\NVT GPDGVPV/EKGSRYAA\DRRRY RRCY\YDR\RRGPPEYV
11748	42116	A	11819	433	866	PPPPAAIDAEEKVLATKVLGTV KWFNVNRNGYGFNRNDTKEDV FVHQTAIKKNNPRK\YLRVSGD GETVEFDV\VEGEKGAEAA\NVT GPDGVPV/EKGSRYAADRRYRR IGYYGKARWPPFANYAGGRR RKGAAQVEGFLPPLPLD

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11749	42117	A	11820	63	484	
11750	42118	A	11821	1	819	
11751	42119	A	11822	150	463	
11752	42120	A	11823	63	594	FAKLNPNGKGGGEATRYMFSR PF*ENHGVVPLGHNN*RFYK GDIVDIQGEWGTLFQKGNCPH KVVTHGQNLGVLPMVTPAML VGHLL*TNQF*GKVSFKRINVR IEPIKHSKRSDFLKRVKEND QKKKEAKEKGTWVQLKRQPA\ PPREAHFVRTNGKEPELEPIPY
11753	42121	A	11824	2	1376	
11754	42122	C	11825	132	341	
11755	42123	A	11826	155	245	
11756	42124	A	11827	3	293	
11757	42125	A	11828	204	467	LRAPHVACSRNQGPGMCNCL NTDQHTQTQRQG*EEKSSSK/ PISSLMEYYKRSQCYSVKARS VF*KLRLAQALLQETKKPVFR L
11758	42126	A	11829	1	768	
11759	42127	A	11830	348	568	REISYKERIGM*MPPSVILNSYV KSMLETYPHPLRLRGVVAPGLK KGFLTESLLALPDPSFSGRMTSF KITPV
11760	42128	A	11831	1	840	
11761	42129	A	11832	2	216	
11762	42130	A	11833	1	726	
11763	42131	A	11834	3	3231	PGGWLRRALPGRERLQSPVHA VPPQHGTSRSLLVTPWAGAG DQDFSSPPLLLGETDHLHDL PLSPPLTSDELFLPGICDPYVKL SLYVADENRELALVQTKTIKKT LNPKNWEEFYFRVNPNSHRLLF EVFDENRLTRDDFLGQVDVPLS HLPTEDPTMERPTYFKDFFLLRP RSHKSRVKGFLRLKMA YMPKN GGQDEENSQDRDDMEHGWEV VDSNDSASQHQEELPPPLPPG WEEKVDNLGRITYYVNNH
11764	42132	A	11835	1	624	
11765	42133	A	11836	2	361	
11766	42134	A	11837	3	432	NSRVDDFVAAQDAKGGKVAP APAVVKKQEAKKVNNPLFEKR PKNFGGQQLRLARA EKAAG KGDVPTKRPVPLRAGVNTVTT LVENKKAQLVIAHDVDPIELV VFLPALCRKMGVPYCIKGGAR LGRLVHRKTCTTVAFT
11767	42135	A	11838	1	684	

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11768	42136	A	11839	9	247	AVTSDEPKGKKAKAKKVAPAP AVVKNQEAKKVVDPLFEKRHK N\FGGQDIQPKRASPRLCLEPR\ YIRLQRQRAILYKRLKGPFCDY PGFTRALDRQTV*SSLKL\AHK YRPETKQEKK\QRLFARAREEG VLAKGDVPNERDPPV\LRARSL TPFHHPWVEKQEKQLV\VNWH TDVADP\NELVLLALPLCREKW GVPIYCN\YRREKARLWDR\VP QERPCTTCPPFTQGELRKTKGG FWLKLGWK\LRITQFTIDQILMR SRRHWG\GNV\G\PKSVGS*SP KLEK\AKAKELAH*TG
11769	42137	A	11840	1	273	
11770	42138	A	11841	1	218	
11771	42139	A	11842	1	1522	
11772	42140	A	11843	136	441	
11773	42141	A	11844	24	274	SRQAWHEAASASARRRGTRSP ALSPARAPAGPIWTNARRSARA NSVSPAAAPPPRRPVSLSDPGE SCTRDPRAPDCGPFRC
11774	42142	A	11845	194	365	
11775	42143	A	11846	1	782	LLVVGTTVVVVFPNGRFKEFM SRHVHLMCYRICVRALTAIITY HDRENRPNGGICVANHTSPID VILASDGYIAMVGOVHGGLM GVIQRAMVKACPHVWFERSEV KDRHLVVKRLTEHVQDKSKLP ILIFPEGTCINNTSVMFMKKGFS EIGATVYPVAIKYDPOGFDAFW NSSKYGMVTYLLRMMTSWAIV CSVWYLPPIID*ERQIEDAVQFA NRVKSATARQGG\VDLLWDGG LKREKV\KDTFKEEQ\QKLYSKM
11776	42144	A	11847	3	916	
11777	42145	A	11848	13	473	DPPTDSLSPDGG\SIEFLAYLAPE PFSMP\LLGAPPY\SLGGVGD YAPLMVLMCRV\LEDKPIKPLP CCKKAVCEECLKVYLSAQIQCP TCQFVWC*CAGCAWKTSPSSPC LAARRPCARSASKST/SSAQIQCP PTCQFVWC\FKCHSPWHEGVNC KEYKKGD\LLRHWA\SEIEHGQ RNAQKCPCK\IHIQRTEGDH MT
11778	42146	A	11849	92	1103	
11779	42147	A	11850	1	516	
11780	42148	A	11851	1	642	
11781	42149	B	11852	200	608	

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11782	42150	A	11853	1	1856	MEETGMCEGHGASPGMEASSG EREKRGTEASPGDREKRGTE ASSGEREKRRTEASSGDREKR GTGKASSGEREKRGTEASYG EREKRGTAAGGQESCAHCGG WLMPRAKPSTHIRETNPRGTEA TAMAMDHVGGQADTTDSTDG SQWDPSEHSPNCGIREVGAGDP DTQQTGRHHCYYPACKETNEKT NTNRNSNTFIEQLLHAKQQRGN SGVPFKPGHMRALTTNALSW AKLYPDPWCLRMGGTGNEVFE NEIKTGSCWIKQEQGPRPQSP RSQVRPEADPGPSPLTKMSAEN EYRPPSPKLAERDKPSRLRP RGVPWRRESRVRAGRECALLR VAAEGARPPPAGMSYDRAITVF SPDGLHFQVEYAQEAVKRGST AVGVGRDIVVLGVKKSVAK LQDHRPVRKICTLHDN\VCMA FAGL/TPADARIVIQTGPGVEFQ SHRA*TVEGPRVTVEYITPLTF ASLKASVYTSQKWGARPFGIS GPHRGFSTFDGTP*LYQTDPSG TYHAWKA\NSIGRGAKSSARS SWEKNYTDKAIETDDL\TIKLV IKALLEVVQSGGKNIE\LAVMR RDQSLK\NLNPEEIEKYVA\IEIK EKEEN\EKKKQKKAS
11783	42151	A	11854	12	432	

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11784	42152	A	11855	1	1775	MSYPADDYSEAAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIVEIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVVEIQDIYENSWTKLTERFFK NTPWPEAAEAIAPQVGNDVFLI LYKELYRRIYAKVSGGPSLEQ RFESYNYCNLFNYILNADGPA PLELPNQWLWDIIEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLLRLHSL GDYYQAIKVLNIELNKKSMYS RVPRVPRSPTYYYVGFAYLMM RRYQDAIRVFANILLYIQRKTS MFQRTTYKYEMINKQNEQMH ALLAIAL/TMYPMRIDESIHLQL REKYGDKMLRM/QKGDPPQVY EELFSYSCPKFL/SPVVPNYDNI HPN/YHKE/PFLQ/QLK/VFSDDEV Q/QQAQLSTIRSLKLLHPCLV AKPGLASDLTEQEFRIQLLVF KHKMKNLRVDSA/VSQALDGEF QSASEVDFY/DKDM/IHADTK VARRYGDFFIRQ/NHKF/EELNPN P*RRMG/QRPWMIFTTHSGNLV
11785	42153	B	11856	1	537	
11786	42154	A	11857	98	334	WATERWKGRKNHEISWKCFFG KAIS*MRSSQMKPNFRCSSIT VLSVRGMVLF/LTACPRFKMSS RTDFRFGNPQVT
11787	42155	A	11858	4	422	
11788	42156	B	11859	1	2567	
11789	42157	A	11860	2	364	
11790	42158	A	11861	1	501	
11791	42159	A	11862	1	402	
11792	42160	C	11863	30	673	
11793	42161	C	11864	195	1263	
11794	42162	A	11865	3	648	
11795	42163	A	11866	200	420	ILPSALRPPNPNWNVG/YVQTQ LVSKPLSLPTGIPCSTTSNLIKPV ITKDARLHRVIVHGWG/KGTIPI AKIAIS

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11796	42164	A	11867	1	502	MQLPGRGHFSVCKANAGSTQA RQGASAGVAGCRGWLNYAAS EQIVLRVPHMRCEIPHKCVRRK SRIRPHSPFRLRNCWKGRSVRA FSLRLQAKGGCAARLSWVT PGFSQSRRCKTTASAKLACLQV RAQSEDISTVPIHYAYNMTRVG RMQMLGKYNPQSAKLVREAIL PTKATLDLSNQNNEDFSAFQLG LAQALHIKVIHMTREVMSDEL TKLLEGNLKPADMMVEFTT GSLPENAVDVLNTALGDRKSF VALMALMEYSRYLVAEDKSAF VTPLYVEADGVTNGPINAMML MTGGFLTPDWIRNIAKGG*FQ YTFTFNRNSRSQCFFHIFQETSCK FFSMCF*SSLLTKHCHSSRDVW VFSTSFQHIRHTLIDGISNRTNQ LTCNTTSTRITIDGNSQVRVLSNTT
11797	42165	C	11868	1	3831	
11798	42166	A	11869	1	5370	
11799	42167	A	11870	1	3999	
11800	42168	B	11871	1	12036	
11801	42169	B	11872	1	16395	
11802	42170	A	11873	1	19997	
11803	42171	A	11874	1	70	
11804	42172	A	11875	44	613	AGTHLRPFSPSLAAMALRYPM AVGLNKGHKVTKNVSKPRHSR RRIGRLTKHTKFVRDMIREVCG FAPYERRAMELLKVSKDKRAL KFIKKRVGTHIRAKRKREELSN VLAAMRKAAAKKDLGPSPCL PEIKDKLDRSPGSPAVRGWVW VCRGPAVPCLVPALSHTLSGCC LVVNQKPWPAHPSRGRSR
11805	42173	A	11876	1	150	FRGRCCVQRYRGCTLASA/CLL VGAEAEPSVPDPLERSRPYAVL RGQNLE
11806	42174	A	11877	447	725	
11807	42175	A	11878	2	206	RPVAYLLLQGWGRCCVQRYRG CTLASA/CLLVGAEAEPSVPDPL ERSRPYAVLRGQNLDQTLH*ST HQA
11808	42176	A	11879	1	413	
11809	42177	A	11880	122	268	
11810	42178	A	11881	1	555	

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11811	42179	A	11882	221	419	LQTLQGYSNQNSMVLVLPKQR YRPMQNRNALRNNAAYLQKSP *ADKQLQQ/ECQDTKSMCKNH KHSYTPITDKQRAKSRVNSHSQ LLQRE*NT*ESNLQGA*RTSSRR TTNHCSMK*KRIQTNGRTFHAH G
11812	42180	A	11883	1	2464	MDEFNLNTYTLPLRLNQEEVESLN RPITGSEIVAIINSLPRKKSPPGD GFTAIFYQRYKEELVPFLKLKLF QSIEKEGILPNSFYEAHILIPKPG RDTTIKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAADKIQQP FMLKTLKKGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKKWNIPCSWVGGRINIM
11813	42181	A	11884	2104	2637	MFQRGHISQWVVVVGALTFTFT SVLDTDPMRDNKRSGEILPFC REHGTSFTYNHAHSPSCSPSCL FSGALALFSPENNSGFLCMTLPAS FTAGNRLFSSAGQPWWIQQGF KAHAKARRLILLAFHHYCCRP LAVELKPSPVSTPTFLFA*LLPP CSVPGAILHESFGAITWDAE
11814	42182	A	11885	69	417	QTHSQHYTEWGWKVESIPPENW NNTRMPIFTISIQHIIRSSSESQNT RERNQGHPNG*RGSQTVAF* YDRIPRKP*RLIQKTPRTASAAD TQANRVWSGPPASSNRPAEAGP DC
11815	42183	A	11886	376	597	ENKIPRNPTYKGCCEGLQGELO TAAQGNKRGRHKHMEKHSRLM DRKNQYPSAADTQANRVWSGP PANSNRPAEAGPD*PGQNFQYH VE
11816	42184	A	11887	5	292	LTVSCPSRMLFLTDTDLPLM FIKKLGANVASPSSKKPLFVIRL VITLTLPLACGLPTSSVSRTTF RTMLPQAVEFAPPSTGTESHYY CCIW
11817	42185	A	11888	320	596	YPGKQGLEWTSSKLQQTCKRY RERHKDTP/TRRATPR/RHNCQV HQS*NEGKNVKGSRERSGYS QREAHQTNRSRLGRNSTSQKRV GASIQRS
11818	42186	A	11889	3	239	EASRGRIRQQLPFCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDK*KEN*QTERSTPKPD LYTHIKDQSL

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11819	42187	A	11890	3	278	EASRGRIQQHLPFCNICCSAAS TGDQTANRVWSGPPANSNRPA AEGLDG*KEN*QTERSTTPKPD LYTIHKDQRLPIGLFTSPWISARI
11820	42188	B	11891	394	1213	
11821	42189	A	11892	856	1217	VDRSRLQKVSNNKLVAQKGGC SNPLQGS*KLDNPKDANS/RQQ PERTWKWIFPQPHR*GAFGPRH C*ESHL YQFGLDLLNSAGSGIG KNEVQEQKRAEVGARAAPKE LPEALSWFLKVLW
11822	42190	B	11893	1	894	
11823	42191	B	11894	93	938	
11824	42192	A	11895	149	508	LLEGKLTNKKDIIHKTPSVRHH HQRPKPKISL**ATSASQDTK SMCKNHKHSYTTITDKQRAINH E*TPIHNCFKESKIPRNPYKRC *G/RSSRTANHC SRK*KRTQTN GRTFHTHG
11825	42193	C	11896	1	1257	
11826	42194	A	11897	183	1065	YWRNCGFLS*YAEAAEEIVDCI TESLSILKTPLPKKMNEEMLCQ EFGFGLASVKIMWPRTEER ARERNCGFVAFMNRDAERAL KNLNATAFRPALSHFPLPMDT TSQIPKHPVTVSSTNKLILIKTH FQAQSSLNQNIHPMDPSHGQY SAFSPSTPNPSHPALP*PLAIQVH HAVCDGFHVGRLNELQQYC DEWQRDKLEEILRGLTPRKNDI GDAMVFCNLNAAEAAEEIVDCIT ESLSILKTPLPKKMNEEMLCQE FGRFGLASVKIMWPRTEERA RERNCGFVAFMNRDAERALK NLNATAFRPALSHFPLPMDTT SQIPKHSRQFNKQAHSDHQD SLSGPVQSESKYPSHGSIPWDSI LSLLTLNTQPIPPSLALTHMEME SGLHFHCFTASPPSAVPPPELE KTTLKFIWNQKRARIANSILSQ KNKAGGITLPDFKLYYKATVT KTAWTGSPTAIRQARTTRQEKE MKGIQIGKEEVKLSLFTDDVNL QVRENK
11827	42195	C	11898	138	644	

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11828	42196	A	11899	2	3088	ADKTPGGSKASSKTRSSDVHS SGSSDAHMDASGPSDSDMPST RPKSPRKHNRYNESARESLCDS PHQNLRLPLENKLKAFSIGKM STAKRTLKKEQEELKKKEDEK AAAEIYEELAAFEFGSDGNKVK TFVRGGVVNAKEEHETDEKR GKIYKPSSRFADQKNPPNQSSN ERPPSLVIETKKPPLKKGEKEK KKSNELEFKEELKQIQEERDER HKTKGRLSRFEPQSDSDGQRR SMDAPSRNRSSG
11829	42197	C	11900	413	823	
11830	42198	A	11901	263	1246	NPGKQGLEWTSSTPADLQLR VLTVRRTNKKQGHPHQNPCT SPSSKTEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDLEERVVPM DQNMENKQEEKFREKRMKRN EQSLQEIRDYVKRPNRLIGVPE SDGEWKEPSWKTLCRILSRRTSP A*QGRPTFKFRKYRECHKDTPQ GEQLQDT*LSDSPKLK*RKKY* GQPERKKYRLPSANTKTSLRK* TRKSRRNG*ITGHIHPPKTPGR S*IPE*TNRL*N*GNN**PANQK KSRTRRIHSQILPEAQRGAGTIP SETIPINGKRGNNPKLIL
11831	42199	B	11902	67	2584	
11832	42200	A	11903	1	3793	MSDAEDERFLQFLRYRYVLT GDCRTVGAGQWVQRTEREPKQ GEALPHPGSARGWGVPPRDD GWHLENRVPTLILRFSHSLSK QHTRRPYSAPGSEGTPTPCSL LAQQSEIKLQDGSEAGGGLLLI PRQTGSGVDLRQTPDMQLRV LTVRRKTNKQKGQPHQNPCTS PSSKTKAPHHTYSKTDHIVGSK ALLSKCKRSEITNCLSDHSAIK LELRKKRIQNRSTTWKLNLL LNDYCVHNEIKAEI
11833	42201	A	11904	1	441	

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11834	42202	A	11905	312	3705	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECLDRDEERAYVLYM KYVTYVNLIIKKRPDFKQQDDY FHSILGPGNIKKAVEEAERLSES LKLRYEEAEVRKKLEEKDRQE EAQRLQKKRQETGREDGGTLA KGSLENVLDSDKDKTQKSNGEK NEKCETKEKGAITAKELYTMM TDKNISLIIMDARRMQDYQDSC ILHLSVPEEAI SPGVTASWIEA IILPDDSKDTWKKRGNV
11835	42203	A	11906	1	609	
11836	42204	A	11907	3	755	LRVDNAPAHASGLFFCAGAAG TVLFAMAPSRNGMVLKPHFHK DWQRVATWFNQPARKIRRI RPRQAKARRIGAPRGGGPIRPI VRCPTGRVHNGSWRPGRGFQP GRSSRVAGHSRKPVPAPDPSGIS VDPKIRRETSSHGSP LQAQAS GLKEVYRSQTQSSSRKPSPAS/PL *GDSSAEELKLATQ/LTGPMVP VRNVYKKEKARVITEEVKNF KAFASLRMARINARLFGIRAK RAKEAAEQDVEKKK
11837	42205	A	11908	1	327	
11838	42206	A	11909	1	756	
11839	42207	A	11910	1	219	
11840	42208	A	11911	2	227	
11841	42209	A	11912	1	567	
11842	42210	B	11913	99	799	
11843	42211	A	11914	61	342	
11844	42212	B	11915	1	945	
11845	42213	A	11916	92	133	DPFSQKLKTLRKD*TNG*LQ*P MKRSP*MT*WS*KP*HENYVTH AQASVPDSINWKKGYQ*LKIK* MK*SKKRSLEKKE*KETNKASK KYGTM*KD
11846	42214	B	11917	1	368	
11847	42215	B	11918	1	106	
11848	42216	A	11919	1	705	
11849	42217	B	11920	1	834	
11850	42218	B	11921	1	1305	
11851	42219	A	11922	1	1187	
11852	42220	A	11923	228	619	

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11853	42221	A	11924	1499	2238	KGKKKVINQISLGQRMRLSQSS HGKVVQACQVPFHPNAPPAVQF QSRELQSGSRPRSCGEKATRCLE RQGPREVPLPKNAWA*QRKQE KKRSRKGS/GREPGLRRPPNAQ ARDRSSRAPATHRKELKPEREH ISCSRSIRYQEWVSLRDTVHR NLVLDTKRHPALILVEYKERTS SPATEQSCMENDFDELREEGFR RSVITNFSELKEDVQTHHKEAK NLEKRLDKWLTRINSVEKSLND WMEKKTMA
11854	42222	A	11925	699	796	
11855	42223	A	11926	1029	1223	ERELPDPLRFPSEGNASALLSAS RTVRASTDLRPLSGTP*RDEPGT SDGNAEITRLRLRRSGWEL
11856	42224	A	11927	186	1597	
11857	42225	A	11928	1	1200	
11858	42226	A	11929	1	600	
11859	42227	A	11930	1	663	
11860	42228	A	11931	908	1331	GDMRGRREGGFGLRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLTMLAPATFL RVNCWAG/RGR/*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEELQAPSPEKRDPL RVKDQGRHPCVV
11861	42229	A	11932	1	1707	
11862	42230	A	11933	1	1012	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLDIYGTLP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEITSYLSDSHAI KLELRQNLQTNHSTTWKLNLL LLNDYWLHNEMKAEIKMFET NENKDTTYQNLWDAFK/RSV*R EIYSTKCPQEKAGKIQN*HPNID QQN**TTSKANKEKKREDSNRC NKK**RGYHHRSHRNANYVQR ILQ/YTSMQIN*KI*KKWINSSTH TLSQD*TRKKLNL*IDQ*QELKL WQ*SIAYQPKRVQDQMDSQPN STRVASKRIKYLGQLTRM*RTS SRRTTNHCSMK*KRIQTNGRTF HAHG
11863	42231	C	11934	1	1788	
11864	42232	A	11935	550	827	DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLQL PQEHTRKTLPLQQTSAWYTRLF HTSCEI

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11865	42233	A	11936	584	1094	NWIPSLHLTKQLIQDGLKT*MLDLKP*KP*KKT*AIPFRT*AWAR TSLCKHQKQWQKPKLTNGI*L N*RVSA/PAKETTISMN/EATYR MGENFCNLI*QRANIQNLQ*T QTNLQEKNKQPHQKVGKGHEQ TL.LKKRHLCQKTHEKMLIITG HQRNANQNHNEMPFTS
11866	42234	A	11937	797	1044	EESIS*KWPVCPR*FVDSMPSPS SYR*VSSQNWKKLL*SSYGTKQ EPTLPSQS*AKRTKLEASHYLTS NYTTRLQ*PKQHG
11867	42235	A	11938	176	374	LTNQKKSRTRWIHSQILSEVQR GADKQPNRE*TPHNCFKENKIP RNPTYKGCEGPLQGLQTTAQ
11868	42236	B	11939	1	1843	
11869	42237	A	11940	3227	3391	DPLPGQRQLLLQKQRRP*TAAG LLSFQPGQPHGSVPPLTSQPW LPGGWPELSG
11870	42238	B	11941	1	1479	
11871	42239	B	11942	1	2097	
11872	42240	A	11943	654	1341	KNRNYNKL.SLRPQCNQTRTQD *ESHKSLNMYMETEQPAPE*LL GT*RNENGRNKDVL*NQREQRH HIPESLGRIGSSV*REIYSTKCLQ E/I/MQERSKIDTLTSQLKELEKQ EQTHSKASRRQE/DN*NQSRTE GNRDTKNPSKNQ*IQELVF*KD QQN**TASKTNKEKKREESNRH NKK**RGYHHRSHRNTNYHQRI LQTPLRK*TRKSRRNGYIPRHH SPKTKTGRS
11873	42241	A	11944	471	611	
11874	42242	A	11945	1	585	
11875	42243	A	11946	3	1029	GRQHGGSQRMGGTASARASSG RLAPRGRGAFARRRCPSPRRW RLTCGPAAVEHSFCHNVGPGV RATADKYTCMFTYASQGGTNE QWQMSLGTSEDHQ/HFT/CTIW RPPRGKSYLYFTQKAEVAGR LRFYRHLGLTFKAA/SLKRES VPLENLRNFEVQNQSSGLTRPG GISKAELSKLIVGGQIRALSCD QQPLLRRGGTFSPPVKLGACVP ERAQHITGFLGTLKFSTWADV ALSRRGFGSWLKPWGREQRVQ GPPGSQQLFRPLPVKLFWTQD RRSRGTKRVGNMGMALGKAA MLPPTSSRASFMSLQNCFFMFT QGTSPQMNWEEKCFFIFK
11876	42244	A	11947	1	1206	

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11877	42245	A	11948	1	654	
11878	42246	A	11949	849	1089	SPEGKHYRCYL VHMPDTERSS L*MRPRAGRSSAEGPGCRQRSL ALDHMVQQAQRWCWRYQWWR RFSKEFNQWWRFEEL
11879	42247	A	11950	5	1376	
11880	42248	A	11951	2	278	VPQPDTRKGSVLK WISKRGKPL AVEIEESHCLCLPLRTECLGKIP VVHLFSCTRPVVPSLELNYDV DSIAHMFVADLLMITLPSYDIP
11881	42249	A	11952	3	267	
11882	42250	A	11953	1152	1338	FKRGQYGRLLRPRFHGQILYA RRQGAIEPLAIQVHHAVCDGFH VGRMLNELQYQCDEWQGGA
11883	42251	A	11954	394	615	ASDPLRGLLCGPSLLDERHPLL HGAQSHRPPKG*GVRANNAGL AGSSIYLQPRCGIHEVKPSGLLS REGLQLQS
11884	42252	C	11955	114	362	
11885	42253	A	11956	1	211	
11886	42254	A	11957	395	547	
11887	42255	C	11958	412	641	
11888	42256	A	11959	3	905	SNNSPTSASRVAGITGVRHCVR NWWVLGLTDFKNEAVDPRAW TTKSKTPPQNKTKQENKNEDV GRDQVVEWLVTEEVSLSLKG EKLHWKEKEVQSTGKETDARS SMRNYLMLLGPEVQEKEPVKR RLARGKAFVELAEPTRAPGNSG FPVSGGVFTPSLGA LTWICKFR VKS WAILNSQLLDTMKKGIV YKNGDRIQGNRSADNRNNGVP LTGARDMQPAMPEPPTHSMGS CAARAFPMASASC FRAPSPIDH PKAEE\WGARRGTGGQ\PTCSP GAGIHWVKPAGLLSREGLQLH
11889	42257	C	11960	482	709	
11890	42258	A	11961	1	734	MRLESD/KHLVQFVPIHKSGL EYPIGPWLPFITNSRVQEAFYH DRHSFEAVLDNAAPESVDLAE AERLAEDLRLLYVALTL SAFAP LVRRRGDKKGD TDVHQSA LGR LLQKGEPQDAAGLR TICIEALCD DDIAWQT AQTDGNQPWQVND VSTAELNAKTLQRLPGDNWRV TSYSGLQQRGHGIAQDLMPRL DVDAAGVASVVEEPTLTHQF PAGASRGTFWHSLFEDLFTQ PVPDNWRL
11891	42259	A	11962	21	898	
11892	42260	A	11963	1	1962	

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11893	42261	A	11964	1	313	MRFYGGLEAEDPGQKAGETTR HTEDYISQLPLQRQGIPELALQK DLFINKIYGKEFNVCSTLEDPR VHVLCRDMDEAGNHSEQTIA RTENQTPHVLTHRRELNNENT WTQGGHEHTPEPVMGWG*RPR AAKSWGNNKAY*RLYFSAFA ETRDPRTPCPSERSFY*QDLWK/ MSSMSAGRL*RIPEFMSFVGW MKLETILSKLLQGQKTKHRMF SLIGGN
11894	42262	A	11965	47	178	QQLVHTAFVIRLIRGTTEGAWR NCKQMAR*QSISLECKFMPRT
11895	42263	A	11966	2	223	
11896	42264	A	11967	2	133	
11897	42265	B	11968	179	6003	
11898	42266	A	11969	1	1125	
11899	42267	A	11970	1	360	
11900	42268	A	11971	677	1238	
11901	42269	C	11972	193	471	
11902	42270	A	11973	17	280	
11903	42271	B	11974	1	654	
11904	42272	B	11975	526	597	
11905	42273	A	11976	1	1261	
11906	42274	A	11977	170	998	
11907	42275	A	11978	1	1130	
11908	42276	A	11979	1	369	
11909	42277	A	11980	1	300	
11910	42278	C	11981	207	451	
11911	42279	A	11982	1	348	
11912	42280	A	11983	2	469	RGIREGEEDVDLAGMEVAVG GWGRGLWLHRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFSSNTTCQQFRDPCFR GRYPASPHTLSPETAHL*LLL CLPAAGVLPHTWPLLDQGWGH RGHAR

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11913	42281	A	11984	1	937	MAAPLVLVVVAVTVRAALFR SSLAEFISERVEVVSPLSSWKRV VEGLSLDLGVSPYSAGVFER QYIPVKMKSKAFWIFSWYAM MYVGS/HSGNHLPLLLPSQLLG FHPRSL/VALYFLFQISLQTLVIF WYFFAEMFEHSLFFVCVFQIN VFFYTIPLAIKLEHPIFFMFIQI AVIAIFKSYPTVGDVALYMAFF PVWNHLYRFLRNIFVLTCIHVC SLLFPVLWHLWIYAGSANSNFF *GITLTFNVGQRPRLKAPRASS AARSDRGPAASPSGDAARPV SGRRPWDAPPHNYLNAVPPPSR
11914	42282	A	11985	1	521	
11915	42283	A	11986	1	207	
11916	42284	A	11987	1	867	
11917	42285	C	11991	1	225	
11918	42286	A	11992	72	425	
11919	42287	A	11993	1	354	
11920	42288	A	11994	460	752	
11921	42289	A	11995	93	401	PQKKYIHIFLDSLALLPRLECSG AISAHCKLHLLVSSDSPASASQ VAGITGARHHAWLIFVFLVEM GFHH/VGQAGLELLTSGDPPAL ASQRAGVSIFILFIF
11922	42290	A	11996	2	315	
11923	42291	A	11997	615	1180	
11924	42292	A	11998	3	151	
11925	42293	A	11999	2126	2241	
11926	42294	A	12000	1	765	
11927	42295	A	12001	924	995	
11928	42296	A	12002	1	789	
11929	42297	A	12003	2	132	FFFFLVEMGFHHVVGQAGLKL TSSDRPPWPVKVLGLQARAT
11930	42298	A	12004	504	755	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
11931	42299	A	12005	1	1322	MAILPKVIYRFNAIPKLPVTFET ELGKTTLRFIWNQKRACIGKSV LSQKNKAGGITLPDFKLYYKAT VTKTAWYVYQNRDIDQWNRT ESSEIMLHIYNHLIFDKPDKNKK WGKDSL FNKWCWENWLAICR KLKLDPLTSTHTKINSRWIKDL NVRPKTIKLTLEENLGNTIQAIG MGKDFMTKTPKAMATKAKID KWDLIKLSFCTAKETTIRLLG RPPALFTASSSVLKQLALEGILI LDSRALLGFLYEARHSHSNPN HDAQNATSKKNIRDGYDKIYR QEQLARMEKTLITAGGNVK WCSHFRKQIGGQWLTETKTK TPQPFSSQISTDKDGLNPQL LKMDPGHMGWCPPGMGIPWQ LSSDDR VVWLAAGSGRHPGS GFKSL/PGLLHEGSYGH***S*I *GGNS*GSSGGPQCISGEERVFR
11932	42300	A	12006	12	143	
11933	42301	A	12007	1	534	
11934	42302	A	12008	1	591	
11935	42303	A	12009	2	353	
11936	42304	A	12010	1	1923	
11937	42305	A	12011	1	465	
11938	42306	A	12012	1	784	PGWEKMRSSSVVNTQELPT AAIPRDAKGRVYYFNHITNASQ WERPNSGNSSSGGKNGQGEPA/R VRCSHLLVKHSQSRPSSWRQ EKITRTKEEALELINGYIQIKQS GEEDFVESLASQFSQCKHQPKA RG/DLGAFOQKVRQLQKPF*RT RFALADGGR*AGPCFTD/SGIHII LPHLSEGWGAQAWPRGRAGRL GRPAPPCPPASGRTPHSLPPSHSI YCSHNGWEGALPDWGPFTGG PGVPHLSVPSWGCDELQTLH
11939	42307	A	12013	1	319	PRERAPRGSVGAGGEICHTSVC CCQPSWTRL.LLLITWMLL/YYS ECKPFHCSREPDNHILLK1*EF GPPSTQGGHAAPLSRSSRYSCCP DRYL.LRKL.GICQEHQL.L
11940	42308	A	12014	1	1058	
11941	42309	A	12015	1	861	

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11942	42310	A	12016	1	431	IVLGGVATTVCQLNEFIMTDNA VPADVLVLTKPLGTQVAVAVH QWLDIPEKWNKIKLVVTTQEDV ELAYQEAMMNMARLNRTGGL LICLPREQAARFCAEIKSPKYGE GHQAWIIGIVEKGNRTARIIDKP RIMEVAHKWPLKM
11943	42311	A	12017	1	1020	
11944	42312	A	12018	247	1436	GERGPRMTMSTRESFNPESYELD KSFRLTRFTELKGTGCKVPQDV LQKLLLESQENHFQDEQFLGA VMPRLGIGMDTCVPLRHGGLS LVQTTDYIPIVDDPYMMGRIA CANVLSLYAMGVTECDNML MLLGVSNKMTDRERDKVMPLI IQGFKDAEEAAGTSVTGGQTVL NPWIVLGGVATTVCQPNFEMIP DNAVPGDVLVLTKPLGTQVAV AVHQWLDIPEKWNKIKLVVTTQ EDVELGLPGRRLMNMARLNRT AAGLMHTFNHAHAATDITGIFG ILGHAQNLGQASRRNDVSFVIF NLPGAWPRWLA VSKACGNMF GLMHVTCPETSGGLICLPRAE QAARFCAEIKSPKYGEHGHQAWI IGIVEKGNRTARIIDKPRIEVA HKWPLKM
11945	42313	A	12019	219	380	RPLQIRSHSELLGVWVPTSEF*E DITTSVVTAGLLEVSWSGRVILC SKSFPALQS
11946	42314	A	12020	1	516	
11947	42315	A	12021	1	228	
11948	42316	B	12022	56	656	
11949	42317	A	12023	1	488	
11950	42318	A	12024	3	419	
11951	42319	A	12025	1	348	
11952	42320	A	12026	1	708	
11953	42321	A	12027	25	213	
11954	42322	A	12028	1	1165	
11955	42323	A	12029	1	411	
11956	42324	A	12030	1	996	
11957	42325	B	12031	1	744	
11958	42326	A	12032	1	444	
11959	42327	A	12033	1	555	
11960	42328	A	12034	1	2241	
11961	42329	A	12035	1	408	
11962	42330	B	12036	1	423	
11963	42331	B	12037	1	507	
11964	42332	A	12038	3	529	
11965	42333	A	12039	191	319	
11966	42334	A	12040	1	660	

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11967	42335	A	12041	1	579	
11968	42336	A	12042	1	2940	
11969	42337	A	12043	1	4280	MEYYAAIKKDEFMSFVGWTW MLEITILSKLSQGRKPKRRMLSL IGSQLLTNKGTSWMENEFDELT EVGFRRTLHPKSTTEYTFSSAPH CTYLLKIDHIIASKTLISKCKRTEI ITNGLSDHSVIKLELKIKKFTQN CITTTWKLKNLLNDYVWNNEI KAEIKMFFETSENEDTMYQNL WDTFKPLCRGKFIALNAHKRR QRRSKIDIQTAQLKELEKEEQQT NSKASRRQEITKIRAEALKVTETR KTLQKINESRSW
11970	42338	A	12044	1	645	
11971	42339	A	12045	3	362	LDQLLDMSYE/QLMQLYSCAQ RRRLNPLGRKKQHSLKRLRK AKK/EAPPMEKPEVVKTHLRD MIILPEMVGSMGVYNGKTFN QPEMIGHYLGFEFSITYKPVKH/G RPGIGATHSSRFILK
11972	42340	A	12046	1	519	
11973	42341	A	12047	2	599	PPRRSSEDPAKMAEVEHEEGSG PFRKFTLPAADVLDQQLLDIVPT KQFDAAVQVAAQRRRLPEPGL RRKQ/HSPA*KRLRKAKKGGPA PWRKPEVVKT/HTLRDYDHSYP EMVGSMGVYNGK/TFNQV GDQGVCGRPCLGWAGVA*CR RDQLTPSFALGLPQPEMIGHYL GEFSITYKPVKHGRPGIGATHSS RFILK
11974	42342	A	12048	8	224	RTASYPRRFPWDHLLICPCQQL LICFLSLWIRLVFTKVSCT*NNH NMFSCVWLLLLSMIFLRFTHIA CIRNI
11975	42343	C	12049	65	163	
11976	42344	A	12050	3	187	
11977	42345	A	12051	3	689	HASDQKEIIIEPFQAVDEVERVP EDYYTGPVYLTEVTTLQQRLLQ PDFQPVCASQLYPRHKHLLIKR SLRCRCKEHNLSKPEFNPTSIFK KIQLVAVNYIPEVRIMSIPNLR MKESQVLLTLNPNVNLTHVTL LECEEGDPDDINSTAKVVVPPK ELVLAGKDAAAEYDELAEPQD FQDDPDIAFRKANKVGIFIKVT PQREEGEVTVCFKMKHDFKNL IAAPISP
11978	42346	A	12052	1	882	
11979	42347	C	12053	152	404	

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11980	42348	A	12054	3	398	LRKIKIDLKGFSDNPDGYIDVLQ GLRQSFDLTWDRIMLLDQSLT PNEKSAAKTAAREFGDLWV/V/S FQN*SCKTNRSSNGAPDAVHD *D/PTADPWTGPLAHALMLMTL KAPLTRKSQLHDPYYAPIQGEA V
11981	42349	A	12055	2	286	
11982	42350	C	12056	261	482	
11983	42351	B	12057	1	1133	
11984	42352	A	12058	438	575	NKTRMPSLTITPLQHSTESPSQSS QTREGNKGYPNW*RGSHTVTV C
11985	42353	B	12059	50	309	
11986	42354	A	12060	1	870	
11987	42355	A	12061	148	368	ELSSCSLMSHRAIHPSEERATT T/NQQSEPGSW*GWVGANRWC HKMSSGSLGTEPCGSLACSA WTVTVQAQ
11988	42356	A	12062	405	707	RLSLQTAGCSDVPVFPSPAGPP SPA*AP*SGSAASPWPFPAPSA HVAMPAPPRHWQQLSKMPPPW PPDSPVPPGCLA*AEAPPHCPV HLPASRSALS
11989	42357	A	12063	90	470	KSVHSLPPSFSSLLPWTCNRTLS KPPALPSPSRQPECRRLHCSG SRHSSCPSSSSPSFSSSPSSSS SASASPPPPSPSPAPP*LWLQPL FCSQ*QLCHCQELVHLESRLTY PYHSSNQPF
11990	42358	B	12064	1	474	
11991	42359	A	12065	1	383	MEYYAAMKNDEFMSFVGTWM KLETHLSKLSQGQKPNACSHS WMDPQRRGKRQSLSISEAGAN QFPKSVFRFFGLGDSKVGSKWS ATCACEPIHTSEYCGDRVICKTT SSLRGASFAWCSSGNGE*WFP SSMSLQRT
11992	42360	A	12066	1	384	MIITGLEDYEMGLRMEGTLEIP GHYQKDKFLAQSTPDLLPKTS LTNPFISNQLAERQIVTFTVYP DTERDRETRNLADLKQIKIDL KFSDNPDGYIDILRGLRQSFDLT WRDIMLLNQTLAPN
11993	42361	A	12067	152	238	
11994	42362	A	12068	89	544	
11995	42363	A	12069	62	199	SWKPSFSANYHKDRKPNTACS HS*DPAFLAPSPVP*SRPLRPPQ D

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11996	42364	A	12070	1	655	SVSGLVEKVTFEQRLLKGEGDS TVGSSGNEIFRQWPCWELSNCG SLQGDAGCSCLVVHVTFPAGSL SGDGLPTAQWLQSLVLGGR RVNSTQGHRCCHWGSVAEPCV LVKRHHAAQEGLCFSQKTPRS QVPFHLFWDPGHHTLLCSYCPS GVAGTQPAVQAVSTAV*TAAE GEPLPMSENMRCLVFCPCDSLL RMMVSSSFRVPTKDMNSSFFM
11997	42365	A	12071	1	987	MLVLGYNRKNTGTOQKQGT NASDFHFLSQLEQVVSPEGSK EAQCCVLRHLGCESSAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLGKERR QREGERRERKREKREKRESQR KERKREKKGKREKREKDRSDL KQIKIDLGKFSPTDGYIDVLQ GLGQPYLTLWRDIMLLDQTL TPNERSAATAVREFGDLWYLS QVNDRKITEEREQFPTGQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPM*SMISTI TQKKEENPTAFLELRREALRKH
11998	42366	A	12072	1153	1379	CLASWKEKSLHCPQRKQRLR GEELEKLLKKWKETATQIKRSYC WI*PSKSPHYLTS*KR*WNY**L GNYSINIPAS
11999	42367	A	12073	1	864	
12000	42368	B	12074	8	441	
12001	42369	A	12075	62	332	TDSPHCTDPPSRPTVPASCLRK CCGSTMPPTARPIMPTLMETR*M PISPRVS WAGPRPTSWPALISST LFPRMANHWRD*SRITWFQGG A
12002	42370	A	12076	34	409	TRAAGIRHEGKPEKTGLKRNFT N/DCRKS*TSG*RSTSSRSRSPS PAPRSRSCSR/RLPAPPPLSRSG DRPQTAPSCPMWRARLPSCPGS AIPIPRPAWTRSAACCGAASRLR PFGSSSTSPQWM
12003	42371	A	12077	1054	1368	
12004	42372	A	12078	298	514	PNWFKHDVSKSESFSNMWIA KILKA/ARPA/TQCV/RNSCFL QCRHLSSVSASDLT*DNVQRQF CVSPHTES
12005	42373	A	12079	2	1613	
12006	42374	A	12080	2	106	

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12007	42375	A	12081	42	305	YNTVLPKACLCGSLICWMN*SH SDQNMQVSVERSRLRVLYAC CGLLCTAYPQHFAHRYVDKIP GYPSRAGTLTGLHPMQVRCR
12008	42376	A	12082	206	6038	
12009	42377	A	12083	1	4316	MQWEEAEKDPGSCVFRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPQASGQLSLSPAPPYVL PGPGKIKAGNPNLSLTSYRSEV FCAHRHLHPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSGQTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSND
12010	42378	A	12084	393	991	
12011	42379	A	12085	324	438	
12012	42380	B	12086	528	598	
12013	42381	A	12087	52	574	
12014	42382	A	12088	1235	1366	
12015	42383	A	12089	1	1800	
12016	42384	A	12090	1	513	
12017	42385	A	12091	3	77	
12018	42386	A	12092	1923	2171	GAFCPTLLHGYQVLQWPGSSL PHKEGPAPALEGGHVPYRWI*A SADSQSTEAGRIGPASTG*RQYP GGEEHACCLPALLHS
12019	42387	A	12093	1	360	
12020	42388	B	12094	21	3636	
12021	42389	A	12095	1	936	
12022	42390	A	12096	1	599	
12023	42391	A	12097	1	248	VGKSSIVCRFVQDHFHDNISPTI GASFMTKTVLCGN/ELHKFLIW DTAGQER/SRQIPPLDPHENGNN GTIKVEKPTMQASRRCC
12024	42392	A	12098	1426	1572	
12025	42393	A	12099	367	513	
12026	42394	A	12100	31	661	APALPGCEHMMMAIRELKVCLL GDTGVGKSSIVCRFVQDHFHDH NISPTIGASFMTKTVPCENDFT KFLIWDTAGQERFYSLAPMY RGSGAAVIVYDFTEAGFHPL KKWVKRLKELGPEINIVMAIA GNKCDLSDIREVPLKGC*RNTA ESIGAIIVVETSAKNAUNIE/LFQ GNSRPDPHPWTPHENGNNGTIK VEKPTMQASRRCC

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12027	42395	A	12101	1	487	MDKFLDITYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAIFYQRLISNFSKVSQYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRIINIVKMAILPKNW KKLL
12028	42396	A	12102	1	1563	
12029	42397	A	12103	1	1449	
12030	42398	A	12104	3	1606	
12031	42399	A	12105	2	402	
12032	42400	A	12106	172	329	
12033	42401	A	12107	1	720	
12034	42402	A	12108	97	206	
12035	42403	B	12109	1	1248	
12036	42404	A	12110	1	1419	
12037	42405	A	12111	1	1387	MDKFLDITYTLPRLNQEEVESLN RSITGSEIVAIINSLPTKKSPGPD GFTAIFYQRYKEELVLLLLKLF QSIEKEATLPSNFYEASIIIPKP GRDITTKENFRPISLMNDAKIL SKILANQIQHKKFVHDEVG FIPRMQGWFNHKSKNVIQYIN RTKDKNYMIISIDAEKAFDKIQ QLFMLKTLKSLGIDGTYLKIIRA IYDKPTVKIILNGQKLEEFPLKT GTRQGCPSPLLFNIVLEVLR AIRQEKEIKGILLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI SNVS*V*GYKINVQKSQAFLY TTNRQTESQIMSELPFTIASKRI KYLGIQFTRDVKDLFKENYKPL LNEIKEDTNKWKIPCSWVGRI NIVKMAILPKPPLLIPRQTGSGV DLQQTPTDLQLSVLTVRRKINK QKGHPHQYLIWTSPPSKTKGRQ LLASNRKLDGE
12038	42406	B	12112	1	711	
12039	42407	A	12113	1694	4489	IYRFNAIPIKLPMTIFFTELEKTTL KFIWNQKRARIKAIRSQKNKS GGITLPDFKLYYKATVITKTAW YWYQNRDIDQWNRTEPSEITPH IYNYLIFDKPEKNEQWKGDSLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLIVRPKTIKT LEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTKWEKTFA TYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDM

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12040	42408	A	12114	1	115	
12041	42409	A	12115	58	414	
12042	42410	A	12116	6	389	VMTTGTNSRVEPRVRGRVYKK KMDKKRQEKITEAKSKDKSQM DEEKTD/DEKPKLQVELEQEQYQ DKFKRLPLEILEFVQEAAMGKGI SEDSNHGSAPI.SLSSDPGKVN KTPSSEELGGDIPGKEFDTP
12043	42411	B	12117	50	5137	
12044	42412	A	12118	1	1194	
12045	42413	A	12119	1	2559	
12046	42414	A	12120	3	406	
12047	42415	A	12121	119	423	TSSCSSEKFVITHLLKPTSVNSS KSFSLQCSIG/VQGAAIL.WRRR GSLVFRIFSFALVSPHLCGFIYL WSLTMVTYFSLNGGRSPCQA AAPQVNLGLLC
12048	42416	A	12122	3	597	ISASADNVFMSVSSPSCSCFF TLRYRLWKSEKPLYYSFVDPK VAYKKREMVVNQKQKHTG RVQSSNLEKKAPSSQFNWT EEDTDRTCFHGSHLQGVLLKEK GQSLLTKNLSLYWLSLTKQF*RCY GHHVPPYEEISYFLSNRNLNLF SFLLRIKTSFL/HEEVSLVEKVL FEEKIQCKERNQDPRKVRTTL
12049	42417	A	12123	1	883	
12050	42418	A	12124	23	362	FAFNMPPEPKIVPAP*KGSKKA VTKAQNKGDEKRLSRKESYS VYVYKVLKQVHPDGTGSSKG MGIMNSFVDDILERIAGEAFRL AHYNKRSTITSREIQTAVRLLLT REMYK
12051	42419	A	12125	2	405	
12052	42420	A	12126	1	398	LHSAMPEPAKSAPAPKKGSKK AVTKAQKDKGKKRKRSRKESY SIYVYKVLKQVHPDGTGSSKAM GIMNSFVNDIFERIAGEASRLAH YNNKRSTITLPREIQTAVRLLLP GELAKHAVSEGTKAVIKYTSA K
12053	42421	A	12127	1	401	
12054	42422	B	12128	48	424	
12055	42423	A	12129	3	462	DAWVSGRLTELPSFCFFPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKDKGKKRKRSRKESYS VYVYKVLKQVHPDGTGSSKAM GIMNSFVNDIFERIAGEASRLA HYNNKRSTITSREIQTAVRLLLP ELAKHAVSEGTKAVIKYTSSK

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12056	42424	A	12130	74	504	FAFNMPEPAKSAPAPK/KGS/KK AVTKAQKQKDGKKRK/RSRQGR AYSVVYVKVLKQVHPDTWHL LLRPWGMELLSFNDIFRNGIAG LRVSLGRl*QQGVSTIHLPGEl HDGPLRLACLPGGVWPSKAVF RGAPRPFNQVNTSV
12057	42425	A	12131	53	471	
12058	42426	A	12132	1	241	FKDTCRMTFIAALFTIAKTWNQ PKCPTMWHIYTMEEYAAIK/SD EFMSFVGTWMKLETITLSKL*Q GQKTKHRMFSLIGGT
12059	42427	A	12133	1	244	
12060	42428	B	12134	1	2142	
12061	42429	A	12135	1	1962	
12062	42430	A	12136	3	393	IWMKLETILSKLSQG*KTKHR MFSLTGGNLTMRITLGHRLPSL PHRLRPCARLHLRCPWPWPPSR RRCARSTTPATPPSTATSRWSS TPPTCTCLWPSTSTGTTWPWRT SSATSCACRTTKWSMPRS
12063	42431	A	12137	2	87	
12064	42432	A	12138	1	270	
12065	42433	C	12139	1	214	
12066	42434	A	12140	1	684	
12067	42435	C	12141	1	333	
12068	42436	A	12142	1	189	
12069	42437	A	12143	215	310	
12070	42438	A	12144	2	91	
12071	42439	C	12145	1	229	
12072	42440	A	12146	1	268	
12073	42441	A	12147	1	278	
12074	42442	A	12148	2	274	WMKLETILSKLSQRQKTIHHLF SLIALFTIAKKWKPPRYLSVDK WIKKLWY/HTYTMEEYSAFKK EAILPIAIWMLKDIMLSEISQ TWP
12075	42443	A	12149	2	136	
12076	42444	A	12150	2	95	
12077	42445	A	12151	1	233	
12078	42446	A	12152	377	484	
12079	42447	A	12153	2	91	
12080	42448	A	12154	1	891	
12081	42449	A	12155	1	1194	
12082	42450	A	12156	785	892	
12083	42451	A	12157	191	317	
12084	42452	A	12158	410	520	
12085	42453	A	12159	683	796	
12086	42454	A	12160	830	927	

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12087	42455	A	12161	18	539	PTDP*LGIVQKEVYKSCYKIDIC T/RVCVPAALFTIANTWNQPKC TSMIDWVKKMWHIYTMEEYA AIKTDEFMSFAGTWMKLETHL RKLSQGQKTKHRMYSLIGGNL TMRTFGHSAGSHHTPGPIMRCG AGGGIALGEIPNVNDELMTGTAN QHGTCPMQQNCTLCTCTLKLK V
12088	42456	A	12162	1	108	ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSLYIYFFLDEFM YFAGTWMKLETHLSKLSQGQK TKHRMFSL*GVSYYVAQAGLK LLGLSLSKCRDYRCEPPCPE
12089	42457	A	12163	1	701	
12090	42458	A	12164	274	435	
12091	42459	A	12165	1	3658	
12092	42460	A	12166	749	856	
12093	42461	A	12167	1	598	
12094	42462	A	12168	538	664	
12095	42463	C	12169	1	873	
12096	42464	B	12170	177	325	
12097	42465	B	12171	1	1245	
12098	42466	A	12172	1	3313	
12099	42467	A	12173	1940	2060	
12100	42468	A	12174	1	1213	
12101	42469	B	12175	155	559	
12102	42470	A	12176	2	321	PAPRGGAYRGRQTSLSGGLHP V*ASWLLCLPKQAWAM/VGRP PQASLLPCSLISDCCASNQRDSV GVGPSEPCAGYNLLLCRFLSQS EKHSIRVGAVDCSCSYLAIL
12103	42471	A	12177	1	519	
12104	42472	A	12178	1	477	
12105	42473	A	12179	119	375	KRTQT*AIAGAPPASLPPCSLIS DCCASNE*GSVGIGPSKPGAGY NLLCHLISPSISPTSSPKSDTCPI ADFSNKS PDRSSAGDILLAMQS LGSMAIFLILILPTREHGKFFHLF VSSFISLSSGL
12106	42474	B	12180	1	363	

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12107	42475	A	12181	1	1309	MAEGEEGTSYMAAGERVVAIA LIDGFRPLTLESTFFNSGSCSKL EQHSTYLGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVPEP KQHGIGPKQKYRSTGPNRALR NNAAYLQFLIFGNLEKTKPWG KDSLLIKVFEEAVLWIECFAFIF YDARGVLIVVQVDSCKLEQHS TLSRALLIYKGFRCFRNHHQTG FSPAGANQRGPLAATLSGPGGE GQSAVARLTGEKKNHPGAQYA NRLSPRVGRFINAAGTTGFTG KRAVSATQLMDFADFGTTIKQ DFRLLGQTSVDRI.LQLSQGQA VKGNNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGHLISDCCASNQPDVSGVG PSEPGAGYNLVVRHFLSPSEKH SIRVGVTRFSRCRPSPLPLTQKG NSLTPCASQLRQCLALLRLR*R AISCCPSHW*KEKPPWRPIRKP LPARWPIH*CSWHD RFPD/CESG HLISDCCASNQPDVSGVGPSEP GAGYNLVVRHFLSPSEKHSIRV GVTRFSRCRPSPLPLTQKGNSLT PCASQLRQCLALLRLRH
12108	42476	B	12182	1	1335	
12109	42477	A	12183	1	1675	
12110	42478	B	12184	57	1530	
12111	42479	A	12185	1	1419	
12112	42480	A	12186	1	574	RVDDFVRQTRPSAQAAAEKM AANQPPPLMMKHSQTDLVSR KTRKILGVGGEDDDGEV/HRSP ISQALGTEIKFTIREPLGLTVWQ FVSAVLFSGIAIMALAFPDQLY DAVFDGAQVTSKTPIRLYGGAL LSISLIMWNALYTAEKVIIRWTL LTEACYFGVQFLVVTATLAETG LMSLGIRLTRSSRRGR
12113	42481	B	12187	79	387	
12114	42482	A	12188	1	908	
12115	42483	A	12189	2	70	
12116	42484	A	12190	1	1158	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12117	42485	A	12191	2	611	FVSVPSVLLGLQFWRSERD/TA RLQ SARWRVERGR LKELLSRQ RPRRREEVVVGREVCRTMEV RASLQKIVSNGDEQLEKAMEEI LRDFEKRPSLLVDCQSSSEISD HISFGDIPASQTNKPSLQLILDPS NTEISTPRPSSPGLPEEDSVLF NKLTYLGC MKVSSPRNEVEAL RAMATMKSSSQYPPFVTL YVP
12118	42486	A	12192	3	497	
12119	42487	A	12193	1	804	
12120	42488	A	12194	1	1243	MAPVEHVADAGAFRLHAAL QDIGKNYITIREVVTEIRDKATR RRLA VLPYELRFKEPLPEYVRL VTEFSKKTGDYPSLSATDIQVL ALTYQLEAEFVGVS HLKQEPQ KVKVSSSIQHPETPLHISGFHLP YKPKPPQETEKGHSACEPENLE FSSFMFWRNPLPNIDHELQELLI DRGEDVPSEEEEEENG FEDRK DDSDDDGGGWITPSNIQIQQE LEQFDVPEDVRVWLA*PPDFA MQNVLLQMGLHVLAVNCMLI REARSYILRCHGCFKTTSDMSR VFCSHCGNKTLKKVSVTVSD GTLHMHFSRNPKVLNPRGLRY SLPTPKGGKYAINPHLTEDQRF PQLRLSQKARQKTNVFAPDYIA GVSPFVENDISSRSATLQVRDS TLGAGRRRLNPNACRKKFVKK
12121	42489	C	12195	164	350	
12122	42490	A	12196	1	378	
12123	42491	B	12197	265	1539	
12124	42492	A	12198	1	2511	
12125	42493	A	12199	1	1077	
12126	42494	B	12200	38	1451	
12127	42495	A	12201	1	207	
12128	42496	A	12202	1	197	
12129	42497	A	12203	1	216	
12130	42498	A	12204	1	335	
12131	42499	A	12205	1	174	
12132	42500	A	12206	1	1309	
12133	42501	A	12207	1	1266	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12134	42502	A	12208	1	590	IDRFDA PCGLEELEDHEDEFNE EDERAIE MYRRRLAEWKATK LKNKFGEVLEISGKDYVQEVTK AGEGLWVILHL YKQGIPLCALI NQNL SGLARKFPDV KFIKAISTT CIPNY PDRNLPATILVYPG DGIN G/QFIGPLSVGGMNL TRDELEW KLSGSAIMTDLEENPKKPIEDV LLSSVRRSGPHEEGQRFGR
12135	42503	A	12209	291	416	SHYLKIHAEKLESEYDQISPPNSQ PDKENPVLST**SIQRRHMTLFLK MNLKILKYRKPEA*SQR LVSK R*KHSIRGSGINLSFVPTGFQIVP FHLFETSLWL
12136	42504	A	12210	437	773	DYTTIGELKTAIQRSKINFCPIH SHSSHNAKSFVITVTL LHRHLL *KVSYNKVQSLFIQC GFSEAGA GVYNYCPPRQRQPGDKPRW RWRGRGNRCSANSHGLQLYA
12137	42505	A	12211	1	1183	
12138	42506	A	12212	1	459	
12139	42507	A	12213	1	513	
12140	42508	A	12214	91	1168	
12141	42509	A	12215	323	429	
12142	42510	A	12216	870	1305	SPGLPHCWQPCRARSRTD VV NVLVSGSGSGAYKEPAILVGPE NLTLTVHQTAVLECVATGNPRP IYVSWRLGWPPNP TKAQEQRRA KTESQRKQPRDKARENQPKAA RPKRAAPKSHEAARKTNPTTAS TKRQAAPTNTPKESS
12143	42511	A	12217	1	2695	
12144	42512	A	12218	1	258	
12145	42513	A	12219	1	624	
12146	42514	A	12220	247	425	
12147	42515	A	12221	31	858	LLEIVNSSIQPEKQAGWLSQAV HGAPDGNRPMLHPETSPGRG HLLAVLLALLGTTWAEVWPPQ LQEQA PMAGALNRKESFLLLSL HNRLRSWVQPPAADMRRLDW SDSLAQLAQARAALCGIPTPSL ASGLWRTLQVGNWMLLPAG LASFVEVVS LWF AEGRYRHA AGE*ARNATCTHYMQLVWATS SQLCGGRHLCSAGQAAIEAFVC AYS PRGNWEVNGKTI VPKKG AWGSLCTASVSSLLKAWDHAR GLLGGPRETLGKEPTEPW TALK
12148	42516	A	12222	1	1519	
12149	42517	A	12223	1	789	

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12150	42518	A	12224	1	505	ATEDPGVAMGRPARCYRYCK NKYPKSRFCRGVPDAKIRIFDL GRKKAKVDEPFLCGHMSVDEY EQLSSEALEAARICANKYMKVS CGKDGFIHVRRLHPFHVIRINK MLSCAGAD/RIHISKKWGFTKF NADEFEDMVAEKRLLIPDGC GV KYIPSRGPLDKWRALHS
12151	42519	A	12225	135	828	RFWVSPHGPAAPARCYRYCKN KPLPKVLRFCRGVPDAKIRIFD PGAERKQKVE*VFRFCGHMVS DEYNQLSS*ALEVAARNLCPIS TMVKS\CGKDGFIHVRRLHPF HVIPHQTRCCSCAGADRLQTG MRGAFGKFPQGTVARVHIGQVI MSIRTKLQNKHEV\DALRRAK YFKFPGRQ/KIHISKKWGFTKFN ADEFEDMVAEKRLLIPDGC GV YIPSRGPLDKWRALHS
12152	42520	A	12226	2	367	
12153	42521	A	12227	2	376	QTYSLRRAIPRHIIIVGFTKVEM KEKVLRAA/NKPIRLTVDSLAFET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFDTKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12154	42522	A	12228	1	714	
12155	42523	A	12229	122	939	YPGKQGLEWTSNKIQQTCS*GS SLLLEGKLTNRKDIHTKTPSVRH/ RSSKAKERVSVIEDQMNKRE EMFREKRVRKNEQSLQEIWEY VKRPNRLIGVPESDGDNGTKL ENTLQDIIQQYFPNLAQANIQI QEIQRMQRCSSRAAPRHIIVR FTKAEKMKMLRAARGKRV THKGKPIRLKVDVLAETLQARR EWGPIFNILKEKNFQPRISPAK LSFISKGEIKSFDTKEMLRDFVT TRPALQELLKEALNMERNRY QPQQKHAKL

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12156	42524	A	12230	1	1043	MGDFLHSTDNRNYLIKFWAKLS AKKTPANSSSPLGDHQHPCITK NLQIPEKWLIGLLLPLKADLLK EDAGTHCKEAKNLDERLDEWL TRINSVEKFLNDLMELKTMQAQ LHYACTSFSSQFDQLEERSVIE NQMSMKREKFRKRVKRNE QSLQKIWDYVVKRPNRLTGVPE SDWENGTKLENSLDIIEQENFP NLARQANIHIQEIQRMPQRYSS RRATPRHLIVRFTKFEMTEKMN RAAREKGQVTHKGKPIRITADI SAETLQARREWGPIFNILKEKN FQPRISYPAKLSFISEGEIKSFTD KQMLRDFVTTRPTLQELLKEAL /NMERNNQYQLQKHAKL
12157	42525	B	12231	1	1275	
12158	42526	A	12232	1	1584	
12159	42527	B	12233	1	1023	
12160	42528	A	12234	1	2052	
12161	42529	A	12235	5160	6183	VSKHPQASAGDTQTNRVWSGP PANSRPAEAGPDC*KEN*QTE RTS/WQNPICMSPSSKTKEAKNL DKRLDEWLTRINSIEKTLNDLM ELNTMARKLRDACTSFSSQFDQ VEERSVIEDQMNMKREKFK REKRIKRNKQSLQEIWDCKVRP NLRLIGVPESDGENGTLENTL QDIIQENFPNLARQVNIQIEIQ RTFQRYSSRRGTPRHIVRFTKV EIKEKILRAAREKGRVTHKGKPI RLTAVLLAETLQARREWGPIFN ILKEKNFQPRVSYPAKLSFISEG EVKSFTDKQMLRDFVTTRPAL QELLKEALNMERNRNYQLLQK HATLSRPSMLG
12162	42530	A	12236	1	975	
12163	42531	A	12237	3	1186	
12164	42532	A	12238	1	906	
12165	42533	A	12239	1	1882	
12166	42534	A	12240	1	1394	

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12167	42535	A	12241	1	4935	MGPGARLALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLLRRYLRGEEARLRDL TRCNDETTITYLLDKRLTVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLRSR WAVGGATG SWVLSKGDRA SLGERVV TGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLPTSTRQRGQ SEKSDANGRRRKQKT
12168	42536	B	12242	88	1014	
12169	42537	A	12243	686	1920	IKPQRWGKKQNRKTGNSKKQS ASPPPKERSSSPATEQSWTENDF DELREEGFRRSVITNFSELKEHV VTHRKEAKNLEKKLDDEWITRI TNAEKSLKDLMEKTTAQELR NECTNLSNRCDQLEETVSAME DQINEMNEMKQEGKFREKRIK RNEQSFQEIGDYVVKRPNLHLI GVPESDGGQNGTKLENTLQDIQ ENFPNLARQANIQIEIQRTPO RYSLLRRATPRHIVRFTKVEMK EKVMLSAAAREKGRVTHKGKPIR LTTADLSAETLQAQKTEWGPIF NILAKEKNFQPRISYPAKLSFIS EGEIKYFTDKQMLRDFCHHQG LPLKELLKEEALKHWKGTTRY QPLAKTLPKYRSTRQKVNKDT QELNSALHQADLIDYRTLHTK STEYTFQHHHTPIPKLTT
12170	42538	A	12244	1	633	
12171	42539	A	12245	3	109	
12172	42540	A	12246	2	575	
12173	42541	A	12247	1	237	
12174	42542	A	12248	1	1065	
12175	42543	A	12249	2	338	
12176	42544	A	12250	1	1319	
12177	42545	A	12251	1	744	MQKALCAAPDLGTFVTVLTPPP GAQIGSRRRERSKVPYIVRQCVE EIERRGMEEVGIYHVSGRVAA DIQALKAADFVN/NRTMHSSWE ESDELLKARDDPHSGQHSRDG ALAKAGMADKKDMSVMMSET DMNAIAGTLKLYFRELEPLFT DEFYPSFAEGIDRLERVAEKEA VNKMSLHNLATVFGPTLLRPSE KESKLPANPSQPTMTDSRSLV MSQVEVLLYFLRLEAIPALDSK RQSILFSTDV

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12178	42546	A	12252	1	507	
12179	42547	A	12253	1378	4280	STPMAVAGPLGRPWSTSPTRAS TSGASWKGRRARARSCAARAPL SRRSALPGPAGTPPPGVLRIEA AIPRTAAPMRTSPPARRTSPLAS PAACPQAPPTACSGTKAALPR RTRNSPSTAAVPPRRSAISGTGT ARLSCPRPPSWASARPGSGPT MTRAPSMETQMARSEHLDTA ALQTGQRSSAGTKMGCPMLMT RPPHRTPTSAARAGAAGMRWSR EP*SPLK/RSELDLEKGLEMRK WVLSGILASEETYL
12180	42548	A	12254	1	1109	MRTPYKTSPMRMLYMTSLMTP TRHANEDAVDDIAYKDTVQDI TSEDAVYDIANEDVYDIANED ALQDIANEVAYDIANEDIVYD IANEDALYDITNEDAVYNIANE DAVYGIANEDAVYEFANKHAV YDIANEDTVQDICKEDAANK CYPPGFFPIRCRHEHLPVCIIDVI CSLIKCRHEHLPSSLIQDRLGA QASRRERSKVPIVIRQCVEIER RGMEEVGIYRMSGVAADIQAL KAAFNVSERCPAQDGMVWVA VVSAMRSQSAPRPHVTSFSVS FLHLSGSSRRPLHFRALSNNKD VSVMMSEMDVNAIAGSLKLYF RELPEPLFTDEFYPNFAEGIGEH WRPWPHGRRLLHVHCCPQRL
12181	42549	A	12255	1351	4308	WKGRRARARSCAARAPLSRRSA LPGPAGTPPPGVLRIEAAPRT AAPMRTSPPARRTSPLASPAAC PQAPPTACSGTKAALPRTRN SPSTAAVPPRRSAISGTGTARLS CPRPPSWASARPGSGPTMARA PSMETQMARSEHLDTAALQT GQRSSAGTKMGCPMLMTRPPH RPTSAARAGAAGMRWSREPWS PLK/RSELDLEKGLEMRK WVLS GILASEETYL SHLEALLPMKPL KAAATTSQPVLTQS
12182	42550	B	12256	1	1017	
12183	42551	A	12257	2310	2834	EEKYNMQTRLRRAEDVFPVIG VAAHKGGVYKTSVSVHLAQDL ALKGLRVLLVEGNDPQGTASM YHGWWPDLHIHAEDTLPPYL MLRLAIETVAHDYDVIVIDSAP NLGIGTINVVCAADVLIPTPAE LFDYTSALQFFDMLRDLKKNV DLKGFEPDVRILLTKYSSNSNGW

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12184	42552	A	12258	106	108	NFLFVLRRLQLVWVGGLCW*AAE LNKVCL
12185	42553	A	12259	1	901	
12186	42554	A	12260	23	482	KPRELGPISPVWLPPDRLPERPQ RRRPSGVDPGWSLWGS GCGSTG CSALMSCSCGSTPLLSLALKVT PGGVVLGAPSGSEDGS*PNRKAC GSEMEICLTTRGVWGPVALG VGGGLQQSCRAPCGGLPKLLRS WSQSSLSPNSPGRGASSGEAA
12187	42555	A	12261	1	1938	
12188	42556	A	12262	1	2235	
12189	42557	A	12263	43	1827	THVRLAGARASPRAPRLRPKP RPQGLPCLPGLRRARLEGGARG RADEMFLPLPAAGR VVVRRL AVVRSGRSRLSTADMTKGLVL GIYSKEKEDDVPQFTSAGENFD KLLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAQCRIQDLELSSVEVDP CG DAQAAAEGAVLGLYEYDDLK QKKKMAVS AKLYGSGDQEA W QKGVL FASGQNLARQLMETPA NEMTPTRF AEIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICS AIVS AAKLNL PINIIGLAPLCENMPSG KANKPGDVVR AKNGKTIQVDN TDAIEGRLLADALCYAHTFNP KVLNAAATLGAMDVALGSGA TGVFTNSSWLWNKLFASMET GDRV*RMPLFDHYTRQVVD C QLADIVNNIGKYRSAGACTAA AFVKEFVTHRKWAHLDIAGVM TNKDEVPQSTGKA*LGPRTRL IEFLLRFSQDNCLVQILKNVFH SVLNWTVELKKVFE
12190	42558	A	12264	1	405	GIRSAEVGKHLAHILLSRQQGR RPVTLIGFSLGARVIYFCLQEM AQEKDCQGIIDVILLGAPVEGE AKHWASL SGRVVS GRIINGYCR GDWLLSFVYRTSSVQLRVAGL QPVLLQDRRVENVDLTSVVSG
12191	42559	A	12265	1	1072	
12192	42560	A	12266	105	514	

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12193	42561	A	12267	44	872	NARPWWVRLGLLIEFRRRGLSCRE RAREMEMGRRRIHLELRNRTSPD VKELVLDNSRSNEGKLEGLTDE FEELEFLSTINVGLTSIANLPKL NKLKLELSDNRVSGGLEVL EKCPNLPHLI*GGNKIKDLSTIE PLEKLENLKSLDLFNCEVTNLN DYRENVFKLLPQLTYLDGYDR DDKEAPDSDAEGYVEGLDDEE EDEDEEEYDEDAQVVEDEEDE DEEEEEEEDVSGEEEEEDEKGY NDGEVDDEEDEELGEEERGQ KRKREPDEGEDDDD
12194	42562	A	12268	1	388	KRGAAMDGRVQLIKALLALPIR PATRRWRNPFPFETFDGDTDR LPEFIEQTGSYMFVDENTFSSDA LKTALPQSLPSIASHRQTAAPS DLDSPRRYLGWQSLDSDSDS WPPPKGSVTFSETYFLPTP
12195	42563	A	12269	1	127	
12196	42564	A	12270	5	434	ISRLYLDGLAGPHTASAAEAS DRSEDLRWTVCAQLIQUALLAL PIRPATRRWRNPFPFETFDGDT DRLPEFIVQTCYSYMFVDENTFS SDALKVTFITRLTGPAQWVI PYIKKESPLLNDYRGFLAEMKR VFGWEDDED
12197	42565	A	12271	515	1137	
12198	42566	A	12272	1	762	
12199	42567	A	12273	1	468	
12200	42568	A	12274	2716	3411	KREEETKKKSKREMEVVKKKQ CTYSFKSQGKFLSTHARQFSIGS QPISASQTVVEIMKSILTLQSQV NSLAAVTLQNR*GLDLLTAEGK GLCTFLGEECCFYTNQSGIA*D ATQRLQEKASEIRRLSNSYTNL WSWATWLLPFLGPVAAILLLL AFGPRIFNLLVKFVWSRIEAIKL QMVLQIEPQMSSNNFYRGPLD *PAGTSPGLESSLKDDTTAKPL LRPYAGSS
12201	42569	A	12275	8312	9221	
12202	42570	A	12276	74	471	
12203	42571	A	12277	4043	4159	LFCQSGFHSLLTPSTATCSTIR* VATSRLRPVFTCRRS
12204	42572	A	12278	1	1332	
12205	42573	B	12279	29	1316	
12206	42574	A	12280	1	580	
12207	42575	A	12281	2	710	
12208	42576	A	12282	1	1559	
12209	42577	A	12283	1179	1490	

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12210	42578	A	12284	2	313	
12211	42579	A	12285	599	743	GALART*PPQQRWVSCPR/GVP/ GAL*REFTMFLSLQAENSIDFVS RELCAHSIRKLQAHVLK*VFI K
12212	42580	A	12286	208	398	
12213	42581	A	12287	716	1069	
12214	42582	C	12288	326	577	
12215	42583	A	12289	188	590	
12216	42584	A	12290	860	1121	VPFLTSWVNVGFKSSALHSSAL LQFWLTLWE*LPAWARCCCL PNGSFWGPSSRLDVAWERPV APGWREVSPLLSELWTAASGP YG
12217	42585	B	12291	1	1614	
12218	42586	B	12292	1	1080	
12219	42587	A	12293	3	219	
12220	42588	A	12294	890	1094	VESGTHLGQYKIYFGFLYQKKF SLQSHGYILFGCPQYW/ITSDC PSIPCMWYSRTL*VTWSKKQVT SE
12221	42589	C	12295	1	3912	
12222	42590	A	12296	881	1151	
12223	42591	A	12297	1	1323	
12224	42592	A	12298	1817	2284	VWDGSILYQKLGALDGLSS*VI PLASSLSQYPLPSSFIQRLNT YSVKGLRSWTVNEDRVDAVSS GGIWLQVEASLVLY*MLYFSIIT LLIILGLVHVNFILDSSSELITD KLCGGLGFTLYTYSKLI*SDVTF PRAFASTQTSMLTKYTVE
12225	42593	A	12299	1	1109	
12226	42594	A	12300	1	367	
12227	42595	A	12301	1	531	
12228	42596	C	12302	1371	1746	
12229	42597	A	12303	1	645	
12230	42598	C	12304	387	680	
12231	42599	A	12305	655	2498	
12232	42600	A	12306	1	528	ENLGNTQDTGMGKDFMTETP KAMTTKAKIDKRDILKLSFCT AKETTIRVNRQPTWEWEIFAVY PSDKGPISRIYKQLKQIYKKKSN NPIKKWAKNNRHRFSKEDIYV AKKHMEKSSSLVIRKMHKTT VGYHLMPPVRMAIHKSGNNRC WRGCGE/C*WEGQLVQPLWKT VWQ
12233	42601	A	12307	1	1359	

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12234	42602	A	12308	1968	2648	TQTNLQEQKNKQLHQKVGKGYE QTLKRRHLCSQQTHMQPTDT WKNAAHQLAIREMQIKTMTMY HLTPLRMAIHKSGNNSCWRGC GEIGTLLHCWWDCCLVQPLWK TVWRFLKDLESEIPFDLAIPLLCI YPKDYTSFCYKDTCTCFIAAL FTIAKTWN*PKCSSVIDWKKM WHIY/TTMEYYGAIKRNKIMSF AGTWMKLDAILSKLTQKQKT KLRMFLLSIRS
12235	42603	A	12309	1	403	
12236	42604	A	12310	3	264	FFYAHIMFIAALFTIAKTWNQS KCTSMIDWIKK/MWHIHTMEY YAAIKR/RGFMFSFTRTWKLEA IILSKLTQEQTKAHHMFSLIRGS
12237	42605	A	12311	79	432	
12238	42606	A	12312	1	933	
12239	42607	A	12313	70	675	
12240	42608	A	12314	1	339	
12241	42609	A	12315	3	422	
12242	42610	A	12316	1	471	
12243	42611	A	12317	1	963	
12244	42612	A	12318	375	542	ENDKARRSDTPSML*WVEGMK *SVKAPHTLHLASDYVLEPWG GESATFIPASWDC
12245	42613	C	12319	1	2148	
12246	42614	A	12320	1	1881	
12247	42615	B	12321	1	1074	
12248	42616	C	12322	143	439	
12249	42617	C	12323	123	362	
12250	42618	A	12324	474	603	NHKNPRRKPRQYHSGHRHGQG LHV*NTKNNGNKSQNGQMGSN
12251	42619	A	12325	5169	5756	CPSLPPPHGKPAACPRSPPGGC CTPRSARTVPRGLSENSQTKCH SADLPPEGPRVFWTPPGTGAAP APPAPAPGARCGPRRCHAWPP QRSSGAGRSPPPRHFAEFLKM VAFLRILILRAVSLRLSLDLLEIS* G*RP*GPSWGGPPQSTPSAASA ASKTSSPRRWSTPAWAFSLARA HPRWVAPSTAAQCTAAP

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12252	42620	A	12326	21	98	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMHDRDSCPLDCKVY VGNLGNNGNKTELEAFGYYG PLRSVWVARNPPGFAFVEFEDP RDAADA VRELDGRTL\CG\CRV RVLELVRMGK\RSRNRGPPPS\ WRRRPRDDYRR\RSPPPR\RRSP R\RRSFS\RSRSRSL*ERVGWC WAGGKREDSSSERVDSRRIF
12253	42621	A	12327	919	1043	
12254	42622	A	12328	460	657	CFSPGMWQKTHSRKHSFGAICP INPVGECLEVRKIKQLD*ITWINA I*LPLRDGLFYFLNFPFCCRG
12255	42623	A	12329	1	2235	
12256	42624	A	12330	1	255	
12257	42625	A	12331	2	429	CRADLNSRIDDFVPNPSVAVSG ASYAVAAVTMAHYKAADSKR EQFRKYFEKSGVLDLTKVLV ALYEEPE\KLNSALDFLKHHLG AATPENPEIELLRLELAEMKEK YEAIVEENKKLAKLAQYEP QEEKRAELGFFSV
12258	42626	A	12332	670	860	
12259	42627	A	12333	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFYSYPLDLLKLHDERVLVAF GQRDGI RVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANY VSIRFGPRLTSNEKLMLASMF HSIKFVVLADP/RQAGIDSLLRK IYEIYSDFAKLPFYSEMP
12260	42628	A	12334	1	2034	
12261	42629	A	12335	1	324	
12262	42630	A	12336	2	694	FGTRGKAAMAIFSVYVVKAG GLIYQLDSYAPRAEAEKTFYSP LDLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTA DGKEVLEYLGNPANYPVSRFG RPR/LTSNEKLMLASMFHSLFAI G/SQLSPEQSSGSIEMLETDTFK LHCYQTLTGK/VVLAADPR/Q AGIDSLLRKIYEIYSDFA/LKNPF IYSEMP/IRCELFQNLKLALEV AEKAGTFGPGS
12263	42631	A	12337	2	1658	

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12264	42632	A	12338	3	997	VQKPNRQWRLVQDLRIINEAV VPLYQAVRNPYTLSSQIPEETG WFTVLDLKDALFCIAVHPDSQF LLAFEDPLNPTSQLTWTVLPQG FRDSPHLFGQALADLSQFSYL DTLVLRVYVDDLLAAPSETLCH QATQVLLNFLTGCYKVKSLK AQICSQQVKYLGKLSKGTRAL SEERIQLAYPHPKTRKQLRGL LGITGFCQIWIPRYSEIARPLHTL IKKTQKANTHLVRWTPEAEEA FQVLKKALTQAPVLSLPTGQDF VSLYVTEKTGIALGVLTQHYGE ERNs*LPTEYLSNIRKPLGDYV WLYRNLKRQSYTARVIRKER
12265	42633	A	12339	3	421	
12266	42634	A	12340	3	4804	KRLNIIQKTEVAFSEAVWMQ PSVLLDDLADIAGLPAVPEHE HSPDAVQSQRALAHNDMIKE FISMGSLVALIATSQSQSLHPL LVSAQGVHIFQCVQHIPPQNQE QRCEILCNVINKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAHSRLSRQSISTREKLVL TTLDLQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
12267	42635	A	12341	1	2223	
12268	42636	A	12342	1	3864	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNPNLSIYRSEV FCAHRHLHPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGT QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTTLTSTRINPLKKEKSPEDL KQIKIDLGKFSND

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12269	42637	A	12343	204	963	DCACTFHCRSATKIVKDLKAQ GLVKPCNSPCSTPILGVQKPNG QWRLVQDLRIIDEVVVVYVDDL LLAARSKTLCHQATQALLNFLI TCDYKVKPKAQLCSQKVLYL GLKLSKGTRVLSEERIQPIAYP HPKTPKQLRGFLGITGFCRIWIP RYSEIARPLYTLIKKTQKADTH LVEWTPAEVAFQALKEALTQ APVLSLPMGQDVPLYVTEKTI ALGVLGVLTVQVRG/LSLQPMAY LSKEMDVVAKGWPH
12270	42638	A	12344	1	1178	MPESPTLLGRDILAKAGAIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFYQRYPLRPEAQQLGQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPGQ FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQOECHQATQV LLNVLATCGYKVKSKQAQLCS QQVKYLGVLKSKGTRAL/QQ*R TDRT*LSSTNSCNLRHSRGPSSRG SLD*SQPOLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIRRRKGL IRIYMLPLILSAPYDHLH
12271	42639	A	12345	1	841	
12272	42640	A	12346	3	1428	
12273	42641	A	12347	2	268	
12274	42642	A	12348	1	897	
12275	42643	B	12349	1	1650	
12276	42644	A	12350	232	1002	TPGSTVHAPEADQGLQKIVKDL KAQGLVKPCNSPCSTPILGVQK PNGQWRLVQDLRIIDEVVVVYV DDLLAARSKTLCHQATQALL NFLITCDYKVKPKAQLCSQKV KYLGLKLSKGTRVLSEERIQPIP AYPHKTPKQLRGFLGITGFCRI WIPRYSEIARPLYTLIKKTQKAD THLVEWTPAEVAFQALKEAL TQAPVLSLPMGQDVPLYVTEK TGIALGVLGVLTVQVRG/LSLQ MAYLSKEMDVVAKGWPH
12277	42645	A	12351	1	2217	

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12278	42646	A	12352	1	6530	MWGSDDLRLAGAGGGGAAVTVA FTNARDCLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSQDQGENVAEINRQVGKQL GLSNGGQELHVAVSLEQHLLDQI RIVFPKAIFFVWVDQQTIFYFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAIEYKKLHS YGRDQKGGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSHFSQSEKKQETSWG LTEINAFKNMQSKVVP
12279	42647	A	12353	1734	4349	MPNRACFQCGLQGHEKDKCPS RKPVQCLTIESQEVNCLLDAGA AFSVLLSCPGQLSSRSVTIRGVL GQPVTRYFFQPLSCDWGALPFS HAFLIMPESLTPLLEIEILVKAG AIIHLNIGEGTPICRLLFEEGISPE VWATEGQYQGAKNHAFVQVK LKDSTSPYQRYPLRPEAQQR LQKIVKDLKAQGLVKPYSSPCN TPH.GVQKPKRQWRLVQDLRII NEAVFPLYPAPSPYTLSSQPEE AEWFTVLDLKDAFFCIPVHPDS QFLFAFEDPSNPTSQTLTWTVLP QGFRDSPHLFGQALAQDLSQFS YLDTPVLQCMDLLLAARSET LCHQATQALLNFLTTCGYKVS KPKAQCLCSQVVKCLGLKLSKV TRALSEERIQPIIAYPYPKTLKQ LRGLGITGFCRIWIPRYGKIAR PLYTLIKETQKANTHLVRWTP AEAFAHFKKALMQAPVLSLL TGQDFSSYVTNKQTKKKK/T* IALRVLALV*GTSLOPVAYL/SK EIDVVAKGQPHCLRVVAVAV LVSEAVKIIQGRNLTWVTSHDV NGILTAKGDLWLSNHLKYQ ALLLEGPMLRLCTCAALNLDTF LPHNEEKIEHNCQQVIAQTYAT RGDHLVPLTDPNPNLYTDGRS FVEKGLQKVGAVVSDNGILES NPLTPGTSACLAKLTRALELGE GKRVNIIYTDSKYAYLVLHAHA
12280	42648	A	12354	5	138	
12281	42649	A	12355	1	909	
12282	42650	A	12356	3	245	
12283	42651	A	12357	1	1080	

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12284	42652	A	12358	3	955	VPRKSVHSGDAEYHKVLKEEA SDSRENKVGTTWLQILSGSFAS RVTEHITQPLQESVSLWISSEQN IPPKFMGRLNKLKATYKRKYS AAKSKVEKKKKEKVFAVTTKP VGGDKNGGTRVVQTRIKLPR YHPTEDVPRKIVEPPQKNLFSQ HVRKTAKTALPPGTILILTG/RH RGKRVVFLKQLASGLVITAP LVLNRVPLRRTHQKFVIATSTKI DISNVKIPKKKDKTPLLTDAYL \KKKKLRKPR/HPRKGEIFDTVK RGNMRITEQRTIDQKAVDSQIL PKIKAIQA/LQGYLRILCLL*RN GIYPHKLVF
12285	42653	A	12359	1	555	
12286	42654	A	12360	1	300	
12287	42655	A	12361	1	588	
12288	42656	A	12362	1	264	
12289	42657	A	12363	1	870	
12290	42658	C	12364	239	400	
12291	42659	A	12365	9	98	SWKPSFSAN*HRNRKPNTTCSH SQVGVDL
12292	42660	A	12366	9	81	
12293	42661	A	12367	3	169	
12294	42662	A	12368	134	481	GCCGGTIKNSFSFPLPNWPRFV MFPSLCVLIVETCETWICTLIVQ LPLMSENMRCLIFCSCVSLLRM MVSSFVHVHDHKVKSHPSP/G NLRKSKEASPSPKTSKVGKLTQV PSVCG
12295	42663	A	12369	41	388	SYGQMMKCPQTFPPSPGYGAG VFSSDKIGQMTFMERT*RMSCK EAAQDHTAREKEKVELKFPSLP FRRKELL*PCTWLGSPISLVTL D FPWPQSGRLSMPVLWTCLPG SLEIG
12296	42664	B	12370	1	909	
12297	42665	C	12371	295	2025	
12298	42666	A	12372	14	260	
12299	42667	A	12373	1	142	TCTCVFIAALFTIAKTWN*SKCP SMRDWIKKNVAHTHHGILCSH KKE
12300	42668	A	12374	1	395	

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12301	42669	A	12375	2	976	REHLAEGMAVGTASADLNISA CWLRRQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQFK EQAAIFAVLQPPLVIPRKIGSGV DLEQTPADLQKRGLTVTRKTN KQKAIASSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSPAR EQNWMEFDELTEVGFRRW VITNSSELKKHVLTCCKEAKNL EKRDMDDEAGNHHSQQTNTGTE NQTPHVLTHKWELNNENTRTRI YKKHGAAICLASGIYHSVDLPF WGLDLFPWDEDSGSTILSGSG QWPSSHSSTRQCTSVDSVWGL
12302	42670	B	12376	1	111	
12303	42671	A	12377	34	346	
12304	42672	A	12378	1	585	
12305	42673	A	12379	3	14703	
12306	42674	A	12380	1	636	
12307	42675	A	12381	1	1626	
12308	42676	A	12382	1	3246	
12309	42677	C	12383	62	202	
12310	42678	A	12384	1	286	
12311	42679	A	12386	1	1176	
12312	42680	C	12387	1	942	
12313	42681	A	12388	785	892	
12314	42682	A	12389	2	91	
12315	42683	A	12390	1	708	
12316	42684	A	12391	3	96	TWMKLEITILSKL*QRQKTKHR MFLIGGN
12317	42685	B	12392	1	1954	
12318	42686	A	12393	1550	1830	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKMMW HIYTMEEYAAIK/SDEFMCFAW TWMKLEITILSKLSQEHKTKHH MFSLTSGS
12319	42687	A	12394	3	553	
12320	42688	A	12395	1	1428	
12321	42689	A	12396	642	753	
12322	42690	B	12397	1	759	
12323	42691	B	12398	1	900	
12324	42692	A	12399	623	775	
12325	42693	A	12400	992	1156	
12326	42694	A	12401	86	349	

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12327	42695	A	12402	1	2521	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIQMGQWFRNRSI NIVQHINRTNDKNHMIISDAEK AFDKIQQRFMLKTLNKLIGDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTROGCLPLLFNIV LEVLAIRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSGYKINVQKSQ AFLYTNRRQTESQIMSELPFTIA SERIKYLGQLTRDVKDLFKEN YKPLLNDIKEDTNKWNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKGARIAKSILYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPKDKKKWGNDS LFNKWCWENWLAICRKLKLDLP FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNITQDIAMGKDFMS KTPKAMATKAKIDKWLINLK SFCTAKETTIRVNRQPIEWKIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAARKHMKKCSSSLAIREMHI KTTMRHHLTSVRMAHKKLGN DWCWRGCGEIGRLLHCWWDG KLVLQPLWKSVMFLRDLELET FPDPASPLLGIIYQKE/YKSCYYK DICT/RVCVPAALFTIANTWNQP
12328	42696	B	12403	80	5612	
12329	42697	B	12404	68	505	
12330	42698	A	12405	1	471	
12331	42699	A	12406	194	430	IAIMRLLQISIIILSSCLREVKSM QAYRKALRKLKADVKRYQKS LVVQKRS*ER*SLVLILILPARTF QSYLAPIC
12332	42700	A	12407	1	546	
12333	42701	A	12408	2	418	
12334	42702	A	12409	302	746	ETSHQVMDRSNPVKPALDYFS NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGLKV LGNLWPPYLMHEHPAYLYS WEDGDCFTPKALDPLPACDLC DQLHLRSRQGGVCGGDPCEQ LLLLVAVSLQAPAIASAAAGRPV
12335	42703	A	12410	83	552	
12336	42704	A	12411	1	459	
12337	42705	A	12412	34	588	

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12338	42706	A	12413	1	466	
12339	42707	A	12414	950	1230	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ
12340	42708	A	12415	497	847	
12341	42709	A	12416	1	337	MGVVPPEELFLEELNLSGLKWD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQHPEFAPP SHGD
12342	42710	A	12417	716	961	
12343	42711	A	12418	1	1218	
12344	42712	A	12419	1	1104	
12345	42713	A	12420	548	1078	
12346	42714	B	12421	83	345	
12347	42715	A	12422	1	681	
12348	42716	A	12423	1	1431	
12349	42717	A	12424	566	871	
12350	42718	A	12425	145	980	
12351	42719	A	12426	2	702	
12352	42720	B	12427	1	1156	
12353	42721	A	12428	188	584	
12354	42722	A	12429	1	1194	

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12355	42723	A	12430	170	1855	LLEGKLTNRKDIPHQNICTSPS SKTKGILPISEPPSNRIFACWGK PAWTACCN/FSQQQAVKGNQL LPVSLVKKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESQGD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KKRKTTLAPNTQTASPRALADSL MQLARQVSRLESQGINHTPNSF HIGAGGSWCLSESPPVVLNYK YPLVCGYTDGNAEVSKFGNFFL DLSRTRCLAEGNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGT ENGYQGEESLFNKAYYGGGTN FFRKESQKLQSQAKKRDAELA NGALGIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKMNGKW YLFDTDSRGSKMTIDGINSNDIY MLGYVNSLTGPYKPLNKTGL VLQMGDLDPNDVTFTYSHFAPV QAKGNVNVITSYMTNRRGFED KKATFAPSFLMNIKGKNTSVVK NSIRREGFCFRNHHQTGFSPA GANQRGPLAATLSGPGGEGQS AVARLTGEKKNHPGAQYANRL SPRVGRFINAAGITGFPTGKRA GFCFRNHHQTGFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGITGFPTGKRAV
12356	42724	A	12431	851	2237	
12357	42725	A	12432	2	2346	
12358	42726	B	12433	329	479	
12359	42727	B	12434	656	2404	
12360	42728	B	12435	486	834	
12361	42729	A	12436	1	693	
12362	42730	A	12437	1	114	
12363	42731	A	12438	152	391	AGGWALPSLGLPSWTSRCPWR RGSAGLLLLASVPVQQ*PKLLD RLSRRWPGEHPRPARVRSCM ALGPRRLGVLCOEPS
12364	42732	A	12439	1	1707	
12365	42733	A	12440	1	897	
12366	42734	A	12441	36	420	
12367	42735	A	12442	2	217	
12368	42736	A	12443	1	903	
12369	42737	A	12444	1	1626	
12370	42738	B	12445	107	757	

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12371	42739	A	12446	1	1655	MGTVPRSAQGETWVWLCEHIIIGG ERSFTEYSLSCHRIESSTSSIKLEL GGNNVEPLESSRVFDSIVQNEE ADAVSTGEEGVTHEGTQGGKV IPQMHHMGSGLQPKSFSQNRSQV NNDMIVTDNNGAVKFPQLCKF CDVRFSTCDNQKSCMSNCISITSI CEKQPEVCVAVCWMSEIECTN VMYSPLPCKFLHLSPIEVLPIRS PVNQSGRCKIRHIGSNNRLQRS TCQNTGWESAHVMKTPGFREY NTSNPDLLLIVFQVTGISLLPPL GVAISVIIIIFYCYRVNRQQLSS TWTGKTRKLMFSEHCAIILE DDRSDISSTCANNINHNTELLPI ELDTLVGKGRFAEVYKAKLKQ NTSEQ*DSGQFKILFPIEYAS WKTEKDIFSDINLKHENILQFLT AEERKTELKGQYWLITAFHAK GNLQEYLTRHIVISWEDLRKLGS SLARGIAHLHSDHTPCGRPKMP IVHRDLKSSNILVKNDLTCCCL DFGLSLRLDPTLSVDDLANSQG CYEVCSSGRFLVTIFKGNRLRE RTEKNTRITPRDWVYEWLW
12372	42740	A	12447	1555	3277	RAAGSAMGRGLRGLWPLHIV LWTRIASTIPPHVQKSVNNDMI VTDNNGAVKFPQLCKFCDVRF STCDNQKSCMSNCISITSEKQP EVCVAVVRKNNDENITLETVCH DPKLPYHDFILEDAAAPKCMK EKKKPGETTFMCSSEDCNDN IIFSEYNTSNPDLLLIVFQVTGI SLLPPLGVAISVIIIIFYCYRVNRQ QKLSSTWETGKTRKLMFSEH CAIILEDDRSDISSTCANNINHN TELLPIELDTLVGKGRFAEVYK AKLKQNTSEQFETVAVKIFPYE EYASWKTEKDIFSDINLKHENIL QFLTAEERKTELKGQYWLITAF HAKGNLQEYLTRHIVISWEDLR KLGSLSARGIAHLHSDHTPCGR PKMPVIVHRDLNSSLNVLKNDLT CCLCDFGLSLRLDPTLSVDDL NSGQVGTARYMAPEVLESRMN LENAESFKHTDVYSMALVLEW MTSRCNALGEVKDYEPFGSK VREHPCVESMKDNVLRDRGRP EIPSWLNLHQGIQMVCELTTEC CDHDPYARLTAQCVAERFSELE HLDRLSGRSCSEKIPEDGSLNT

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12373	42741	A	12448	3	1354	
12374	42742	A	12449	1	168	
12375	42743	A	12450	2	147	
12376	42744	A	12451	3	523	LQFFRRSEVVKMKNHLLFWGVL AVFIKAVHVKAQEDERIVLVN KCKCARITSRIIRSEDPNEDIVE RNIRIVPLNNRENISDPTSPLR TRFVYVHLSDLCKK\CDPTEVEL DNQIVTATQSNICGWMVTPQS TCYTLSTGKNKCYTAVVPLVYVG GETKMOVETALTPDACYPD
12377	42745	A	12452	3	274	
12378	42746	A	12453	1	120	
12379	42747	A	12454	119	461	PVPQDLQA AVLGRITLALFKVAV KTGTLQVCKRLLLSFVCL/CPA PRGRQASLSCGGLHPVRASWLL CLPKQAWAMAGAPPPAWLPCC SLISDCCASNQRDSVGVPRSEPG VGYSLV
12380	42748	A	12455	2	370	
12381	42749	A	12456	1	3135	
12382	42750	A	12457	1	942	
12383	42751	A	12458	1	462	
12384	42752	A	12459	1	297	
12385	42753	A	12460	935	1338	CTDGLFVWMSFLVFSFPLPPCS LISDCSASNERDSVGVPSEPG AGYNLVVRRFLSPSEKRSIRV* VTRFSRCRPSPLSLTRKGNSLTP CASQVRQCLALFRLAHGVRTH SPAPT VWHSLPKVGPFLSNSVP
12386	42754	A	12461	1	268	
12387	42755	A	12462	3	479	
12388	42756	A	12463	1	262	
12389	42757	A	12464	1	304	MAGAPAPASLPPCSLISDCCAS NQRDMSGVGPSEPGAGYNLVP V\EKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLALL QLAHGRGSPNPRP
12390	42758	A	12465	1	512	
12391	42759	B	12466	1	1257	
12392	42760	A	12467	1	705	
12393	42761	A	12468	1	3039	
12394	42762	B	12469	66	467	
12395	42763	C	12470	360	747	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12396	42764	A	12471	3771	4703	SFOQFCVSFSPSLWFYLLLVFDD GDVQMRFCGCPFCFLVFLTD RTLSCRSVGPICRVRCQCA/LLG GASQLGCSGVKGSRDPLEEAV CPFS/DLQLRAGGNTALFKAVR QGHLSLQRLLSFVCLCPAPRG GAYRGGQASLSCGGLHPV*AS/ RLCLCPKQAWAMAGAPPPASL LAPC/LISDCCASNQSDSVGVGP S/ERPGVGYSLVVRFLSRSEKR NIRGGVTRFSRCPSPSLSTRK GNSLTPCASQSEGNAGPAGF AHGARTHWALRPVTVHSLCE MNPVPQMEMQKSPVFCVAHA GGCRPEL
12397	42765	A	12472	1	1038	
12398	42766	A	12473	27	428	LADRSAIPGFAFAVTFLLALVG AVLYLYPWTLKPC*SHY*GIN LVVAV*VKTT*GKNCMKMV*L IL*RVTLPS*RFGLRLEKAF*M GHLIKT*LGKNNMKMPCSNWS LF*GTS*KNEKEGTSVNIFSLTP
12399	42767	A	12474	107	362	NKPCFEFYLAALIYLLYHGRK KADTKIPP*ISRFLLIYPSHELTI FIVIHIMCDLGCTWAICFLTISE EVQKKLYEENQVFG
12400	42768	A	12475	193	637	TSSEVVKKQIAQVHNFVIMQL ARENILSS/EDLLVIKVPVLY*GV NENMLTEVPFSFFYDVP*NRL QLHEGIFILFFPSHFVFIK*PI*KAF SNLRPNCAMILLEANDFLIIFKC TTHYHLCNRLHSTKTKHMLAEG HVLGLVWVGEPFI
12401	42769	A	12476	1	1930	
12402	42770	A	12477	1	362	
12403	42771	A	12478	58	160	GVSLQSTSEEGRMQRQE*TERE IKVTCRSHYRLA
12404	42772	A	12479	3	410	
12405	42773	A	12480	1	807	
12406	42774	A	12481	154	375	
12407	42775	A	12482	2	512	
12408	42776	C	12483	29	455	
12409	42777	A	12484	209	433	
12410	42778	A	12485	1	1546	
12411	42779	A	12486	3	931	
12412	42780	A	12487	1	363	
12413	42781	A	12488	1	351	
12414	42782	B	12489	82	263	
12415	42783	A	12490	1	1878	
12416	42784	A	12491	24	242	
12417	42785	A	12492	1	3558	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
12418	42786	A	12493	2	478	HNSLKSNDKENSFSADHVTTA VEKSKESQVTADDEEEKAKA ELIMDDDRVTVDPLLSKSQSILIS TSATASSKKTIEDRNKNNKKSTN NRASSASARLMTSEFLKKSSSK RRTPSTTTSSHYLGLTKVLDQK PFTEEA*EPDRADNIRGSCLFR
12419	42787	A	12494	1	1047	
12420	42788	A	12495	1	1055	
12421	42789	A	12496	212	611	
12422	42790	A	12497	2	195	YVMGRNDGGYLMIDSKTAEIK FVKNNMRDSTFVNKTITAEVL AIDRYSGKNCLLSWSYICG
12423	42791	A	12498	1	429	
12424	42792	A	12499	1	503	
12425	42793	A	12500	3	825	GTTKWQTVRRQKREWIKFAAA CREGEDNSKRNPAAK*SDLQNS LLPALY*KHURSDCESNQKITY RISGVGIDRPPYGVFTINPRTGEI NITSVVDREITPLFLIYCRALNS RGEDLERPLELRVKVMDINDN APVFSQSVYTASIEENSADANTL VVKLCATDADEENHLNSKIAY KIVSQEPGAPMFILNRYTGEV CTMSSFLDREQHSMYNLVVRG SDRDGAADGLSSECDRIKVL VNDNFPT/FRENFKQNSRFSNS LLSSFDQWRKL
12426	42794	A	12501	986	4030	KQRLTWTFSPGKSETMMGLFP RTTGALAIFFVVILVHGLRIET KGQYDEEEMTMQQAQRQKR EWWKFAKPCREGEDNSKRNPAA KITSQYQATQKITYRISGVGIDQ PPFGIFVVDKNTGDINITAIVDR EETPSFLITCRALNAQGLDVEKP LILTVKILDINDNPPVFSQQIFM GEIEENSASNSLVMLNATDAD EPNHLNSKIAFKIVSQEPAGTGM FLLSRNTGEVRLTNSLDRQQA SSYRLVVSGA
12427	42795	B	12502	1	3572	
12428	42796	A	12503	1	594	
12429	42797	A	12504	1	612	
12430	42798	B	12505	200	532	
12431	42799	A	12506	2	735	
12432	42800	A	12507	5	400	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in UNSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12433	42801	A	12508	2	1260	GQAASPASPASPAMAWAA LLGLLVALLLLLLSRRRTTRP GEPPLDLGSIPWLGALDFGKD AASFLLTRMKEKHGDIITLVGG RYVTVLLDPHSYDAVWVEPT RLDFHAYAIIFLMERIFDVQLPH YSPSDEKARMKLTLLHRELQAL TEAMYTNLHAVLLGDATAGS GWHMGLLD/CLQLPAQSRPL DSLRN*GAATHP*KPGPGPRPLS *CLPHLSPARPAAPQTGPWLPV SGGQGPVHVCQKSPVEAIPSQ AGQAGPPEQMAGELPAAPGGD GCVRGDAGTGPAAA VGHTGE YGSRCLLAPALPSQES*SPGCCP RRAREYPLASGAACLDHDSPT EGSRQHTC/DLIAC*VRASGLQL PPSSPARL/GGPGHAHGRERIQ PATW*PPPLPLPEPPERPRNLH RPRGI
12434	42802	A	12509	3	466	
12435	42803	A	12510	1	1134	
12436	42804	A	12511	2	1211	
12437	42805	A	12512	2	405	HEMLLASEIKHLPRLLIGQERE TQTSELKIKRRGNEEAPS/PPSS AYERGTKRPDYDTPTSKKK VRIKDRNKLSTEERRKLFEQEV AQREAOQKQQMQNLGTMSP LPYDSLGYNAPHHFAGYPPGY PMQA
12438	42806	A	12513	191	898	
12439	42807	A	12514	1	270	
12440	42808	A	12515	2	1328	
12441	42809	A	12516	1	2868	
12442	42810	A	12517	1	1254	
12443	42811	A	12518	1	576	

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12444	42812	A	12519	1919	3044	HQGPSTPPSWAMSGPPTPLSRE DWHQGPSTPPSWAMSEPT/SSI QGLASGAVHTJLLGDVRATYTS IQGVTSQVSVQSRRAAQMAVPSS RILQLSKPKAPATLLEWDPVP KPKPHVSDHNRLHLAKVPRK EGSGKKVGAFPEIKGPEAFRDK ARAMESQSNMDMPFDELLALYG YEASDPISDRESEGGVDVDPNLP DMTLDKQIAKDLLSGEEEEET QSSADDLTPSVTSHEASDLFPN RSGCLLAGAEASSRGLLPRAQP VPRGAGLADNSRGALLRAHGT VRVGTATVVKPADAPPESPRDR RSRNDSHRPTGPSESERQPQSN QPTLLLRGHGTIRVVRTATVVKP ADAPAESPRDRSRNDSHGQSS
12445	42813	A	12520	413	1412	
12446	42814	A	12521	293	412	NHLSVAGNGSSPCGL*AGALGL LLWLLASSGHRVLSGMI
12447	42815	A	12522	2	181	
12448	42816	A	12523	1	277	
12449	42817	A	12524	1	739	
12450	42818	A	12525	1	326	
12451	42819	A	12526	3	566	
12452	42820	A	12527	1	465	
12453	42821	A	12528	1	1167	
12454	42822	A	12529	260	395	EVATATPTLSNHYPDQSAAIN/D QG*PLHQKQDHILKQAQMNISIF
12455	42823	A	12530	209	958	FRCVLISFWSHKLHLWYHEGRI VPSDRIVPPHGI/VSSHGVALPQR ILMRQFTLLEGLNKDGRFLIQLS GTAPWSSYFNSVAKFGVIHRIH SFFLSHNGHKAVALDLLSNVG GSCLCGDASSFTTPSRITMTSK SWLARSVAEMSYR/WTALVNH VADDQRGHQKNVIALDWVINR NVQLVNRNHLPRFCSCFLDHL AHRGTNDHAFQVTHSEHAQ LAISDGNHSMMAENQSFPCPSVS LSCFHENAA
12456	42824	A	12531	1	1965	
12457	42825	C	12532	520	684	

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12458	42826	A	12533	701	1307	GRHLTTNHTAAVVFPPFRPLCS SFFRYSGRFVAGATASGRGQG PAG*DNCQRAWRGAFYKFQAT LSAGAGTRAEEGSDGDGEAAE PGAGTAREPARLRGVRSRFVL DGRRCCLCYFKNPHDPLPLGHL DIAEACFSYQRADEAAEQPAHF QVRSAGAATVLEVGTRALRGV HLIRAHRGIAQAWSPVSFLQ AVLPAWLL
12459	42827	A	12534	1	1356	
12460	42828	B	12535	1	1449	
12461	42829	A	12536	3	2449	
12462	42830	A	12537	1	3327	
12463	42831	A	12538	1	1359	
12464	42832	A	12539	1	672	
12465	42833	A	12540	1	1281	
12466	42834	A	12541	1	399	
12467	42835	A	12542	1	399	
12468	42836	A	12543	171	426	PVSCATGEEEDNVLPFKGDDL R**PGKLWCEFHASSISQALGQ HPRRSVLDTQDSHVLVRRKTT CFSQRAMISPDPPSQEAGALS RNNLLAPYSALTFMENGNCLL QLFQLGKLLVQASHLHGQLLV FVQKIIISM
12469	42837	A	12544	1	988	
12470	42838	A	12545	3	129	LFHPCQDSQHH*CVCCRLTGH GAA*VHGPGCAVQTYRASH
12471	42839	C	12546	532	1101	
12472	42840	A	12547	197	355	
12473	42841	A	12548	1	1275	
12474	42842	A	12549	3	131	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
12475	42843	A	12550	1746	3504	ESDPSNSTTSM DRTLL/MSSIVP RLPSACRILPTGTIPE*SCVHRT ASLIPLPPGSRKYSPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTS PDISHQQA AALLRTY LKNLSPIYNSTPIFGPLTTQTTI PVAAAPLCISWQRP TGIPLGNLSP SRCSFTLHLRSP TTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCLSLHPWLS SPSSDSDP PRPSSCLLIPSPENNSERLLVDT RRFLIHHENRTFPSTQLPHQSPL QPLTAAALAGSLGVVWQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAGISTSM TFRSLSNDFS ASITDISQTL SVLQA QVDSLAA VVVLQGGRLGLDLLTAEKGGLCI FLNEECFFYLNQSGLVYDNIKK LKDRQAQLANQASNYAESPWA LSNWMSWVLPVPSLPIPIFLLLL FGPCIFRLVSQFIQNRIQAITNHS IRQMFLLTSPQYHPLPQDLPSA
12476	42844	A	12551	2	394	
12477	42845	A	12552	1	882	
12478	42846	A	12553	45	409	
12479	42847	A	12554	1	1035	
12480	42848	A	12555	118	312	
12481	42849	A	12556	1	1083	
12482	42850	B	12557	1	1122	
12483	42851	A	12558	97	439	
12484	42852	A	12559	1	450	
12485	42853	A	12560	1	471	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
12486	42854	A	12561	2	1407	WGKNRAEKLETLSRVPLLLQ RNAVPHQQWNKAGRRMTLS* EKKASDD/PNYSKLQEEIQTGK KEVKHFEKNLDECITRITNREK CLKELMELKAKARELREECRL RSQCDQLEERVSVMEIEQTTIRE YYKHL YENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPIGTSE IVAHINSLPTKKSPGPDGFTAKF YQRYKEELIPLLKLFQSEIEKEGI LPNSFYEA SIIIPKQGRDITTKK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSRNVJHHNRTKDKNH MIISIDAEKAFDKIQPFMLKTL NKLGI DETYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTQRGGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDIMIVYL ENPIVSAQNLFELISNFSKVSGY KINVQISQAFLYTNYRQSAKS
12487	42855	A	12562	1	846	
12488	42856	A	12563	1	1281	
12489	42857	B	12564	1	274	
12490	42858	B	12565	1	2265	
12491	42859	A	12566	1	2742	
12492	42860	A	12567	1	1272	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
12493	42861	A	12568	222	2130	RKKNNKKK*TKPPRNMGLEKT KMSDWCT*K*GEWNQV/AK TLCRILSRRT/YPNLAQADIQIQ EIQRTPQRYSSRRATPKHIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLTADLSAETLQARRE WGQIFNII.KEKNFQPRISYPAKL SFISEGEIKPFTDKQMLRDFVTT RPALKELKKEVLNEMERNRKK LNRPTIGSEIVAIINSLPTKKSPG PDGFTAEFYQRYKEELVPFLLK LFQSKEKEGHIHPNSFDEASIIIP KAGRDTTCKDNFRPISLMNIDA KILNKILANQIQHIKLIHHDQ VGFIGMQGWFNICQSNVIQHI NRTKDKNHVVISIDAEKAFDKIQ QRFMLKTLNKLIDRMYLKIIR AIYDKPTANIILNGQKLEAFPLK MGTTRQGCPLSPLFNIVLEVLA RAIRQKEIKHIIQLGKKEVILSL FADDMIVYLENSIVSAQNLLKLI SNFSKVSQYKINQKSHALHT NNRQTESQIMSELPFTIASKRIK YLGIIQLTKDVKDLFKENYKPLL NEIKEDTKKWKHIPCWSVWGRIN IVKMAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRAHT AKSILSQKNKAGGITLPDFQLY CKATVTKTAWY
12494	42862	A	12569	1	474	
12495	42863	A	12570	1	1197	
12496	42864	A	12571	1	1518	
12497	42865	A	12572	1	3189	
12498	42866	A	12573	1	2199	
12499	42867	A	12574	3	2820	ENKDTTYQNLWDAFKAVCRG KFIALNAHKKRQERSKIDTLTS QLKELEKQEQTHSKASRRQET KIRAELEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKREK NQIDTIKNDKGDITDPTETIQT REYYKHLIYANKLKNLEEMDKF LDITYLPRLNQEEVESLNRPIITG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIIIPKGRDITTK KENFR
12500	42868	B	12575	1	1593	

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12501	42869	A	12576	1	3549	MGDFNTPLSTLDRSRRQKVNK DTQELNSALHQVDLIDYRTLH HKSTEYTFPSAPHHTYKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQNRSTTWKLN NLLNDYWHNKMKAIEIKMFF ETNKNKDDTTYQNLWDAFKAV CRGKFIALNAHKRKKQERSKIDT LTSQLEKEKQEQTHSKASRRQ EVTKIRAEKKEIETQKTLQKINE SRSWFFERINKIDRMLARLIKK KREKNQIDTIKNDK
12502	42870	A	12577	1	2724	
12503	42871	A	12578	1	3567	
12504	42872	B	12579	709	2064	
12505	42873	A	12580	1	3370	
12506	42874	A	12581	1	2024	MGFYHVGQAGTELLTSNDPLT SASQASRITGKALQKPTVPVP YEKMLQDQSALIVQGLPEGVA FKHPENYDLATLKWILENTAGI SFIINSATIEPPAAQPMSTHMG HSLCVLVVETHAKPVAVQSSSF TRNPEVISLEVAAVTVKEESD PDYDYITFKDLPGLIAYETKAYV LWPQLSKICKSNGDKNKAYRG QQCRLRQQNPLAALTGKISVSV YVSHPSLRVSIGWTRQVARQT MQKDRDGPLKNEGECNCAGSE KNTLTSQLEKEKQEQTHSKAS RRQEITKIRAEKKEIETQKTVEK INESRSWFFERINKIDRPLARLIK KKREKNQVDAIKNDKGDITDP TEIQTTHREYYKHLANKLENY EEMDKFLDITYTLRLNQEEVES LNRPIITGSEIVAINSLPTKKSPG PDGFTAIFYQRYKEELVPFLK LFQSIKEGILPNSFYEASIIIAK PGRDITTKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSNVIQHIN RAKDKKHMIISIDAEKAFDKIQ QPFMLKSLNKL/DIGKNYFKVH MGPKKSPCRQVNPKEQSWR HHST*LTQILQGYSNQNSMVLV PKQRYRSMQNTALRNATYL QLSDL*QT*EKQAMGKGFI**
12507	42875	A	12582	722	4214	

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12508	42876	A	12583	228	1152	KNRDYKNKLSLRPQCNQTRTON *ESHKPLNYMETEQPAPE*LL DT*RMKAEIKMFFETNENKDT TYQNLWDAFKATASKTNKEKE KNQIDTIKNDKGDIITDPTIEQT TIREYYKHLKYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGAIEVAIINSLPTKKSPGPDGF TAEFYQRYKEELIGWLRRESVSK ICLKFDHQVQVITGRLIIRFQIAF GTVVLCQLTRHIDVFVGKRLA NARFAPSLGGAPDLFTLKPCFV AVETQGDLPQATTVDIDGCL GKPANVQVALDIDVKGFGQQW
12509	42877	A	12584	1	2028	
12510	42878	A	12585	2	2264	
12511	42879	A	12586	1	2130	
12512	42880	A	12587	1	2900	MENDFDELREEGFRQSNYSER EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELTKAQELR EEWRSLSRSCDQLEERVSAME DEMNMKGEGKFKREKRIKRN QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLTYN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPIITGAE
12513	42881	A	12588	1	2745	
12514	42882	B	12589	1	3288	
12515	42883	A	12590	1090	2526	
12516	42884	A	12591	1	3242	
12517	42885	A	12592	3862	8976	RAKSPANIIMTGSNSHITILTN VNLNSPIKRRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFPSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSHSAIKL ELRIKNLTQSR
12518	42886	A	12593	1	1000	

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12519	42887	A	12594	1	979	MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFQVDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGNRQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRLQVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDL MEL KTMARELRDSCSFQRQDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLFADNMTVYLENPI IS/PKISLS**ATSASQDIKSMC KNHKHSYTPITDKQRAKS
12520	42888	A	12595	1140	2210	KPWHKNEFVTHAQASADLIKW KKGYQ*LKIKLMK*SKKTRNTN YHQNTINISMQIN*KI*KKWRNS WTHTLQY*TRKKLNL*IDQ*Q ALKL/QAIHYSLPTKNVQGMQD SQSNTRVWGILARAIQKEKEI KDIQLENEEVKLSLFADDMTVY LENSIVSAQNLLKLRKLYLGIQL TTDVKDLFKENYKPLLNIKIED TNKWKNIPCSIRGINIMKMAI LPKLIYRFNAIPIKLPMTFFTELE KATLKFIVNQKRAHIAKTILSK KNKAGGIMLPDFKLYYKATAT KAAWYWYQNRDIDKKLTQIYK KKTNNPIKKWAKDMNRHLSKE DIYGANRHMKKCSSSLVIREKQ IKTTMR
12521	42889	A	12596	520	697	GLCSVPLLCISVLVPVPCFCGYC SLVV*FEVR*SDASSFVLLA*DF LGNVSVFLVPYEL
12522	42890	A	12597	1	1410	
12523	42891	A	12598	1	1461	
12524	42892	A	12599	77	457	QALKLRQ*LIAYQPKRVQDQM DSQTSNARGTKRSWYHSF*NYS N/PTEKEGILLNSFYEAIGIIPKP GRDITTKKENFRPISLSINAKIL NKILANRILQHIKKLNTIKSASS LGCKAGSTYANQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
12525	42893	A	12600	1	919	MGDFNTPLSTLDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNCSTTWKLN MLLNDYWEHNKMKAEIKMFF ETNKNKDDTYQNLWDTLKAVC RGKFKALNAHKRKKERSQIDTL TSQLEKEKEQEQTSHKASRRQE ITKIRAELEKETETQKTLQRLMN PGAVLEVLAARIRQEKEIKGIQL GKEEVKLSLFADDMIVYLENP MSQPKISLS**ATSAKSQDIKSIY KNHQHSYTPIRDQKRAKS
12526	42894	A	12601	1	1264	MDKFLDTYTLRLNQEEVESLN RPTGSEIEAINSLPTQKSSGPD GFTAIFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIIIPKPG RYTHKKNNFRPISLMNIDAKIL NKILANRIQQHHKKLIHQDQVGI IPGMQSWFNHKSINVIQHINRT KDKNHMIIISIDAFAFDKIQPF MLKTLNKLKIPKNPTKYGCE GPLQGELEQITAQNRKGRHKQM EEHPMLMDRKNEYHKNNGHTPK VIYRFNVIPKLPMTFFSELEKST LKFIWNQKRARIATILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEM TPHIYNHLIFDKPDKNKQWGW DSLFNKWCWENWLAIGRQLKL DPFLTPYTKINSRWIKDLNVRP KTIKLEENLGNTIQDISMGKDF MSKTPKAMATKAKMDKWDLI KLKSFACTAKETTIRQSWPEMTK FTFSNTDVKNWKGKNNIGR HKTSVNTCKMDSGLVLERWM EWNPGFPLSIDAKCHKDLPRDI QFDSEKGVDFVLNYSKANMR WAGSMFL*FIESF*HEWLLNFV KGLFCIY*DNHVVVFVGSYYML
12527	42895	B	12602	1	1827	
12528	42896	B	12603	13	1377	
12529	42897	A	12604	557	664	KTPLSQPKISLS**ATTAKSQDT KSVYKNQQHSYT

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12530	42898	A	12605	77	1866	QAPKLRQ*LIAYQPKKVQDQTD SQPNSTRGTTKSWYHSF*NFSN/ PIEKEGIFPNLFYEANILIPKPGR DTTKKENFRPISLMNVNAKILN KLLANQIQQHKKLIHHNVQGF PGMQGWFNICKSINVIQHINRT KDKNHRSSISIDAEKAFNKIQPF MLKTLNKLDDMIYVLENPIVSA KNLLKLISNFSKVSQYKINVQK SQAFLYTNNRQAESQIMSASF TIASKRIKYLGLQTRDVKDLFK ENYKPVNLNKIKEDTNKWKNI LWIGRVNIMKMAILPKVIYRFN APIKLPMTFFTELEKTTLKFIW NQKRAHIAKTILSKKNKAGGIT LPDFKLYYKATVTKTAWHWY QNRDIDQWNRTEPSEIPIHYNH LIFDKLDKNKTLGKDYLFNKRC WENWLAICRKLKLDPLTRYT KINSRWIKDLNIRPKTIKLEEN LGDITQDIGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWENIFAIPYSDK GLISRIYKELKQIYKKSSNNPIK KWAKDMNRYFSKEDIYAANR HMKKCSSSLALREMOIKTTMR YHLIPVRMAIHKSGNNRCW
12531	42899	A	12606	67	243	GLCCVFLIYISVLVPVPCCFGYC SLVV*FEVR*HDASSFVLA*D* LGDVGSFLVPYEL
12532	42900	A	12607	1554	1692	
12533	42901	A	12608	640	816	GLCSVALVCISVLVPVPCCFGY CSLVV*FEVR*HDASSFVLA*D *LGNVDSLVPYEL
12534	42902	A	12609	1626	1739	

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12535	42903	A	12610	1	2014	MKREGSLEKKRIKRNEQSLQEI CDYVKRANRLRIGGPESDGENG TKLENTLQDMQEKFPNLRQA NIQIQEIQRTPQRYSSRA IPRHI IVRFTKVEMKEKMLRAAREKG QVTHKGKSIRLTADLSAETLQA RREWGPIFNILKEKNFQPRISYP GKLSFISEGEIKSFDTKQMLRDF VTTTPALKELLKEALNMEKNK QYQPPQKHAKLTREARANTFK PSRRREITKIRAELKEIETPKTAQ KINESRSWFSERINKIDRPLARL RKKKREKNQIDTIKNDGDDITT HPTIHTIIEYYKHLYANKLEN LEEMDKFLDTYTLPRPNQEEVE SLNGPIAGSEIQAIIINSLPTKSP GPDGFYQRYKEELVPFRLLKFQ SIEKEGILPNSFYEAIIILPKPGR DTTKKENFRPISLLNINAKILNKI LANRIQQHIKKLMHHDQVGFIP GMQGWFNIRKSNVQIHINRTK DKNHMIISIDAEAKFDTKIQQPF MLKTLNKLGDGTGTHKIJIRANY DKPTANILNGQKLEAFPLKTGT RQGCPLSPLFNIVLEVLARAIR QEKETEGIQLGKEEVKLSLFAD DMIVYLENPMMSQPKISLS**ATS AKSQDTKSMCKNHKYSYTPIT DKQRAKSSVNSPFTIASKRIKYL GIQLTRYVKDLFKERSMK
12536	42904	A	12611	1	700	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLSTKKSPGPD GFIAQFYQRTKDKNHMIISIDAE KAFDKIQQHFMLKTLNKLGDG TYLKIJIRAVYDKPTASIIINGQK LEAFPLKTGTGRCPLSPLFNIV VLEVLARAIRQEKEIKGIQLGKE EVKLSLFADDMIVYLENPMMSQ PKISLS**ANSAKSQDIKSMCKN LKHSYTLITDKQRAKSSVNSHS QLLQRE
12537	42905	A	12613	1	1765	
12538	42906	A	12614	1	2310	

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12539	42907	A	12615	1	836	MENEFDELTEVHFRRWVITNSS ELKEHVLTCCEEAKNLARRNK LENLEEMDKFLATYTFPSLNQE EVESLNRPTSSIEAAINSLPTK KHGPGDGTAKFYQRYKEELHI NRAKDKNHMIIISDAEKAFDKI QHPVKLIKILNKLGI DGTLYKIIIR AIYDKPTANLILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSL FADDRLYI*GTPLSQPKISLS** ATSAKSQDTKSMYKNHSHSYT PTTDKQRAKS
12540	42908	A	12616	355	4502	QSARFRGRRTLRRPGVGYSLVV *FEVR*CDASSFVLLA*DCLGN AGSFLVPYEL
12541	42909	A	12617	248	362	
12542	42910	A	12618	529	680	YYTRCSKWWNCVLP*YIYNF HLPHGKLKNTDYIKKKLHDFFF KNSKHI
12543	42911	A	12619	1	641	
12544	42912	B	12620	36	48	
12545	42913	A	12621	1	326	
12546	42914	A	12622	1	444	PGSTHASAHACERLQTRTLRAF SSQRRFPATASRASLSSNMAKIS SPTETERCIESLIAVFQKYAGKD GYNYTLSTKTEFLSFMNTELA TKNQKDPGCP*PHDGRKLGQPT VDGQLDFSEFLNLIGQAMAC HDSFLKAVPSQKRT
12547	42915	A	12623	2	6008	
12548	42916	A	12624	530	856	

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12549	42917	A	12625	1	952	MAARGTGDKVKPGCEEAGAAF ELPPSVYAAALHESHQHQPCPA GGARAQRVPGGIVTEPLCTTP KDMVFLSDDGDDDDDDNDND GGGDDDDNDGNDNDGNDNDGND DDGDDDDNDGDDDDNDNDGND NDGNDNDNDGDDDDNDNDND GGDDDDGVDGDDNDSDGNDG DDDDSDDDGDSNGYDDGDD GNDDDGDDSDDDSDNDGDD NGDGGDDGGGGDDDDNGHDD DGDMMMMIIVMMVMVMV MMVMVMVMVVVQLRKRAEA SVSEAKCSINVSDDNDGDDGND DGDGDDSDGDDDDGGDGGD SELTNQFPTNHSGMKASKLRK DSDHREW*W**WWWCN*GR EQRPVFLKQSAQLMSVMIMMM VMVMVMVMIMVMVMVMTMV VVMVVIVNSPINSRLITQA
12550	42918	A	12626	3	380	
12551	42919	A	12627	5	765	RQWEVGRWSGTTFSCFKKTL YFTNPSPSSSLVTVILRREVT CGGAPEQRYQIIPVCVAARLPT RAQDVLDAHLSEVNAVRFGN SSLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDFDPS VRNSAPVAVDCALSDLHTGQG YQVLAATYNQAAQLWKVGEA QSKETLSGHKDKVTAAKFKLT RHQAVTGSRRDRTVKEWDLGRA YSPKRQRPSTGHDDGGFVE KKRGKCGEKRDQIVTVSV
12552	42920	B	12628	1	2802	
12553	42921	A	12629	458	708	QNRHRHHGPFMSVAVSSQLLD TPAERLSLHTWKIAQRPGRGTP HFPDGA/VQAETLPQTGRPR GTPHFPDGAASSFGYCCLVA
12554	42922	A	12630	2300	6491	EGLEALIHQERLSYWANQVSED RPVCKAIQKQFEGLVDTGAD VSIHALNQWPKNWPKQKAVTG LVGIGTASEVYQSMELHCLGP DNQESTVQPMITSIPLNLWGRD LLQQWGAEITMAPLYSPTSQK IMTKMGYIPGKGLGKNEDGIK VPVEAKINQEREGIGYPFLGAV TVEPPKPIPLTWKTEKPVVWNQ WLPKQKLEALHLLANEQLEK GHIEPSFSPWNSPVFVIQKSKGK WHTLTDLRAVNAV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12555	42923	A	12631	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDKAKACRSIYPLH DVFVRKVVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
12556	42924	A	12632	1	642	
12557	42925	A	12633	260	534	
12558	42926	A	12634	1	438	
12559	42927	C	12635	391	750	
12560	42928	A	12636	199	451	
12561	42929	A	12637	120	992	RDRIPGPVCKGKWKNERILIFS SRGINFRTRHLMQDLRMLMPH SKVHDTNMARSDNLSVINEGCE MNNWLRCIYFEAKKKQDLYM WLSNSPDGSAKFLVQNIHTLA ELKMTGNCLKGSRPLLSDPAF DELPHYALLKELLIQIFSTPRYH PKSQPFVDHVFTTILDNRIWFR NFQIIEEDAALVEIGPRFVLNLIK IFQGSFGGPTLYENPHYQSPNM HRRVIRISTAAKYREKQVQKDV QKLRKKPEPKTLLPHDPAADV VTPAEKPIEQVVKPETKVDL KASV
12562	42930	A	12638	1	342	
12563	42931	A	12639	1	580	PGWEKMRSSS/GVNTQEALPT AAIPTDAKVRVYFNHITNASQ WERPIGNSSSGGKNGQGEPARV RCSHLLVKHSQSRPSSWRQEK ITRTKEEVALELINGYIQIKSGE EDFESLASQSDCSSAKA/RGD LGSFSRGMQKPF*RTPRFAL RTGGDERGPCFTD/SCIHIILPHL SEGKPRPLGAGQGG
12564	42932	A	12640	3	116	
12565	42933	A	12641	2	253	
12566	42934	A	12642	3	512	EDYLERKRQ/VPTQCQTHSKLG GPMTLKREVKP/KVDVSPSKKG PLQHIHTLLVCHVRIFYPGSIQ/ VRWFLNGRKKTAGVVSNNLIR NGDWT/FQILVMLEM/TPQQGD VYTCCQVHTSLDSPVTVEWKA QSDSARSKTLTGAGGFVLGLIIC GVGIFMHRSSKAFNEDLHKQG
12567	42935	A	12643	1	363	
12568	42936	B	12644	70	1229	
12569	42937	A	12645	1	430	
12570	42938	B	12646	1	1321	
12571	42939	A	12647	3	446	

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12572	42940	A	12648	1	417	
12573	42941	A	12649	269	452	TILRSFGYFFRRINIMLTEEKIKS DHRKISQLIFLQKLCQTLQSENV SQGGMLYRAKA*H*T*TLVVW *HVMSPYHKGLGLMLSLCSVK HSTLRDVFTL
12574	42942	A	12650	83	1385	
12575	42943	A	12651	1	974	MNPLECVDRSSQPWGNPTWTS SGMRSVTLVGVFKLTLFALAQT LNAAASLTGQELLAGFPFVGINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMKNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLKFANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCIGLQMGNTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGLPPCLGPSQE
12576	42944	A	12652	1	1103	MNPLECVDRSSQPWGNPTWTS SGMRSVTLVGVFKLTLFALAQT LNAAASLTGQELLWNFPLLMF AWKIAPALCCGNTVVIKPAEQT PLSALYMGALIKEAGFPFVGINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMKNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLKFANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCIGLQMGNTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGLPPCLGPSQE
12577	42945	A	12653	1	729	
12578	42946	A	12654	259	390	SFCSANFEVFRLLTAQQ*FVR*H ALSHIF*G*V*SFPKSTKRVNF
12579	42947	A	12655	68	735	
12580	42948	A	12656	1	825	
12581	42949	A	12657	3	470	
12582	42950	A	12658	1	1683	

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12583	42951	A	12659	1	1748	MNKPPIRNLSENAAPLDLEGIL KDAKIPVSGPFLVKIGYAFVDC PDEIWAALKAEIALSGKIELHGK IEVEHSVPKRQRIKQLQIRNIPPH LQWEVLDS*LVQYGVVESCQ VNTDSETAVVNTYSSKDQAR QALDK/LLDKLNGFLENFTLK VAYIPDEMATQQNPFQPRGR GLGQRGSSRQSGSPGVSQKPC DLPLCLLVPTQFVGAIGKEGAT IRNITKQTQSKIDVHRKENAGA AEKSITILSTPEGTSAAKSILEI MRKETQDVKFTTEIPLKILAQN NFVGRILIGKEGRNLKKIEQD TKITISPLQELMQYNPEHTITAK GNVETCAKAEIEIMKKIRER*E NDITSMN/LQAHLIPGLNLNAL GLFPPTSQMPPTSGPPSAMTPP SPQSEQSESETVHLFIPALSVRA LISKQGQHIKLSRFAGASSKIA PVEAPDAKVRMVMIAAGSPEAR FKAQGRIRYKIKKEENFVSPKEE VKLEAHIRVPSFAAGRVIGKGG KTVNELQNFSSAEVVPVRDQTP DENDQVVVKITGHFYACQVAQ RKIQEILTQVKQHQQKALQSG
12584	42952	A	12660	3	803	
12585	42953	B	12661	1	330	
12586	42954	C	12662	127	342	
12587	42955	A	12663	324	491	
12588	42956	A	12664	1	891	
12589	42957	B	12665	1	1869	
12590	42958	A	12666	2	136	
12591	42959	A	12667	108	355	
12592	42960	A	12668	2	811	FGMRGSRGGWAGEMAASGES GTSGGGSTEEAFMTFYSEVKQ IEKRDSVLTSKNQIERLTRPGSS YFNLNPFVQLQIDPEVTDIEIKK RFRQLSILVHPDKNQDDADRA\ QKAFAVDKAYKLLDQEQKK RALDVIQAGKEYVEHTVKERK KQLKKEGKPTIVEEDDPFLFKQ AVYQTMKLFALIEIKRKERE AKEMHERKKQREEEIEAQEKA KR/EEREWQKNFEESRDGRVD SWRNFQAQFRRGKKEKKNRTF LRPESKNGSNVE
12593	42961	A	12669	731	850	
12594	42962	A	12670	201	377	LMTLPCKIPSPGSSWLKISPIEHL MTPTPASQRTTPDCNFPLPTQI L*NGPTPISLH

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12595	42963	A	12671	742	2982	KIPFFDASFLPCLHKFNLKGGK NSKGFKMAEFESLMNIHGFDL GSRVMDLKLPGCGGNGLVFSA VDNDCDKRVAIKKIVLTDPSV KHALREIKIRRLDHDNIVKVFE ILGPSGSQLTDDVGSLETNSV YIVQEYMETDLANVLEQGPLLE EHARLFMYQLRLGLKYIHSAN VLHRDLKPANLFINTEDVLKI GDFGLARJMDPHYSHKGHLSE GLVTKWYRSPRLLLSPNNYTK AIDMWAAGCIFAEMLTGKTLF AGAHELEQMQLILESIPVVHEE DRQELLSPVPIRNDMTEPHK PLTQLLPGISREALDFLEQLTFS PMDRLTAEALSHPYMSIYSFP MDEPISSHPFHIEDEVDDILLMD ETHSHIYNWERYHDCQFSEHD WPVHNNFDIDEVQLDPRALS VTDEEEVQVDPKRYLDGDREK YLEDPAFDTNYSTPCWQYSD HHENKYCDLECSHTCNYKTRS SSYLDNLVWRESEVNHYEYEPK LIIDL SNWKEQSKEKSKDKKGS KCERNGLVKAQIALEEASQQLA GKERENKQGFDFDSFIAGTJHLA SSQHEPTDVGDKLNDLNSSVS QLELKSLSKSVSQEKQEKGMMA NLAQLEALYQSSWDSQFVSGG EDCFFINQFCEVRKDEQVEKEN TYTSYLDKFFSRKEDTEMLETE PVEDGKLGERGHEEGFLNNSGE
12596	42964	A	12672	826	1041	WKITVKGGVFLWWAGVGDTK VLSGGAF*ARMSQEEDFHKVM SSVKARTGHLHFFCGGMSSVK AGQGPFSVLL
12597	42965	A	12673	1	1482	
12598	42966	A	12674	3	488	
12599	42967	A	12675	2	114	

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12600	42968	A	12676	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSTIRRIIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSSDFCHWGQRFR YYSYDESQGEIY* SIEHLDKMG MSHIEQLDPVSFSNYLKKYHNNTI CGRHPIGVLLNAITELQKNGM NMSFSIFLNYAQSSQCARNWQD SSVSYAAGALT ^{TVH}
12601	42969	A	12677	2	114	
12602	42970	A	12678	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSTIRRIIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSSDFCHWGQRFR YYSYDESQGEIY* SIEHLDKMG MSHIEQLDPVSFSNYLKKYHNNTI CGRHPIGVLLNAITELQKNGM NMSFSIFLNYAQSSQCARNWQD SSVSYAAGALT ^{TVH}
12603	42971	A	12679	1	912	
12604	42972	A	12680	1	156	
12605	42973	A	12681	112	1120	
12606	42974	A	12682	33	415	NMNKPIPTSTYVRCLNVGLIRK LSDFDIPQEGWKKLAVAIKKPS GDDRYNQFHIIDAVPKTANTLP SKEAITVQKQMPFCDKDRTL MTPVQNLEQSYMPDSSSPENK SLEVSDFRHSFSFYELKN
12607	42975	A	12683	3	311	
12608	42976	A	12684	1	1125	
12609	42977	A	12685	1	1365	
12610	42978	A	12686	3	141	VVSTVVPDS/AHKLFIGGLPNYL NDDQCHGLSKGAFCEYVDIN VT ^V

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12611	42979	A	12687	1	1255	GTRSTSSLRRQMKNIHVHNYSEA EIKVREATSNDPWGPSSSLMSEI ADLTYNVVAFSEIMSIWKRL NDHGKNWRHVYKAMTLMLEYL IKTGSERVQQCKENMYAVQT LKDFQYVDRDGKDQGVNVRE KAKQLVALLRDEDLREERAH ALKTKKLAQTATASSAAGVS GPPPEAEQAWPQSSGEEELQLQ LALAMSKEEADQEERIRRGDDL RARRWQSRARRGLGARRSRPS WTLTSSRPQLLPRPQTGGAQ HPWLLPSPRLPPRTPGAAPLSL QLLIPGEVQPPRRPLGTGPGLLP LQDPQLTLGVGPQLQLGRGPR LIHGEVPMVGSRSVGPQPPIGH RPRPSQIPGEGHLPSPAPMAQQ QPGDSTRSPTSSLTLTDSARHCR PPGAAQESWSCWQERCPRPEAL
12612	42980	A	12688	116	1541	
12613	42981	A	12689	3	415	
12614	42982	A	12690	1	1440	
12615	42983	C	12691	117	314	
12616	42984	A	12692	3	120	
12617	42985	A	12693	1	729	
12618	42986	A	12694	79	870	EWSSVRRSLVEKRALRRPHPC LCFRMKTILSNQTCRPFPEINVD ITLKGRAVIV*GPAEGTLR\RDF \NHLQW*NLSLSWKEKKRGRS VDK\WWGNRKGNWPT\VRTYL VVHVQNMIKGVLPGLPVTKD EGLVYA\HFPHPTLVIPGRNGSS LLKSRNFLGVKNTSRRVSG*RP G\VACS\VSSSPRKDEFNPLKGN DIGACFQISAGFGFQQAPTHCL KTRDIQGNFWDGYPMVLWKK GTVSARAGWNKDLKEFTWATE RKMPG
12619	42987	A	12695	2	293	
12620	42988	A	12696	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPKIVLAT LKMS
12621	42989	A	12697	1	1308	

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12622	42990	A	12698	124	1135	DKNSMGLPGVIPSAAVLSWSI HLSSALSPITISACRHPMEDSM DMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTV SLGAGAKDELHIVEAEAMNVE GSPKIVTLATLKMSVQPTVSLG GFEITPPVVLRLKCGSGPVHISG QHLVAVEDEADESEDEEEEDVK\
						LLSISGKRSAPGGGSKVPQK\
						KLAADEDDDDDEEDDDDD
						DDDDDFDDEEAEEKAPVK\
						RDTPAKNAQKSNQNGKDSKPS
						STPRSKGQESFKKQEKTPKPK
						GPSSVEDIKAKMQASIA/EKGG
						LPKVEAKFINYVKNCFRMTDQ
						EATQDLWQWRKSL
12623	42991	A	12699	201	416	
12624	42992	A	12700	2	678	
12625	42993	A	12701	3	2149	
12626	42994	A	12702	1	219	
12627	42995	A	12704	267	437	
12628	42996	A	12705	507	845	
12629	42997	A	12706	426	704	SRRWGGVHSCPPSPPTAGHWT LLILCAKARRSEAAAMVLASRRR RPGPRPRRRRLPVLGSRGGAG PARGRGPGSGWGPLRAAPSP
						SSTV
12630	42998	A	12707	195	892	
12631	42999	A	12708	1	893	
12632	43000	A	12709	1	777	
12633	43001	A	12710	1	439	KTQVAPSTDGIQIPSSNSRTDE REFFIASYNRKKEDEGEGNVWIA KSSAGAKGEGILISSEASELLDFI DNQAQVHVQKYLEHPLLEPG HRKFDIRSWVLVDHQYNIYLY REGVLRTASEPYHVDNFQDKT CHLTNHCQKKKKK
12634	43002	A	12711	1	394	SGTRPVFLVPHTIGIPHPAIVTP QVQKEHPHTDSDLMHVQKQHE QRKEQEPKRPKPKPLNAFMLY MKEMRANVVAECTLKESAAIN QILGRRWHALSREEQAKYYEL ARKERQLHMQLYPGWSARDN
12635	43003	A	12712	1	789	
12636	43004	A	12713	1	870	
12637	43005	A	12714	1	729	
12638	43006	A	12715	1	828	
12639	43007	A	12716	1	213	
12640	43008	A	12717	1	664	
12641	43009	A	12718	1	695	
12642	43010	A	12719	96	269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
12643	43011	A	12720	3	241	
12644	43012	A	12721	213	660	EGPARHRLSPVRSKMTKKR RNNGRAQKRAARHVRGPSPLK/ CFPSGLPPNCAICVPKDKAIK KFVVRNIVEAAAR/DISEASV FDAYL/LPKL/YVKLHV/CVSCAI HKQK*SGNRSS*SPAKTRTPPR FR/PGG*LPHGPPTKSP
12645	43013	A	12722	1	303	
12646	43014	A	12723	610	928	FLSLPTFLFV/IFSGEELLVLALV FLSLFFFFFFLRWSEFVVAQAV/ VQW/INLSSLPFGKQFSCLSLP SSWDYRCPPPRPANCFITRDG VSPCCPGWSRTSDLR
12647	43015	A	12724	1	2775	
12648	43016	A	12725	1	6039	
12649	43017	A	12726	2	3661	
12650	43018	A	12727	1	1173	
12651	43019	A	12728	1	1632	MPNPKNSKGGRKNKRANSSGD EQENGAGALAAAGAAAGAAAG GALAAAGCGAAAAGAPGAG GAAGAGGAGTGAANAAAAAG AAAAGDAKNEAPCATPLCSFG RPVDLEKDDYQKVVCNNEHC PCSTWMHLQCFYEWESSILVQF NCIGRARTWNEKQCRQNMWT KKGYDL/AFRCSCRCGQGNL KKDTDWYQVKRMQDEKKKKS GSEKNTGRPPGEAAEEAKCRP PNKPQKGPSHDLPRRHSMDRQ NSQEKA V GAAAYGARSPGGSP GQSPPTGYSILSPAHSFGRSSR YLGEFLKNAIHLPEHKKAMAG GHVFRNAHFDYSPAGLAVHRG GHFDTPVQFLRRDLSELLTHIP RHKLNTFHVVRMEDDAQVGGQ EDLRKFILAALSASHRNVNCA LCHRALPVFEQFLVDGTLFLSP SRHDEIYDVPCHLQGRMLHL YAVCVDCLEGVHKIICIKCSR WDGSHWQLGTMYYDILAASP CCQARLNCKHCGKPVIDVRIG MQYFSEYSNVQQCPHCGNLDY HFVKPFSSFKVLEAY
12652	43020	A	12729	1	1485	
12653	43021	A	12730	1	1074	
12654	43022	A	12731	2	3394	
12655	43023	A	12732	1	2190	
12656	43024	A	12733	1	1251	
12657	43025	A	12734	1	1710	
12658	43026	A	12735	3	679	

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12659	43027	A	12736	209	337	
12660	43028	A	12737	365	538	
12661	43029	A	12738	2	196	
12662	43030	A	12739	1	2639	
12663	43031	A	12740	3	173	
12664	43032	A	12741	1	1479	
12665	43033	A	12742	1	921	
12666	43034	A	12743	1	798	
12667	43035	A	12744	2	773	
12668	43036	B	12745	75	321	
12669	43037	A	12746	321	738	
12670	43038	A	12747	1	3190	
12671	43039	A	12748	287	1636	ACGAMERAPPDGPLNASGALA GDAAGGARGGSAAWTAVL AALMALIVATVIGNALVMLA FVADSSLRTQNNFFLLNLAISDF LVGAFCIPLYVPYVLTGRWTFG RGLCKLWLVVDYLLCTSSAFNI VLISYDRFLSVTRAVSYRAQQG DTRRAVRKMLLVVWVLAFLLYG PAILSWEYLSGGSSIEPGHCYAE FFYNWYFLITASTLEFFTPFLSV TFNLSIYLNIGRRTRLRLDGR EAAGPEPPPEAQSPPPPGCWG CWQKGHGHEAMPLHRYGVGEA AVGAEAGEATLGGGGGGGSVA SPTSSSGSSRGTERPRSLKRG KPSASSASLEKRMKMVSQSFTQ RFRLAIRDKEAKSLAVIVSIFG LCWAPYTLMIIRAACHGHCVP DYWYETSFWLLWANSVNPV LYPLCHHSFRRAFTKLLCPQKL KIQPHSSLEHCWK
12672	43040	A	12749	1	2142	
12673	43041	A	12750	3	711	VWWSNDLMVINRSTTELPLTV SYDKVSLGRLRFWIHMQDAVY SLQQGFSEKDADEVKGFVDT NLYFLALTFVAAFHLLDFDLA FKNDISFWKKKSMIGMSTKA VLWRCFSTVVIPLFLDEQTSLL VLVPAGVW/AAIELWES*/RK/ VI*RWITIFWRGLMPEFQGTYS ESERKTEEYDTQAMKYLSYLL YPLCVGGAVYSLNLIKYSWY SWLNSFVNGVYAFGLFMLPQ
12674	43042	A	12751	1	2025	
12675	43043	A	12752	494	747	ATVKWITLCNRNRIKLPFIKKE GTGKAPKSRKSVLGLGP*VHT SPGDPAEGEGLPAGERPDGNLS QSPNSLRFYIKKKKAYK
12676	43044	A	12753	9	731	

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12677	43045	A	12754	143	641	RSWVLLGVGARGSTPRTYQVP SPSLAPSALC*VS*VPLESLSCH ADNWKQELTKFISPDQLPVEFG GTMTDPDGNPKCLTKINYGGE VPKSYYLCKQVRLQYEHTRSV GRGSSLQVENEILFPGCGCLRVL RFYNTYSLVHSKRISYTVLELL PDQTFMEKMEKF
12678	43046	A	12755	1	1506	
12679	43047	A	12756	2	526	CQPVRAA*RHGNTPLATV*PAS T/WWWSEKQKEEQEMQNW ESAS/VSGYPDILSCAMSONPR KRRKPRNVSAAPPVHQAQMNI SVEQMETSQTHQATPLTWGQM KRLAHVAEENLRSONKPLTTSN LMVAMMVVISLAVSLPVAGAD QNYIYWAIYIPFPF
12680	43048	A	12757	1	1443	
12681	43049	A	12758	3	766	
12682	43050	A	12759	29	253	
12683	43051	A	12760	34	252	
12684	43052	A	12761	1362	1611	SSVLHPWDARLVQHTKSIHH HINRTNDKNHMIISIDAFAFD KIQQDFMLKTLNKLGDGTLYK IVRATYDKPTASILNG
12685	43053	B	12762	1	1755	
12686	43054	A	12763	1	2109	
12687	43055	B	12764	1	1497	
12688	43056	B	12765	1	1527	
12689	43057	B	12766	1	1746	
12690	43058	B	12767	1	2853	
12691	43059	B	12768	1	1479	
12692	43060	B	12769	1	1932	
12693	43061	A	12770	1269	1581	NTGKPNPAAHQKGYPPRSSGPH PWDARLVQHTKSIHHHINRT KDKNHMIISIDAFAFDKIQLPF MLKTLKSLGVSYNMFRTLTIPI AQVDTRGNQLPSYLI
12694	43062	B	12771	1	4404	
12695	43063	B	12772	56	2080	
12696	43064	B	12773	1	5445	
12697	43065	B	12774	295	2831	
12698	43066	A	12775	89	459	
12699	43067	A	12776	2	980	
12700	43068	A	12777	1	378	
12701	43069	A	12778	1	363	PGVALPGRRCRQAPADLLP*MR AYWPDVIYSFANRSRFBKHEW EKHGTCAAQVDALNSQNYFG TSLELYRELDLNSVLLKLGKPS INYYQVADFKDALRNVYGVIP KIQCLPPSQDEDRQ

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12702	43070	A	12779	1	577	QRFKNDRCRDPRTGPIHGLWPD KSEG/CNRSW/PFNLEEIKDLCP EMRAYWPDVIHSFPNRSRFWK HEWEKHGTCAAQVDALNSQK KYFGRSLELYRELDL/NQVADF KDALARVYGVIPKIQCLPPSQD EEVQTIGQIEICLT.KQDQQLQN CTEPGEQSPKQEVWLANGAA ESRGLRVCEDGPVFYPPPKTK
12703	43071	A	12780	1	624	MRPAALRGALLGCLCLALLCL GGADKRLRASVSRPFSLEHPEP GHCLDLHLRAYPAR/WSS*PWP QDFWVR*PTWES/VSDLLPEMR AYWPDVIHSFPNRSRFWKHEW EKHGTCAAQVDALNSQKKYFG RSLELYRELDLNRGERVPTQFP RELVVNRSLAPPTPGFLSGHVI SVHTSSPLPSAMSGSFLRPLPEA ESGMLLGQPADP
12704	43072	A	12781	1	612	
12705	43073	A	12782	113	1149	RGAPRGPGRQGCCGHSRSPAR GPRDTGLGRPRAPGAPGGRCCS GGSAARAAGLGDVSPGSLPRAA GGKWEPERQLAAFSQVGTMR PAALRGALLGCLCLALLCLGG ADKRLRDNHEWKKLIMVQHW PETVCEKIQNDCRDPDPYWTIH GLWPKDSEGCNRSW/PFNLEE KDILLPEMRAYWPDVIHSFPNRS RFWKHE/WPKRHGTCAAQVD ALNSQKKYFGRSLELYRKLDL NSVL/LKLGKPSINYQVADFK DALARVYGVIPKIQCLPTSQGE EVQTIGQ/IDLCLIKARTQLQN CTEPGEQSPKQEVWLANGAA AESRGLRVCEDGPVFYPPPKKT
12706	43074	A	12783	2	515	
12707	43075	B	12784	62	359	
12708	43076	B	12785	219	523	
12709	43077	A	12786	1010	1550	DTENIPSSRRRERSKVPYIVRQC VEEIERRGMEVGYHVSGR/V AADIQALKAAFNVSECRPAQD GMEVWAVVSAMRSQSA PRPRH VTSFSVSFLHLGSSRRPLHFRA LSNNKDVSVMMSEMDVNAIA GSLKLYFRELPFLTFDEFYPNF AEGIGEHWRPWP HGRRLLVH CCPQRL

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12710	43078	A	12787	2	951	GSNLYCTLEGDSFGYFVNKAK TRVYRD/THADPNWNEEFIEL EGSQTLRLCYEKCYNKTKIPKE DGESTDRLMGKGQVQLDPQAL QDRDWQRTVIAMNGIEVKLSV KFNSREFSLKRMPSRKQTGVFG VKIAVVTKRERSKV/PYI/VRQC VEIEPPKALEGGWASTACPAG VATDIQALKAADFNNKDVSV MMSEMDVNAIAGTLNLYFREL PEPLFT\DEFYPNFAEG/IRVAEK EAVNNM/SLIINLATVFGPTLLR PSEKESKLPANPS/QPITMTDSW SLEVMQVQVLLYFLQLEAIPA PDSKRQSILFSTEV
12711	43079	A	12788	3	644	
12712	43080	A	12789	168	378	
12713	43081	A	12790	1	486	
12714	43082	A	12792	83	536	
12715	43083	A	12793	1	662	
12716	43084	A	12794	3	357	
12717	43085	A	12795	2	421	
12718	43086	A	12796	2	908	
12719	43087	A	12797	1	846	
12720	43088	C	12798	87	413	
12721	43089	A	12799	1	508	MCQGDYAWGGHMCRRGHLR RGHSHERDTPRGPERPPRPAR DRESKDERRRPPPKDPPAVRT\ PDSPTATPPPPPPPPPPPPPPPP PAAPSAFAALRLRGPGRKWT RGQLPLPATAPPEARVRALPRGG YSSPGRATSARGAPWPLPSRT GKPPRPCSANTQEHC
12722	43090	A	12800	1	393	
12723	43091	A	12801	1	582	
12724	43092	A	12802	1	1422	
12725	43093	A	12803	1	1080	
12726	43094	A	12804	2	261	SCPFGGNCFYKHAYPDGREET QRQKVGTTSSRYAQRNRHFW LIEERENSNPFDNDEEVVTFEL GEMLLLMLAAGGDDDELNTS
12727	43095	B	12805	60	802	
12728	43096	A	12806	2	238	
12729	43097	A	12807	1	1017	
12730	43098	B	12808	1	939	
12731	43099	A	12809	1	708	

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12732	43100	A	12810	1	2653	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDYRNHLP ESTEYTFPSAPHHTYSKIDHILG SKAPLSKYRSEIKINCLSDHSA IKLELRIKKLTQNRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDDTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLARLIKRR EKNQIHAIKNDKGMSTNHTIEI QTTIREYYKHLANKLENLKEI DKFLETYSPLNQEEVESLNR PITGSEIEAIIISLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSEL PFTIASKRMKYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNI PCSWVGRINIVKMAIL PKNWKKTTLKFIVNQKRARIA KSILSQKNKAGGIMLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEIMPHIYNHLIFDKPDK NKKWKGKDSL FNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK DLNVRPKTIKLTLEENPGNTIQDI GMGEDFMSKTPEAMATKAKID KWDLIKLSFCTAKETTIRLNR PPTEWEKIFAIYSSDKGLISRIYN ELQQIYEKKTNNPIKKWAKDM NRHLSKEDIYAAKRHMKKCAS
12733	43101	B	12811	1	2748	
12734	43102	A	12812	1	1962	
12735	43103	B	12813	1	1833	
12736	43104	A	12814	176	421	QQPASPTRSVLLFPKTAHISGSP APPNVGLLNPSTGAQKKTMT SAGLGRLSL*K*LNLPCEVACA GETWVTSMMSGNQCN

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12737	43105	A	12815	1	1615	LISNFSKVSGYKINVQKSAFL YTNNRQTESQIMSELPFTIASKR MKYLGIQPTRDMKDLFKENYK PLLNEIKEDTNKWKNI PCSWVG RINIVKMAILPKNWKKTTLKF WNQKRARIAKSILSQKNKAGGI MLPDFKLYYKATITKTAWYWW QNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGDLSFNK WCWENWLAICRKLKLDPLTP YTKINSRWIKDLNVRPKTIKTL ENPGNTIQDIGMGEDFMSKTPE AMATKAKIDKWDLIKLSFCT AKETTIRLNRPPTEWEKIFAIYS SDKGLISRUYNELQYIEKKTNN PIKKWAKDMNRHLSKEDIYAA KRHMKKCASSLAIREIQIKTTM RYHLTPVRMAIKKSGNNRCW RGCGEIGTLLHCWWDCCLVQP LWKS VWRFLRDL EIPFDP AIP LLGIYPKDYKSCCYEDTCTHMF IVALFTIAKTWNQPKCPTMIDW IKKMWHIYTM EYYADIKKDEF MSFVRTRMKLETIILSKISQIEK KTKHRMFSLIGGN
12738	43106	A	12816	1	996	
12739	43107	A	12817	1	756	
12740	43108	A	12818	1	1428	

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12741	43109	A	12819	1	2377	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPMGQWGFNIRKSI NIVQHNRTNDKNHMIISDAEK AFDKIQQRFMLKTLNKLIGIDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTTRQGCPSPLLFNIV LEVLAIRAIQKEFIKGIQRKFE IKLSLFADDMMVHLENPIVSAQN LLKLIDNFSKVSQKINVOQSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGIGLTRDVKDLFKEN YKPLNDIKEDTNKWNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIVN QKGARIAKSILYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKGWNGDS LFNKWCWENWLAICRKLKLDLP FLIPYTKINSRWIKDLNVRPKTI KTLLENLNGTIQDIAMGKDFMS KTPKAMATKAKIDKWDNLNLK SFCTAKETTIRVNRQPIEWEIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSLAIREMHI KTTMRHHLTSVRMAIIKKLGN DWCWRGCGEIGRLLHCWWD KLVQPLWKSVMWFRFLRDELET PFDPATPALLGIYPKDYKSCCYK DICT/RVCVPAALFTIANTWNPT
12742	43110	A	12820	1	4840	
12743	43111	A	12821	578	630	EYKNR*GLSLNPWGKTVHISW DVWSVGSSKAKRNWESWES*C RGIQKASLSRSTGNHSASSGI* ESRV*GLGTTGYRGITASLSML RSCTRLH
12744	43112	A	12822	8	214	EEWPKRKSEIRERPRP*SWPSDK QTLVVQRGQKMEQANHPDPTD HMSQLMWTACPKGLGIALICL VRH
12745	43113	A	12823	33	240	GGGRTNLQAVPGFPGW*RTL RTAVWDRRLTLRKP HHCPGGS QFPGPQRQVIGLLHLFSSLNHQ GWFV

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12746	43114	A	12824	1	411	MSTITQRKEENPSVFLEWLWEA /CKKIYSPVTRLTRGSDPKR*V YYAISHRYQQKAPKPSGPG*TK SGGIIKPGNLGVLY*GPRGTGQ KGKARSEKGCSSLHGPTQNK WWFREDRKWSRPITWYGFSLV WFARTP
12747	43115	A	12825	1	611	
12748	43116	A	12826	120	493	KYRAQRMMIARWLPQDLERGE AMLPNSSGWYKSLKGI/VLISEA FSCCKRAASLTADWL*VKQHS SPKKVQSPFSAVRRSKPWQFW RVTAAKQSIWDCRVRFIDVISC KLRLPLRVCGSRILK
12749	43117	A	12827	1	2195	VGEEGPAGVEGLNFFPAQSRRLP GPQQCSPGAEGGASARARRPRP RPRPAAAMVPGVPGA/VLTCLW LAASSG/SWRPAPARL/CAAAG RVAVCRERPARS/CASRCLSLQI TRISAFFQHFNNGSLVWCQNH KQCSKCLEPCKESGDLRKHQ QSFCEPLFPKKS YECLTSCEFLK YILLVKQGDCAPEKASGFAAA CVESCEVDNECSGVKKCCSNG CGHTCQVPKTLVKGVPLKPRK ELRFTELQSGQLEVKWSSKFNI SIEPVIVVQQRWNYGIHPSED DATHWQTVAAQTTDERVQLTDI RPSRWYQFRVA/VNVHGTRGF TAPSKHFRSSKDPSPAPPANLR LANSTVNSDG/AV*TVTIVWDL PEEPDIPVHHYKVFWSWMVSS KSLVPTKKRKRKTTDGFQNSVI LEKLQPDQDYYVELQAITYWG QTRLKSAKVS/LHFTSTHATNNK EQLVK/ITRKGIGITQLPFQRRRP TRPLEVGAPFYQDQQLQVKVY WKKTEDPTVNRVHVRWFPEAC AHNRITGSEASSGMTHENYIIL QDLSFCKYKVTVPQIRPKSHS KAEAVFTTTPCSALKGKSHKPI GCLGEAGHVLKSLVAKPENLS ASFIVQDVNITGHFSWKMAKA NLVQPMTGQVTVAEVTTESR QNSLPNSHSQSLPSDHYVLT PNLRPSTLYRLEVQVLTGEGG
12750	43118	A	12828	1	1410	
12751	43119	A	12829	2	299	
12752	43120	B	12830	81	510	
12753	43121	A	12831	3	436	
12754	43122	A	12832	1	769	

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12755	43123	A	12833	15	413	ERM CAGPWRKGAETGPYFCND TVRHRKASLLCPF*RMNGDQN SDVYAQEQDQFVQHFSQIVRVL TEDEMGHPEIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFRELE VEPRKQDADSLQRAWTVGWC VELLQA
12756	43124	A	12834	1	795	MNGDQKSDVYAQEQDQFFQH SQIVGVLTEDEMGHSEIGDAIA RLKDVLEYNAGGKYHRLGLTV LVAFQELDAINYAILLEACIYYL LKLYCQAQPYLYNLIELFLQISC QPEIGQTLDLITAP/QDNVDFGR FT/EKQHANA*KILLEI/GEFFQI QDGYLDLFGDPTVTRKVGTDIQ DNKCSWL VVQCLQRSTLEQYQ ILKENYGGKKAKKV VQVKALY EELDLPVFLQY EEDGYSHIMG LTEQYAAPLLPAMFLGLVYKIY
12757	43125	B	12835	1	328	
12758	43126	A	12836	2	868	
12759	43127	B	12837	118	1138	
12760	43128	A	12838	100	374	KHISPALKALELPFERNLI/PLQ LLKVRILKEGEM/LDI*HWFL** GMGT VQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV
12761	43129	A	12839	1	1035	
12762	43130	A	12840	13	600	INPPPPFRPELPSSNSPKMTDH KGERGEATRYMFSRPFKKTMG VVPLGHNN*RFYKKGDDIVD/IK GMGYCVQNGMP/HKCYWPVKL EGVLQLLPQHA\VAIVVNQPV GQSFFPRE*IVRIEHIKHF*EPEIS FLK/RVLKENDSEKERSPNEKG TWGSNLKRILAPPQKKHTL*R TNGKEPELLEPIPEFHGHN
12763	43131	A	12841	1	317	QRPSEAKEIKLYAQIPPIEKMDA LSMLANCEKLSLSTNCIEKIAN LNGLEAVGDTLEELWISYNFIE KLKGIHIMKKLILYMSNNLVK DWGTPVIKGDDEEDN
12764	43132	A	12842	155	588	
12765	43133	A	12843	1	954	
12766	43134	A	12844	1	486	
12767	43135	A	12845	1	367	
12768	43136	A	12846	1	190	LISRAKEDMTLNIAEGVHPSY NIVLNTLHTCGISVKSTWRPSK GAAP*ARMPGGTAGPCLAS

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12769	43137	A	12847	1	2376	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFNDRDAVSRKENGKENG GQARRYADLFSRTKKNYPVQD LRLHQAQLTFHPTVNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA/WQQLPC*YKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
12770	43138	A	12848	1	636	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFNDRDAVSRKENGKENG GQARRYADLFSRTKKNYPVQD LRLHQAQLTFHPTVNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA/WQQLPC*YKKQIS
12771	43139	B	12849	180	811	
12772	43140	A	12850	1008	1265	FLGVPTLGGWRPIQHRLK/PRE VTPVLLRDLIRRFPLWIGSDN GPAFLAALVQKTAQGIQNNITG GVYTLCDIDSHILFRSGY
12773	43141	B	12851	1	996	
12774	43142	A	12852	1251	1424	DSPRGEAES*A*LPEKLEMSG NRLVDNKDPGKKQTQRRIPHSP SQIPVPLPEIWCT
12775	43143	A	12853	1	1121	
12776	43144	A	12854	189	621	
12777	43145	A	12855	2207	2308	
12778	43146	A	12856	1	762	
12779	43147	A	12857	1	678	
12780	43148	A	12858	3	496	
12781	43149	A	12859	107	258	NALGKRSTFTNRNFLASGRFLD SVTYARRLQYQYAPAL*KTAI*SF SLLNH
12782	43150	A	12860	2	410	SPDPVWVSTYKSTCHIAQEAKEI HLRNQYERKGE*APRSNLMSE DANGGAPNPWFEEPEETIGW GFDEIRQQQHNIIR*QDAGLDA LSSHSRQKQM/GIEIGNELHEQN EIHDDLANLMENTDEKLRNETR RVN
12783	43151	A	12861	3	1402	

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12784	43152	A	12862	1	711	MAPDPWFSTYDSTCQIAQIEAE KIQRNQYERKGEKAPKLVTVI RALLQNLKEKIALKDLLLRAV STHQITQLEGDRRQNLDDLVT RERLLASFKNEGAEPDLIRSSL MSEEA KRGA PN PWLFEEPEETR GLGFDFIRQQPKINQEQDARL DALSSIISSQKQ/MGQIEGNELD EQNEIIDLANLVENTDEKLRN ETRRVNMVDRKSASCGMIMVI LLL.LVAIVVVAVWPTN
12785	43153	A	12863	1	936	
12786	43154	A	12864	1	1023	
12787	43155	A	12865	1606	2238	
12788	43156	A	12866	3	347	
12789	43157	A	12867	1	1665	
12790	43158	A	12868	1	589	
12791	43159	A	12869	19	1677	
12792	43160	A	12870	1	906	
12793	43161	A	12871	1	228	
12794	43162	A	12872	1	320	
12795	43163	A	12873	1	398	TSKAPGAQGEQGFEECLAVAL AGRPLPSLWALFQATTPVLQ LKEAFFRPEVPLRRDLPLLLFR TQTSDPAMLPTMIGLLAEARR AGCLSYQTSLSVDGETWHVMG ISSLLPSLEGWKQHVTEAFQF HF
12796	43164	A	12874	3	322	SAGGSGRRTLHSRTMAQFVRN LVEKTPALVNAAVTYSKPLRAT FWYYAKVELVPPTPAEIPRAIQS LKKIVNSAQTSFKQLTVKVTT G*MKT DVHNRKCLPLGFF
12797	43165	A	12875	91	425	WTFHPTTMAPFVRDLGEKTPA LGKAAVTVLKPRLAAFWYYH QVELVPPTPAEIPRAIQSLKKIV NSAQTSFKQLTVKEAILLNDL VATEVSTWFYVREITGKRGIIG* NV
12798	43166	A	12876	179	664	HSSPAVPGRTDFSHSQNPWPQF CPVTLVGEDPRALVNAAVT/YT RKPRIGLHFYYA/KVELVPPT PAEIPRAIQSLKKIVNSAQTTG LANSSHVKEA/VL*NLVATEV LMWFLCSERLLGKRGHSLGYG CFEDQSFNIIWILFILELFVW DHVDPDC
12799	43167	A	12877	25	164	
12800	43168	A	12878	2110	2260	
12801	43169	C	12879	32	1429	
12802	43170	A	12880	172	322	

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12803	43171	A	12881	1060	12039	
12804	43172	A	12882	1	810	
12805	43173	A	12883	3	146	
12806	43174	A	12884	1	1211	GPQDGNQQAPPEKVGWVRKF CGKGIFREIWKNRYVVLKGDQ LYISEKEVKDEKNIQEVFDLSD YEKCEELRKSKSRSKNHKFT LAHKKQPGNTAPNLIFLAVSPEE KESWINALNSAITRAKNRILDE VTVEEDSYLAHPTDRRAKIQHS RRPPTRGHLMVA VASTSTSDGM LTLDLIQEEDPSPPEPTSCAESFR VDLDKSAVQLAGSRRRADSDRI QPSADRASSLSRPWEKTDKGAT YTPQAPKKLTPTEKGRASLEEI LSQRYAASAHTLQLRAEEPPTP ALPNPGQLSRIQDLVARKLEET QELLAEVQGLGDGKRKAKDPP S/RSPDPSES/EQLLETER/LLG EASSNWSQAKRVLQQVRELRLD LYRQ/MDLQTPD/SHL/RQTTPH SQ/YRKSLM
12807	43175	A	12885	617	1041	TTLINPGGPAPLLSLPTSSITGFT TFYHPNLKPLRTCPSPVQAWPC RHP1*SRDYQRDAEPTTCISKLL GENIRRDDEFWKVQIKARSGETE QNPRSTAFAGELPLANREELN LLLNKGILPLCDQRQEIESECAF TIFCAGDANCFFPSPHTLPLTAL QQRPCGLSGSASKEAWGNSLV CGPRGDTLPMAIAKPHRSASKH STLHQYPTPPRSLCHQHRDEQP TNHLQTLNTIPA WHITKWVPL DHINKPWRS CSSQSAYLFYHW LHYFLPPKLKTSKDL SILSAGLA MSAPHILFRVSAITNSNCKPSS TSKACEELFKHQCLGSTDIPHI IQGGAPFSAVSPQRLVLRGSQD GSHMVRPRLPPFDSAGLANFHL FSKFLD
12808	43176	A	12886	1	606	
12809	43177	A	12887	174	350	VSWRFVQVFI*VAGGSRICAAA GLSPGTPPCATSLIGACSLIFIP RLLSLFCGDEAL
12810	43178	A	12888	3	265	
12811	43179	A	12889	1	1209	
12812	43180	A	12890	53	369	VAHQEKGIAEPLRPTGDSRQT HRRLDVERSTSVQEHMGGCHF SPFPEREKLSTLRGIHQAPAL WQATDQWIDIEF/GLGQPEESL GR*ITRLQGGKTLFPFGSPIC

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12813	43181	A	12891	1	345	
12814	43182	A	12892	2	451	
12815	43183	A	12893	2	286	
12816	43184	A	12894	217	1071	GENPRSENTRLATILEVACCHF GSSPPPSIGSSGRKDPPLTFGDH EGTSKAEPSPALGLTPEHKGNV GHAARIQQPGPLSLWSRKAGK GVQDCYIDLKQIKIDLDFSDN PDGYIDVLQGLGQSFDTWRNI MLLLNQTLTPNERSATTTAARE FGDLWYLSQVNDRIAAEKREK FLTGGQAVPSVSGSIHWDTESEH GDWCCRHLITCMLEGLRKRTRK KPMNYSMMSTITQKKEENPTA FLERLREALRKHTSLSDSIEGQ LILKDTFITQSAADIRK\NFKSPP
12817	43185	A	12895	1	756	
12818	43186	A	12896	473	1015	
12819	43187	C	12897	152	322	
12820	43188	A	12898	146	1079	PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAPWKIPFLGIREAKN PRSENTRLATILEAGHRHLGTS VSKDHPVTFWRPRRDLQSDLK QIKIDLKGFSDNPDGYIDVLQEL GQSFDTLWRDIMLLLNQTLTPN ERSATITAAREFGDLWYISQVV AAVAGLVSEAVKIIQGSYCVDI HDVNGILTAKGDLWLSDNHLL KYQALLLEGVPLRLRATCATLNP ATFLPDNEEKIEHNCCQVIAQT
12821	43189	A	12899	189	1798	

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12822	43190	A	12900	194	1729	NPAAQTFFVVKKGGRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSSPCNTPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEAEWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVL PQGFRDSLH LFGQALAQDLSQFSYLDLTVLQ YMDDLLLVTHSETWCHQATQA LLNFLATCGYKVSQKNAQLCS QQVKNLGLKLSKGTRALSEERI QPILAYPHPKTLKQLRGFLGITS FCRIWIPRIKAVKLQILQMEPQ MQSMTKIYHGPLDRPTSPSSNV NDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAAP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPIN*SMISTI TQKKEENPTAFLERLREALRKH
12823	43191	A	12901	1	642	
12824	43192	C	12902	54	254	
12825	43193	A	12903	32	221	NGVGHNRMTNGSGGGGEWGP PAPASA*GCSLASAFASAPRW WFEMGCRGIYDAQVALSRSF
12826	43194	A	12904	203	538	
12827	43195	B	12905	131	536	
12828	43196	A	12906	1	1251	
12829	43197	A	12907	38	475	ESERRGEFCLCKIIEQGRVAVCV EDEQTSHFALTGNNGIYRKSSQ QWQQLSDLARDPPAQCSAGP VGDDMFHWQATIMGPNDSPYQ GGVFFLTHTFPTDYPFKPPKVA VTTIRIYHPNINSNGSICLDILRSQ WSPAFNQFPKSS
12830	43198	A	12908	282	849	QSCPAAGIISFGRTFEHTPREV RKPDCKHTLLALKRINKDLSDL ARDPPAQCSAGPVGDDMFHW QATIMGPNDSPYQGGVFFLTHT FPTDYPFKPP*GLHFTTRFYHP VINSKWAACFLRYS*DSQWSP ALTFKVLLSICLLCDPNPD DPLVPGDWHGYS*NRGTGDKYN RISREWTKQYAM
12831	43199	A	12909	1	397	
12832	43200	A	12910	245	535	
12833	43201	B	12911	68	333	
12834	43202	A	12912	265	562	

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12835	43203	A	12913	1	872	MVNTCEQLDWIEGCKVLILGVS KEASQGLGGRSRGRNVQRSTD ADIRPTSEKDARSLMTTRQEDN ISVDQRGFLSGVQKKGSCANGL KGSVCGGFYVWMAVIRMGVG KAMGLNLKLGKFEIKKGYLKG CRDSLRLSPTGFGKFTATSHV AATVPKVVLELTLQTHKILRG VFAHLTSLQLHSLPPGSSMDS AKARRQLQVAGQGHSLVKQK GFHVEAPDHHVPQLSDISCKSY RWGHKLIKINFLIPPLWYYDL EEVKREQSEKQQAQIMADIIIG DALNAQKAFKGNPKGHKPLPF SAGQMENW*CCECPKSI
12836	43204	A	12914	7	231	
12837	43205	A	12915	1	223	MEILITCDKGLIFTGNTRKSETS TSECTCPDLINCSLSHSPSPSDE ETQHHTDLSLHVRPRKGYLLCIY HIPDIVAVMVNIQCQLDWIEGC KVLFLGVSVKVLPEINTGISGL GKADPPSIWKS*QHVTKDLYLQ VILENQKLVANALVRWLTVP FPTLLRALQMRKHSTTLTVCMS DRGKDICYCASTIYQI
12838	43206	A	12916	1083	1273	NKMSFKLKEDCFGRSKCNLT* CWKSINEA*/K/DLELQLQFGPQE KLFALEQQVKKKLNLPDA
12839	43207	C	12917	1	1506	
12840	43208	A	12918	3	1219	
12841	43209	A	12919	1	735	
12842	43210	A	12920	2	94	
12843	43211	A	12921	362	460	WLILSVNLIGLKDAKYCSCVCL *GCCQRRLTF
12844	43212	A	12922	1235	1474	
12845	43213	A	12923	1	250	
12846	43214	A	12924	1	261	
12847	43215	A	12925	2	85	
12848	43216	A	12926	1	291	
12849	43217	A	12927	1	321	
12850	43218	A	12928	1	370	
12851	43219	A	12929	1	684	
12852	43220	C	12930	1	210	
12853	43221	A	12931	2	91	
12854	43222	A	12932	1	243	
12855	43223	A	12933	2	353	WMKLETHLSKLS*GQKTKHRM SSLIGSTDQQLRVVKNVQGRVC PGSTGHGAWEAWTAMRKVDS PLQTGSLRPGWCRQVGSNARS GSAEAGNPGIHPGICPRVEDG IQVAENFFEV

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12856	43224	C	12934	1	289	
12857	43225	A	12935	1	1194	
12858	43226	A	12936	140	237	
12859	43227	A	12937	1	292	
12860	43228	A	12938	2	178	
12861	43229	B	12939	1	1245	
12862	43230	A	12940	2	241	
12863	43231	A	12941	1	675	
12864	43232	A	12942	1515	1920	TPTNLQEKNKQPHQKVGEGYE QTLKRRRLCSQKTHGKNAHH HWPSEKCKSKPQWIPSIHQLE WQSLKSOETTGTWWMKLETHLS KLLQGQKTKHHMFSLIGGNRT RRTHGHRKGNITLWGLSDSV NCASSG
12865	43233	A	12943	608	891	
12866	43234	A	12944	1	3956	MGSCPGGFTAIFYQRYKEELVP FLLLKLFQSEKQGTLPNSFYEAS IILIPKPRDRTTKENFRPISLMN IDAKILNKILTNRQQHIKKLIHH DQVGFHGMQGWFNIRKSNVI QHINRTNDKKHMIISDAEKAF DKIQPFMLKTLNKLGTWWMKL ETIILSKRSQGQKTKHRMFSLV NIIPITIKILKQNMAMETLCPIF KLEGDTMDNPIANRRVRTAVP TSVVCLHVGTEPEARLPHGPMI TAQSPFG
12867	43235	A	12945	1	855	
12868	43236	A	12946	1	255	
12869	43237	A	12947	273	3484	
12870	43238	A	12948	3	377	
12871	43239	A	12949	85	333	
12872	43240	A	12952	22	308	
12873	43241	B	12953	30	383	
12874	43242	A	12954	3	448	
12875	43243	A	12955	1	453	
12876	43244	A	12956	3	491	
12877	43245	A	12957	2	749	
12878	43246	A	12958	155	637	
12879	43247	A	12959	1	510	
12880	43248	A	12960	2	559	RPHASAHASGRQSQDVTTMV WALLLLTLTQTGTGSAQSAL TQPPSASGSPGQSITISCTGLIND VASYNFVSWYQQHPGKAPKL MIYEVTKRPSGVPRDRSGSKSG INTASLDHLWGSRLDEADYYC LLICRRLHPGGIRRDWRPRTV LGSAQRPTPTVTSGSRPSSEGAP SQQGHTSVSDQ

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12881	43249	A	12961	1	1958	MSVQRKDRVRTQQGGSVASSM LTQEPVGSVALGQSARDRDPD CSDSVSVYLMMDTWQSVIIGFAE SAATLGDPPELPMHPEGSEASY ELTQPPSVSVSPQGTARITCSGD ALPKQYAYWYQQKPGQAPVL VIYKDSERPSGIPERFSGSSGTT VTLTISGVQAEDEADYYCQSAD SSGTYPTVTQADRETPTHQYSR HPSYAKGFVFLWGSWAQSALT QPASVSGSPGQSITISCTGTSSD VGSYNLWSWYQQPQKAPKL MIYE/VDSKRPSGVSNRFGSKS GNTASLTISGVPGLRDEGDDY CCSYAGSVASYELTQLPSVSVS PGQTARITCSGDVLGENYADW YQQKPGQAPELVIYEDSERYPG IPERFSGTSGNTTTLTISRVLTE DEADYYCLSGDEDNPSVTQAD GEDTGIRSHYEGTLALYLYPEP VKATCSVTSYVLTPPPSVSVAP GQTARITCGGNNIGSKSVHWY QQKPGQAPVLVYVDDSDRPSGI PERFSGSNSGNTATLTISRVEAG DEADYYCQSLSTLGPCTLGDTV LRPMIYSVSIQASGVDPGFSGSK SGNTASMTISGFQAEDEADYYC NSHRRGSVVSSELTDPAVSVA LGQTVRITCQGDLSRYYASW YQQHPGKAPKLIYDGH
12882	43250	A	12962	2	367	
12883	43251	A	12963	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12884	43252	A	12964	2	1178	
12885	43253	A	12965	1	732	
12886	43254	B	12966	99	716	
12887	43255	A	12967	1	1011	

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12888	43256	A	12968	3	1263	GRTIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERSAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTQRYSS RRATPRHIVRFTKVEMKEKMG LLVPNWTNHSPLFRAILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSPGPGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQERQRTQRY YSSRRATPRHIVRFTKVEMKE KMLRAAREKGRVTLKKGPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTTPALKELL KEALNMERNNRYQPLQNHAK
12889	43257	A	12969	1	1392	
12890	43258	A	12970	1	1224	
12891	43259	A	12971	1	970	
12892	43260	A	12972	1	954	MDGDLHKGVAVFWPPDAAGG HTCCRSMVCRSLGGAQWKFH SFRCRIRFELIHHMIQERNISIN QKDVHTETPSETHHHQRPKVD KSMKMRRNQCKKAENSKNQK ASSPPEKHNWSRAREQNWTE EFDKLTVEGFRRWVITNSSELK EHILTQCKEAKNLEKTLEELLT RITSLEKNINDLMKLKNTA*EL REAYTSINSQISQAERISEIEDQ LNEMKHEHRIREKRMKRNKQS FQEIWDYVKRPNLRLISVPESD GENGNK*ENILQDIIQENFPNL ARQANIQIQEIQRTPQRYSSRRA TPRHIVRFTKV
12893	43261	B	12973	1	1346	
12894	43262	A	12974	1	318	GSRGELLSLCYNPSANSIIVNII KARNLKAMDIGGTSDPYVKVW LMYKDKRVEKKKTVTMKNRL NPNFNES\FAFDIP\TEK\LRRETTII ITVMDKDKLSRNDVIGK
12895	43263	A	12975	17	389	SWGPHCTHKLKSFSLMPMT DAMDREMR/RGSKKDVR/*VLG GCAATWTPRAGGRQQSPGTTV DKREDTPDCAMDQSTSHIPISA SSPSLLPGSSFTQTTPPGIAHYR ASFLIVAYYPSNKNKSK

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12896	43264	A	12976	84	282	GEGQVGWVPQGEVQQDEEVIEE VGA* [*] DAGSGYQEEEEGPQLRR EVVGVELVVGADPSGEGPKED
12897	43265	A	12977	1	1179	
12898	43266	A	12978	3	634	
12899	43267	A	12979	234	619	CYVVQEVLPDLLCHLVICSRP GRTAEWPPG*GF*SPHRGW/ GC*GHD/HRRGTSIFPH/V* [*] SPP ASYPGSLCRPGGQEEREREGEW QREGRRPGTR*CGAAEARGW RAAAKATAVAGARRRRPGISG
12900	43268	A	12980	1	1182	
12901	43269	A	12981	3	763	
12902	43270	A	12982	32	949	
12903	43271	A	12983	1	1299	
12904	43272	A	12984	1	1176	
12905	43273	A	12985	1	421	
12906	43274	A	12986	81	404	VKFGPEIWCRRSDQGRGGVGT SLGRSIPCPALCSVRKIYLRPL VLRPTSPRNPILNRDPTVQLT WQPLPEPLELWPKAL* [*] LTPSQIY SA* [*] RLKTDAAARLPKPPR
12907	43275	A	12987	1	378	
12908	43276	C	12988	1	751	
12909	43277	A	12989	302	629	ICLSYPAPPKCRFPHYTRVLYH* SLFNENTSQSCFTSR/WKLESFT TRAIERHQIFLL* [*] ATLTLIRWLD KKLAFQLLSLTASFSPSYQLSP TPPLKLPIISSHTRQMV
12910	43278	A	12990	14	380	
12911	43279	A	12991	189	608	QSDLSASQHGFLPLATEVRSSG AASCPDSDSICPAPTAPGRATP PQANCWASEGLTRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLSNLQGP RSRPVAFLSKQLDLTVLWGPSC LVVQQLPP
12912	43280	A	12992	1	513	
12913	43281	A	12993	2	462	WSMGLPRRSGCVSLQPLSQEDL GRSQSES LGPEFQGLWEWLPEQ LPRSFQALGSLSYFPRTLNLNLS WPLCLRKGWYL/SLYLPFQVGL PSTVPWPLILPSKVPEEEGQLQS TLPCGIKLLPVFTSHHAF LGVFC NQWVSDVFLALFLMKLLGAQ
12914	43282	A	12994	59	213	
12915	43283	A	12995	1	1159	
12916	43284	C	12996	1	864	
12917	43285	A	12997	1	1155	

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12918	43286	A	12998	879	1163	SRRPLFMGLVRVLCCKMSGRGP LCFPGGHWIVFLWGGTVLWLW T*SPHWHRRKAN*DLFLQKLPRL *VSHQCDPCLPVCHLWNCLFL PLWGPPAG
12919	43287	A	12999	1	179	
12920	43288	C	13000	1	410	
12921	43289	A	13001	42	365	FGLRLSLAPPFCMFPLTT*HS*P SVLPASFPAAALGIPQARAVTFV SP*LLASLSFWAPPCSLCLDASV *HGSHLWHAQSSCRLRWSFGL AASQMQPPEPSHGPRRK
12922	43290	B	13002	1	741	
12923	43291	A	13003	8	265	
12924	43292	B	13004	1	646	
12925	43293	A	13005	1	1158	MKLVTIFLLVTISLCSYSGYWFE NEQMSVGGGDDNGEVLYSALR GASEVIGQCQSATKPRRSKGE SVREPWARVPGALGVGVREID QTLGIDTILCHHERLLQSHYGI HKSSLSMVGNSQVAALYQLNV YVVADTVGLIKNSISLDSVQPN YCSNKHIELRTQVGGARNLRA NSPMTSSYNQESSSMENVVALS LLTVESPTSMFDYCDDSLRLVK SALDIFSMIIYTVTFGLAGNG LVIWVVGFMHSCVTNTCLPSPDP HLHGPLTCDPVANLVLEQLHTS KGNsgaledlafgnlflcslld LQGNswwkvpsllynqydlq NETQGSQHLWKEIHPW*PSAFV V/SSGYWPENEQMSVGGGDDN GEV/RVFRPEGGFRGDRAVSFV SH*AEKIWEGISQRAL/VPEFQG LWEVW/CREIDQTLGIDTILCHH HERLLQSHYGIHKSSLSMVGNS QVAALYQLNVYVVADTVGLII KNSISLDSVQPNYCSNKHIELRT QVGGARNLRANSPTSSYNQE SSSMENVVALSLLTVESPTSMF DYCDDSLRLVKALDIFSMIIYT VTFGLAGNGLVIWVVGFMH SCTVNTCLPSPDPLHGPLTCDP VANLVLEQLHTSKGNsgaled LAFGNLFLCSLLDLQGNswwk VSPSLYNQYDLQNETQGSQHL WKEIHPWHQTLVTTAHFFFGFF

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12926	43294	A	13006	3	371	AGARFNVRSR*RNDRVRPHRD VYSLQGRSLSDHSPTFGCQQTQ GRLPWSFTLSGKFRFSGEGATT SPAHIKNFQTPEPQWP GIPPEPPP TGACYTCRKS GHWAKECPQAR IPPKPHPICVGP
12927	43295	A	13007	77	332	RWKKNCNLSPPRMS*QR*WKP* MQQAACSVGETQPPCTQVK*T ALLLTQSLFGGLFTRTHMKFGA VTRIGGPPLDQSPVLLLFAP
12928	43296	A	13008	1048	1349	RVVEQDDAERLFRFRFAA/GDL PYGAFFEIF*ETQCEMQQLAE DHASVTMISLEAWRLYRKMVC RIWASMLRLSVCHLCAPKR VV SLISRNGYHLP GSIH
12929	43297	A	13009	213	499	PEQRTSHRQQRRQPPQSRSP FCPLSPRSALSLFLCDGYAAP* AYRE*IPVTEDHFAE*/ISWCP *YREALGQLLAKMRR*SARKRF QLSP
12930	43298	A	13010	2	431	
12931	43299	A	13011	2	367	
12932	43300	B	13012	1107	2083	
12933	43301	B	13013	1	627	
12934	43302	A	13014	712	2671	AHVGRGST*ALPRAMGSDAF*C PLQ*MTPASFGSKAALS RVFIKE ALMMEDPCVVRKPLSAHMTA WWCRIWKAYLESV
12935	43303	A	13015	50	1362	WEQIPHGLVLSLQQLPRRSGSIS LQPLSQEDLGRSQSESLGPEFQ GLWQWLSDFQT*HQWVVS GFQ AFSDRLKAALSASLLRF GDSD WLPS SACKCLMLGLHFVIVGN ICATLKEKYSSMLHLDVTMKK NGEKRTLQKRKKGMPPHPAY EDLNIAAITLPANVVLHQPSGFR TSGQLDPVWWSLDTDAHEIWC QDPGLGSGDFPWEITPLSSYSLL HEKDPPTTSGPQTDQPKKHLTN FKSKTKETGFIHGPKTPAPVTD WEGSLPLVFNHCRDTS LIIHPCF KGVRRRDACLGPSPLAASPAF LEKGQDLINLAFKVYNNRKKL QFLASTVRQTPATSPA HKNFQT TEPQQPGVPPPEPPTGACYMCR KIWPLGQANARSPGFLSRVPS VWDPTGNRTVQLTWQPLPEPL ELWPKALCLTDSFPDLLGLAA
12936	43304	A	13016	1	507	
12937	43305	A	13017	5	271	
12938	43306	A	13018	1	618	

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12939	43307	A	13019	1	429	
12940	43308	A	13020	1	3567	
12941	43309	A	13021	1	353	
12942	43310	A	13022	1	338	
12943	43311	A	13023	1	1175	
12944	43312	A	13024	3	326	
12945	43313	A	13025	150	494	PSPSLGYLVGTRGTALRL*DAR AAMRPFDPSTLLPTCWDYWTY AGSLTTPLTESVTWIIQKEPVE VAPSQLSAFRTLLFSALGEEK MMVNNYRFLQPLMNKRVWAS FQATNEG
12946	43314	A	13026	2	975	DSREHHPLQTGVSGNRPKMLG RNTWTKTSAFSFLVEQMWAPLW SRSMRPFGRWCSQRSCAQWTSN NTLHPLWTVPVSPVGGTRQSPI NIQWRDSVYDPQLKPLRVSYE AASCLYIWNTRYLQVFEFDDA TEASGISGGPLENHYRLKQFHF HWGAVNEGGEHTVDGHAYP AELHLVHWNSVKYQNYKEAV VGENGALVIGVFLKLAGHQT LQRLVDILPEIKHKDARAAMR PFPDSTLLPTCWDYWTYAGSLT TPLTESVTWIIQKEPVEVAPSQ LSAFRTLLFSALGEEKMMVN NYRFLQPLMNKRVWASFQATN
12947	43315	A	13027	1	1233	
12948	43316	A	13028	761	1000	IPFISFSLIALARTSNTMLNKG ERGHPSLVVPFIGNASSFCPVSM ILAVGLS*IALILRYVPSIPNLLR VFSMKGC
12949	43317	B	13029	697	1527	
12950	43318	A	13030	1	1695	
12951	43319	A	13031	434	925	VAKIFSHFVCCFLTLMVVFAV QKLFSLIRSHLSILSFVAIDFGVL DMKSLPMPMS*MYMPRFSSRV FIVLGLTFKSLIHLELIFV*GVRK GSSFSFLHMASQFSQHLLNRE SFPHCLFFSGFSKIR*L*ICGIIE GSVMFH*SIISLFWYQYHAVLVT VAL
12952	43320	A	13032	1124	1234	KITPKKQIRQSPNLTQNTGQQ*S LQLWEHFQISTHF
12953	43321	A	13033	929	1261	
12954	43322	A	13034	1118	1354	IPFISSCLIALARTSNTMLNRSGE RGHPCLVPVFKGNASSFPFSMI LAVGLS*IALILRYIPSIPSLLRV FSVKGK

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12955	43323	A	13035	2	348	HQHLLFPDFLMIALTGMRWYL IVVLCISLRASDDEHF/YHVS GCINVFF*EISVHILRPLFDGVV* FFLVNLFKFFVDSGYEPFVRWV DCKNVLPFCRLPVIHSDGSFFCC AFAAL
12956	43324	A	13036	578	712	LISNFSKVSQYKINVPKSAFLY TKNRQTAKS*VNSHSQLQRE
12957	43325	A	13037	1	1833	
12958	43326	B	13038	1	1587	
12959	43327	B	13039	1	1851	
12960	43328	A	13040	1349	1444	
12961	43329	A	13041	953	1277	MVLPRESSRVFVVLGLTFKPLI HLELIFV*GVNFV*GSSFSFPHM ASQFSQHLLNRESFPHFLLSG LSKIR*L*MGHISEGSLFHW ESLFWYQYHVLVTVAL
12962	43330	B	13042	804	4236	
12963	43331	A	13043	1	744	
12964	43332	A	13044	137	797	
12965	43333	A	13045	210	418	
12966	43334	A	13046	1	927	
12967	43335	A	13047	1	1415	MGFLGTGTWILVLPQAFPK PGGSQDKSLHNRELSAERPLNE QIAEAEEDKIKKTYPPENKPGQ SNYSFVDNLNLLRAITEKEKIEK ERQSIRSSPLDNKLNVEDVDST KNRKLIDDYDSTKSGLDHKKFQ DDPDGLHQLDGTPLTAEDIVHK IAARIYEENDRAVFDKIVSKLLN LGLITESQAHTLEDEVAEVLQK LISKEANNYEEDPNKPTSWTEN QAGKIPEKVTMPMAIQDGLAK GENDETVSNTLTLTNGLERRTK TYSEDNFRDFQYFFNFYALLKSI DSEKEAKEKETLITIMKTLIDFV KMMVKYGTISPEEGVSYLEGL DEMIALQTKNLEKINATDNIS KLFPAPSEKSHEETDSTKEEA KMEKEYGSLKDSTKDDSNPG GKTDEPKGKNRSPWPKIRKNI EWLKKHDKKGNKEDYDPFQR* EVSPNNKADAIYVEKGILDK AEAIRIYSSL
12968	43336	A	13048	1	879	
12969	43337	A	13049	3	640	
12970	43338	A	13050	134	382	DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPPWMN/WPPH*IKHIQS
12971	43339	A	13051	87	500	

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12972	43340	A	13052	1	1356	
12973	43341	A	13053	1	447	
12974	43342	A	13054	3	107	
12975	43343	A	13055	3	2377	
12976	43344	A	13056	1	2193	
12977	43345	A	13057	1	2724	
12978	43346	A	13058	253	490	QSSIPAIMSSFLGTGAETMPVPL GAGMRRTSTEPQVCFCTGIIF KTSSLREAPRKKSMSISLMGR E/WMPVTKLGRLLVKDMKIKSLE EIYLFSLPIKESIIIDFFLGASLKD EVLKIMPVQKQTRCGSVLVRLLI PAPRGTGIVSAPVPKLLMMA GIDDCYTSARGCTATLGNF/AK ATFDAISKTYSYLTPDLWKETV FTKSPYQEFTHLVKTHTRVSV QRTQAPAVATT
12979	43347	A	13059	1	819	
12980	43348	A	13060	1	623	MARRKNGKWESEIIDFCLGGSL KDEVLMIMPVQKQTRAGQC FKAFVAIGDYNHGILGKCSK E/LATAIRRAILLAKLSIVPCRG YWGNKISKPHIVPCRGTGIVSA PVSKLLMMASINDCYTSARG CTAILGNFDKATFDAISKTYSYL TPNLWKETVFTKSPYQEFTHLV VKTYTRVSMQSTQAPALAKLP RVAVQPAEAV
12981	43349	A	13061	1	949	KWRITPVPTGRP/GGPGGPGMG KPRCF/RGEVFGIVIRAGSPGPG TGPGRG/GEAAGAKAED*E/W MPVTKLGRLLVKDMKIKSLEEIY LFSLAIKKSEIMSFLGLLRSRDE VFE*LCPVQEQ/TRAGQ/RATRF KAFVALTTLGTTNG/HVGLGC* VPPREVATGNSWGPFLGQALH SSPVRRGLLGGTKNSAKPPTLV PWQR*PRAACGLCAGYAFIPLQ PRGQLASVSA/PVP/KKLLMMA GTDG/CNNSQRRGCTATVG/NL AKATTFDAISKTYSYLTPDLWK ETVFTKSPYQEFTHLVKTHTR VSVQRTQAPAGATT
12982	43350	A	13062	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIIDCGQLE

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12983	43351	A	13063	2	797	NRVLLAMVNPVTFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIGLFAKVPKTAENFR/A L*SIEEKGFGL*GVPCFHRLFPR VLCVRGGDFHTAINGTGGKSI\ YGEK\FEDENFILKHTGPGILSH GKMLDPNTNGSQFFICTAKTIE WLDGKHV\VFVGK\KEGMNIVE AMEA\FGSRDCKTSKKITIA\DF GQLRIKFDFVFLSLTTKIISFCAL LSGEHPLHPIWLGVILESMWLS LAVPFWVPCFCSLPCLAGLQS
12984	43352	A	13064	1	720	
12985	43353	B	13065	98	2074	
12986	43354	A	13066	596	841	
12987	43355	A	13067	66	326	
12988	43356	A	13068	1	441	
12989	43357	A	13069	2	325	WCPSQAAAAGARATRDMPEGS MTCLCRALWWLFSWLKVHR*R QQQQGRPAAPSAGPAKPTPTRN SSWLLAAPVPTRTSPSTPPCKL REPAPALASPERGSHSAAVG
12990	43358	A	13070	38	1066	
12991	43359	B	13071	1	324	
12992	43360	A	13072	2	680	
12993	43361	A	13073	2	165	
12994	43362	A	13074	1	1110	MASLLKSARPTQHWKEETPETS KRLKEQTPDIPSLRAVTLIAKVH SFIPEVCETKNPLEGIHSGHILAP NVGSPSPRRQARVQVFENVSVR ATKSDLPQSSLWSRRKTTVSAA ASKKTSKEISKGPQKPPGY/PVT SPSSCRGRGIWPNP/EYMTSPS LI*/SQIKVDLGKISDDPDRYIDV LQGLGQTLDSLWRDVMLLLDQ TLAFNEKNAALAAAEQFGDTW YLSEVNDRMTAEERDKFPTED GEPIKDCQQIIVQTYAAQDDIL EVPLANPDNLNLYTDGSSFVENG IRRAGYAIVSDVTILERPNLFRA IQQVVKACEVCQRKNPLVHPP NYLYKTLNLTHSLNLQSNPSLA NDCWLCSSLSVSAEPPYN

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12995	43363	A	13075	450	1776	RGGRACLRP*AA/SPGPSTP*WP PPRGVQAAAILSGPPRPAPPKG AASQRLCGGFVEARQAWVGRR GRRGVPVGETQPPPSVIQPPSRG AG/PRDQQPAMPEPPTPSVGSC AARASQISAAPCSTAPSPIDHPR AEECRRTVWDWQAAPPAQV RDPLGEASWAPESGGDVENLY VLLRDCKYTSQHPVSSSGSVNA PIDTLYLATLLRDCKYTNRHVS SSSRFVNTPISTVSSEFANAPID TLHLATLKEETPNTSEHQKEQT PDMPLRTVTVTARVRGFILDV SETKNPPIPDITWRPWRDLRQS PSNQTLAFNEKNAALAAQEF GDTWYLSQVNDRMTAERDKF PTEFIPSSGFLVLLTSRMKPQTF AASVTALKDGVSRVCSFRCVQS FFLPSADWCIYKPLARYALIG AFLQSAHWCVYKPLARHSVL GAFTNL
12996	43364	B	13076	1	1999	
12997	43365	A	13077	3	469	
12998	43366	A	13078	224	410	
12999	43367	A	13079	478	675	
13000	43368	C	13080	55	237	
13001	43369	A	13081	109	239	
13002	43370	A	13082	2	88	
13003	43371	A	13083	2	178	
13004	43372	C	13084	278	460	
13005	43373	C	13085	50	217	
13006	43374	A	13086	3	251	
13007	43375	A	13087	1	759	
13008	43376	A	13088	2	604	
13009	43377	A	13089	1	558	
13010	43378	A	13090	3	1055	
13011	43379	A	13091	1	466	MDKFLDTYTLPRNLNQEVEESLN RPMITGAEIVAINSLPTKKSPPGD GFTAIFYQRLISNFSKVSQGYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGGRINIVKMAILPK
13012	43380	A	13092	2	848	
13013	43381	A	13093	458	625	
13014	43382	A	13094	482	745	

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13015	43383	A	13095	1	742	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIWHINRTKDKNHMIIIDAE KVFDKIQQPFMLKTLNKLIGDG TYLKILRAIYDKPTANIILNGQK LEAFPLKTGTRQGCPSPLLFNI VLEVLAIRQEKEIKGQLGKE EVKPSLFADDVIVYLENPIISVQ NLLKLISNFSKIKYLGQLTRNV KYLKFNKYKSLLEIKEDTNK WKNIPCSWIGRINIVKMAILPK
13016	43384	A	13096	1	1458	
13017	43385	A	13097	2	1624	
13018	43386	A	13098	1	1095	
13019	43387	A	13099	1	2913	
13020	43388	A	13100	2	1887	
13021	43389	A	13101	1	972	
13022	43390	A	13102	1	873	
13023	43391	A	13103	1	1365	
13024	43392	A	13104	1	867	
13025	43393	A	13105	1	591	
13026	43394	A	13106	1	990	
13027	43395	A	13107	1	2109	
13028	43396	A	13108	1	843	
13029	43397	A	13109	1	1203	
13030	43398	B	13110	1	1221	
13031	43399	A	13111	1	1092	
13032	43400	A	13112	1	931	
13033	43401	A	13113	1	1293	
13034	43402	A	13114	1	544	
13035	43403	A	13115	3	718	
13036	43404	A	13116	693	1397	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLKLLISKFSKVSRKYNV QKSQAFLYTNRRQTESQIMSEL PFTIATRKIKYLGQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFPIPTKINSRWIKD LNVPRKTMKTLEESLGNITQDI GIGKDFMTKTPKAMATKAKRA SAQQKKLPSE
13037	43405	A	13117	1	2814	
13038	43406	A	13118	1	1302	
13039	43407	A	13119	1	1542	
13040	43408	A	13120	3	1327	
13041	43409	A	13121	1	1023	
13042	43410	A	13122	1	1448	
13043	43411	A	13123	1	1038	
13044	43412	A	13124	3	1711	

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13045	43413	B	13125	1	1756	
13046	43414	A	13126	1	923	
13047	43415	B	13127	1	1515	
13048	43416	B	13128	1	1560	
13049	43417	A	13129	1	4032	
13050	43418	A	13130	1	2684	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRKLNLTQSRSTPWKLN NLLNDYVWHNEMKAEIKMFF ETNNKNDTTYQNLWDAFKA CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTSHKASRRQ EITKJRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDITIKNDKGDITDPTIEQ TTIREYYKHYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAIFYQRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIQKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTKNRQTESQLMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNKIEDTNKWKNI PCSWVGRINIVKMAILPKVIYR FNAIPKLPMTFFTELEKTTLKFI WNQKRAIAKSILSQKNKAGGI TLPDFKLYKATVTKTAWYW YQNRDIDQWNRTEPSEIIPHIYN HLIFDKPEKNKQWGKDSL FNK WCWENWLAICRRLKLPFLTP
13051	43419	A	13131	1	1149	
13052	43420	A	13132	127	329	
13053	43421	A	13133	1	1132	
13054	43422	A	13134	1	1020	
13055	43423	A	13135	803	2009	
13056	43424	A	13136	1	1944	
13057	43425	A	13137	1	1282	
13058	43426	A	13138	1	2423	
13059	43427	A	13139	1	2694	
13060	43428	A	13140	1	1195	

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13061	43429	A	13141	6082	6984	KLAQDRDALSPPLLFNIVLEVL ARAIQKEIKEIGIQLGKEEVKLS LFADDMIVYLENPIV/SAPKSPL RLISNVSVK*GYKINVQKS/QA FLYTNNNTDKQESQIMSELPFTT ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWNIPCS WVGRINIMKMAILPKVNYRFI NSMPSIPIKLPMTEFTTELEKNYF KVHMEPKKSPHCQVNPKTKEQ SWRHQRYLTSNYLQGYSNQK STISMVLVPKQHGTGTKEIIDQ WNRTEPSEITPHIYNYLIFDKPL LEKNKQWGKGFI
13062	43430	A	13142	193	335	MVEEKLTLPKDEK*KSKQRSY RKTLLQELKNKNEKRNKKNKW QVKTH
13063	43431	A	13143	131	427	
13064	43432	A	13144	1	360	
13065	43433	A	13145	2	376	
13066	43434	A	13146	1	360	
13067	43435	A	13147	2	376	
13068	43436	A	13148	3	469	
13069	43437	A	13149	224	410	
13070	43438	A	13150	478	675	
13071	43439	A	13151	32	161	
13072	43440	A	13152	1	1671	
13073	43441	A	13153	1	1656	
13074	43442	A	13154	62	1295	
13075	43443	B	13155	149	320	
13076	43444	A	13156	12	89	
13077	43445	A	13157	28	417	
13078	43446	A	13158	2	440	
13079	43447	A	13159	190	553	EIVREGASFIRHLRWSRHRKC RFSVKTLTGEDPSTLEV/EP/DT IE/NVKA/IQDKEG/PPDQQR/L/ VSFAGKQL/EDGRDSLGSY/NIQ KGSLLHPCV*DFRGGAKKKEE ESLYTTSRPRKD
13080	43448	A	13160	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVFPPVECRIG RDILSSWQNPHGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY

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13081	43449	A	13161	5	405	HCCGIPHSIAEQDTYFMAKEV WQWAHAHGIHWSYHVPHHLE AAGLIEQWNGLLMSQLQHQLG DNTLQGWGKVLQKVYYALNQ RSIYGTVSPIRIHGSRNQGVVE EVALLTVTPNDPL/GKY*L.PVPV TLHSDR
13082	43450	A	13162	138	387	
13083	43451	C	13163	184	297	
13084	43452	A	13164	1	430	
13085	43453	A	13165	1	867	
13086	43454	A	13166	35	601	CLSRRAAPVYLASMSGRGKGTG G/KARAKAMSRSSRAGRPSQ VGR/VHRLLRKGHYAERVGR QPCCYLG*CMYELT*ESWS MAGNAARN\KKTRIPIRHLQ LAIRNDEELNKLA WAALTIAQ GSR/VLPNIQARCCGPR*TSATV GPKAPSGGEERATQASARSTK RARAAAGRPSVPMPPQRP
13087	43455	C	13167	11	313	
13088	43456	B	13168	1	552	
13089	43457	A	13169	1	621	
13090	43458	A	13170	55	296	
13091	43459	A	13171	959	1182	WVYLF*PSCKGVIYP*AAGFESI FWWVTINKNIDWINIYYNQ QFMNYTRDAVKGIAEQLGTNC QMAWENRIALDMILAEGRGVC IMIKTECCAFIPNNTAPNGSITK ALQGLTALSNELASSSGVNDPF TGWLEKWFGKWGITASILTSL TAVMGVLILVGCCVPICGLV QRHRGPPLVVIETKPLGLERLA GLPVGHALKLSGIQATPQNGE NADRREAFPAAS
13092	43460	A	13172	1	540	
13093	43461	A	13173	2	142	
13094	43462	A	13174	42	384	
13095	43463	A	13175	102	329	
13096	43464	A	13176	1	1257	
13097	43465	A	13177	1	378	
13098	43466	A	13178	1	1143	
13099	43467	A	13179	1	481	SDSELNRPVMTMKNFPVFTSDR SKNRKRHFNAPSHVRRKIMSSP LSKELRQKYNVRSMPIRKTDEV IQVYVRGHYKGQIQGQSPRCTR KKYVIYIERVQREK\ANGTNC TWGISPKARWLFTRLKLDKDR KKILERKAKSRQVGKEKGKYK EELIEKMQE

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13100	43468	A	13180	39	556	AAAGYFAEDCEASCVCVKHPP SVKKARCFLSELIKKPSGGSVTL SESTAIISHGTTGLVTWDATLYL AEWAIENPAAFTNRTVLELGSG AGLTG/VAICKMYRPRAFIFSDC HSRVLEQLRGNVLLNGLSLEAD ITANLDSRVTVAQLDWDVAT VHQLSAFQPDVVIAADVLY
13101	43469	A	13181	46	231	
13102	43470	A	13182	1	1503	
13103	43471	A	13183	3	340	FFFANTFYCVFNVLVNAPLRF SLPSTQSLKLRDSSDSELRRD ILQKVRIPESLGLMTLPPESLRK T*EKNRRCACTL*K/TPVQRTKP LSQHCRVWVWAPPTAPALSFSTK
13104	43472	A	13184	2	594	
13105	43473	A	13185	1	1470	
13106	43474	B	13186	79	1355	
13107	43475	A	13187	248	540	
13108	43476	A	13188	386	1388	
13109	43477	A	13189	386	1334	
13110	43478	A	13190	3873	4070	
13111	43479	A	13191	146	510	PPCAVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAWPKIPFLGIREAKN PRSENTRLTT
13112	43480	A	13192	21	95	KCSSNGAPDAVHE*DLPWTPGP AC
13113	43481	B	13193	1	477	
13114	43482	A	13194	228	935	PLSSSMAAELEFAQIIIVVVTV MVVVIVCLLNHYKVSTRSFNIR PNQSRREDGLPQIMHAPRSRD RFTAPSFQIRDRFSRFQPTYPYV QHEIDLPTTISLSDG/EEPLLYQV PCTLQLRDPQQMELNRESVRA PPNRTIFDS/IDIAMYSGGPCP PSSNSGISASTCSSNGRMEGPPP TYSEVMGHHPGASFLHQRSN AHRGSRLQFQQNNAESTIVPIK GKDRKPGNLV

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13115	43483	A	13195	526	1629	FYSFDSARGEAPRPWRVRGLEGRVELGQQLGLLTLGPAPFPGGLG GTQRVGLPGPAGPGAGEGQA GPAAEQQVPVGGLADEAVEHG VGDAVEAGEQEGEVVGVENAL GEVAAGLPDAAHQQQHVVGQ EAGQEDDHGAHQPLDLVLA LLGAVAPAHGAQDALVGRQQ QADGEEELPGSGSS*WHAAM PGWGSAQSTRGAGSRPR*PPRA SGSRCWSAAPWR*PR*RRRPP SGSGTGGSGRDPQPGSGRPT MQQRKPTLM*MFYRRIRTPG RTGRRETSCRAAARTAAARRA SRCRRGRPPSGCTGRPARSGP* SAGSEVEGQAVGREAHHQHG NIDHRGQRLVDGMVDGTAHRG VVCSDVPH
13116	43484	B	13196	2699	7361	
13117	43485	A	13197	67	1523	
13118	43486	A	13198	1	287	
13119	43487	A	13199	2	563	
13120	43488	A	13200	96	401	
13121	43489	B	13201	1	480	
13122	43490	A	13202	1	924	
13123	43491	B	13203	13	1512	
13124	43492	A	13204	1	402	
13125	43493	A	13205	609	803	RDPRNPSSA\FQAGGIALMLI TRGEDLTGGVIHQYPPGGMNL WMQGTAGNQRRRAENAAQQQ
13126	43494	A	13206	3	526	VTETALTPLYLVAKHGYFLPQD LAKRTETMNWLFWLQGAAPFL GGGFGHFYHYAPVKIEYAINRF TMEAKRLDLVDKQLAQHKFV AGDEYTIADMAIWPFGNVVL GGVYDAEFLDAGSYKHVQR WAKEVGERPAVKRGRIVNPTN GPLNEQLHERHDPDFQNTNE NNRQG
13127	43495	A	13207	1	250	
13128	43496	A	13208	1	489	
13129	43497	A	13209	209	601	
13130	43498	A	13210	1	96	
13131	43499	A	13211	1	1110	
13132	43500	A	13212	1	595	
13133	43501	A	13213	1	240	
13134	43502	A	13214	1	675	
13135	43503	A	13215	1766	1957	
13136	43504	A	13216	1	426	
13137	43505	B	13217	94	3238	
13138	43506	A	13218	1	2370	

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13139	43507	A	13219	1	2796	
13140	43508	B	13220	43	566	
13141	43509	A	13221	1	903	
13142	43510	A	13222	3	110	
13143	43511	A	13223	2	755	
13144	43512	A	13224	1	1338	
13145	43513	A	13225	1	807	
13146	43514	A	13226	1	918	MARADTVSVPMFMGLAAKPC WRDTEPNTGYRGPHVNRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDAC/LSNAILVHNKKGPP LADGIVITPSHNPPEDGGIKYNP PNGGPAVPTSLKWWKTGPTH WPMA*KA*SVSPARRSDGIRSKN DVIDTSDDDM**QCLSRSSNG HPGAKVANLVPKTTTFIDGVDQT SFFLGTNGQSNRKAHEYFLNGK LAAVRMDEFKYHVLQQPYAY TQSGYQGGGTGTVMQTAGSSV FNLYTDPQESDSIGVRHIMP PLQTEMHAYMEILKKYPPRAQI
13147	43515	A	13227	1475	2904	FWRAAAPIDCWRSQAVKKQH VEVTQLDWTTPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGGTGT MQTAGSSVFNLYTDPQESDSIG VRHIMPVFLQTEMHAPGLPLA SSMKRWIRRTGFIKGKEQFED VVPVLGSKVNGVQFNALVAD SLGISQIRCRCAIFLTVVFPVLH KQAFDLISLLQQPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAF LTVQGSPELHQAQVADDERPH ANRFLPPDEIEQSLNGVHYQH IQPITLWFDALSAMRSLKGIG ATHLHEGRDPRILTRSLOQLQ LAWPQQQGRYPLTYHLFLGVI
13148	43516	A	13228	215	525	LAWARRCRLLAKATSLIRAPS SEMRASTPCRQRRPSGYSWY GRSPRAVLEGLRVGAHLSTRAN CPWPSR/SQVVELIPDGPVFLD FTKIPGRDTQNEHIVLLH
13149	43517	A	13229	1	942	
13150	43518	B	13230	1	1201	
13151	43519	A	13231	685	921	

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13152	43520	A	13232	2	251	
13153	43521	A	13233	2	100	
13154	43522	A	13234	5	1093	
13155	43523	A	13235	2	482	
13156	43524	A	13236	1	2496	
13157	43525	A	13237	572	912	RCRPDKAFTPHPAIGARCLMRR LRVLSCLQPLPNVGWIRRLRRIR QFSAPDEGAKCRVAIQ/DFDA QYGRFLEVTSGAQQRFQTD*K HAAALPFFFPSSAYSLAAISVVF GFR
13158	43526	C	13238	5	127	
13159	43527	A	13239	1	444	
13160	43528	A	13240	17	261	
13161	43529	A	13241	173	397	
13162	43530	A	13242	169	421	LKPKNLDEKLLPASSSSCRIWA TSPVHHLWQVLKKILFGWNP KSPRCLS/TRQAMFSLSKKASLP WTIAARSADQRCRTIAEL
13163	43531	A	13243	17	744	RPHQEORAGCGVNALSSLRSA TAVGMIRASVASG/DRAPIAG CGVNALSGLHRHFIEVTC THFL LVRYEGIAIFRGGKFRLHLFLN VVLHTLALGIGVCQVKHVEPH AVDTCQGDEL ELVAHIRQLLLE AGNSFVVEVYLPVERRRAVISQ QFARIFRVDSLCKATRFQIRRG RSHQTGQHMGI RRQVDAAHAD DRRTSGRVFPPLIQVC PAHSSEA VVVVDVDVDVDVDVDVIGAV
13164	43532	A	13244	954	1104	
13165	43533	B	13245	54	1169	
13166	43534	A	13246	35	3066	VGHSTRPAASGPAAGIGRSPA RLVQQPQORSLAKPLNRPAAQR GLLPQRHPKRTKRRKQAQN PQKRLPHRPQVRRRRHHRRLL QKMRRPDKRQORRAAPRRHPR RRQRLLA VRRRLRAKVR RNP RQRA PQQLNGQRILHPPWR LR MQVRRKRG*YSSAVRPTVRLK RWRQRQRQ*NQPM TMQRNV C RKTRTALIYP/YKGCFLNNINAV SKDTFADKRGMRVYRVNAPAG ATSGKYYPPVVVMRSAGSFHI
13167	43535	A	13247	1	2919	

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13168	43536	A	13248	1	3211	MEFTSLTPDDLRLVLELYRTPFS DGYVFHSMQFHIFDLLKSGQN VVLASPTSMGKSAIVDSLLGMG TLKRLVLVPTVALADETRRRL QERFGDRYQIIHSSQVCHSDQ AVYVLTQERVNERDDIVIDLF VIDEFYKLAFRQLKSGDIDHQD ERVIELNIALSKLLKVSRQFYLT GPFVNSIRGLEKLGYPHTFVST DFNTVALDVKTSASKRMTTKP SSKRWGKSRTCVDADHIKNGIG LHFGALPRALQQYT
13169	43537	A	13249	486	3882	LRLRGEALPVASGCLANATDTP AGTTLWADTERHAVQ**TCEA DTLGSCGYAAKPCLSPPVAVWQ MLLTRLLEQHYGLTLNDTPFSD EPVLTAPIDAAALRGIEFGKFQ GNMVGDIIECGSDVTDYAVG DSVCGYGPLSETVIHNAVNNYK LRKMPQGSSWKNAVCDPAQF AMSGVRDANGARRGFWWGGL GAIRVQLAFKWLNAAGRLPGG GLGGPIPSAHRCDIARRHGAD FCLNPIGTDVGKEIKTLTG
13170	43538	B	13250	1	1116	
13171	43539	A	13251	729	985	SAPPQLAPSLPDRATDPDTCWP PG*RP*RYLPSRQIDCFNTRFRLL QRLTASQCAEAVDVAFRLTV QQTPHFRCAQLRQRAFRID
13172	43540	A	13252	395	605	
13173	43541	A	13253	1	1140	MIYVFVTVKHRNDHFTKNTLA SYRGRTLLGLTFKGVYHLYKD ETYLQSGKGHTIQEVRIKGL NNPDLDAAVGEDLAQQLRDEL ELVKGASNEFDKELFLAGEITP VFFGTALGNFGVDHMLDGLVE WAPAPMPRQDTRTVEASEDK FTGFVFKIQANMDPKHRDRVA FMRVVSQGYEKGMLKRVRT AKDVVISDALTFMAGDRSHAY PGDILGLHNNHTIQIGDTFTQG EMMKFTGIPNFAPELFRIRLK DPLKQKQLLKGLVQLSEEGAV QVFRPISNNDLIVGAVGLQFD VVVARLKSEYNVEAVYESVNV ATARWVECADAKKFEFKRKN ESQLALDGGDNLAYIATSMYV LRLAQERYPDVQFHQTREH
13174	43542	A	13254	1	1495	

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13175	43543	A	13255	372	1365	IRYFENRGLFAHCATRTGQFPP HCILASYKCGEQPDSSSNHPRN LFVWRSNLLGSSG/KGHEYMQ KYL LGTESGIQGEELGASDGIKP EEVEWQTA AIEGKLDLVLTLDF RMSSTCLFSDIVLPTATWYEKD DMNTSDMHFPFIHPLSAAVDPA WESRSDWEIYKGIKAFSQCVCV GHLGKETD VVLQPLLDHSPAEL SQPCEVLDWRKGECDLIPGKTA PNIVAVERDYPATYERFTSLGP LMDKLGNGMDLTDYANMALSI PSANTDIWNLEQDVTGTRLTNS RHGLADNGGAWSYFGGNFN GDNGTINYDQDVNGIMGVDT KIDGNDG
13176	43544	A	13256	3	1444	
13177	43545	A	13257	61	1058	LPYLIALLARAWFNGLLTSRTR LYIKGNIGIVL PKLQEMVADVS HHFPLRLPAPT PKALYSPCEIRH LAINVNLEYDPTAAFRNQVVHF DFRKL DVFSFGENQNC LVGNV DLLYRNSWNEVRTLHFNGEQS MIEALKTILGKMHQDAAPPDSV EVFCYSQHLRLIRTRVQQLVS ECIELRLSSTRQETGRFKALRVS GQTWGLFFERLNVSVQKLENAI EFYGAISHNKLHGLSVQVETNH VKLPA VVDGFASEGIIQFFFEET QDENGFN IYILDESNRVEVYHH CEGSKHEELVRDVS RFYSSSHDR FTYGSSFINFNLD PPLYLARVSI
13178	43546	A	13258	1	1133	
13179	43547	A	13259	2	240	ISSARHFGALACTLELGKALT GQNDLRQFAVTA SAIAALL/SR HSPSFEMHMASD TLNFMPEFK GTLLAQDGEERFTVTH
13180	43548	A	13260	1	358	LPFLPSGLRGLA AENKIRRP GSFLGPCCGLRGKL V/ISAALM STTIPISRVQGLLQFLNSKSPISR AERSWSTFGASA AFLTTLASLL FLFPPLA ISSLANSAFAVFPPTPC AGSP
13181	43549	A	13261	1	1635	
13182	43550	A	13262	1	1363	
13183	43551	A	13263	5	249	
13184	43552	A	13264	15	280	
13185	43553	A	13265	6	363	

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13186	43554	A	13266	78	346	TRYAMLTRHDNHLKSFYLARG RYRADFHAPETNTGERCYRYK PLPYWLE*RRGRNRYPALQ*TM FLPADGPARCLSRQAAILKESV LPK
13187	43555	A	13267	568	831	ELQRHVLVVFAGFWIVKNSRN LFLVCAEHRKSVVKGLLRQQ GQGFWFHFQDGFAVEVGNAN VIGSE*IVFGIVFPHRERCLVDK
13188	43556	A	13268	3	419	
13189	43557	A	13269	1	561	
13190	43558	A	13270	1	741	
13191	43559	A	13271	2	1040	
13192	43560	B	13272	1	1974	
13193	43561	A	13273	2111	2340	EVFIRDKLMERRNRRTRGTEKA /RDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPVKVLQSQCI
13194	43562	A	13274	470	813	KTTSPAKLFNACRISLLASAEV NPNISAYLATWISQIPSCSRVP SDFLIWSNTRYRIR*SRERLVG EAV/AAAAADGVTFSVPVTPHT FRHSYAMHMLYAGIPLKVLQS LMGH
13195	43563	C	13275	440	1180	
13196	43564	A	13276	1	1290	
13197	43565	A	13277	1	1036	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPKARKITRRWRIG EAADLVGVSSQAIRDAEAKGR LPHDPMENSRRDRFEQGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMLVKNVRETDEVG KDPRPLPYLGHDEPYTFDINLS VNLKSMVVG GTDMGQEPKQ MGAWGPLSLKAMGFFIRGYG FFTPFGRITLPLGFGSTPPFTPL LTKTIGVFILDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA GAAAAADGVTFSVSVTPHTFR HSYAMHMLYAGIPLKDLQSLM GHKSISSTEGYTKDFSLDVG/AR HRVQFAMPESDAVAMLKQLF
13198	43566	A	13278	366	672	RNGTHPRYIEAVPWGALPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSRRLALRELQAV HAGLPQAKILFDGGSEIGKIPH IVLYKPVQCSSLWAFVH
13199	43567	A	13279	2602	2976	
13200	43568	A	13280	982	1347	
13201	43569	A	13281	1	780	
13202	43570	A	13282	568	891	

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13203	43571	A	13283	1	718	MKEKPSSPRQYSYSLSSMILLG GGESWNLRLADQRLIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEA VAAAA ADGVTFSPVPTPHTRFSYAM HMLYAGIPLKVLQSLMGHKSIS STEYVTKV/FALDVAAPHPSTP VHLPSPRENKIPPPIMRIPCGLPTS PIEQKQGISATGTQWRRLKQE TRLSSVSARLMSYVGVCMC
13204	43572	A	13284	1	496	AMFGFFIRGYGFFTPFGRTLFLP FGGSTPPFTFPLLTKTIGVFILDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEA GAAAAADGVT FSVSVTPHTFRFSYAMHMLYA GIPLKDLQSLMGHKSISSTEGYT KDFSLDVGARHRVQFAMPES DAVAMLKQLF
13205	43573	A	13285	2	545	
13206	43574	B	13286	1	735	
13207	43575	A	13287	1	1599	
13208	43576	A	13288	583	1005	
13209	43577	B	13289	31	1239	
13210	43578	A	13290	1	1023	
13211	43579	A	13291	1	933	
13212	43580	A	13292	1	1278	
13213	43581	A	13293	1	705	
13214	43582	A	13294	2	893	
13215	43583	A	13295	88	429	
13216	43584	B	13296	1	1419	
13217	43585	A	13297	1	2784	
13218	43586	A	13298	163	416	RNGTHPRYIEAVPWGALPAD/G VTFSPVP/TPHTFRFSYAMHML YAGIPLKVLQSLRALRELQAV HAGLPQQA KILFDGGSEIGKI
13219	43587	A	13299	740	1431	CCQTLPVFHPHPSHLGPRPCPP TH/HLPSEHRS/LFLEAACHDS LEPLNLSGSKTSKPSLPPKAKK PKGLEISA/RPAGALRHRRLHR PQQSPPLGIPHPSL/TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEA VAAAAADG VTFSPVPTPHTRFSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13220	43588	B	13300	1	858	
13221	43589	B	13301	1	1098	

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13222	43590	A	13302	1	1047	MNRQLSDSYTEDTKPESDVTTT ETRSPPGSAKTTMIDTLKKLQ DVLKTEDSKNPTKSAADLLEQ YVKATGPHEILQKATKTMEMI MIVEEKASDELQDPPELQQRVI HSVRGKPGLVKQRTQEITRLR LAGLTVSSPLKRSHSLAKLGSL TFSTEDLSRPPGPPGPPGLHP GPPRRPPKLPAPPGCSVHC CHYPLHFVVSPLGFGYCSLMRI QIVFVTFVHHDSALLPLDASL APEALQNFQRYTGQIHVIRIGM AERMWCDNRNRHTVSSSGGN RLPNPAPLPNPGVL SAPPNLIQR PKADDTSAATIEKKATATISAK PQITNPKAEIT*NPVRVWQGSWI GEAVAAAAADGVTFVSVPTPH TFRHSYAMHMLYAGIPLKVLQ SLRSQ*SVRGKPLVKQRTQEI ETRLRLAGLTVSSPLKRSHSLA KLGSLTFSTEDLSRPPGPPGPP PPGLHPGPPRRPPKLPAPPP GCSVHCCHYPLHFVVSPLGFGY CSLMRIQIVFVTFVHHDSALL PLDASLAPEALQNFQRYTGQIH VHRIGMAERMWCDNRNRHT VSSSGGNRLPNPAPLPNPGVLS APPNLIQRPKADDTSAATIEKK ATATISAKPQITNPKAEITRFPCL
13223	43591	B	13303	1	1185	
13224	43592	A	13304	529	774	
13225	43593	B	13305	1	1089	
13226	43594	A	13306	712	1024	GVESNLVVVVVALCHRLIYLVW GTRTVRTWIGEA VAAAAADGV TFSVAVTPHTFRHSYAMHMLY AGIPLKVLQSRVVALDVAARH RVQFAMPESDAVAMLKQLS
13227	43595	A	13307	556	1040	
13228	43596	A	13308	1	984	
13229	43597	A	13309	95	428	
13230	43598	C	13310	1	426	

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13231	43599	A	13311	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIERVQLPQSYQLY YFELAIPIVGYFYPGFSFSTASRL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHSISTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVRETDEVG KARLTWIGTINVVCAADVLI PTPAELFDYTSALQFFDMLRDLL LKNVDLKGFEPPDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
13232	43600	A	13312	1	1593	
13233	43601	A	13313	1	2536	
13234	43602	A	13314	887	1205	RPEKAR/IWGVTDRTVVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAAR RHRVQFAMPESDAVAMLKQLS
13235	43603	A	13315	79	351	
13236	43604	A	13316	1	2320	
13237	43605	A	13317	187	798	
13238	43606	A	13318	2089	2610	
13239	43607	A	13319	1	1407	
13240	43608	B	13320	154	3682	
13241	43609	A	13321	1	1206	
13242	43610	A	13322	1	255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \=possible nucleotide insertion)
13243	43611	A	13323	3058	3160	GSAA*LPPLPAAFSGCWLSQLRHPDLHV*NEIYHLLH*KSFTSC*HNLSS*PRYPYLSSEVLW*CLSFISKI*SVTMP*DLISLW*KLEPLTCRSTSHFRQKLAQ/RLP/AYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEKARIWEVTDRTVRTWIGEAVAAAAADGVTFSVPVTPHTFRHSYAMHMLYAGIPLKVLQSLMGHKSSISTEYVTKVFALDVAARHRVQFAMPESDAVAMLKHYPEINALALYLKCGTEWIC
13244	43612	A	13324	1	1812	
13245	43613	B	13325	1	1776	
13246	43614	A	13326	583	751	
13247	43615	B	13327	826	2097	
13248	43616	A	13328	1810	4163	
13249	43617	A	13329	686	2939	
13250	43618	A	13330	1085	1690	SYFIMVKVGTSYVPINVSFSPKVGPASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRUIYKARIWEVTDRTVR/TWICRGLLPAAAAADGVTFSDPGPPHTFRHSYAMHMLYAR*YR*KFLQSLMGHKSHPINGKATPKVFGPGMGLARA/HRGAGWQWPKSDAVG\MPKQLSLRINALGLYMETGKPEGIMLFFGC
13251	43619	A	13331	3	327	
13252	43620	A	13332	3	337	
13253	43621	C	13333	167	413	
13254	43622	A	13334	1	1256	
13255	43623	A	13335	1	1078	
13256	43624	A	13336	3	976	
13257	43625	A	13337	1	1004	
13258	43626	A	13338	2	291	WRKIYEANGKKRKRLQSL*SLMKQTLNQQRSKETKKASA/SMRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWSVG RINIVKMAIPPK
13259	43627	A	13339	1	2022	
13260	43628	A	13340	1	2262	
13261	43629	A	13341	5	283	
13262	43630	A	13342	1	1245	
13263	43631	A	13343	1	1203	
13264	43632	A	13344	1	687	
13265	43633	B	13345	1	1371	
13266	43634	A	13346	1	2241	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13267	43635	A	13347	1	832	LKKCIKTPEIPSKHVRNWVPKV LEQRRQGLETYLQVASITLIPKA DEDTPKKKTTDKNSWTGTD AKVFNKILEIKFSSILKRLYWPVLE VLARAMRQEKEIKGIQLGKEEV KLSRFADDMIVYLENPVSAQN LLKLLSNFSKVSQYKINQVKSQ AFLYTNNRQ/TESQIRIKYLGIGI Q/LTRDVKDLFKENYKPLKEIKE DTNKWKNNPCSWVGRINIVKM AILPKRYPPCQLCHQSAISTTKG VFTSILPLLMIEQLVSGRSCPSV AWSSMECTTV
13268	43636	A	13348	1	1314	
13269	43637	A	13349	1	843	
13270	43638	B	13350	1	1011	
13271	43639	A	13351	1	173	
13272	43640	A	13352	1	323	
13273	43641	A	13353	3	2020	
13274	43642	A	13354	1	1473	
13275	43643	B	13355	1	636	
13276	43644	B	13356	1	456	
13277	43645	A	13357	1	619	
13278	43646	A	13358	1	1293	
13279	43647	B	13359	79	1041	
13280	43648	A	13360	3	718	
13281	43649	A	13361	1	612	
13282	43650	A	13362	1	992	
13283	43651	A	13363	1	1236	
13284	43652	A	13364	1	1071	
13285	43653	A	13365	359	1250	KLPMGVAVVKLLHLPKVIIVFW LASWMMSRWLHYDPDWVTIIAQ QVLMNVVSVMQADCRMNLLLEI FLRWLMRKIFHVRLLPAVSTPP NCLNQLLLFLLTPVNYLPGQVM HFKKPLQIKRNYLSSRHFTFMS RKKLKGKVSQYKIHVQKS/QAFL SANSQGOTESQIMSELPFTMASK RIKYLGIQLTRDVKDLFKEKYK SLLNEIKEDTNKWKNNPCSWV GRINIMKMAILPKVIYRFNAIPI KLPMTFFTELEKTTFKFIWNQK RAHIAKSNLSQKNKAGGITLPD FKLYYKATVTKTT
13286	43654	A	13366	1196	2132	
13287	43655	A	13367	1	2271	
13288	43656	A	13368	2	1105	
13289	43657	A	13369	1	2117	
13290	43658	A	13370	1	1447	
13291	43659	A	13371	1	1669	
13292	43660	A	13372	1	2823	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13293	43661	A	13373	1089	2539	
13294	43662	A	13374	1	1787	
13295	43663	A	13375	1205	1207	
13296	43664	B	13376	1	2745	
13297	43665	A	13377	1	2063	
13298	43666	A	13378	1	4380	
13299	43667	A	13379	1	3347	MGDFNIPSLDRLSTRQKVNKD TQELNSALHQADLDSYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEITNYLSDHSA IKLELRINKLTQNCSTTWKLN LLNDYVWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKA VCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQEI TKIRAELEKETQKTLQKINESR SWVFERINKIDRLARLTKKKS EKNQIDAINKDK
13300	43668	A	13380	1	2367	
13301	43669	A	13381	1	1116	
13302	43670	A	13382	1	1095	
13303	43671	A	13383	670	1500	QTESSTSKSLSTMIKWASSLG WQGWFNIRKSINVIQHIKGIQR QKPHDYLNRCKSL*QNSTTLH AKNSQ*IAQNLLKLISNFKVS GYKINVQKSQAFLYTSNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNI PCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFTELEK TTLKFIWNQKRAHIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYVYQNM CYRSMEQNRALS YYVAYLQPSDL
13304	43672	A	13384	441	3131	
13305	43673	B	13385	1	5688	
13306	43674	B	13386	916	2165	
13307	43675	A	13387	1	1529	MDPPAGAARRLLCPALL*LPAG *PLRPRLAGAAPAGTALLHER AMPL*LRPGLHDVHGVDPDL
13308	43676	A	13388	1	714	
13309	43677	A	13389	3	457	
13310	43678	A	13390	2	492	
13311	43679	A	13391	3	1201	
13312	43680	A	13392	1	309	
13313	43681	A	13393	2	1073	

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13314	43682	A	13394	3119	6984	CIVKHAAMRSAMTSLAARITVL NPTRATTPTNT/RVADDQGFLRQ WSKVAKERKLQRLYIGEPSAEA VAAQMPDLILISATGGDSALAL YDQLSTIAPTLIINYYDDKSWHPR LSFNKADEITTVCFSKSLAN GIPMANILFPTSVIATQQTQHFR FVDDFNAQFLRFASLDPAASPA ITISGKATLEIPGTGVFYAAALE KKLNKPGQTTDFGRFTLLPTC CLGNCDKGPNNMIDEDTHAHL TPEAPELLER
13315	43683	A	13395	3	587	
13316	43684	A	13396	1	315	
13317	43685	A	13397	430	636	
13318	43686	A	13398	1	84	
13319	43687	A	13399	1	1647	
13320	43688	A	13400	1	2652	
13321	43689	B	13401	1	1494	
13322	43690	A	13402	1	750	
13323	43691	A	13403	1	513	
13324	43692	A	13404	1	2254	
13325	43693	A	13405	1	746	
13326	43694	A	13406	3	428	LGDDFVRAANIILHCEGKVVS GIGKSGHIGKIAATLASTGTPA FFVHPAEALHGDLMIESRDV MLFISYSGGAKELDIIPRLEDK SIAL/GKPTSPLGLAAKAVLDIS VEREACPMHLAPTSSTVNTLM MGDALAMAV
13327	43695	A	13407	1	1431	
13328	43696	A	13408	943	2481	
13329	43697	B	13409	1	783	
13330	43698	A	13410	3	729	
13331	43699	A	13411	1	843	
13332	43700	A	13412	3	128	
13333	43701	A	13413	1	136	
13334	43702	A	13414	1	492	
13335	43703	A	13415	3	619	

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13336	43704	A	13416	1	1600	GQACHASSSPLKSGRGSPPNFEI LYGPIFEDSLAPD*PKVIAGQIT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLDFALYFFHNYQA LLAKGSGPYFYLPKTSQWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDIELHALR DHIVGLNCGRWYIFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTCRKGAFAMGGM AAFIPSKDEHNQVLNKKVA DKSLEANNHGDGTWIAHPGLA DTAMAVFNILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKQSQNLWKFA VYSGLRHGELAAALAWEDVDLE KGIVNVRNLTILDMFGPPKTN AGIRTVTLLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFA SQMGHETAQMVVEIYGMWID DMSDEQIAMLNARVM
13337	43705	A	13417	2	278	
13338	43706	A	13418	3	662	GHLWIRIDLSQSAVSHSVKELE NHTGVRLDRITREVVLTADG QQIALRLERLLDELNSTLRDTG RMGQQLSGKVRVAASQTISAH LIPQCIAESHRRYPDIQFVLHNR PQQWVMESIRQGDVDFGIVIDP GPVGDQLQCEAILSEPFLLCHRD SALAVEDYVPAALPLPEGSPLVV KRITPVVERQLMLVRRKNRSL TAAEALWDVVRDQGNALMAA
13339	43707	A	13419	1	646	GQQLSGKVRVAASQTISAHLP QCIAESHRRYPDIQFVLHNRPO QWVMESIRQGDVDFGIVIDP VGDLQCEAILSEPFLLCHRD LAGGDYVPWQALQGAQLVLQ DYASGSRPLIDAAALARNIQAN IVQEIGHPATLPPMVAAIGISIL PALALPLPEGSPLVVKRITPVVE RQLMLVRRKNRSLSTAAEALW DVVRDQGNALMAIGRE
13340	43708	A	13420	1	1068	
13341	43709	A	13421	1	381	
13342	43710	A	13422	3	938	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
13343	43711	A	13423	595	1630	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESQGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESQGDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLES GHYDHDYEFELGTR FRAVIIKLCNGDSLRFHMTSVY ALVKCFHEGDP LHKTG CQHLIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVEMLLREAGKAGFC RFRNHHTGFSPAGANQRGPL AATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGNSYDHDYEFELGTHQ RLGAVARI VGDDLNLRRDV VDARAGDVDQHAHAKEKGDFR
13344	43712	A	13424	1	1395	

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13345	43713	A	13425	1307	1992	DKLNPVAHQKAYLAQSSQCHP QNARLVQHTQIRILPISEPPSNRI FACWGWKPAWTACCN/FSQGGQA VKGNGQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQLKHKEVESPNRPI TSSEIQVLKLSPIKKSPGPDGFT AEFVERYKEELVPFLKLFTQIE QERLLPNSFYEASILTSPSRD ATKKNFRPTSLMNIYAKILNK IGQTESSSTSKSLFSTIKSVSSPE CKAGSTYANQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNGQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQETTPWSPFSDPVLAFDY KVFMFVYNNVVRVSRQRMVVA GCISAFNDKLLNDLICFPVAPVS SKQIFPSDVKVAEPDHSCVSSY RIGSMAPNLTISEMPRHNYFPA GNSVDHDNEFEL
13346	43714	A	13426	560	844	
13347	43715	B	13427	200	1519	
13348	43716	A	13428	950	1230	CSWIDRFDPWKAGRILPISEPPS NRIFACWGWKPAWTACCN/FSQ QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVK NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, ~ =possible nucleotide insertion)
13349	43717	A	13429	695	1060	FRQRSVAFPTVPNACVSVRSR ERDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQ* AQR N*CRKHRLSIPRK
13350	43718	A	13430	1	1558	MRDIFWVPDICKVMLYL VFRS MGTPPLRAVAMGLVITSWKIAQ KPRDFADFGTTINQDFRLLGQT SVDRLQLSQGQAVKGNQLLP VSLKTDTKAKNLYLT KAYYGG GTNFFRKESQKLQSAKKRDA ELANGALGIIHLLNDYTLKKVM KPLITSNTGFAFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMLQARQVSRLESG Q* AQRN
13351	43719	A	13431	391	1676	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQ* AQR N
13352	43720	B	13432	1	1638	
13353	43721	A	13433	1	2430	
13354	43722	B	13434	1	1282	
13355	43723	B	13435	1	1225	
13356	43724	A	13436	350	709	
13357	43725	A	13437	1	2236	
13358	43726	A	13438	548	1698	RSWLRSSLSGSIPIATEISCSTCE ASTSS/VRDFPGVKDLTFQWHD RLIFAIALRLGRSACGVTFHKEQ LGTVKVLRGTISQFARQRAAG QLFTHHFFGRHTALGAGNRH LRQQFSRLNVLVQPQDKGIFHH ARNECALTRRETPAFFRIRAVF NSQLSQTQLHIFTARPAGLAS KCRKPPQACYLWDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMLQARQV SRLESGQNIESAKGLHVWDSW PLHNADGTVDEYNGYHVVFAL AGSPKDAADTSIYMFYQKVG NSIDSWKNAGRVFKDSKDFDA NDPILKQDTQEWSGSATFTSDG KIRLFYTDYSGEHYG
13359	43727	B	13439	448	1116	
13360	43728	A	13440	97	1636	
13361	43729	A	13441	1	1296	
13362	43730	B	13442	1	2160	

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13363	43731	A	13443	485	865	FIRDFADFGTTIKQDFRLLGGQTS VDRLLQLSQGQAVKGNQLLPV SLVKKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQS*NSS KTKNTKCLNSINQRLKILSLQK DLMCGTAGRCKTLTEQ
13364	43732	A	13444	816	1194	SLILFLRRRRRAVEKRKGKVVWQDS CPNGTTTLTSGAIFLFIREFADF GTPITQDFRLLGGQTSVDRLLHLS QQGQAVKGNQLLPVSLVKKRKT LAPNTQTASPRALADSLMLQLA RQVSRLESGQ*AQRN
13365	43733	B	13445	1	2710	
13366	43734	A	13446	2027	2934	NPRILPISEPPSNRIFACWGKPA WTACCNFSQQAQVKGNNQLLP VSLVKKRKTTLAPNTQTASPRAL ADSLMLQLARQVSRLESGQDFA DFGTTIKQDFRLLGGQTSVDRLL QLSQGQAVKGNQLLPVSLVKKR KTTLAPNTQTASPRALADSLMQ LARQVSRLESGQSRVHSHSLGP LPTTTTGLSLNQKGGVSGGPG SKEQAEISCLKERKDLGLGILGS TVGILKVKHQGASTKQGHSD LIKILLSDTSLTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWWSGNE RDQELLTEDALDDLPSFLLTGQ QTPAFGRRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDQ MAALSRLGNDYRPTSAYERGQ RYASRLQYMNLLPIFLRWLMR KIFHDEHVPQDQEEPISEITII EEEIPINSIDLGNELYFVKLPKF LSIEPKDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKKRKTTLAPNTQTASPR ALADSLMLQLARQVSRLESGQP HSTDASATHRKMTLSLADRCST QKIRILPMAGRDPECORTEMIK SSDLMAEIIQEHKEDQLPELEQL EHIGLFSHAEIKAIKKASDLQY RIQERALFKDDFINYVLHEIPLF EQIQRRTIGYSLKHGIRAVKA TIVRALYGRIPAGVVVTRSV
13367	43735	A	13447	1	5240	
13368	43736	A	13448	4733	4753	

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13369	43737	A	13449	299	761	LNTTATLCLLLREARKLTMTHT QSTCFIKRDFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN**PVPKEKRRRGDRQE HQQPCRNTEGTALRVWAARDQ
13370	43738	A	13450	3925	4190	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQ*AQR N
13371	43739	A	13451	2	1040	
13372	43740	A	13452	58	350	HLASWVVALVLHWGCVVWTA ESSTSKTRSPFRARSWIGEAVA AAAADGVTFSPVPTHTFRHSY AMHMLYAGIPLKVLQSLMGH KSISSTGVPSSNS
13373	43741	A	13453	1	1290	
13374	43742	A	13454	289	1338	
13375	43743	A	13455	1	732	
13376	43744	A	13456	982	1347	
13377	43745	A	13457	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSPV VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPIVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRRAVNNDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEVDV RILLTKYSNSNGSQSPWMEEQI RDAWGSVMVLKNVRETDEVG KARLTWIGTINVCAADVLI PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEVDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSVM LKNVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMKLQLS
13378	43746	A	13458	1	780	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
13379	43747	A	13459	116	396	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYVTKVF ALDVAARHR
13380	43748	A	13460	3	514	
13381	43749	A	13461	2	545	
13382	43750	A	13462	1	1110	
13383	43751	A	13463	1	870	
13384	43752	A	13464	1	1422	
13385	43753	A	13465	1	1599	
13386	43754	A	13466	614	1236	TARVAAARRRCQCWGSACGS ALTLPTSSLTLTETPIVQQTRM VVRCPTASLPQWRSPSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVDTRTVRTWIGEAVAAAAAD GVTFSPVTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13387	43755	A	13467	1	1023	
13388	43756	A	13468	1	699	
13389	43757	B	13469	1	1281	
13390	43758	B	13470	77	751	
13391	43759	A	13471	1	705	
13392	43760	A	13472	2	893	
13393	43761	A	13473	206	837	CAGAGGIARRRAEKEKALSAV NLDPTSSRLSSTSLPGAPPNPRV AAAGLSRRRPTSPSAGRKS/GR WPRASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVTRTWIGEAVAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYVTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13394	43762	A	13474	1	1416	
13395	43763	A	13475	1	765	
13396	43764	B	13476	1	519	
13397	43765	A	13477	1	2784	
13398	43766	A	13478	1	624	
13399	43767	A	13479	2089	2454	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, ~-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13400	43768	A	13480	740	1431	CCQTLFVFHPPHPSHLGPRPCPP TH/HLPSEHRSFLFLEAACHDS LEPLNLSSGSKTSPSLPPKAKK PKGLEISA/RPAGALRHRRLHR PQQSPPLGIPHPSLUTAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAFAAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13401	43769	A	13481	2	2309	
13402	43770	A	13482	1	603	
13403	43771	A	13483	1	762	MVPHSTGKSWNGCDPTSATLD QLVTVFFMKLFSIGDARIPCLGP RSHSYRRSDYYSGTIIHSCRA DYWSGTTAHLRCRSDYHPVPS FILVTSTTNHQPLKPSISEASWN PLFASL/HHLQLITES/W/YMSLA TTVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAFAA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYVTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13404	43772	A	13484	1	762	
13405	43773	A	13485	1	615	
13406	43774	A	13486	887	1203	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYVTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
13407	43775	A	13487	1	855	
13408	43776	A	13488	1	927	
13409	43777	A	13489	1	921	
13410	43778	A	13490	1	3216	
13411	43779	A	13491	1	1974	
13412	43780	A	13492	1	1221	
13413	43781	B	13493	1	2337	
13414	43782	A	13494	1	1273	
13415	43783	A	13495	1	1251	
13416	43784	A	13496	1999	3237	
13417	43785	A	13497	1	1773	

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13418	43786	A	13498	1	633	AQALIAITYGRDRDPGRPLWLGLSVKSNIGHTQAAAGVAGVIKMMAMMRHGQLPRTLHVESPSPEVFIRDKLMERRNRRTGRTEKARFWEVTDRTVRTWIGEA VAAAAADGVTFSVPVTPHTFRFSYAMHMLYAGIPL/*VLQSLMGHKSISSTEYVTKVFALDVAAHRVQFAMPESDAGGPGTCACSQQCRLRGSSVSPGRQHPQPHVRV
13419	43787	A	13499	101	1943	
13420	43788	A	13500	686	3925	
13421	43789	A	13501	1	2084	
13422	43790	A	13502	734	834	
13423	43791	A	13503	1	1075	
13424	43792	A	13504	1	357	
13425	43793	A	13505	795	1273	SHPFSTDWSTDTGFRSKSIWCHRNCRW/RVAVVKLLHLPKVII VFWLASWMMRWLHYDPWVTIIAQQVLMNVVSMQADCRMNLLLEIFLRWLMRKIFHVRLLPAVSTPPNCLNQLLFFLTPVNYLPQVMHFKKPLQIKRNYLSSRLHFMSSKKLG
13426	43794	A	13506	344	449	SHPFSTDWSTDTGVRSKSIWCHRNCRW/RVAVVKLLHLPKVII VFWLASCMMSRCPHYDPWVTIIAQQVLTPRKDVMQADCRMNLLLEIFLRWLMRKIFHGFGM
13427	43795	A	13507	1197	1511	WHYREPLLRAQLTNPPSGQLVSITKYLQPVVE*AYVLE*QAHLHYQLKSVQDQWPVQKQFSSGSDLYQLHPFHVQHLEPCFPRHPEFAPPSTGTESHYYCCIW
13428	43796	B	13508	1	1494	
13429	43797	A	13509	1	554	MTARKARKITRRWRIGEAA DLVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMRDVFGRLLRAEDVFPPIGVAA HKGNDPQGTASMYHGWVPLDHIHAEDTLLPFYLGKDDVTYAIKPTCWPLGDIIPSCALHRIETELMGKFDEAQPNLGIGT/N*CRMCC*CADCSHAC
13430	43798	A	13510	1771	2068	DTYSVSWIGEA VAAAAADGVTFSVPVTPHTFRHSYAMHMLYAGIPLKVLQSQYPIFKLSYKNPVTQTA WFWFFNRIFGPVPIVNSFS PKVGPGLPGII
13431	43799	A	13511	65	277	

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13432	43800	A	13512	327	748	VHQFHGSLHEGFCAGCGCPAP GTVCDAGGFCFRFRNHHQTGFSP AGANQRGPLAAATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AKSIWCHRNCRW/RVAVVKLL HLPKVIIVFWLAS
13433	43801	A	13513	512	580	
13434	43802	A	13514	2096	2272	EWRNVCGVTGTENVTPSAAAA QPPQSRPFSWILRPF*RP*RKIS TSFIRPLFTFLPA
13435	43803	A	13515	402	2784	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI*HTQNQRSGRSQSD F*RRRNISERSAAYR*RQLYIR RQPYAERPSHVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIHELNNDYTLK KVMKPLITSNTVTDEIERANVF KMGKGYLFTDSRGSKMTIDG INSNDIYMLGYVNSLTPGYKP LNKTGLVLQMGLDPNVDVFTY SHFAVPQAKGNVIVTSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQQGLTWLQVA KRAGLGGGQSGRTVLRERLPN YKNFKGTIQELGQNYAVSGEI FVVDNRNTEITELPVRTWTQVY KEQVLEPMLNGTDKTPALISDY KEYHTDITTVKFVVKMTEEKLA QAEAAGLHKVFKLQTTLTCNS MVLFDHMGCLKKYETVQDILK EFFDLRLSYGLRKEWLVGML GAESTKLNNQARFILEKIQKKT IENRSKKDLQMLVQRGYESDP VKAWEAQEKCDNLKTCHTSH GSVMAETA VINHHKRNKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGDICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRLS
13436	43804	A	13516	2	199	WRKKSLDIPPLIIPNGIVKNILRH FSQLLNVPIRPFWSWILRPF*RP* RKISTSFIRPLFTFLPA
13437	43805	A	13517	1	1887	

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13438	43806	A	13518	125	828	ECKRHTKLKLPQTIWHVLI/Y NSEKLLVYRKLLQVLTLGYKRS NLGVRLYACCGLLCPAYPQH FAHGYYVDKIPGYGRAGTLTGL HPMQCDNLKTCHTSHGSVMAE TAVINHKKRKNSPRIVQSNLDT EAAYSLSRDQKRMVLYFVDQIR KSDGTLQEHGDCIEHVAKYAE IFGLTSAEAILRVFIKHSADMEA ITNGMMNLNRQRHQHLVALRII FAHGENGGEEVVHIGHV
13439	43807	A	13519	504	755	EPCFPAIPEFAPLSTGAESHIIY CCIW*AKYVHQARTL*DQRS*A DHEAYRKTA VRRCSTTQQAWE EQLVHQHILPSSCRYPG
13440	43808	B	13520	1	1980	
13441	43809	A	13521	923	1063	
13442	43810	B	13522	1	1932	
13443	43811	A	13523	383	1383	RKVFFIALKRPAMKKAMNLF LGLSNVRTVHIEGFTVYISTHIS FPLSGYKTRLSFGLVKQKKS PILLEVLAREIQE/KEIKGIQGF KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRKYLGIQLTRDVKDL FKENYKPLLEIKEDTNKWKNI PCSWVGRINIVKMAILPKLSRM HGRPHQPPNAASTLPFKRRSH YGQKSERLSRSGDNRKSHPECR HWQSCAKKSRCLAFTRTVRHT PRSAYLRTTIELLESSALWHV QTRQRIYAPLYETLDPGNRTHCE
13444	43812	B	13524	107	1000	
13445	43813	A	13525	1778	1897	
13446	43814	A	13526	273	421	SHPPFSTDWSTDGTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFSSAS
13447	43815	A	13527	273	697	SHPPFSTDWSTDGTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMSRWLHYPDWVT IIAQVLMNVVSMQADCRMN LLEIFLRWLMRIIFHVRLLPAVS TPTNCLNQLLFFLTPVNYLP QSGTTVPLVSSV

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13448	43816	A	13528	273	688	SHPPFFSTDWSTDGTVRSKSIWC HRNCRW/RVAVVKLLHLPKVI VFWLASWMMRWLHYDPWVT IIAQQVLMNMGVSMPADCRMN LLEIFLRWLMRKIFTTGLRSFGL VKQKKSPIRMPCVYTNPVCVSIV SRMGQASSL
13449	43817	B	13529	1	1053	
13450	43818	B	13530	1	1869	
13451	43819	A	13531	120	430	EDLSDTGVRSKSIWCHRNCRW/ RVAVVKLLHLPKVIIVFWLASW MMSRWLHYDPWVTIIAQQVL MNVVSVMQADCRMNLEIFLR WLMRKIFHSSLEDPRNWHL
13452	43820	B	13532	148	334	
13453	43821	A	13533	2	147	TSMDBKLGQALKKKI*DL*KK* LKNIPVDKWITPREVFSGIVCK QNI
13454	43822	A	13534	151	325	KAICHNTFSKPSMDKGL/LRRS KKEGFKTYKKNIYKNIPVDKWI TPREVFSGIVCKQNI
13455	43823	A	13535	283	406	HRTKISIVPEGIFKSFSPLAGIM TEQYFL*TLHRLRLIM
13456	43824	B	13536	1	1902	
13457	43825	A	13537	508	1041	LWREASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPW/C YQTWHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIDWIIERYQLPQSYQRPDPF RRRFLQVCVNEINSRTPMRLSYI EKKKGQRQITHIVFSFRDITSMIT
13458	43826	A	13538	1	1422	
13459	43827	B	13539	1	1002	

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13460	43828	A	13540	1	160	MVLIVAATV VVVVVVGLCWM AKSECRSAMRLSSLQVRIFTYLI GREAAFADNLKWMACANKES ALLDRFIFLILLCKEPWECHCL PLFKVAMP SKCDIPVICA HINIG FTLRQLRGFGPCNIGSFEAKDS KNPQVRVISQKHKALRCIWFIT CSICNPEFTEGALQGNKQRKRQ CLQWFRKALESNEPGFEFIQD KLLTQSLCFFPYTFLWLTGPHPS GSSYTDPCSSKADVTPSSAVQ EHSSALELKTIVSPITRQQHGF FTQISTLADVQENVMEYLHVLS RPKVIDQEHDVVWTEAYIDSTV CRVKRRQLLLQVPLTRKQQF LPAPYVDLDSARTRTNKQQQN PIIYTGSKQGSVILFHYGESWN LLRADQRLIFAKSWPRASRYQQ GHQDLFILRSDLPSQVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYVTK VFALDVAARHRVQFAMPESDA VAMLKQL*QPQWWWSW*D CAGWRKVNAAPCVCLPFRFA SSHTSLDERLRLQTI
13461	43829	A	13541	48	668	
13462	43830	A	13542	1	1278	
13463	43831	A	13543	100	157	
13464	43832	A	13544	1	1122	
13465	43833	B	13545	1	1131	
13466	43834	A	13546	273	812	SHPFSTDWSTDTGVRKSIWC HRNCRWESPS*SC/WHLPKVILV FWLASWMMSRWLNYPDWVTII AQQLVMNVVSMQADC/KRIC WKYFCAG*CGKIFTYQ**TWN NTETSM SQPKCKMKRI/YSREE LAV*KMDHSDLSLW*KLEPL TCRSTSHFRQKLAQGFVPSTGT PGFIYS AK
13467	43835	B	13547	1	987	

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13468	43836	A	13548	246	2065	LVGWLGDGWLGDGWLIVLALPFM MIPWHSSIQPFTHPFNWNFG*M PELCPQIGMDSWLAGWM/CWL DGWLGDG*MAKLRKPVL*PD KEGNEIWDVMTVKPSGWTVR TFDKPRKRFIFFIAGILFRAIKN HFLPRETLQCLPYILTGFRGQS EYFSIFSNDMLADTVMFILVAL PFMMIPWHSSIQPFTHPFNWNFG
13469	43837	A	13549	2	118	
13470	43838	A	13550	397	729	THGIRIGDFFCFTKRKLKRPVL* PDKEGNEIWDVMTVKPSGWT VRTFDKPRKRFIFFIAGILFRAI KNHFLPRETLQCLPYILTGFRGQ QEYFSIFSNDMLADTVMFIL
13471	43839	A	13551	147	417	SSSWGRSSPQLVCGIFQTAGPQS LCKWNQ*VLAQTNKKTAGTSA DLVVPV*QL*RKAVVLPNTAP WRFWRTRQEWFSRRGRSGYQS QET
13472	43840	A	13552	1	2418	
13473	43841	B	13553	1	1848	
13474	43842	A	13554	188	490	EWRNVCGVTGTEKVTPSAAAA ATASPIQVLTVLVSQSIRAFSV LPVRLRRSMLSRLNTCVNRF CNPICKGMRYGLICPL*SLLDGL CARLINQKGDS
13475	43843	A	13555	83	440	SLLFKCSGVIVLRRPLGYRQVM NVTTRCCLLRTHWMISLLFY*L VNRHRRSVEEYLVSYTLPMGV AVVKLLHLPKNFVSLITPRGRL EKERAFLFQHMRISITGLKIFV MHTSCPMVVC

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13476	43844	A	13556	1337	2583	QQR*MCQNLMT*HQNRSGR SQNDF*RRRNISERSAVYR*R QLYIRRPQYAEPSVHVDEKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFRKESQKLQ SAKKRDAELANGALGIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYTK VFALDVAARJIRIKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLIPFFIGLQNR TQFRLSEKTIINPYAMRVTNP CVSIVCVNEINSRTPMRLSYIEK KKGRQTTHIVFSFRDITSMITG
13477	43845	B	13557	1	696	
13478	43846	A	13558	326	1577	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQR*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHHRH
13479	43847	B	13559	1	3822	
13480	43848	A	13560	848	1476	VNVTSFGSRPICSTSPVLSGL* GPVKEFDT*PSM*ISFELIPSVIF EPRESVNYHLPILKTFARSISS VTVEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFYEVVMAFVFNVV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
13481	43849	A	13561	1	2196	
13482	43850	A	13562	326	3746	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRS*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHHRH*SCRYPS*ARCQ*LTG QIVHREGKEQQLI
13483	43851	A	13563	3802	4075	IRCFYSPAPGYVFPFRFRAVHKL NGDSLRFHMTSVYALQEA VRHTLVTLRQLVTLDPVDFQ RDDA*AIRAYDTDTGIRINAWH TDW
13484	43852	A	13564	1708	3198	
13485	43853	A	13565	1	1401	
13486	43854	A	13566	1214	1357	NKINMFIAALFTIAKT*WNQPK\ CPTMIDWIKRGSSRVASSSSPT RTR

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13487	43855	A	13567	3363	3852	SHPPFFSTDWSSDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMRSRWLHYPDWVT IIAQQVLMNVVSMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLFFLTPVNYLPG QGFAGFRNPPSNRIFACWGKPA WTACCNLSLRARR
13488	43856	B	13568	350	742	
13489	43857	A	13569	248	599	HRDSYKRMAYGLVISVVSLSR KLRKPVL*PDKEGNEIWVDMY TVKPSGWTVRTFDKPRKRFI FIAGILFRAIKNHFLPRETLQCLP YILTGFRRGQSEYFISFNMDLA DTVMFL
13490	43858	B	13570	1	2148	
13491	43859	A	13571	3064	5069	RSDPDENCC*TGH*STLFNWC WRNALSIWEPVCNEIFYRLIKPR WEIRWGKRAPVIPKHTLNTQPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSLTGTQQTP AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGELDDQMAA LSRLGNDYRPTSA YERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSPHRQ APCMKSNNALIVILGTVTLDAV GIGLVMPDLALKGLRVLLVEG NDPQGTASMYHGWVDPDLHIHA EDTLLPFYLGEKDDVITYAIKPT CWPGLDIIIPSCALHRIETELMG KFDEGKLPTDPLMLRLAIETV AHDYDVVIDSAPNLGIGTINVV CAAAHALIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPPD RILLTKYSNSNGSQSPWIEQIS DAWGSMVLKNVHAIVTGDVAV GMDDIPQEARQYRHNQAYAYS IQGDGAEDDDERIVRFHTRVT DSDTLASDAARLTCRHGLGNQ RNGGVLIEDKFECFFSLTA VFA TRAYYAVYHLTGARHSDIVVA HGYAGCNVRFVALLGTNTTLE TYLSNQGSNGFSLHFEGDVGGQ

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13492	43860	A	13572	1408	5578	CSHLIIQLANQNTHITFGKCSF TTATPIGNFYDTRYSSSTERRCLL TSQ*KRRDEIIQCVLKQLRAR SLPDPTRKVFSTLSRSTFRVNF TSRPHTGKVFVAFREPFLPPHL RKPDITDTGYLYKRMAYGSVIS/ ICFTKPKLRKPVL*PDKEGNEIW VDMYTVKPSGWTVRTFDKPRK RFIAFFIAGILFRAIKNHFLPRET LQCLPYILTGFRGQSEYFSIFS NMDLADTVMFL
13493	43861	A	13573	2678	2884	SAPLQRNTARRFLFLKACSNR FCYRWRHMTAIPSYNRSKLREI KGGLYHMGIFRRFLASKETPTF CY
13494	43862	B	13574	1	7903	
13495	43863	A	13575	1	880	
13496	43864	A	13576	1	996	
13497	43865	A	13577	763	778	NRCEPPV*GTRFSQQLLLAKA TLLIEELYALTVHSWRPKW
13498	43866	A	13578	2	254	
13499	43867	A	13579	1	2358	
13500	43868	A	13580	206	382	
13501	43869	C	13581	1	1137	
13502	43870	A	13582	79	906	
13503	43871	A	13583	2	383	SPPEVVRLLGYHPPRHGHQ*HLF ASCRKGDVGRVRP*TRPDPGSD LLPAQVPAGAARRGGTMPACV GTRSWYSTFWMEPAARPTPS MVSAASMGGH*VTPSAGLYAITS RSRLPAGGGITMTTSCSGF
13504	43872	A	13584	1	1092	
13505	43873	A	13585	173	262	
13506	43874	A	13586	898	1391	QLGILRVNLLGIDLRVTGHQAA PPLHLLDLLQMH/SSPPCRPQ*A TSPPPSLRCRAPHR*SLAAP*A PPPRPFLSAGSPHRKGGPGPAPT GSWSSGNQAGLPCCLGWASVF LCPSHLPPHLPQSSASLAFHRV KHLHLHNSVIDKMKYQLKFLC LLGEYLSV
13507	43875	A	13587	1	960	
13508	43876	A	13588	1318	1369	RDFHPK*HTGIQYIWQQLEINQ CDTSLSMVLPR*RDHFHPKSHLL PGAAQIQ
13509	43877	A	13589	212	385	
13510	43878	A	13590	377	505	
13511	43879	A	13591	69	193	CSLRSLAQMLPFYPRRSCLSCS L**PHCCLWLAALRSESK
13512	43880	A	13592	1	230	
13513	43881	A	13593	2	341	

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13514	43882	A	13594	1	2421	
13515	43883	A	13595	1	623	
13516	43884	A	13596	1	906	
13517	43885	A	13597	1	568	
13518	43886	A	13598	107	199	
13519	43887	A	13599	42	328	GGASGVCSF*CSE/LSSFWWVR GLAGSGVKLQTFATQEPSWLH PVPDPVGLQVELPASPAPCART PQPLGGRWDSAPWSRGRSSG AHGIDVALLP
13520	43888	A	13600	5	124	IWLWFFVSLT*RSRGSQ*VLQ LIKAPHVDLLVVTFC
13521	43889	A	13601	827	973	HHQSALCI*LKFYTSLTHPVISLV VETLVVW*YLYKM*KKLWSWI RGRG
13522	43890	A	13602	2	503	
13523	43891	A	13603	56	792	
13524	43892	A	13604	1	411	
13525	43893	A	13605	1	1554	
13526	43894	A	13606	1	363	
13527	43895	A	13607	1	966	
13528	43896	A	13608	932	1189	
13529	43897	A	13609	146	323	
13530	43898	A	13610	1	1827	
13531	43899	A	13611	2	412	
13532	43900	A	13612	1	2238	
13533	43901	A	13613	2	411	GATDCVCYYTVGFNDTKTSAL HMVVGDSLAMDVSSVHIINSTL LRYSVTLGFGFYGDIIKDSDK KRRRLGLARYDFLCKTFFSHH* YEGTVTFLPAQHTVGSPRDRKP CRAGCFVCRQSKQQLLEEQKT ALYGLEL
13534	43902	A	13614	3	2185	
13535	43903	A	13615	206	1568	
13536	43904	A	13616	165	417	TWDYIRPNE*YM*MAKKKMP MD/VWCNGKNWRPAG.EFVDD GVTETHFSIGNHDCYKAVSSGK RKEGIIHTLIVDNREIPEIAS
13537	43905	A	13617	463	837	
13538	43906	A	13618	1	765	
13539	43907	A	13619	3	510	AGVHKIEFEHGTSGKRVVVV DGKEEIRKEWMFKLVGKETFY VGAATKATINIDAIISGFAYEY TLEINGSLKKYMEDRSKTTNT WVLHMDGENFRJVLKEDAMD VWCHGKGIKRRPAGFVDDGTE TPLQYPGPMTCYIKAVSSGKR KEGIIHTLIVDNREIPEIAS
13540	43908	A	13620	342	585	
13541	43909	A	13621	1	1119	

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13542	43910	B	13622	48	1104	
13543	43911	A	13623	656	916	GWRKYLQGAADMGIAEGGGS VWSSWASSLSISVPVR*LCES TSQ RSAPGWPLTGGSCSEVALWL CVNDFEFQMRLMPSRDSEPA
13544	43912	A	13624	179	682	
13545	43913	A	13625	1	7511	
13546	43914	A	13626	56	8669	
13547	43915	A	13627	42	8716	
13548	43916	A	13628	1	2457	
13549	43917	A	13629	3	571	
13550	43918	A	13630	1	867	
13551	43919	A	13631	1	2238	
13552	43920	A	13632	171	396	
13553	43921	A	13633	1	3940	
13554	43922	A	13634	554	619	
13555	43923	A	13635	1	1359	
13556	43924	C	13636	208	359	
13557	43925	A	13637	2	513	PSHDHSLKGLTRASGKVLHGEH AAVHGKVALAVSLNLRRTFLRL QPHSNGKGDLSLPNIGIKRAW D VARLQSLDTSFL/RWTKEDLELI NKWAFQGERMIHGNPSGVDNA VSTWGGALRYHQKISSLRSP ALQILLTSTRG/PNRIRALVGGG RNRL/LEVPMGGPILLSW
13558	43926	A	13638	3	1331	RVDDFVGELLRLRRGGADVE AAAAAGFPAGMLSQVLLVSAP GKVLHGEHAVVHGKVALAVS LNLRTFLRLQPHSNGKVDLNL P NIGIMRAWDVARLHSLDTSFLG ECKEEKPEQGDVTTPTSEQVEK LKEVAGLPDDCAVTERLAVLA FLYLILSICKRQALPSL/DIVV WSELPPGAGLGGSSAAYSVC LA AALLTVCEEIPNPKDGD/CVN R/WTKED/LEL/NK/WAF/QGER MIHGNP/SGV/DNAVQHLGEGA LRLPSRGRFSFL*RGSPVFQI/LG LTNTKVP/SAITRALVAGVRNRL LKFPFIVAPLLTSIDALSLEC ERV LGEMGEAPAEQYL/VLEELIDM NQHHNLALGVGHASLDQLCQV TRARGLHSLKTGAGGGGCGITL LKPGLEQPEVEATKQALTSCGF DCLTSIGAPGVSIHSATSLDSR
13559	43927	A	13639	1	950	
13560	43928	A	13640	1	1653	
13561	43929	A	13641	1	2601	
13562	43930	A	13642	2	513	
13563	43931	A	13643	47	367	

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13564	43932	A	13644	1	633	
13565	43933	B	13645	1	1110	
13566	43934	A	13646	172	1095	
13567	43935	A	13647	1	855	
13568	43936	A	13648	3	440	
13569	43937	A	13649	2	230	
13570	43938	A	13650	2	606	AEFDLCCSPCRRRLLGREEAGE EPTSPVTQYLQPRSPPECKMFA CAKLAICTP*SLJRAGSRVAYRPI SASVLSRPEASRTGEGSTVFNG A\QNGVVSQ/LIPKGSFKTSAISKK TLDTA\AKFIGAGAGNS*GVG WFLVAGIG\TVFWASLIHWVM ARKPFRWKQQLFSYA\ILGICL VLKAMGSPFVLMVAFILFAHV TEITA
13571	43939	A	13651	200	2320	
13572	43940	A	13652	224	640	
13573	43941	A	13653	1	357	
13574	43942	A	13654	43	183	
13575	43943	A	13655	3	478	SSAGREPDPSDLPRRLCFTHRLP AARRVWVQLCVHASPEPGGQGV CPGRSERMVRVFIASSGFVAI KKKQDQVVRFLANKIEFEEVD ITMSEEQRWMYKNVPPDKKP TQGNPLPPQIFNGDRYCGDYD RLFESKESNTVFSFLGLKPLAS KAEP
13576	43944	A	13656	2	428	CRDGKDVVSLVRATVWALSKR KLQPTR/ALTPPSAVNLIKQF LKDKPELVDVKVGVRTGCNG LSYTVETKTKGNSDEVIQDEA RVFIEKKAQLTPLGTEMDYVED KLSSE/FMFNNPT*TCGCGAPGK LVETLGLTEIM
13577	43945	A	13657	1	1377	
13578	43946	A	13658	1	1215	
13579	43947	A	13659	1	452	REAEAADLRSEAPGRDGEDV GFLSSGQLSLGCKRKLQPTR ALTLPSPAVNLIKQLLKE*P*AC R\LKVGVRTRGCNGLSYTLEYT KTKGDSDEVIQDGVVRVIEK\K AQLTLL*TEMDYVEDKLSKGV GVH\SPNIKGTCCGESFNI
13580	43948	A	13660	3	763	
13581	43949	A	13661	1	306	
13582	43950	A	13662	738	1022	GQHHPETKAWQRHNKKREF*T NILDEH*CKNP*NTGKPNPAT HQKAYPP*SSGLHPWDARLVQ HTKINKCNPAYKQNRQKPHD YLNRCRKGL

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13583	43951	A	13663	2	516	QKIDLPYQGEPEISIQKCQEA VRQVQGPVLVEDTCLCFNALG GLPGPYIKWFLKLPGLHQ FLAGVEGKSAAYALCTFALSTG DPSQPVRLFRGRTSGRIVAPRA CQDFGWD/PCFQPDGYEQTYAE MPKAEKNAVSHRFRA/LELQ EYFGKFGQLDFCKLEAGPFR
13584	43952	A	13664	7	227	
13585	43953	A	13665	1	415	
13586	43954	A	13666	234	510	
13587	43955	A	13667	2	402	
13588	43956	B	13668	530	1544	
13589	43957	A	13669	1	603	
13590	43958	B	13670	1	1527	
13591	43959	A	13671	1	1179	
13592	43960	A	13672	2	413	
13593	43961	A	13673	100	374	KHISPAKALELPFERNLI/PLQ LLKVRILKEGEM/LD/*HWFL** GMGTQVQKGMPHKCYIIGKTGR VYNTQHAVGIVVNVKQV*VV
13594	43962	A	13674	1	1035	
13595	43963	A	13675	2	564	GPFGRRNRHLPVIRQNDGPQRGK RRGTPKYVF*/RPFRR/HGGGPL GPPYMRIVRKGDIVD/LKGMG/ TVQNGMPHKCYHGGKTGRVYN VTQHAVGIVVNVK/QVKGKILA KIRINVRIE/H/KHSKSPR*ASLK/ RVLENDQEKERSPKKGTWG SNLKRHPAPPQKKHTL*RTNGK EPELLEPIPYEFHGHN
13596	43964	B	13676	68	391	
13597	43965	A	13677	1	404	PTRTWTRGRIPLSAPPSSRGAR GTMA DPRVRQIKIKTG/VKRL VKEGVLYEKEPKQ/QEEKIEKM RAEDGENYDIKKQAEIL/QESR MMIPDCQRRLEAA YLDLQRILE NEKDL/EAE EYK EARLVLDSV KLEA
13598	43966	A	13678	1	436	LLACRSMDCYLAIVHATRTLT QQRHLVKFICGLRNLFLLLSL RILLFRRTFYPSNVSPVCYEDM GNNTANWMLRLILPQSGFIV PL/LIMLFCYRFTLH/LFKAHMG QKHWTMWWIFADVLI/LLCWL PYNLLADTIMGT
13599	43967	A	13679	1	705	
13600	43968	A	13680	292	1489	
13601	43969	A	13681	434	1205	
13602	43970	A	13682	1	390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13603	43971	A	13683	21	479	TYPEAWKLYYRSR*SRDLRKY HAHSVSP*QDQRYTS*KILKCD EHIKLGLGSCITDPGNRETSGNT MHTVFHRDKTKDTHPESCCSSE KGGQPLPWFEHRKNVPQFAEP TETLFGPDSGKGAKSLVELLDE SECTSDIEIFISQDEIQSFMANN QSFYSNREQYRQHLKEKFNKY CRLNDHKRPICSGWVDNGWEA
13604	43972	B	13684	32	438	
13605	43973	A	13685	533	1226	
13606	43974	A	13686	1	1566	
13607	43975	A	13687	215	453	
13608	43976	A	13688	1	553	RRPARAAVIKQPPAPGASQHAA TPTQTPLCTPARPLPPMAHVQQ LEGRWRLVDS\KGF**NTMKE\I GVT\IALRKMGRNAQAQICIT\TS DG*NPSP\KTESTLKT\TQFSC\T/ LWGEKFEETTA\DGQKKLTNCL STFPDGA\ALVQHGEWDGERKS TVTKKN*KDGEISWLECVMMN\I VTCTPDSMKK
13609	43977	C	13689	11	106	
13610	43978	A	13690	3	155	LCELQKAIDLFTDAIKLNRLAI LYAKRASVFVKLQKPNAAIRD CDRAIEINPDSAQPYKWRGKAH R*ILAWPFCMPRGVSSSNYRS QMLPSETVTEPLK
13611	43979	A	13691	1	1732	
13612	43980	B	13692	95	1715	
13613	43981	A	13693	1	446	
13614	43982	A	13694	1	786	
13615	43983	A	13695	88	828	

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13616	43984	A	13696	157	1515	RREKMAELKYISGFGNECSSED PRCPGSLPEGQNNPQVCPYNLY AEQLSGSAFTCPRSTNKRSLWLY RILPSVSHKPFESIDEGHVTHNW DEVDPDPNQLRWKPFEPKASQ KKVDFVSGHLTLCCGAGDIKSN NGLAIHIFLCNTSMENRCFYNS DGDFLIVPQKGNLLIYTEFGKM LVQPNEICVIQGMRFSDIVFEE TRGYILEVYGVHFFELPDLP ANGLANPRDLFIAPWYEDRQV PGGYTVINKYQGLFAAKQDV SPFNVVVAWHGNYTPYKYNLKA NFMVINSVAFDHADPSFTVLT AKSVRPGVAIADFVIFPRWGV ADKTSGPPYYHRNCMKRFME LIRGQFEQKQGWFLPGGRG/SL HSTMTPHGPDADCFEKASKVK LALKRIADGTMA/FMF*SSFNLA GPKWGLQAPRVLDKNYPKCW EPLKSPFVTPNSRNPAPEN
13617	43985	A	13697	1	156	
13618	43986	A	13698	8	306	
13619	43987	C	13699	1	1143	
13620	43988	A	13700	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPFEDQEGGQRLRSSHIR LGQFLLIEDCKTPSPSLGADAI AKQRKTSVSAASVSATIPIRR VQGPVTVGSWARGVSAASGP RGTGPKGKARSEKGCSSLSHGPQ TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSH LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAIYMNMGKGL PIWCHLLEEGIYLEVWALEGQF GRAKNACPQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGWQKP NGQWSLVQDLRLISEAVIPLY VVPNPYTLSSQIPEAEWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPGQFR DSPHLFGQALAQDLGHFSPGT LVLYYVDDLLLTSSSEASCQQA TLDLLNFLANQGQYKASRSKAQ LCLQQVKYLGILARGTRTLGK ERIQPILAYPHPKTLKQLWGLF QIT/GFCQLWIPR*SKI
13621	43989	A	13701	188	688	

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13622	43990	A	13702	636	2628	SNDRTEDDCGKHPPMSSPPTEP WVCLIEGQEIDFLDTGTTFVS LIPCLGRLSSRSVTIQGILGQPV RYFSLHLLSCNWETLLFSHAFLV MPESPPTLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDP SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLISQVPEEAEW FTVLDLKD
13623	43991	B	13703	302	619	
13624	43992	A	13704	1	5172	
13625	43993	A	13705	1	2091	
13626	43994	A	13706	1	1754	GPRGTGPGKARSEKGCSSLHG PQTNKPLVVQKGQKMEQANHP VGLVISVYKDIKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIYMNMG KLPIWCHLLEEGIYLEVWALEG QFGRKNACPVQIRLKDPPTTF YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILG KPNQGWSLVQDLRLISEAVIPL YPVVPNPYTLISQIPEEA VFLDKDAFFCIPLHYDSDSQF LFAFEDPTDHTSqliwTVLPQ FRDSPHLFGQALADLGHFSSP GTLVLQYVDDLLATSSASCO QATLDLLNFLANQGYKASRSK AQLCLQVKYLGILARGTRTL GKERIQPILAYPHPKTLQWL GLEITGFC* LWIPGYSKIARPLYT LIKETQRANTHLVEWESEETA FKTLKQALVQAPGLSLPTGQNF SLYVTERAGIALGVLTQTRGTT PQPVAHLKETDVAAGWPHC LRVVAAVLVSEAIKIQGKD LIVWTTHEVNGILG/AGKSLWL SDKRLFRYQALCLEGLVLIQRT SCGSHLAVTRLWALYF
13627	43995	A	13707	2	887	

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13628	43996	A	13708	3	1750	GWAVPRPGPRGLTVATEAAAA AAAAAAAIISSRTRAPQAEGR NRRLEKMADDIDIEAMLEAPY KKDENKLSANGHEERSKKRK KSKSRSSHERKRSKSKERKRS RDRERKKSKSRERKRSRSEKRR RSRSRSDRRFRGRYRSPYSGP KFNSAIRGKIGLPHSIKLSRRRS RSKSPFRKDKSPVREPIDNLTPE ERDARTVFCMQLAARIRPRDLE EFFSTVGKVRDVRMISDRNSRR SGIAYVEFVDVSSVPLAIGLTG QRLGVPIIVQASAEKINRAA AMANNLQKGSAGPMRLYVGSS HFNITEDMLRGIFEPFGRIESQL MMDSETGRSKGYGITFSDSEC AKKALEQLNGFELAGRPMKVG HVTERTDASSASSFLDSELER TGIDLTGTGRLQLMARLAEG TGLQIPPAQQAQMSGLAF GAVGRNLCYRFKQDFSHQT ETSALSAASVQPLATQCFQLS NMFNPQTEKEVGWDTEIKDDV IEECNKHGGVHIHYVDKNSAQG NVYVKCPSIAEIAAVNALHGR WFAGKMITAAYVPLPTYHNL PDSMTATQLLVPSRR
13629	43997	A	13709	141	343	LHEGLLP*RGHALLSGALHG*C VGSLFSTPRCLTSSACGYPS CTPGSCTAWCPASRRRLSCWT
13630	43998	A	13710	5	426	
13631	43999	A	13711	1	1188	
13632	44000	A	13712	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEDP NCHEQHLSNTATHLGTQDEAVI DGRRKPEESRTTSHICRCS
13633	44001	A	13713	1	700	
13634	44002	A	13714	3	483	
13635	44003	A	13715	2	361	RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNLKIIISNA SCTTNCLA/PPASTGAAKAVGK VPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13636	44004	A	13716	2	249	SADAPMFDMGVNHEKYDNL NII/SVMKAGPVEKRPAPWHMPD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDFNGIVEGLMV

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13637	44005	A	13717	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKGVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQERYPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPADAPM FVMGVNHEKYDNSLKIIISNA/S CTTNCLT/PLAKVIHDNFGIVEG LMTTVHAITATQKTVDPGSGKL WRDGRGALQNIIPASTGAACA VGKVIPELNGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVKQA/SEGPKLGILGYTEH QVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13638	44006	A	13718	3	483	
13639	44007	A	13719	2	361	RRFRAGAGYVVESTGVFTTME KAGAHQGGAKRVIISAPADT PMFVMGVNHEKYDNSLKIIISNA SCTTNCLA/PASTGAACAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13640	44008	A	13720	2	249	SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRP/WHPM D TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
13641	44009	A	13721	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKGVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQERYPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPADAPM FVMGVNHEKYDNSLKIIISNA/S CTTNCLT/PLAKVIHDNFGIVEG LMTTVHAITATQKTVDPGSGKL WRDGRGALQNIIPASTGAACA VGKVIPELNGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVKQA/SEGPKLGILGYTEH QVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13642	44010	C	13722	40	243	
13643	44011	A	13723	2	2972	
13644	44012	A	13724	1	602	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13645	44013	A	13725	1	325	MGRNQSRKAENTKNESASSPP KDRNSSPVREQSWTENEFDEL EVGFRKLVTNFSELKEHVLTD HKEAKNLEKS\LEVVAAREISQ KEIKVFN*EKRKSNCPCLQMT
13646	44014	A	13726	1	981	
13647	44015	A	13727	1	739	MGRNQSRKAENSKNQSTSSPPK DCSSSPAREQNWTKNEFDELTE VGFRRLIANFSKLKECVLTHR KEAKNLEKSDRENGTKLENTL QDIIQENFPNLRQANIQIEIQ RIPQRYSLRRATPRHII\VRFTKV EMKEKMSRAAREKGRVTHKG KPIRLTADLSAENLQARREWGP VFNLK\NFQPRIPYPAKLSFISG GEIKSFDTKQMLRDFFTTRPAL QELLKEALNMERNNQYKPLQK HAKW
13648	44016	A	13728	1	1277	MKEQNGGGGREEDHKDKGIRQ LPSSLPSAGEAKSDKPEHHNRY RKEIASFEDEKRAMGVAKMAE QEQLQSAAPSMTNAEVGTAHG GRAEAGRGVDSGPKRKVLGDF PFLAKGSRDRLPGKAGHSLPKY YAFTKVLATGRQERNINISKK VIYTKTTSTGHQHQRPKIDKTT KMGRNQSRKAENSKNESTSSPP KGHSSSPATEQSGTENDFDEL EVGFRRSVTTNFYELKEDVQTH RKEAKNLEKRLDKWLTRINSV EKTLSDMELKTMARELRDTC SSFKSRFNQVEERVSVIEDPIYE LSREDKVRDKKVRNKQSLQEI WDYVVRPNLRVIGVPESDGEN GTKLENMLQDIIQENFPNLRQ ANIQIEIQRTQRYSSRRATPR HII\VRFTK\VEMKQKVLRAAREK GPVTHKGNSGSL
13649	44017	A	13729	1	1584	
13650	44018	A	13730	493	575	SHPMPNPANTRSQRNPTKKKQ KKNV\CDNIRELEQQMEDAYR GTRKRMPLSSSSMRSDGFDEE SQRYYWRPKNEISGTLDDFLK AKSWNRKFYDYANMPDRWG\ QVAIKSYTLKNLQTVVISIKLP TGRKHLPR*SHPMPNPANTRSQ RNPTKKKQKKNVCG
13651	44019	A	13731	1	655	
13652	44020	A	13732	2	1664	
13653	44021	A	13733	1	2364	
13654	44022	A	13734	1	224	

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13655	44023	A	13735	1033	7511	
13656	44024	A	13736	56	8669	
13657	44025	A	13737	42	8716	
13658	44026	A	13738	1	5046	
13659	44027	A	13739	1	2298	
13660	44028	A	13740	1	2362	
13661	44029	A	13741	1	2046	
13662	44030	A	13742	1	1503	
13663	44031	A	13743	1	813	
13664	44032	A	13744	185	735	
13665	44033	B	13745	317	910	
13666	44034	A	13746	1	867	
13667	44035	B	13747	1	2325	
13668	44036	A	13748	1	430	
13669	44037	A	13749	1	867	
13670	44038	A	13750	35	518	CLSRASPVLASMSGRGKTG GKARAKAKSRSSRAGLQFPVG RVHRLLRKGHYAERVGAGAPV VLAAWLEVAQPLRVLELAGN AA/RSNKKTRIIPRHLQLAIRND EEL*KLPGLP*RIAQGSRLVLPNI QA/VLLPKKTSATVGP/PAKPSG GKKATQASQEY
13671	44039	A	13751	1	937	
13672	44040	A	13752	1	1096	
13673	44041	A	13753	85	1512	
13674	44042	A	13754	3	2377	
13675	44043	A	13755	1	1134	
13676	44044	A	13756	49	408	
13677	44045	A	13757	47	2603	
13678	44046	A	13758	1	378	
13679	44047	A	13759	1	696	
13680	44048	A	13760	3	401	
13681	44049	A	13761	882	1106	KLHPYTTRQYCHFRI*TDVMAK RSRNAVKGSLVWCAISDFA AGFTPDGCTRAFTFTGGWRK RDCRGAVAGG
13682	44050	A	13762	688	1100	
13683	44051	A	13763	476	552	
13684	44052	B	13764	178	1107	
13685	44053	A	13765	1	198	
13686	44054	B	13766	94	625	
13687	44055	A	13767	1	732	
13688	44056	A	13768	1	4443	
13689	44057	A	13769	216	575	PGAGDRYVGKPVSAVGTAVSC GVWSSMPDATLIASYQAYTSH VGRIRRSRRIR/TNTARADYPAL TALPFNNFRTHNRFGNAAVSL ASIGIGSSLICARISAHSGAEH KPPEPKAANIK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13690	44058	A	13770	1018	1489	KLPGQRRFVQTPSHVLHTLSYPTAPAQSSYPAPLSPSQDRAPTLAHQTT*FSASYTANAQWQRVAADHLKSVRETYAHVRQFSPALGNAPPDQLPLS*ASCVPKSGARYSSVIRQNRDRFFRATDHMYVTVPTRPKMWNPNVTQMNSFRA DTCE
13691	44059	A	13771	1013	1755	GSPGLRPGGAAGKALAPSGCTGNSHRAMP*PGAQAQTRPEKW A*QRP/HVSTGARGARVRALAA VAAAEAQRAAGAAVRAAALHTRAAVSAGAAARAVVQVVLAA RTREAGAAAAAQGVAQVQAES AIAAWLQAAPVHPLLTVGALE TGWAVADVGRVRVCTPDTQA AVEAGSICTCHPAHLTPQPVEPTRAGAFKGPGLTTAASIGTRVPVTGPRPRDKASGGSRGRAPGA EAAAGGDRDRAEGSSPAL
13692	44060	A	13772	1	1236	
13693	44061	A	13773	1	456	
13694	44062	A	13774	1	219	
13695	44063	A	13775	1707	1853	
13696	44064	A	13776	1	615	QLATFFFGGLPGGSAPWDPPGEACLWVLVRLPGRTVWVIQFVQLRSFFAPPFANHGRASSGRVSVHYGIAQTAEWAAEICGVGAR KIRELAAIFHQNTIMHFANGG/NPTRRS AVLSSMQGSLPGGCDAVDIHPVARIVEALENPGGAYQHNGMNRHFPDIRFIWWAGGANFTHHQDTRNLIRAWQNDYSYFRKGRIKAKMGPKLF
13697	44065	A	13777	407	661	ANWIKWRWIIRAMIHSSSSMWQTANSLASFISAPVTSSACRSTLPATRYWCI*WRSSAIWKWVILSGPVATRICTATIWIQLICN
13698	44066	A	13778	1	2448	
13699	44067	A	13779	3	1612	
13700	44068	A	13780	1	1626	
13701	44069	A	13781	3	118	
13702	44070	A	13782	1175	1396	
13703	44071	A	13783	197	933	
13704	44072	A	13784	2	64	IILLNSAPAWM*TFKLPGVDVNYMLHTQNK
13705	44073	A	13785	1	855	
13706	44074	B	13786	1	1605	
13707	44075	A	13787	1	588	
13708	44076	A	13788	1	2769	
13709	44077	A	13789	813	1341	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
13710	44078	B	13790	1	999	
13711	44079	A	13791	1	281	
13712	44080	A	13792	1	1332	
13713	44081	A	13793	1	1384	MPITLRRSVEKEQLIEANTIMPF GKYKGRRLIDLPEEYLLWFARK DEFFPAEARYTHIDLHVPAPLLV MFTLDTRQSAACDRNP.H.PIHVC SSWTSKCAPRLWTRALLPRTR TPPYATGTTIGSRASWFVTFPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLHKM VEVNACLKQLDNKDIADYEHN QLMRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSVVVEETR EAVDTSQPVAT
13714	44082	A	13794	1	2004	MTQQITLIKDKILSDNYFTLHNI TYDLTRKDGVEVIRHKREVVYDR GNGATILLYNTKKKTVVLIRQF RVATWVNGNESGQLIESCAGL LDNDEPEVCIRKEAIEETGYEV GEVRKLFELYMSPGGVTLEIHF FIAEYSDNQRANARGGVEDEDI EVLELVQCGGQIGVDPDTVLAVF ATGIGFLAMSVTKPRINAQPPY MPWRNLAQLVEHINRTRIHRNL QFTDAFKRRLIDNICRKNNIIGT HTGQSKFSGQTQIFGEIPQVVP ASELAAMKQIKELQRLLGKK TMENELLKEAVEYGRAKKWIA HAPLLPGDGERTDDWMDGRRS RHTDDTDVLLRIHHVIGELPTY GYRRVWALLRRQAELDGMPIAI NAKRKYRIMRQNALLERKPA VPPSKRAHTGRVAVKESNQRW CSDGFECFCDNGERLVRTFALD CCDRLSSRGRNAAAKRQRDDP LRWKFRLPSSGTLKLLMPLDQQ APARFAPVFTCTLTILCGTHV VYTLPIHYDVAIKNNIRPERPM AASSIGAQMGHASPVSVAVVS VAMLGNVTFDGRHLEFLDLLAI TIPSTLIGILAIGIFSWFRGKDLD KDEEFQKFISVPENREYVYGD ATLLDKKLPKSNWLA MWIFLG AIAVIALLGADSDLRSSF/GGKP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
13715	44083	A	13795	3	918	DKTRKRRIRQ*IPNATSFYQNS PGLSE*LAAGTWTFAGNAPASS CGFRDRYLIVCSHQTPHVPQGI TVAAPDARAQAIRIVRQLQRF FHRFEGGHRQHRAKNLLLEHP HIVLTQKNRRFEADALQPDPA WQQGTLSNGLQWQVLTTPQRP SDRVEIRLLVNTGSLAESTQQS GYSHAIPRIALTQSGGLDAAQA RSLWQQGIDPKRPMPPVIVSYD TTLFNLISLPNNRNDLKEALSY LANATGKLTITPETINHALQSH DMVATLVFRYLKKGWWRYL KGSTLLSHDPAHPLKQVVEAK
13716	44084	A	13796	1	1368	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAVYGIAWMA ETMFAPACYGYILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVCVFGWIFAAIKRDA AAGRAKENVIFHHFPQSVKAD IATNPFKRPGGAFIRITQFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNPLDSSVLSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTGAIPFAAADPLR/PSFGG KPLSMVLVIQMFMLLTGALIIIL TKTNPASISKNEVFRSGMIAIVA VYGIAWMAETMFAPACYGYI LPTYPSDLAAIQFDRSGTTHIGR FVINHSFILPGLIGVSVCVFGWI FAAIKRDAAGRAKENVIFHHF PFQSVKADIATNPFKRPGGAFIR ITQFRTVQTFRLSAYRLDFAG DRLRISTPRAKMRTAFKKDHLR QRRRCIRQAPPARHNLVGAV ALPATVAGVNFTFSNPLDSSV LSLLTDFSTAVGSIVMLAVIM GLMLAFDMGGPVNKVAYAFM LICVAQGVYTVVAIAAVGICIPP LGMGLATLIGRKNFSAEERETG
13717	44085	A	13797	3	2185	
13718	44086	A	13798	1	920	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13719	44087	A	13799	251	479	TQRVDWRSRSSISPGDGLHAFP AFGKEGGKMLDRLRERRDVKT LQSGSAAAGAEFALAGAHPT GTTA*IQAINV
13720	44088	A	13800	1	939	
13721	44089	A	13801	1	386	
13722	44090	A	13802	3	524	
13723	44091	A	13803	1	548	
13724	44092	B	13804	67	1144	
13725	44093	A	13805	811	974	VSRRIKLDVTEEFARAGDNRKC ICQ*RHGLAERDIARLLVEIVVI WCDIGVIQA
13726	44094	A	13806	1164	1262	
13727	44095	A	13807	2	894	
13728	44096	A	13808	1	1587	MVKEGTFREDLFYRLNVIHLIL PPLRRDRREDISLLANHFLQKFSS ENQRDIIDIPMAMSLTAAWSW PGNIRELSNVIERAVVMNSGPPI FSEDLPPQIRQPVCNAGEVKTA PVGERNLKEEIKRVEKRIIMEVL EQQEGNRTRTALMLGISRRAL MYKLQEYDATGFFRDMGTIMV GGFMGIGTPSRLVEALLESQVR DLTLIANDTAFVDTGIGPLIVNG RVKRVIAISHIGTNPETGRMRMSG EMDVVLVPQGTLEIQRGCGAG LGGFLNPTGVGTVVEERQTSID TSTRKRPFELGRPSRNNDKGIRP VDQALDRKNIRE/ALHDSLKRRLQ TDYLDLYQVHWPLRPFYCFGK LGYSWTDSPAPVSQDLTDLAL AEYQRAGKIRYIGVSNETAFGV MRYLHLADKHDLPRIVTIQNPY SLLNRSFEVGLAEVSQYEGVEL LAYSCLGFGTLTGKYLNGAKP AGARNTLFSRFRYSGEQTQKA VAAAYVDIARRHGLDPAQMALA FVRRQPFVASTLLGATTMDQL
13729	44097	A	13809	1	618	

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13730	44098	A	13810	80	952	RPGIVALNAILPLSRTQSKPTR LKKRAIANCAPTWKKRFVALV YRTA*RFPSITLSVAVT*PASAK NKAIKMTQKIEQSQRQERVAA WNNRAECDLAAFQNSPKQTYQ AEKARDRKLKANLEAIRRSG LQDGMTVSFHHAFRGDDLTVN MVMDVIAKMGFKNLTLASSSL SDCHAPLVEHIRQGVVTRIYTS GLRGPLAEISRAYCADSHHGP FAMVNNMTDLTAQEPAWQTR DHLDDPVIGELRNRFQPDFTV QATRTGVPPVWIKREQLLEV GDFLKKLPKPYVMLFDLHGMDE RLRTHREGLPAADFSVFYHLISI DRNRDIMLKVLAENDLHVPT FTKLFPNANWYERETWDLFGIT FDGHPNLRWIP
13731	44099	A	13811	92	735	RLRLPLQPRESSVLPLGTTFHAS STSETRQSKPTRLKKRAIANCA PTWKKRFVALVYRTA*RFPSIT LSVAVT*PCVNIITIGQVKTVT TIATAQIQRTFRNFHSRFQYFR NSPKQTYQAEKARDRKLKANL EEAIRRSGLDQDGMTVSFHHAFR GGDLTVNMVMDVIAKMGFKN LTLASSSLSDCHAPLVEHIRQ GVVTRIYTSGLRGPLAEISRGLL AEPVQIHSHGGRVHLVQNGEL NIDVAFGLVPSCDFEGNANGYT GKACCGSLGYAIVDADNAKQV VMLTELLPYTDNPEA
13732	44100	A	13812	1	1113	
13733	44101	A	13813	5121	6228	LRRDSGRLRSCWHPRSPSTMG SGLQREDLQEDRNSGADPGQR GRCSIHLEGGPGQPCQLQRAVQ EGDPVLAKEEIQDQCHPHGQV QLLLVPAEPPVRAVPPRVQPV PHHHHPAELSGIREE*GNQND EN*TISTTRTGSGLESSR*M/SILP LSRTRQSKPTRLKKRAIANCAP TWKKRFVALVYRTA*RFPSITL SVAVT*PYWSGAPGPGCRPPYC HFRHRGARGSGAPGDGGEAPP AAAFGGDVGFGL
13734	44102	A	13814	56	196	CRGDGGKLIHQCRMRMG*PCG* LRQRKAELFQHLPLC*FWRPEI GTVCSGSIDNGSDRLRR
13735	44103	B	13815	64	2373	
13736	44104	A	13816	3	403	
13737	44105	B	13817	55	1040	

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13738	44106	A	13818	587	1533	VLLTAKFFPSMYSPIKTAGGPA ST*VL*MIISIDAEKAFDKIHQPF MLKALNKSENKIPRNPPTYNGCE GPLQGELQTTAQGNKRGYKQT QQHDMHMTKNQYHENGHTA QGMKGITQPSAFIPTAESNSFQP QVKTLPSPIDAKQQLQRKIQKK QQEQKLQSPLPGESAAKKSESA TSNGVTNLPNGNPSILSPQIGIV VAAVPSPIPVQTRQLVLTSPSP MSSSDGKVLPLNVQSHQNCW WTRFNMSLNVVKMTTISLTPS NSNTPLKHSASFISATGTTEESR SVPQIKNGSVSLQSPGSRSSSA GGTSAVEVKVEPETSSDEHPVQ CQENSDEAKAPQTPSALLGQKS NTDGAQKPSNEGVEIKATKE RRSSPAEQSWMENVFEEQREE GFRRSNHSQIREDSQTKGKEEK RLKELMELKTKVRELREECRL RSRCDQLEERSVAMDDDEMNE KREGNFRKRIKRNEQSLQEIW DYVKRPNLRLGVPESDGNGT KLENTLQDIIQENFPNLRQANI QIQEIQRTP
13739	44107	A	13819	590	817	
13740	44108	A	13820	107	410	KGRNIQLNGPSSRVSLWRSLYF LNLNTGLPC*IGEVLLDNILQSV FQLGSILPITFRYTNQT*1WSFHI VPYFLEALLISFYFFSKLPFSLH FIHFIHFR
13741	44109	B	13821	1	3735	
13742	44110	A	13822	922	1137	HFFLHFNFGESDNYVSWSFSSR GVSLWRSLYFLNLNVGLPC*IG EVLLDNILQSVFQLGSILHITFR YTNQT
13743	44111	B	13823	1	954	
13744	44112	A	13824	3	156	
13745	44113	A	13825	683	972	SHRLLRLHSSRSSPGLVSSSISS FKHFSVLVILFTLMIVSFAVQKL FSLIRSHLSILALVIAFGLVLM KSLPTPMSSMVLRS/SFF*GFYG FRSYI
13746	44114	C	13826	1	895	
13747	44115	C	13827	372	1727	
13748	44116	A	13828	705	1072	LALLVELIPLPLCNGLLCLF*SL LV*SLFYQRLGLQPLPFFVFHLL GRSSSILLF*AYV*LFWHDFAA AGTGCSFPCLALPSGALVGQA WW*QKSLICLSVKDFISPSLM KLSLAGYEILG

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13749	44117	A	13829	1	1136	
13750	44118	A	13830	547	675	
13751	44119	B	13831	144	1877	
13752	44120	A	13832	1	441	
13753	44121	A	13833	27	344	
13754	44122	A	13834	287	600	GPGLQSSPLLSPWPWRASSPLL LRPSVRGWHLGEP*NCFPSPLA AS/EQAPKRSS*PQCNRH*RETA ARGLAYPPDRPLPSMLSCESPE TPAKAGPGRERGCEKC
13755	44123	A	13835	2	226	
13756	44124	A	13836	2	226	
13757	44125	B	13837	45	518	
13758	44126	B	13838	1	699	
13759	44127	A	13839	3	362	
13760	44128	A	13840	2	130	
13761	44129	A	13841	3	96	
13762	44130	A	13842	1	545	
13763	44131	A	13843	2	144	
13764	44132	A	13844	2	91	
13765	44133	A	13845	1	370	
13766	44134	C	13846	1	214	
13767	44135	A	13847	215	310	
13768	44136	A	13848	2	91	
13769	44137	A	13849	1	289	
13770	44138	A	13850	1	997	
13771	44139	A	13851	1	192	
13772	44140	A	13852	2	267	
13773	44141	A	13853	2	181	
13774	44142	A	13854	1	171	MESYAAIKNDEFMSFVGTWMK LETILSKLSQGGQKTKHCMFSL TDVIARRRSWTSI
13775	44143	A	13855	92	244	KRRRRRGQIRKMKEEENRRT WMKLETILSKL*QRQKTKHRM FLLIGGN
13776	44144	A	13856	146	382	
13777	44145	B	13857	124	1215	
13778	44146	B	13858	1	628	
13779	44147	A	13859	377	484	
13780	44148	A	13860	2	220	WARTSCLKHQKQWQKPKLA NGI*LN*ASAQQKLPSEWTG TWMKLETILSKLLQGGQKTKHR MFLIGGN
13781	44149	A	13861	965	1150	GVDQRAVCSSRIW*SHLFLFHS VVVHLPWAGTWMKLETILSK LSQGGQKTRHRMFLIGGN
13782	44150	A	13862	254	571	YSYKLEIIGKQPEIYRDCYRP AV*SQTAVLASEAPWA*DLPS QVSDTISWWTVC*AHWKSAVL GWE*PGFPGTWMKLETVSLSK LSQGGQKTKHHMFLIGGN

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13783	44151	A	13863	62	214	
13784	44152	A	13864	274	435	
13785	44153	A	13865	1	294	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSLVYIFFLDEFM YFAGTWKMLETHLSKLSQGOQK TKHRMFSLVGGN
13786	44154	A	13866	663	1266	PPLTCQCSHLCVTLVGH/WIKLE THLSKLSQGOQKTKHRVFSLIGG AGALAKECMSLYPGCKITVFDI PEVVTWAKQHFSFQEEEQIDFQ EGDFFKDLPEADLYILARVLH DWADGKCSHLLERIYHTCKPG GGILVIESLLDEDRGPLLTQLY SLNMLVQTEGQERTPTHYHML LSSAGFRDFQFKKTGAIDAIL
13787	44155	A	13867	1	681	
13788	44156	A	13868	1	247	
13789	44157	A	13869	2	178	
13790	44158	B	13870	1	2042	
13791	44159	A	13871	1	378	
13792	44160	A	13872	1	683	
13793	44161	A	13873	1	972	
13794	44162	A	13874	308	406	
13795	44163	C	13875	177	653	
13796	44164	A	13876	1	465	
13797	44165	A	13877	3	1175	FFSSQAAALLVVLGSSHTLQRA RKHSAPGLPDTCALLQPPAASA AAAPSMSPDVPETPSAIQICRIM RPDDANVAGNVHGGTILKMIE EAGAIISTRHCNSQNGERCVA LARVERTDFLSPMCIGEVAVHS AEITYTSKHSVEVQVNVMS ENI LTGAKKLTNKA TLWYVPLSLK NVDKVLEVPVPPVYSRQEQEEE GRKRYEAQKLERMETKWRNG DIVQPVLNPEPNTVSYSQSSLIH LVGPSDCTLHGFVHGGVTMML MDEVAGIVAARHCKTNIVTAS VDAINFHDKIRKGCVTISGRMT FTSNNSMRFKVLLDPAPVVD S FQKRYRGRQCLSS*VSLSQER QV/PLPVPQLVP/ETEDKKRFE EGKGRLYQMKAKR/QGHAEPQ
13798	44166	A	13878	121	361	SLFELENRSKFSVATAGLVPSR RLSINCIRRAFITSSNGFPLWFCL HQKGPVDCCVAVY*CGTEDGS WAPTHPGVGPSLP
13799	44167	A	13879	1	462	

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13800	44168	A	13880	3	287	PCSLSSDCCASNQRDSVIGIPSE PRVGYNILVIRFLSPSEKRSR\IV GVTRFSSAWEPSQLAGILPISEP PSNRIFACWGKPAWTACCNLSLR ARR
13801	44169	A	13881	1	1332	
13802	44170	A	13882	1	753	
13803	44171	A	13883	1	516	
13804	44172	A	13884	71	277	IYFNTQESFCPPRPLK/LCDGRG CHKGL*NAFKAFSPFSWPLALG SFLLMQISAACLNSFPENGLFFS TT
13805	44173	B	13885	1	1095	
13806	44174	A	13886	1	741	
13807	44175	A	13887	264	2880	WLLQKHKLHVSRLGLPDTSW ILPSRPDAGGRFPRTPPCVL VV HKPSRHCREWTA NTVPK GAL AKWLLEPKADLQGWHL PADG QYTKPSISYNIKLYINCYNRTVT TAAQHQQVQRKHGASIFLAEN VAVREKDKEEKVTRAPTEQA WTAGSWIETAYREIKGVGQES VCITVMHLEELVYELAWIUMSA VVEAFDPVAPSSKRLNPD PDP YCCTPYTLHTSPPPSPCTPYT LHTGPPPTPFCTPYTLDTSPS PQTHSCCTPYTLHTVPTFHLPA AHPHLLHTIPPQTQGGQFVSED EYLEISDIKRDQSGEYECALND VAAPDVRRKVKITVNYPPYISKA KNTGVSVGQKGLSCEASAVP MAEFQWFKEETRLATGLDGM R IENKGRMSLTFFNVSEKDYGN YTCVATNKLGN TNASITLYVD HIVGSKALLSKCKRTEIITNYLS DHS AIKLELRINKLTQNHSTTW KLNNPLLNDYVWHNEMKAEIK MFFETNKNKDDTTYQNLWDAFK AVCRGKFIALNAHKKRQERSKI DTLTSQLKELEKQE QTHSKANR RQEITKIRAELEIETQKTLQKI NESRSWFFERINKIDRLRLRIK KKREKNQIDA IKNDKG DITTYT TEIQTITREYKYKHL YANKLENL EEMDKFLDTYTL PRLNQEEVES QNRPTTGSEIVAINSLPTKKSPG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13808	44176	A	13888	1	629	AMAGSPPASLLPCTLISDCCAS NQRDSEGVGPSEPGVGYSLVV RRFLSPSEKRSIRVGVTFRSRR PSPLSLTQKGNSLTWSAQVLT PAPEKQPDNKLPLPRGSRDPT EYFHGQEVDRKSDHEVHDHVSQ IHSFRDEVKRLGAEDSSNAETP TELHEFNTGGVYRPPNSTSVIQP LDQGVIRTFKPCYTKYSLEKIVS AVEENPDRT
13809	44177	A	13889	1	1452	
13810	44178	A	13890	167	309	
13811	44179	A	13891	3	386	SVGALQKQGGWHQRRCSLHF PSFLCVFSLAKSRRADHNQDPR ASRMASFSLTSSPLARSAASAVA AFGGCTSGNGRFSSVP*AYRQV FQRIAIAYVGPLMRDR*AHPVK TPDAIDCRIRQPAIPRLQ
13812	44180	B	13892	121	298	
13813	44181	A	13893	473	1826	
13814	44182	A	13894	1	270	
13815	44183	A	13895	3	3706	
13816	44184	A	13896	1	1464	
13817	44185	B	13897	591	729	
13818	44186	A	13898	1	1326	
13819	44187	A	13899	1	1152	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13820	44188	A	13900	1	2524	MREEFAHRWLARAGEKTPFDA LEKLTDPMLFAAAMVSAGKAD VCIAGNLSSTANVLRAGLRIIGL QPGCKTLLSIFLMLPQYSGPAL GFADCSVVPQPTAAQLADIALA SAETWRAITGEEPRVAMLSFSS NGSARHPCVANVQQATEIVRE RAPKLVDGELQFDAAFVPEV AAQKAPASPLQGKANVMVFPS LEAGNIGYKIAQRLGGYRAVGP LIQGLAAPMHDLSPIAATDAG SAAQIRIGDLVSVHVIRPHVD LEQVFPGLKAYTATCNHPVSL RFTIKSSDRIKLSNQTLSQKNL FIMRFYCFSLCLSLSAFYHCRGV IVNIQAVFWLQKGTEAADILTT CAQLWIMMYALLSVFSLDVL NLAQKFPAASQLPLKGIFQGIKL IGAILVGILMISLLIGQSPAILISG LGAMAAVLMVFKDPILGLVA VRNWDNTITTTIPTWSLVSDSFK NWSGMSASGGRIKRSISIDVTS IRFLDEDEMQRNLKAHLKPYL TSRHQEIENWNRQQGSTESVLN LRRMTNIGTFRAYLNEYLRNHP RIRKDMTLMVRQLAPGDNGLP LEIYAFTNTVVWLEYESIQADIF DHIFAIVEEFGRLRHQSPGTNDI RSLAGVTINKAPGDDEILKNTV DFVSFSYYASRCASAEMNANN SSAANVVKSLRNPLYQVSDWG WGIDPLGLRITMNMMDRYQK
13821	44189	A	13901	1	2370	
13822	44190	A	13902	1	282	
13823	44191	A	13903	1	714	
13824	44192	A	13904	3	506	
13825	44193	A	13905	459	551	
13826	44194	A	13906	401	492	
13827	44195	B	13907	479	702	
13828	44196	A	13908	120	256	

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13829	44197	A	13909	16	1249	SKSGAIEIARLAGRVHGVVVQI TSEIGPLTLLTANFAFSAS*STA WKATSMDEGVLS*YSTASAS AERQSTHQ*TGFAPLCR*PLPMI /VAQRADDVGFSEVHGQVRV RPVAQHAQTDKVFALTYNLGR RVFAALGAELGGARSAVRPVP ECYAVRETLALLQKIFPIRQCEN SVYRNRSRFLQYQIGRCLGPC VEGLVSEEEYAQQVEYVRLFLS GKDDQVLTLQLSRMETASQNLE FEEAARIRDQIAVRRVTEKQF YSNTGDDLDVIGVAFDAGMAC VHVLFIHQGKVLGSRSYFPKVP GGTELSEVVETFGQFYLQGSQ MRTLPGEILLDFNLSDKTLAD SLSELAGRQINVQTKPRGDRAR YLKLARTYAATALTSNFRSIYR SPATDRACQRVETAGNER
13830	44198	A	13910	1	438	
13831	44199	A	13911	1	1200	
13832	44200	A	13912	1	300	
13833	44201	A	13913	1	431	
13834	44202	A	13914	2	1465	
13835	44203	A	13915	1	513	
13836	44204	A	13916	3	535	RDKILVFKDENFWMIRGYAVLP DYPKSIHTLGFPGRVKKIDAAV CDKTRTKTYFFVGIWCWRDFE MTQTM/EKGFPQVRVVKHFGPISI RVDAAFQYKGFFFFSRGSKQFE YDIKTKNITRIMRTNTWFQCKE PKNSSGFGFDINKEKAHSGGIKIL YHKSLSLFIFGIVHLLKNTSIYQ
13837	44205	A	13917	1	876	
13838	44206	A	13918	23	414	
13839	44207	A	13919	2	425	QERGPHQVIQRKECLREYSPVV S*AKGTGVAVGQKGTQLQCEAS AVSSAEFHWYKDDKRLIEGNK GVKVENRPFLSKLIFFNVSEHD YGNYSVCVASNKLGHNTASIML FGPGA VSEVSNGTSSRAGCVW LLPLLVLRLLLKF
13840	44208	A	13920	1025	1270	
13841	44209	A	13921	370	701	
13842	44210	B	13922	1	660	

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13843	44211	A	13923	1	432	RFSRVDDFVLTMDDGPPRRAR GDLTHSGLWRVCCIEGIYKGHC FRINHPEDNDYDHSSEYLLRI VRASSVFPILSTILLGLLCIGA GRIYSRKNIVLSAGILFVAAGL SNIVGIIVYISSNTGDPDSKRDE DK*NHYN
13844	44212	A	13924	1	1093	
13845	44213	A	13925	1	1203	
13846	44214	A	13926	1	1353	
13847	44215	A	13927	2	445	
13848	44216	A	13928	1	227	
13849	44217	A	13929	1	840	
13850	44218	C	13930	120	356	
13851	44219	A	13931	40	342	
13852	44220	B	13932	403	473	
13853	44221	A	13933	70	2169	
13854	44222	A	13934	1428	1905	RCAATSGYGERVQRITV/PTHV W*ASLSQSSAHRVVAINSIANK RSSMPPKSWATVALTSTKLKCR FMAKVRNKSFSLVHNV*MTISI/ SPWVILSSGVDEKLPRAVRVA MTAGASGFLAGRAVWASVVG LPDNELMLRDVCAPKLQQLGDI VDEMMAKRR
13855	44223	A	13935	227	342	VHSWQRYSGR*RGY*PQNQSA TDQTRRWQSLKTAGAVA
13856	44224	A	13936	480	928	FFADLQQPVCADSYPLLVMQK LAPHKS*NAVWQRSATKSFSV L/AQGLNDHINMPWVILSSGVD EKLFPRAVRVAMTAGASGFLA GRAVWASVVGLPDNELMLRD VCAPKLQQLGDIVDEMMAKRR FIPLLRWVDLALTRWLITVSK
13857	44225	A	13937	564	1185	WLHASAALLRW*YQLPGQPHH RRCRSADGSHVPSLCAAVPDQR VPLITVRRIGMQAMTTSTTGDRQ RSWQIAMDGSQKLQRMMLDSV RWHLAHDSKFDLLALGVAGW MRYVGGVDEQGNPIESDPLL RMAANRFVHITQLPVIYRAFRN SFTQVARLQLCHKRFQQRHTSV REQIVTVLSGIRDNVHVFVQTL TGDGVGNQRLVQ
13858	44226	A	13938	228	424	HRFCPAARH/RSWSGLREMAVS ISMRRRIINSGRYCAICWYKRRS RCARNMLIFVARSTPIPGPS
13859	44227	B	13939	128	1670	
13860	44228	A	13940	2	2367	

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13861	44229	A	13941	1	921	ELPASPAPCARTPQPLGGRWEA ARRKERVLCDFVDGTLTPAR/ QGRITLKIGSSHRECHADTPAE CGVCSSVTEVRAKWSQTC*KP ECYASPLPP*KIDPEVA AFLQKL RSSYLPVGSQTWSHTLSSSCPLC DPEVIGRDTVPVSGSGSPGHAQ SPVFLGQTIQNLGPGGARFEF RA/CSGSLWLALPHH/RGT FIEF RNGNCVPSPQGLAHSRSELPSA PSPLQKEQAALLALASPPSRE* QSPPLPTGGMISFDFPEGWDK QVRSSQCGEGLHNLNIPPLPILCV QGGNDFEIFADPRTVGHS
13862	44230	A	13942	105	416	HSVLEVGPWVEVFGSWGQILH SLVSSHVRHWLLPSPSAMTES SLTFQKQPSRCQHHASCKAYHS HQLLLVPTAGRLEDRSHH*IPC KHSPAPAWSLAAPVGN
13863	44231	A	13943	191	573	SSSGGYQQLMRVIGTRDTAV NKASNVPSFGA*/IPSGRGQAK LIALTRALTLAKELHVN IYADC KYAFHILHQHDVIWAERGFLT V QGSSSIINASLIKTLKATLLPKE AGVIHYKGHKASAPIA
13864	44232	A	13944	1	1065	
13865	44233	A	13945	321	537	
13866	44234	A	13946	346	1260	GGPARAEFSRHLGCKGHHPLPK DVASEVPAGSSTSVSLIRTNCG PGLGSWEPP*FFSENKRLSTLMS FTLRDSKMFSQSGFLGCSAG EHSALRDPTASGLPGTASGVRP GR/RQRVGS DIEASTQGESKPCI LSI*TL PNA*LKTKLTLPLEAAC TNPHFSITARIGPAHLAAPRPV TPAGRGRGARAPGR*CAAAARPPP ASQ*VSGSPAPGGGSPYAPAAAR TS*PSSLAPGAKRLRFSRVATFC CSFLAWSSSSNKAFC*EHMSL LSSWISQSLKVASCCPCEQFDS WKRENILLFS
13867	44235	B	13947	1	459	

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13868	44236	A	13948	63	1263	V E A A K K A H H A A C K E E K L A I S R E A N S K A D P S L R P Q A H T Y A L S P L F L T A M P S V * Q G E H V I Y T R V R H S D Q V S E S S G K L S L P L E P G I W A F E A A Q V P P R W D Q V R S L E P T T E W E A P G L K K R R V S Q G L N G N E P L S C A W I F L * T K E Y E K S L K E L D Q G T P Q Y M E N M E Q V F E Q C Q F E E K R L G W D K G * L A P A F * K S H V S L * F S Y K A I Y H D L E Q S I R A A D A V E / D R R G F R K * * T F G F S P S A P V A * E W S A D L N R T L S R R E K K K A T D C Q D P H G P L Q S W D P L K A L S L H S T L N V P S N P A Q S A Q S S Y S N P R G P H T L C R P V L R A L W P L S C S V S S Y E K T Q S Y P T D W S D D E S N N P F S S T D A N G D S N P F D D D A T S G T E V L C S P P S V S Y L S W R R L P L C L A G D E L T K M E D E D E Q G W C K
13869	44237	A	13949	2	485	A A A F G T R L S R R R G R G C G V T G S G G G R R R V P A P R R P R S P L Q P P H Q / P P R R P S R R T P G C G S R G A / P S R G R R L V P P P P E P P R A A Q Q R A R H V H R T S / R P A A R Q P P R R P P A Q P R S C P R R V R P T P A W S P P G R R G P R R S R R R R R R G G R A R A R R P R R R G Q V P R P Q S A T G A G H A R
13870	44238	A	13950	1	207	
13871	44239	B	13951	1	5297	
13872	44240	B	13952	1206	1360	
13873	44241	A	13953	46	369	N E G K N A K G S Q R E R S G Y P Q R E A H Q T N S G S L G R N P T S Q K R V G A N I Q H S * R K E F S T Q H F I S S Q T K L H K * R R N K I L Y R Q A N A E R F C H H Q E G S T K H G K E Q P V P A A A K S C Q N V K
13874	44242	A	13954	476	868	K Y D C C I S S T F C R A L V H F S R T T F Q V N S P L S P N I S A F G Y M P L K Y S I Y F L H H L R P N I L * A A S Y F L K Y K G T L K L P A L R G C L S * S T R C W C K I H I C I * N D / E C L Q F L G P W F E N E F C F L P S T S Q F V E F V L D I L V L Q N E P

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13875	44243	A	13955	1770	3003	PANIIMTGSINSHITILTLNVNGV LNAPI*RHRPAIA/S/WLSQDPS VVVICIETHLTCDRDLTHRLIKG WRNIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMAK GSIQEEELTILNIYAPNTGAPRFI KQVLSDLQDRLDAHTIIMGDFN TPLSTLDRSTRQKVNDIQELD SALHQADLIDYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALL SKCKRTEITITNCLSDHSAIKLEL RIKKLTQNHSA TWKLNLSLLND YVHNKMKAEIKMFFETNENK DTAYQNLWDTFKAVCRGKFA LNAHKRKQERSKIDILTSQKE LKKQEQTNSKATRRQEITKIRA ELKEIETQKTLQKKQPNKDPAM EKNKNTDRVLARLIKKKREKN EFSAHILYKFSKQNGS
13876	44244	A	13956	105	392	RSRKPRGNPKSHPEDTDPTKAP RKQRQISSRGHRSR*EPGPQSA PGFREQRRRGQMG*IWYLTPT PGGQRPSSAASPRGFPTNNSR LPAAEPE
13877	44245	A	13957	55	403	SEGMSGKASEKQEAFCPRHLT RAVDGPS*SGLLGSRLPPSCSPG KEAPGGSELYLCLMRGLQTL*A RSGTGLR/PNPAEIR*EPGPQSA APGFREQRRRGQMG*IWYLTPT PPGGQ
13878	44246	A	13958	217	444	RSRKPRGNPKSHPEDTDPTKAP RKQRQISSRGHRSR*EPGPQSA APGFREQRRRGQMG*ITPCRP ALPKSKPRPL
13879	44247	A	13959	309	670	PCPRASSQGLKATHGQR*SSEP PGASFGLQDGGRRPRRPD*D GPSTGLVRCLGHANVGDPLK VFVFFKNLSPTYLRASAEQTLPL LLPLHLGLCLHQLHLGFTAA WAQLTFWEASQ
13880	44248	C	13960	392	760	

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13881	44249	A	13961	24	915	HAGRHRGSLFPGARPSETRAH CVRTARPNCKEEDTPMVRGKN SGGEHCTWGPSLAAGG*GIGDP GGLPGTTPHPLQLLLHGFAGP HMASLCCGVSSPAGVQRWPA* GSGNHQVKS WLGLPKNV S*AP SML*NPQMQLMKAQPHGRCE VRRGRVCSALGP/IGMSGKASE KQEA*DEGHPHLHAPGT*QDQ VDGPS*SLIGSRLPPSCSPGKE APGGS ELYLCLMRGLQTL*ARS GTGLRANPAEIR*EPGPQSAAP GFREQRRRGQMGIWYLTPTTP GGQRPSAASPRGFPLV
13882	44250	A	13962	397	612	RPQHHTFCCDGRVMMARQKGI FYLTFLILGTCTLFFAFE/CSFG *VELPDYGYFGSRGRTCFGLSL GLVLG
13883	44251	A	13963	125	1298	FQSWAQPLFLLSCNRKTHFGTR IPIMSVMVVRKKVTRKWEKLP GRNTFCDDGRGMMARQKGI/ YLTFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSMAT LRLTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGRPPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHC PW VGCNCGKRNRYFYFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTLEVLICFFTLWSV VLTGFHTFLVALNQTTNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVL CGPLPPSVLDRRGILPLE ESGSRPPSTQETSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPPEP PEPPQEA AEAK
13884	44252	A	13964	44	647	DYSAQH GKASQKHVARLISSGT FQGATVSRPFQLSTSSSFCSSSS SLSSSSSLSSLLSCSSSVFLS LSFFFCSEASFLPFC SRLYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFFIAKLLAQDVAYSTKT LAAREIGAPGLLDVDVTRELR GDRG*AKLPFQHLPSPCPFVRPP RAAHRLLDDPGDHGIGQV
13885	44253	B	13965	158	1075	

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13886	44254	A	13966	125	1297	FQSWAQLFLLSCNRKTHFGTR IPIMSVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKGI YLTFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSMAT L/LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGORPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHCW VGNCVGRNRYFYFLFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTVLEVLCFFTLWSV VGLTGFHTFLVALNQTTNEDIK GSWTGKNRNVQNPYSHGNIVKN CCEVLGCP.PPSVL.DRRGILPLE ESGSRPPSTQETSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPPEP PEPPQEAEEAEK
13887	44255	A	13967	247	850	DYSAQHKGKASQKHVARLISSGT FQGATVSRPFQLSTSSSFCSSSS SLSSSSLSLSSLLSCSSESVFLS LSFFFCSEASFLPFCRLYASRA SFNGVTNRVNSISSMAESTSLA FSVFRFPFIKLLAQDVAYSTKT LAAREIGAPGLLDVDTVRELR GDRG*AKLPFQHLLPSCPFVRFP RAAHRLLDDPGDHGIGQV
13888	44256	B	13968	298	380	
13889	44257	A	13969	48	252	QRAGSPHSRSLAPLPPLPLW RHLRSPSAHRCTVGAPFWDGQ G/LEPAPSAALAAFPISRARDLQ LA
13890	44258	B	13970	1	447	
13891	44259	A	13971	236	559	MWLEPMQMGLHMEKMAA RTSAILD*GTLK*FHFTLTSLK ALSSHTPIFPGTGELQLPVSPV CLDQGMQLKPSTSSHLLKTVKP RMKRQSLHMKQSFEPKIYL
13892	44260	A	13972	1	645	MKPQTLTVSVTAFKVAHLEFVP SDVQMCSEFLPSGGFVVSLSAG VKLQTFVAVSFTAHKSSVDPKNS EAQLASPSGFCTRAADGAACQS LPCTCTPQPLGGRWDWALWS RGW/LLVEEA WAAQEPTEELRE RALALASPERGSHSAVVGQAP QVPPKWEPRQRRRRERARAVR TASTLSPLNPPSKQDITLTVGN LADHSSYFLLDRGEAGLQL
13893	44261	A	13973	28	322	
13894	44262	A	13974	1760	4426	
13895	44263	B	13975	942	3414	

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13896	44264	A	13976	1	274	
13897	44265	A	13977	545	1150	RISGPGAVLLPVPMPALWRLRHR MFSLTKK*HLPAPHRSLAEGYLL YQPQLDTLKARLTQKYQELQV LFEAYQIKKTKLDRQSSASLET LLALLQAEGAKIEEDTENMAEK FLDGELPLDSFIDVYQSKRKL HMRRVKIEKLQEMVLKQGR/L TRPWPRCPGPCPNWHLPPFPPT LPQSQWASCRCTSAHPPTTPG AAGRL
13898	44266	B	13978	213	611	
13899	44267	A	13979	1	639	MEAVTVVPVGTEEGMGEEQD SGTTTGCGLPSEVKMLATNPGK TPISLLQKYGTTRIGK\TPVYYLL KAEG\HQPNTFWV\VGNTSCT AQGPCKKVVVKHKAEEVALRHL KVESMLEPAPEDSSFSPLDSSL PEDFPVFTAAAAATPVSSVFLT RSTPMEKQPPLL\QQSECIPVG ALQKLVVQKGWWLPEHTVT*E SRPDQHEELT*RVERFT
13900	44268	A	13980	361	894	AFFPMSTAGVCGNVEGEPETP WSLPLSQVPFSPNA/CPQGTGLGR S*AGVAGAPGPGVPGRSPAA/GI PEPAARPGRPALSRPLGLGGAG ARSGAA*G*GSRPGG/PLPAADP VQSWG*EAPSH*PGTSADSP PSGVSGATGDCLWGSRAELF GFATTSSAAPPGLPTFFFPVSP
13901	44269	B	13981	1	3842	
13902	44270	A	13982	3	407	DAWAAARPGRSCALPPPAGA/PE EPGHVPGAAG*G*GSRPGGRFQL PDPVQSWG*EAPSH*PRNFQ TRRHLGVKQHGCSQSPHGSRA SQAHPGISGLF/GPHHPGPPLFIH GPRCCCAQATASNHLFACGTSS DP
13903	44271	C	13983	127	297	
13904	44272	A	13984	3	1920	

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13905	44273	A	13985	3	2271	GQGRRTAGGGGGGAGVGAG AGAMEAERGPERRPAERSSPGQ TPEEGAQALAEFAALHWVSGE GIGVGSPAHTPADGNSGPQVFD AGEVFGIMQVEVEEEDEAAR EVRKQQPNLAPPTSLCPMPTR QPHIVACARSIFLDHAWTCRV EHARQQLQQVPGLLHRMANL MGIEFHGELPIWVPEGSSGGW MGEREVPYVLCQTAEEKMPV WYIMDEFGSRIQHADVPSFATA VPLEEGPQSPVSPPLMGTH/DL GTEEVTRDFAYGETDPLIRKCM LPLSSSHRGMETPCVHTSRASL PLQACELPSWSLLINEPPRPAF PSLP*PHLYFRCVSF*AIPGLVLE SRLDTWEPGSPSSGSPHRVYTD VQQVASSLTHPALPVRASRHC PPLELAHLPPPCRKLSSQERPGVL LNQFPCENLLTVKDCIASIARR AGGPEGPPWVVLGWHLGTQ APGAPQTALLPRGEDNHWICK PWNLGLCVLGSPLGCPGHQR ACTCVLQVVSKEYIESPVFLRE DVGKVKFDIRYIVGGTSLAGTR PLKNPYVSAHLSSRAFAQGRRG RGGPTWSGWLLARDPARV*DL LSSLVHVSVERCPMQWALSEWQ LHHLSTWSSGLCGLAG**VFQM HRTPTP**QAACSRPSGGLYR A*WALCLLPGAADPLLRCGSEQ AS*LRLPGPQAEIFRAFTFLFQV
13906	44274	A	13986	1	600	MEEQRVQFTLWLHFSPHGICQF ESGRQEAKKLKGSGQPLKTGEI KTGIQKYRREALQHYLGPSAL AGRSKALTGTAERSCSSGSDSI FTLCVNYNDSRAIMKTLAIGT GFDCAKAEIQLVQILGMPPER FMYANSCKQMSQIKYTANNGV QMMIFGNEVKLMSVARTHSKQ P/CHISVKS GAMLKASRLLE*A KEL
13907	44275	B	13987	1	2040	
13908	44276	A	13988	205	438	LYFLETGVFCVQVPAQQC*CSV PGSCRRPLEEAGWRGLGSLGRL AGTGLPSGSRGNRTREGERGKL VRGRRGVTRWLS

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13909	44277	A	13989	284	632	KTGVFCVPGPRPTVLM*CSFVG GKKNQYCLTGDAGCLQEKHSL GPAGV/HLEEAGWRGLGSLGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSFPFEP
13910	44278	A	13990	594	1003	VRKGHHAVRGLCGRAQFRCIS GDPGKRPLG/LPGGNAPKSGSL ARRPQPVRIPIGSRPQ/RGSVSHL GPAGVH*/RAGWRGLGSLGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSFPFEP
13911	44279	A	13991	1	1500	VRVAHIPIAAEIAAIPDRGGHL SVGKRRLTFWFFYGVLPPFRDV AIEFSPEEWELDSAQQHLHRD AMLENYGNLVSLAAGDQSLPG DAAASAVCRQLSPSACGAILGL PPVNGVAPVRLRGEIVTYTWSQ LTGLALALSKDGADGLRRLTRP TRRAPPALLAPQTAAERWRG KCDPRHGGGICALALQGWTLYP RESPSRESKELGGLWSFRADLD SRRQGFEEQWYPRPLRELGRG GRRPEARRWEGSGPGCRLLPL SAPELAPYRKLVNGLRGAGL GDGETGGTGEGRGRRRKRCC RTLSRDEGFNDICQDWLWRQF VGWVLYEQEVTLPQWQTQHLR TRVVLRASAHSYATVVSAAARS RQGRIGGLIYTLGMPFFLSGW QVPEPHAAGYVRECLIAGPLLM P/TTCCPLLISPVSAVGEWRGHA RA*GADSSSLVQNTDFDFNYA GLQRSVLLYTTLTYYIDITITT GVEHDSAEIPFPEYLRVNTGN
13912	44280	A	13992	2	307	
13913	44281	A	13993	220	427	MSTLPFSLQMFRRPPYGSPTC RSQDNRSYSRVTEELQERRRW NSGDAN*QDSPEARQRPRHIE EAA

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13914	44282	A	13994	1	2832	MGKYYTQGDKVLMLAIQVH HACDGFHVGRMLNELQQYC DEWQGGAYPKGYFVQNTDFDF FNYAGLQRSVLLYTPTTYDDI TITTGVEHDSAAAPMVDSLAR VGVMARGNAITLPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLPSFLLTGQ QTPAFGRRVSGVIEADGSRRR KAAALTESDYRVLVGELDDDEQ MAALSRLGNDYRPTSAYERQQ RYASRLQNEFAGNISALADA
13915	44283	A	13995	1	2934	MITFDFMSHIQVTLMQEVSFHG LGQLRPCFAGYSPPPGCFHRL ASSVCSFSRCTVQAAVDLPFWG LEGTSPLLAASLGSAPVGTLCG GSDPTFPSWTALADVLHEEGHT PASNFCLRNLAGESQSWRKE GLGTPRPTASSTEELQTLNEDSR LMTSPHINLETRDCDELPKKS LGWKEIRVYGGNKTGLFWLQA QLLICDGGNLRMFRLPYGSPS TCRSQDNRYGGVTEELMERK RWNSTDGFHIQGVLE
13916	44284	A	13996	68	425	SHILPGAPGAPAWWTRWPSTLP EPFPRGRGSPAGTSPISRPLVQ SS*ASRGSDSRLPV/GPASCQAS GPGPDSRRPPCTPA/GPHHGSL PSAGRVGASAAAAGPPSPAVPL PPAERPAP
13917	44285	A	13997	324	723	TAFSLNFQGGVEGEVWAGTRA ARGACAGERGLGGSRTSGW/P GTAGPGQAGHGTCSLPCPSLPP AMGSCVSEPPRQAPPAPWRLV PSTAQGLRSVGTQCGTGGSSAC GPC/GDPGF*THQSAPCQNGPIS SL
13918	44286	A	14000	39	383	

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13919	44287	A	14001	181	1446	EDLLQEAAQLAEVTAQGKGLG QVRSLLDLSLEACAGSPPLQVLD LQDREPRSLTSLPSSAANRGLK EKAQSNPCGHRRHQAAGLKL LFSQAQPGQPTAPRFRAATR KPGTAQSHAPLWSPAMSFPEL YFNVDNGYLEGLVRGLK/ALGE LSQADYLNLVQCETLEDLKLHL QSTDYGNFLANEASPLTVSVID DRLKEKMWVEFRPHEGTMYP EPTSPSP*TSITLQFT*FDNVIL WLIHRARLHRSIAELVPQVAH PLGISFEQMEAVNIAQTPAELY NAILVDTPLAFAFFQDCISEQDLD EMNIEIHRNTLYKAYLESFYKFC TLGGTTADAMCPTLEFEA/NR RAFINTVFFGATKTPVKKDRCP AFFPH/CGAGFFPEGPAAMGFG LNNLLTGAKKRGPNFPEVQL AFLRGDG
13920	44288	A	14002	1	1182	
13921	44289	A	14003	26	342	ARFLAGP*LPSRRTGLRDLQPA MPEPPPTPWAPVRPEPPRRAAP PAPRRPVSTGKEQTQGLRSA GAGHRDWQAAPAAPVRDPLG EASWAPESGGDVESLYV
13922	44290	A	14004	66	463	
13923	44291	A	14005	3	1446	
13924	44292	A	14006	221	852	NSFLMVGFPPFSL/CAAFDTKT GLRVAVKKLSRPFRLRPDGYYTE FNIYLLNFYILTSSAV*VVLSH SVVIECLLSIRHCSRYFRKSSD KNFLRGSRLLCNFSLISRYLVTH LMGADLNIV*RYR*YK**FFK MNSPFLPLPVGGELIMHHKVDP VCFVFFSLPVYSK*QFVCSSAL *ILDFGLARHTDDDEMTAKGQPE CFVRWACAS
13925	44293	A	14007	55	784	RHIQDPASQRLTNWNSPKSVLV IKMMDASLLQPFKELCTHLM ARGAGGGHDARSLLTAPVSRE PPCRRVGSAGGMSRLALCFQEN MIVYVEKKVLEDPAIASDESFG AVKKKCFCTFREDYDDISNQDIF ICLGGDGTLLYASSLF/QGNAA VVLRSRLKVRVVKELRGKTA VHNLGEGKSQAAGLDMDVVG KQAMQYQVLNEVVIDRGPSY LSNVDDVYLDGHLITTVQGDGVI VSTPTG

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13926	44294	A	14008	155	1592	PESRHQCFSDRSANFLTMEMEQ EKMTMNKELSPDAAAYCCSAC HVGDETSYNNHPIRGAKSRSL SASPALGSTKEIRRTSLHGPCP VTTFGPKACVLQNPQTVIMHIQD PASQRLHVEQRPRTVLVIKKM RDASLLQPFKELCCTHMEENMI VYVEKKVLEDPAIASDEISFGA VKKKCFCTFREDYDDISNQIDFII CLGVDGTLLEYASSLFGQPSP VMAFHLGSLGLATPISFENFQS QVTQVIEGNASCCSGSRLKGQ GW*RLRGKKTAVHNGLGKEK G/SQACRPGTMDVGKA/QAMQ VPRS*NEVVIDRGPSYLSNVD VYLDGHLITTVQGDGKARSTV LGP*ASLGRE*RLRLSLSGVIVS TPTGSTAYAAAAGASMIHPNVP AIMITPISRSVLTAGGPHLSLL DPQIMLSPEARNAGGGPFWKP WLRLLLRSPSISITTSYCLPSIC VRDPVSDWFESLAQCLHWN
13927	44295	A	14009	327	466	
13928	44296	A	14010	2	196	
13929	44297	A	14011	923	1776	WRKCGCETAGSASATRAAATE KMEAPRNKMRDQENSAWRN AVPGP*E*RQPEEFPRITSILAEP TVLSRRKCRPSEKRGSAATEKFG ATSAVTENPPLGAAGERANKTL GAATVPTLGP RPMEKGGTR CPSTL*PSVQERQEPSPSGNHPE TQKIEFAGRRVTFQHRWATTLR TRISGTGASPRDRSAFFGFPWC G/AAQPSDEESTPATQEEAQAQ AGVAAAASSEEPGHCA PRPPHA PRSA LFEDWSREPERSDDGDL ECRRPAT EPWRPPGSAWRLPCA A
13930	44298	A	14012	568	1223	SARGLLPGSGPLSHAGPQLQVE WFGCLPPDSTLELVVCGTVAI SRVRMSAVCVLRTWS/RNAG/Q L/CFTVFQPCSNVHVL/KGPNY VCFGGYPSFKYSHP/HNLFKTI NA VCGQLVQRFDPDTEEGIRK VTV/KCYVKEGDTV/SQFDNIGK VQSDKASVTIASPYDGV/RLK* HSLDDIAYVGGPLVNIEIEALK GTVNLFYQIDYCPFFVIGSQLK

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13931	44299	A	14013	5	296	LFSRVPSKGPPRYHHTSSRG*TR AD*LISS/IGNS*AHCIPSGLQGM LNLLPTPRAPVRPEPPRRAPPPA PRRPVPFDHPRACGTGRQLHLQ PRCGIH
13932	44300	A	14014	1	376	MQAVLLTVLQKHNQSVIYWY MKYIYYEGLVIMDDYDYVIMD YMTMETEKSHDLQAGGPGKPV VQFQFKPKILQASRGNGVKSWS KSKGLRTRCANVQGQENREGP AKHSPFLCLFVLFSSSTGRMIPN HTGDTSKVIAGTEERGVPKKVT LKFDACAIDRPWAHQLDCTY HFKGSNDEHDSRLHTNAG*L*L C/RLWIT*LWRLRNPMICRLEA QESQWYSFSSSPKSCKPVEAMA LSPGPSPKA*EPGVLMMSKGRKI GRAQLSIHLSSAFLFFSAPQOVE
13933	44301	A	14015	1638	2289	VEKKKKPMSAPALRLPLDTKLF TLVYVSETKKMAVRVLTQTVP WPRPVALLSKQLEDEVSKRWPP CPKSLVAIALLAQEAADKLTQR NLNIKSPCAVVILINTKGHH*LM NARLARYQSLCEHPRITLGLSL QHNLNPAFTLPVSESPVKHNCVE VLDSVYSYVGPNNRHDPLNISR LGAVTWMGSSFHQLQSDTLK KTTSPGSSHTRKLTPRTAEA
13934	44302	A	14016	1	675	MAPPLRLPLARLRPPGMLLRALL L.L.L.L.SPLPLGLREGIGELITPIGT SLPDLDPARRRWEIGIGRVGSE VADLCPGKEGGKVPEAEKEGV WCFSELSFVKEPQDVTVTRKDP VVLDCQAHEGVPIKVTWLKNG AKMSENKRIEVLNGLSLYISEV EGRRGESQDEGFYQCLAMNKIF *AILNQKAHLALSRIGST*RRRP DRP*EDEAFVMTTHCFQDLLTS
13935	44303	C	14017	18	329	
13936	44304	A	14018	391	895	WASSDTPGTQQRWRPDWAGG GGGEERGDGTGVVWEGEKVY FRFRVTGGSSFPSPAVLVRAPN TGMPKLTYYIT*GPLGERGKEP VPPNPTLPQTFEGGLNASVVRK TEIPSPSPPPVCYLRAAERQ/PA GGSPQAKWRAASSPPPLPPVH LPPPPPPPPPPPPPP
13937	44305	B	14019	1	1110	

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13938	44306	A	14020	282	710	YPEPQGWVVAHTVQYPIHIQPL KPGPRGR*SIMDIQVPPKEGGV LILKNSSRLNNSWTQGCQISA FSPTSSLPGTPWSNVGPYKIA ITSFGE/PFIRVIWKQLPSWSIIQ V/SHKQ*QIHRVDIGWSPGQEC GPKGCFV
13939	44307	A	14021	1	1416	MIILDAEKAFDKIQQPFMLKTL SKLGTDTGYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTQGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS KINVSQSAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQW/GKDSLFFHKWC WENWLA VCRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWLILKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHKMKCSSLAIREMDIKTTMR YHLTPVRMAIKKSGNNRCWR GCGEIGTL
13940	44308	A	14022	1	3450	
13941	44309	B	14023	1	3171	

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13942	44310	A	14024	1	2433	MRTKTQHTRISGTHSKPVCRGK FIALNAHKRRQEKSIDTLTSQ LKELEKQEQTTHSKASRRQEITKI RAELKEIDTQKTLQKINESRSW FFERINKIDRPLARLIKKKREKN QTDTIKNCKGDITDPTEIQTTI REYYKHLYANKLENLEEMDKF LNTYTLPRLNQEEVESLNRPTG AEIVAISSLPTKESRTGWIHSRI LPEVQGGTEKEGILPNSFYEASII LIPKPGRDATKKNFRPISLMNI DAKILNKILAKRIQQHIKKLIH DQVGFIQGMQGWFNIRKSINVI QHINRTKDKNHMISDAEKAF DKIQQRFLKTLNKLGDGTYP KIIRAIYDKPTANIILNGQLEAF PLKTGTRQGCLPPLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL LSLFADDMIVYLENPIVSAQNLL KLISNFSKVSGYKINVQKSQAF LYTNNTQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKDDTNKWKNIPCSWSVG RINIVKMAILPKNWKKTTLLKFI WNQKRAHITKSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHTY NYLFDKPEKNQWQKDSLNF KWCWENWLAICRKLKLDPLT PYTKINSKWIDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLSFC
13943	44311	A	14025	1	1023	MGAIFYDKPTANILNGQLEAF PLKTGIQGCPLSLLFNIVLEV LARAIRQEKEIKVIQVGKEEVK LSLFADDMIVYLEDPIISAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNTQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWSVG RINIVKMAILPKAICRKLKLDPL LTPYTKINSRWIDLNVRPKTIK TLEENLGNTIQDIGMDKDFTSK TPKAMATKAKIDKWDIIKLSF CTAKETTIRVNRQPTWEKIFAI YSSDKGLISRIYNELKQIYKKKS NNPIKKWAKDM/NRHFSEKEDIY AAKRHM
13944	44312	B	14026	1	2206	
13945	44313	A	14027	1	1689	

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13946	44314	A	14028	1	2523	MKQFLLYLDESNALGKKFIIQDI DDTHVFFVIAELVNVLQERCHTR LGYTEFLVAVRVTFGLCVAV TLHLKYQILIRGLLEMMFSFDA DILKQLPVTVPGLFPASLSPSSL LGNSPPSWLRHNSSEKVSVAVSS PSATKTLSTGIGKIDPGHKEMA EESLLKNKMQAPPLSRCPESQ KCQHQRLRLHHWKPSVRHQVKR RSPAVLRSAMPADCPAVLEAT TATHPEKGTALSKHLPSDDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKQKQKGLDKKKKK GKLPKNYDPKLPDPERWLP QECSEFYQGRKKGKKKDQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIPRH QRPAGAPATKKKQKQKQKKG GKGFVPLREITVVKVDTLVVFG ILEERLSVFHIIQYDTSYFPSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQQPFMLKTLNKFVGVDGY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNTV LEVLRARIRQEKEIKGIQLGKEE VKLSLFGAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTEQSIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL
13947	44315	A	14029	1	2868	
13948	44316	A	14030	1	3099	MGELITPLSTLDRSTRQKVND TQELNSALHQGLDIDIYRTLHP KSTYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRINKLTQNRSTTWKLN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTSHKASRRQEI TKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
13949	44317	A	14031	2	3419	

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13950	44318	A	14032	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFSSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRKIKNLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDDTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQKLEKQEQTHSKASRRQ EITKIRAEKKEITQKTQVKINES RSWFFERINKIDRLARLIKKKR EKNLIDAIAKNDKGDITDPTIEQ TTIREYYKHLYANKLENLEEM DKFLDITYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAEFYQRAIRQEKIKGQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFFTELKKTTLNFIWNQK VRAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD
13951	44319	A	14033	845	1616	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWGRINIVKMAILPKVIYRF SAIPIKLPMFTFFTELEKKNWLA CRKLKLDFFPIPYTKINSRWIKD LNVRPKMTKLTLEESLGNTIQDI GIGKDFMTKTPKAMATKA/KKS FCTAKETTIRVNRQPTWEKIF AIYPSDKGLIS

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13952	44320	A	14034	707	2878	TLMQKSSIKYWNQNESSSTKSL STMIKWASSLGCKAWFNIRKSI KVIQHINRAKDKNHMIIIDA EK AFDKIQQPFMLKTLNKL GIDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPVSAQN LLKLIRNFSKVS GYKINVQES/Q AFLYTINRQTESQIMSA LPLTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNK/WKNIPCS GIEGRNIVKMAILPKNWKKTTF IRFIWNHAKRACIAKTILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNIDIDQWNRTEPSKIIPRI YNNLIFDKPDKNKKWGKYSLF NKWCLENWLAICRKLKLD PFL TSYTKINSRWIKDLNVRPKTIKT LEGNLGNTIQDIGMGKDFMSKT PKAMATKAKIDKWDLN NLKSF CTAKETTIRVNMQPTWEKIFA IYPSDKGLISRIYNELKQIYKKK TTNPPIKKWAKDMNRHFSKEDI YAAKHKMKCSSSLAIREMQI KTTMRYHLTPVRMAIHKSGNN RCWRGCGEIGTLLHCWLDCKL VQPLWKS VW**FLRNLELEIPFD PAIPLLGIYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTII DWIKMMWHIYTM EYYAAIKND EFVSFVGTWMKLEIIILSKLSQE
13953	44321	A	14035	869	3869	RHKKPFKKLTNPGA EIQTIREY YKHL YANKLENLEEMDKFLNT YTLPRLNQEEVESLNRITITGSEI EARINSLPTKKSPGPDGFTA EYF QRYKEEMVPFLKL FQSIEKEGI LPNSFYEASIIIPKGRD TTKKE NFRPISLMNIDAKILNKILANQI QQHIKNLIHHDQVGFIPGMQG WFNICKSVNVIQHINRTKDKNH MIFSIDA EKAFDKFQQLFMLKT LNKLGIDGMYLKIIRAIYDKLT ANIILNGQ
13954	44322	A	14036	2	99	

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13955	44323	A	14037	1	914	TVTVIHTVARVGNLDIQQRKS ELFLSLVVCEAIKNEMNMVLMKS SPVDLVTATDQKVEKMLISSIK EKYPSHSFIGEESVAAGEKSILT DNPTWIIDPIDGTTNFVHRFPFV AVSIGFAVNKKKKVDETYLG VKETCFPLQIEFGVYVYSCVEGK MYTARKKGKGAFCNGQKLQVS QQEDITKSLVLTELGSRRTPETV RMVLSNMEKLF CIPVHGJRSVG TAAVNMCVLATGAGADAYYE MGIHCWADVAGAGIIVTEAGGV LMDVTGGPFDLMSSRVIAANN RILAERIAKEIQVPLQRDDED
13956	44324	B	14038	91	1959	
13957	44325	A	14039	28	152	LPSPSSKDTDS/AASCCAPRGRA KGSVNSNRLSFPSSVPLP
13958	44326	A	14040	35	879	GSQCSPPPASRCGSCSSAPSRH CPCRDPEPAVAGLARTPVLT TNPSPPARTGLNAPSMGTSLI/P ALCCFPLYQGSTEQLQCKAP**LP SPSSKDTDS/AASCCAPYFLVLL KVLSSVDNSSIWCSAGPPAQ/S SLYTIPMSSMSAKNCSVLRSGT WASFTCS*GSQRVSLGTPEALG TEDHTSRSLGHSVCHVDLSPA TASCSFQTASSEVSPATASCSF QTASSEVSPATASCSFQTASSE VSPAATASCSFTFSFFVCALWF GICPSCSAAVLST
13959	44327	A	14041	3	159	EHQCENPQ*NTGTPNPAAHQK AYPP*SSGLHPWDNRQKQPHD YLNRCRKGL
13960	44328	A	14042	54	245	GGGGGEAEDRLREPETEKALSS SL/RRAPDQC/RALIMQLFQAHC FFLST/QATAALQAHYAHIFPSK
13961	44329	A	14043	903	1205	WDVSQNNKSYL*QTHSQYHTE WAKTGSIPFENWHKTGMPSLT TPIQHSVGSSGQGNQTNREPNH E*TPIHNCFKENKIPRNPYKGC EGPLQGEQLQITAQ
13962	44330	B	14044	1	339	
13963	44331	B	14045	1	1547	

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13964	44332	A	14046	807	1440	NTGKPNPAHRKAYPPRSSRLH P*DLQQTPTDLQLSDLTGPKRT NKQKGIASPSKTRISTPKPHLQ ANAQRFCFHQACVTRVPGGST KHGKEQLVPATAKTQIVKNIN AMKKLHQLTEIQTIREYHKHL YANKLKNLEEMDKFLDYTLPL RLKQEEVESLNRPMGSEIEAII SLPTKKSPGPDGFTAKFYERYK EELVSFLKLFQSEIEGILPNSF YEASHLIPKGRDITKKENFRPI SLKNIDAKILNKILANRIRQPIEK LIHHDQVGFIPMKGWFKCKCS INVIHINQTNNDKNHMIISIDAE KAFDKTQPPFMLKTLNKLGTIR QKKEIKGIQLGKEEVKLSLFAD DMIVYLENSIVSAQNLLKLISNF SKVSRYPKINLQKSAFLYTNNR HMESQITSELPFTIDTKRIKYLGI QFTRDVKDLFKENYKLLNEIK EDTNKWKNI PCSWIEESIS
13965	44333	A	14047	603	764	LPLFLIEYPLFLSLA*LPWPKLPT LC*IGVVREGIPVLCFCSKGMPL VFAHSV
13966	44334	A	14048	1566	1865	MQSIRKTIGIHAKYDKACRNGE DICLRETNAAADTQAKRV*SGP PANSNRPAEAGPDC*KEN*QTE RTSTPKPHLYVTIHKDQRGTQLL TNNGTKLDRE
13967	44335	B	14049	I	1932	
13968	44336	A	14050	711	1575	TRKFRNRNG*IP*HIHPKTKSGR SRIFNRPI TGSEIEAII NSLPTKK PGPDGFTA EYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPGMQGWFNIRKSI NVIQHVNRTRDKNHHMIISIDAE KAFDKIQPPFMLKTLNKLGDIG MYLKIIIRAMYDKPTANIILNGQ RLEAFPLKTGTGRQGCPLSPLLFN IVLEVLAIRAGQEKEIKGIQLGK EEVKLSLSADDMIVYLEKPIISA QNLFLKLISNFSKVS DTKSMYKN HKHSYTPITDKQRAKS

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13969	44337	A	14051	1	1579	MQGWFNVNRKSLNIIHINRND KNHIIISDAEAFDKIQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRO GCPLPLLFNIMLEVLARAIQRE KEMKGIQLGKEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKINVQKSQAFLYIINRQTESQ IMSELRFTIATKRIKYLGIHLTR DVKDLFNENYKPLLNEIKEDTN KWKNI PCSWGTGSINIVKTAIPLK VIYRFNAIPIKLQLTFFTELEKTA LKFMWIQGYSNQNSMVLTLV IPRKMRS AVELQQTSTDQLRD LTVRKKTNRKATASTSQKH LHQNPICRSPTSKTKEVGFRSV ITNFSCLKEDVRTYHKEAKNLE NRLDEWLTRINSVEKTLNDLKE LKTMRDLHDACTSFNRRFDQ VEERVTVTEDQINEINDGNGT KLENTPDIIQENFPNLAISRPTF KFRKYREHYKDTPREEQPQDT* LSDSPRLK*RRKC*RQPERKVE LPTKGSPSD
13970	44338	A	14052	50	1105	TRKSRRNG*IPGHIYPPKTKIQE EGESLNRPIGTGSEIEAIIINLPTK KSPGPDGFTAKFYQSTNNKNH MIISDAEAKAFHKIQQPFMLKTL NKI.GIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLPFNIVLEVLARAIQREKEIN CQLHNEEVKLSPFADDMIAYL ENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYITINRQTESQI MSELPFTIATKRIKYLGIQLTRD VKYLFKENYKPLLNEIKEDTNK WKYIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTLSSQNWKKT TLKFIWNQKRARIKSISSKKN KAGSIMLPDFKL
13971	44339	A	14053	1	764	MQGWFNVNRKSLNIIHINRND KNHIIISDAEAFDKIQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRO GCPLPLLFNIMLEVLARAIQRE KEMKGIQLGKEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKI*FPLFLIEYPSFLSLA*LPW PALPTLC

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13972	44340	A	14054	1	344	MGINQRRKAENSKNSASSPTK DCSSSPAKEQSWTENDFEELTE VGFRQQANAERFCHHQVCPKR APEESTKHGKKQ/RSISHCKNM PNCKDHRCYEETASTDLSAETQ QQKREF
13973	44341	A	14055	301	370	DDGVF*IDNHVICKQRQDFDLFS
13974	44342	A	14056	1	1418	MVREGFPPEEVTFLKNELEISK GQQMGKNIPDTGASSAKALGE RELGTLDKMKNSPSDGSKKDIR THRKEAKNLEKRLDEWLTRINS VEKTLNDLMQLKTMARELHDA CTSFNSQFDQVEERINKIDVRLA RLIKKKREKNQIDAINDKGDIS TDPTEIQTITREYYKHL YANKL ENLEEMDKFLDTYTLPRLNQEE FESLNRPIIGSEIEAVSNSLPTKK SPGPDGFTAIFYQRYKEELVPF LLKLFSQIEKIGILPNAFYEASII LIPKPRDRTTKENFRPVSLMNI DAKILNKILANRIQQHIKKFIHH DQVSFIPRMQGWFNICKSINIHH HINRTNDKNHMIISIDAIEKAFDR IQQPFMLNTLNKLGDGMYLKI RTIYDKPTANIHLNGQKLEAFPL KTGTRQGCLPS/ATPVQHSVGS SDQGSQARERNKGYRIRK*GSQ IVSVCR*HDCIFRKPRLSPKSP
13975	44343	A	14057	1240	1596	CYSFLFVRCPDSQVPQLQVC/C EFAGGPLQTVFAWVSPAEEVE MFLQG*RPFFYMSY/TSFEMAL MKVWTMVRTSASPVGDVFRGR GWSPFFTSTVGALTTFGVSPGS CRSSPLPSERLWV
13976	44344	A	14058	507	971	PANQKKSRTTRRIHSQILPEAQR GAGTIPSETIPINGKRGNNPKLIL *SQHHPDTKA WQRHNRKREFY TDIPDDH*CKNPQ*NTGKPNPA AHQKAYPPRSSWLHLWDARLV QRTQISKRNSSYKQNRQKPHD YLSRCRKLGLQNSAALHAKNS
13977	44345	A	14059	561	758	
13978	44346	A	14060	2364	2663	DGQLTLVSLNHYSLAQSCY* DGEFCFLHCSASPFL*EGAQST ACTAPCECFASDLGAV*LPQHS WCSTLLLEGAPWPGTLGTAQPF QHRKLGTLNLAG

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13979	44347	A	14061	1	64	MPIGKVGEEYIKGLTRATKESE QQSSALELSSDRVYLNEKEPGD QPWNAAFVFRGCCGVALALRPP HLGWGEPRWAGFRGAFGFPPS TLNPSNWSLTLIIQGCKQEGFYS PSMRPRVVPKRGSA PKVRAEEN AALPSRCPPGPLPVAQP/TGPAD GGSCEQCPCSCGCCQLPPPLP WFPR*TPCDKRV
13980	44348	A	14062	1	774	MFVWSNVEGHSVAMFPWYSIP FLNPPCSHTRPSNLPTQWPPTR ENNLPWSQLLLTSIHQAQLSA LHKEQGSSEKDGSRPNKWDK DHIRCPMSAVMIFSKRHQAL/V RAHQGHFNQDNWTVSQMLSK WWYTLGPNERQKYHELAFQAT AALQAHYVHIFPSKGRWELLH GSQRLDWGRQQLKLLGQQGQ DVLHTNLGKEENSSCWGYKME CEEFGPGQGDGCLGGVHAPL LSPEGLDSEQNTLIMDIFHCA KKLP
13981	44349	B	14063	1	753	
13982	44350	A	14064	2	1457	YPRRRPSRAGVLAGPAVLAGPP SSGRRPRRAAFPAEPFSARRS PRRAAVLAVPPSPRRRPRRAA VLAAPRVLAAPPSPRRRPRPP PSSPRRRPRRAAAGSLPGAELP QSSRLAAHLAAD*PDS*IAAGA VPRGWGLTIMAEGKEEQVTF YVDGSRQRAYAEKPPVVKTI RS CTV/SGHSRHNSSSGM*/SSPNP /IPFQFTFQIPSLQAALWLCL*V TWHFFVR*PVLSSRHCFSPGGLF SLSLQSGACPGSLQAEFVALP PGGQSRLHRTRAS*VPGAFQEK CPLERVWPFHPSKQHPRNGLAF PLP*APQRTQPAEDTLPRHPEM GLILSQGTAG/PGRECATQLPA QHSHAEVLHFGGAMSGQLSLV GPQDSKRTARLTDSQLHLSPT* QPPGLTEGTSLEQG**S*MGWM VGVIAGAPSGWSGSGPSEGTP LFSSPA*LPWPELPTLC*IGVVR EGIPVLCQFSKGM L PVAHSA
13983	44351	B	14065	72	1235	
13984	44352	B	14066	1	2715	

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13985	44353	A	14067	50	1304	TRKFRNG*IP*HIHPKTKSGR SRIFNRPITGSEIAIINSLPTKKS PGPDGFTAEFYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPGMQGWFNIRKSI NVIQHVNRTRDKNHMIIISDAE KAFDKIQPPMLKTLNKLIGIDG MYLKIIIRAMYDKPTANIILNGQ RLEAFPLKTGTGRQCPLSPLLFN IVLEVLARAIGQEKEIKGILGK EEVKLSADDIMIVYLEKPIISA QNLFKLISNFSKLSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ATKRKYLYGLQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKCKTVGLLS NISTHKSVAHVLAEGGIPSLIN LLVCDEPEVHSRCVILYDIAQ CENKDVIAKY
13986	44354	A	14068	1	1155	MFVWRNVEGHSAVFPWYSIP FLTPPCSHMRPSKLPVTQWPPT RENNLPSWQLLLMSVHQASL SALRKEQDSSSEKDRSPNKW DKDHIWWPMSAVIIFSKQHQA L/VRAHQGHPPNQDNRTISQMLS EQWYTLGPNEMQKYDLAFQN VEARIRY/CHRPKRARFLSHAS PPWRQLPAAGAEASGAWNLP GGG*HDYNRCSVPVFRTEVSTR PRPSEICGLTQE*TLSSAKSQVG NTFGAGHTISDTTTCGLCTSK AAIEVPEADTLPHICSWHKGEE CGLRGPEPSPPPRPSLAARVSA GRGALRRRRRPEVPPSRAPRSA ATATPANEQRAVADVGQWAR ARGGRVRAAGRSGLLRVKMM KMKTVMIHFLMKDEYIFSS
13987	44355	A	14069	1331	1584	SLQRKKAARFASSTVPRRPQGIL PIHSFNVPPVGSRRLLKAPLVFIGP G*ITLNRIPYLPHSAARDPFTWN TFSFLLPCEEVPT
13988	44356	B	14070	1	1248	
13989	44357	B	14071	1	459	

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13990	44358	A	14072	1	2156	MGKKQSRKGTGNSKNQASPPPK KERSSSPAMEQSWMENDFDDL REEGFRQSNYSELKEEVRTGK EVKNLEKKLDLWLTTRITNAEKS LKDLMEKTTARELHDECTSLK RVSVTEDQMNMKREEKFREK RIKRNEQSI.QFIWDYVKRPNLH LIGVPESDRENGTKLENTLQDII QENFPNLVRQANIQIEIQRTPQ RYSSRRATPRHIIVRFTKVEMK EKMLRAAREKGRVTHKGKPIR LTADLLAETLQARREWGPIFNI LKEKNFQPRISYPAKLSFIDRST RQKVNKDTQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHHTY SKIDHIVGSKALLSKCKRTEIIT NCLSDHSAIKLELRICKLTRNHS TTWKLNNLLNDYWVHNEMK AEIKMFFETNENKDKTYQNLW DTFTKTVCRGKFIALNAHKRKQE RSKIDTLTSQLKGLEKQEQTTHS KASRRQEITKIRAEKIEIETQKT LQKINESRSWFFKINKIDRPLA RLIKNKREENQIDAIKNDKGDIT TDPTEIQTaiseyYKHLyANKL ENLEEMDKFLDTYTLPRLNQEE VESLNRPIGTGEIAIINSLPTKK SPGPDGFM/RRILPEGQGGAGTI PSETVPINRKRGNPP*/PHFM/SA SIMLIPKPGRDTTKKENFRPISL MNIDAKI/RQ*NTGKPNPAAHQ KAYPP*SSGLHPWDARIVQLTQ

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13991	44359	A	14073	3	1794	AMLPMELGCGPLPEPLPVGCSR FSLFK*QTCISTVP/GYMVTAQS MSSTPPPPSPSTLPSSPPPPPLPQ PLPPPPSPPTLSSLSSPSPPRPPL VSPSTLPSQPSSPQLLPSSSP SLSPPPPPSPLPSPPSAIPLPPP SPQPLPPPPSSPPSLPSPLPPP PLSSSPSSPLSPSPPPPPSLPPS PPPSPPPPPQPPSPSSSLSSPP LSSSQPSLLPPSSLPLPSSPSPL LPLSLPLSIPP*LSLLSPLPPSPS LPSSFSQT*TIQCFSL/VMWH VAPCTYLALAGNTLMAWPLMS ASSKASGGVSMFVWRNVEPCS VAVFSWYSVPFLTPPCSRVRPS NLPVTQWPPTRAKNLPSRQLLL TSVHQAQSLSALCKEQDSSSEK DGRSPNKWDKDHIIWPMSSGG HDLQQAAPGPGRAHQGHYPYQD NWTISQILSERWYTLGPNEMQK YHDLAFQHMAGEDIASDEEHM VIHEEEGVMSLLMTALAPLTL ISSSRIFGKVYGPPTSSSYTSD ASSSTLAPTSFLLPGGAFKAQES GEEAEDGLRELETEKALSSSL/R RALDQ/*LALIMQLFQAHCFFLS T
13992	44360	A	14074	1	2496	MLLSIDAEKAFDKIQPFMLKT LNLGHGVEQHHLHTTNDVDE EDLSDAASKGDDFALSEQSQD AHFLQPEAYGLGEGAETAATGT AHQGNHVRVEECGRSLCGCVP LVLHPLPDPSLQPEAAQGPASH SVACNQRKQPAKLPAVAHERP PGGTGSVDPRPPGATCPESPG PATPHTLGVVEPGKSSPPTMEE EPWAPQGSPCWTAQSLSALRK EQDSSSEKDGSRPNKWDKDH WWPMSALMIFSKRHQAL/V
13993	44361	A	14075	4317	5099	KMFVFLCISALSLQCFRGSFHF IKIYDFSQFLFLFLELPYLLLLN HFKMLELVLQQGHPNQDNWT VSQMLSKWYTLGPNRQKY HELAFQVKVAHCKND*KKFSS EAKPTSQGLAGGNKGSWEWS MSETGTATAPGVSSSELLSVAQ TLQSSDTKSSFCGAEWGHP*GI GCDDVIADDGFSTTDLDLKFKE WVTDAESGDNSGEEPEGNGKFG GKVFAPVIPSSFT/HCRPLLDPE/ PPGSPDPPAAFGKVYGPPLSSSY

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13994	44362	A	14076	1	637	MSRVGSCRWVCGLADFKNKGT DLCDKSLHNRELSAERPLNEQI AAEAEEDIKKITYPPENKPGQSN YSFVDNLNLLKAITEKEKIEKER QSIRSSPLDNKLNVEKDVDFNQ EFGKLIDGYDSTKEWDVWHKF QDIPNLVVGTA FNVDGNGGF VVHWNKKEFHFTSSTEVMFH QLRKLSDKQVDHENDADRED EEHSQEDRERGLHMKLDH
13995	44363	A	14077	448	464	KKRA*GSVSQRFP AET*LAD*VI NTGSQEA KRREQR
13996	44364	A	14078	179	382	NTPNQRSVASNR FVKCTHQHS VKCTQSALCKMHQSAGFLKVD NHRED*KKGHS DRAKTEHGRG QIRE
13997	44365	A	14079	697	1654	PKPSVGRMGFLGTGTWILVLV LP IQAFKPG/GSQDKSL/H**ED LSAERPFELNRLLEAEGRTFK KTYPPENKPGQSNYSFV/DNL NLLAITEKEKIEKERQSIRSSP LDNKLNVEDVDSTKNRKLIDD YDSTKSLGDHKKFQENETADNSF SQEEEPV VAGEDLPPSPQESD VQPVQPEEVSARDFLQRLDLQI KLSTQA AKKLKESSSLERMRE ETLSPTVPTKRWDTRILLIGAF YRVLIGAFYRVLMGAFYKPIAS YRALIGVFYRALMGAFYNPLV RQKSSPRPHSTQEVQLASPLTN TQITYYVIFTV
13998	44366	A	14080	72	1117	ILENHLSDRVAEGGPLQGLRLG VQGEAVPPGLVHQRGGLGPLD GELIGSVGQQVSDVEGAGSHR G*RHTGRTPAVSAGPAA*SATH TAPMWLAGWYEPAPQGPVLV SPPTPFQGT RQASWCSA*ARCA GSWWH*HQTPGGA*RV AAPAP SWSRSCP*RPTRSPAAAPAPSR PGRVGLATGAGHPAQHGHGR AVPTGPRAAGAGSWSELCPPSS CAGTSRGR*AGTRR*AAPAGSG RPGPGA WAGPRCSRSTYAAAA CGRGGA*AGADSGPRSGTHAG HCGARCRSSTPLVPAAAGHLPP PGPGRTGD CPASSCPGGLPHG CSLSGSWGEGWVSAARQAGLP WAVA
13999	44367	A	14081	2	269	
14000	44368	A	14082	1	591	
14001	44369	A	14083	2	477	

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14002	44370	B	14084	237	419	
14003	44371	A	14085	2	1220	LPPGFVMAAAAAARNHVVWG TETGILKGVNLQRKQAA NF TA GGQPRREEAVSALCWGTGGET QMLVGCADRTVKHFSTEDGIF QGSETLPGVGEGMFRGLAQT DLITCVDSGILRVWHDKDKDTS F*PTPGTESGPGVCGCAKTQA HPHVVCHRLGKRMILKIWDLQ GSGNLCFKAKNVRNDWDLR VPIWDQDIQFLPGSQKLVCTGT YHQVRVYDPA*SPORRPVLETT YEEYPLTAMTLTPGNSVIVGN THGQLAEIDLRRQGRLLGCLKGL AGSVRGVAVHPSKPLT*PPVRL DRVLRHRIQNPRGLEHKVYLK VSIE/RALLLSGRDNLGG*APEP SKTQTRCP*EDTEDR*TLGDPW RQLPSGKLFVWSSPKELSKRD GERRSGLGPPADPAVPPTL
14004	44372	B	14086	96	592	
14005	44373	A	14087	102	612	HCAGSPHSPRSLSGTLPGLPL WRHLRSPSAHRTCTVGAPFWAG QDRSQLP*LAGRCGGRGPGSGNP GCA/PACGPAGVPGGRGLGGPR TRSSQALPAPGNEGLSTRASG CRGRTGSPSSASPPLGLSCLPAG QGWGP/GSPPCVSLPPTPWAPV RPEPPG*AAPPAPRRPV
14006	44374	C	14088	1	636	
14007	44375	B	14089	31	612	
14008	44376	A	14090	234	504	SFYHLGAGE*PGKSRVPIPFQS PWGPYQCGRARGGEVCHLQAV PPRGAGAARTLSGHPLGSPEQL PQGPAAELPGGVVPRSTPPCP
14009	44377	B	14091	1	924	
14010	44378	A	14092	11	354	RLSTSPDSSGAQLASPSGSHTRA AGGAACQSAVRSP/PEPSPWV DGTGCGGAGGARWGGSGCT GAHGVGGR*PGMAG/*GPEPCP EGRQLRPLAPVGCQ*REP/G*K NSMGETTT
14011	44379	A	14093	147	513	GSASGVVRLSRWARGLAGFRS EAADLRGECYSS*GSASGVVRL SRWARGLAGRSEADLRGEC YSS*KQRGPKELRSPAGFT*WIP /LPLQLVELPASPAPCAPTPQL SG*WDIGRRGAGGGARRGSG RTGALGVGGSGMAGCRSRA LPPREGS

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14012	44380	A	14094	418	1026	WNP HQGRW SCLPVRHALAF LSPWVIDGTGRHGAGGGALWG GSGRTGAHGVGGS*GMAGCR SRALPHGKAAKAR*EIERASG/ TG TAGGPSTPSAATGPGAKSLI ARGQGWPAAPSAGPAKPTPT GNSSWPASAAGSSGSCSRLS/SP HLPAS*GSGLQWPWPAQKGAPTV QQQAEGLPRLPEEWISL PFLG HQGEHSGMA
14013	44381	A	14095	897	2111	PPLLQSSPNFFLICYPWHNSHE NTHRTGRRGAGGARRGGSGR TGAHGVGGRRLRHGGLQVPSA PWEGS*GPARNRAQRRYHCSCP GLQSGLPHYSGYHT*PDEKEKN GREGOKLER
14014	44382	A	14096	1304	1922	KLNI GVIYSSEIPDSGAQLASPS GSGTRAAGGAVCQSCALRSHSS ALGWSMG/PGRRGAGGGARW GGLQRTGAHGVGGRRLRHGGLQ VPSAPREGS*GSVRNPAQRRW AGTAGGPSTPSAATGPGAKSLI TRGQGWPAAPSEGPAPKPTPTR NSSWPASAARS PGSRSR/RLPPH LPAS*GSGLQWPWPAHYFEFFLP GQNAQTEVSY
14015	44383	A	14097	318	533	MVCFD GADCPWVVDGTGRRG AGGGAHRRGSGRTGAREAGGR LRHGGLQVPSPARREGS*GPAS PAGCLAHL
14016	44384	A	14098	346	957	ARYTLHIPTRLGSPAGFTQWIPH RGC RW SCLPVRPRRALAFLSPW VVCSPVVDGTGRRGAGGGARR GSGRTGAHGVGGRPGMAGC RSRALPRGKAAKARREIERSAG G/TGTAAGPSTPSAAGPGAKS PFARG/LAGPAAPSARPAKPTST RNSSWPASAARSPGSRSWKMS LYMKKSASGQSAQWIAKMW KSPRFKPLWLTS
14017	44385	A	14099	124	663	SCLPVLRLALTFLSPWVVGNGTG RRGVGGGARRRGSGRTGAHGV GGRPGMAGCRSRALPRGKAA KARREIHSAGG/TG TAGGPGT PSAATGPGAKSPIAPGQQGWLA ALGINGAGERLFMKVAFSLKTC SLSCSYLRLLTLRGGSVHVLRG NLTVCKQPQALLRVVFIHQHQ ADCGALPVP
14018	44386	C	14100	1	672	

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14019	44387	A	14101	3	1759	RPLRGWRRTRDARAPRRRCRG SHGARRCLRKTAATSRCCGAP GP/RSRPPSTGQAAEAGDW/PAG CNP*GGLRAADGPGSRPPRGS GLLCGGGGGGSSPWWVHGTG RCGAGGGAPWGGSGRTGAHG VGGRLRHGGLQVPSAPQEGS* GSARNRAQPRWAGTAGGPTP SAATGPGRDGEGETGAHVSA LKGTPTGETWPAHGLVPSIGDQ TCLIFKVTFKAVVLKCGPQTTS STSISCPGSAN/SPSPAG*/GSSG CGSSSLCSAHSVQEDSQPQ*KR TGLQSVTYGRSGSSNEPRYHSD LPTSRSKLRNEDTFFGRKKLS EVQRTGQDPA*SHHTSSYTLPG L*TAEGKDRVENAA*KGSPNFQ RSGTFNPKGGARKTRQAWHPR APNCQAGTPPREGSSGPRTSL AAFRIPQEVVNFLLISGPITRAQR HGEPESPRGQTGSPPLGKTGSE GTDKSTGADKKSTGDRQEV EPTESQGLDRKPTGMDRRSTG NRQKVRQIGSPLGLNRKPNGT DKKSTRNRQEVRRRQASAGARQ ERAGSSTFLRLSALCGLLVVDVN REQVAKQKWDLYSSRFTSGNR
14020	44388	A	14102	1879	2607	GKPSLSLHPGHKCGISRCNGNV SSRLRSPAGFTQWIPHRGCRWS CLPAPRCALALLSPWVVDGTG RHGAGGGARRGGSGRTGAHG VGGRLRHGGLQVPSAPREGS* GPARNRAQRRWAGTAGGLSTP SAATGPGAKSPIARGQGWPA APS/IGPPSPPPGTAGPQAPH AAPVPAR/PLPPH.PAS*GSLG PWPAQKGAPTVQGGG*RAPQM PPKWEPRQGRIVAFTEVGVV
14021	44389	A	14103	2	272	GHWGMVNSPCRASATVSRGSP LPGVLPTSPSATSTCRMCHPR RCPLPFRRLSPPSLTPP/PGKPPL LPRPHSMPGLGLPLGGLPVFHP

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14022	44390	A	14104	101	1815	Q SARQLR PCP GAPSLAGVENRR K KTTNLTSLAAPDTQSTCGQSC GCLHSMGSSCMQHSYYTGFLR SLWPCRCRHS AFSGRRSEK D SKSVRERSGRSQNV PARPALTS PLTQSPGPLAPGAGSWRSRLG TGTGVLWWQRESATGDFRTES ARSSDPSRRDWP GAKRKR EEG AATVLWACATASTAIICQDNAI SPLKSGNSPSNHLWRPQGQLPP VLGLAQPKRWRPNLTTSPSPS RMMARPVD PQRS PDP TFRSSTR IISGKLEPMEATAHLLRKQCPSR LNSPAWEASGLHWSLDS PVG\ PCR P*GLRPSTHGAR/TFSGARP GLGGYSPPEAMPFEFDQPAQ RGCSQLLQV PDLAPGGPGA GVPGAPPEEPQALRPAKAGSRG GYSPPPEETMPFELDGEGFGDD SPPPGLSRVIAQVDGSSQFAAV AASSHQCLSIHIMPMSVGRNG LLTKPPSTSRRGKLT KRDDMY Y FVFPFRSLNDMMHMLPFIEDSR WTHNLDINREQKTNP LAGPKG RPISRTQAAASTNSKTESIQIE KTEEAPFSLRYINNNRSM DPLN
14023	44391	A	14105	39	877	AGPGPRPLPPRSSEGGPGASISL CSEVPGPSCQGRFRGGRDAMS MPWREERSLAGE*PS*GG*S GRGVSRKCS*PGRGPVPRPL RSRPRAASSELDQNSPLDQSLHR TRKTIPSSGGSTAIMPRRGSSSE TFFSAPSKTWVLGIPGETFISGP AAFPVAPGGPRAAPRFSPLNSL *SGGNGGPGPRLHFSSCGKGP PRPSNSRNGGQSACQGGSHLV C*SHRGSLGEGHAYQGDPCSPG HPAKAPRAHAQARRSAHAAS LTSGPCDASCQAW
14024	44392	A	14106	358	546	CFPSRIRLALSRA PKWPAKRSPS EPEMS/PPVWSHPDPNNTAPPK EQPPSSPGRVGRHGNWSV
14025	44393	A	14107	22	549	DHCLCSVVRNKRDSVYPLPIPP CCKTSTISPP/LVDAVRP*DISVS KRVTSCAPLEQPHPLCLPTINAG R/TLARPQGAPT PNKEEGQAPG RATASGQAAPATTVLGDTTK/G PQGRHRTSASAA GPAPFAVA DQLPPEDRAASAEGRK*AAAFP FCHRLVQDGGPPPPAAGVPGA GES

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14026	44394	A	14108	146	2616	LAAVGMASHCFRQRRQSQSPA/ GLRGAGSAYSPA\EGARSSHGQ/ PPWRGRRRGPGDPVRGAARCR RPRAAAQPARPAARPPARPRPA P* AACCE/VPSAANSVAPSAAM *SSAGRDGASSQSRPPHAAPP RSSALPANGK/PPSPVTRAARTC GARSSNTGA*SAARPKHSAASS RHPPPA/MPLPARHA/PGGTSG RPLPTPQGSAPTSSASPRGPA TP PPAGPRAPPPSPRRAAAPRPPGR QLSPA PGTPAAGGGGPPFPALR *SGSVFGRQLVGDGERGRACG ARGSAAPALRTFVVSPSTVVA GAACPLAVALPAPDPLPCSE* A PLRSG*VPQASLFCSQFRPQA WQHP*LLRAPCPRLGAAPVCV WCHSRALDSATPRWM*G*RLP AVWL\PAFSPPPFNQAFVPPCQO NCSLQNRQTLASAKIGTEEWD IAIKIPENVEVTELGNEQRLEE FGGLRRRQDEDEGKFGTPTDWL NGCDQNADSNMDSGQGEDG GCSFGGAGLRGSGWGDQRET FLALKANLRWPFRRSAQSQTSTQ EGAAGARSGLGKGGKKNPLKLP KKQAKMKNKAFKQKQEKERK KHKELKAKASWKGLRPQVEFK NLAEERRGEAAVPGCPVVAGHS WRLSLARGCAKRARQLLFPSE KLLAALREGSTRGGGAASQPQ RKLRVCMRVLDSVDFHMDG
14027	44395	A	14109	1	885	MIISIDTEKALDKILHPFILKTLN KLIGDGTYLKIIRALYDKPTANI IMNEQKLEAFPLKSNTKQGCPF LPLLFNIVLEVLARA/KQEKEIK SIQIGREEVKLSLFADDMIVYLE NPIISAPNLLKLIISNFSKVSQYKI NVQKSQAFLYTSNRQTEIQMM SELPTIATKGKLYLGINHPLTRD VKDLFKENSKPL/KELEKTTLN FIWNQKRAHIAKTMLSCKNKNA GGVMLPDFKLYYKAAVTKTA WLGDDQVFLIPRGHISDYHMG KNLGQYPAFQDRGPCGFPQCIV PLVYRD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
14028	44396	A	14110	453	891	LIHLSTDALRVSGWGTVRSFSS HEAIFQTIAWGETLDNTLLSRA EVPAAFHGALCPWFETREWQ* LLQSILLVNIWLTRHVLHSPRSL KP*FYTT*VFVCSKLGQSGWGK VAGAKLQMNINISAKQLFKVQV LFKIESLMSSLST
14029	44397	A	14111	452	2922	KMGLAREWILRFLVLILQEIRS MRQKENKDQDLNSALHQAADL IDIYRTLHPKSTEYTFPSAPHC/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKLTQ/NRS ATWKLNS/YLNDYWVHNEMK AEIKMFFETNENKDDTTYQNLW DTFKAVCRGKFIALNAHKRRQ ERSKIDTLMSQLKELEKQEOTH SKVSRRPITG/SEIEAINSFTNPK RVPGPDGFDEPNFYQRYKQEL VPFLLKLFQSIKDGILPN*FYE ASILIPKPGRGTTKK/EENFRPIS LMNIDAKILNKILANRIQOHKK LLHHDQVGFIPGMQGWFNICKS INVIQHINRTSDKNHTIISDAEK AFNKIQQLFMLKTLNKLGTNG MYLKIVRAIYDKPTANILNGQ KLEAFPLKTGTROGCPLSPLLF NIVLEVLAIRQEKEIQGIQLG KEEVKLSLFADDMIVYLENPV SAQNLLKLISNFSKVSQYKINLQ KSQAFLYTNNRQTESQIMSELP FTTASKRIKYLGIQLTRDVKDLF KENYKPLLNEIKEDTNKWRNIP CSWVGRINIVKMAILPKVTYRF NAIPKLPMTFFTELEKTLKFR WNQKRAHIAKTILSQKNKAGGI RLPDFLKFYKATVTKTARYWY ENRDIQWNRTEPLEIMPHIYN HLIFDKPDKNQWGWKDSLFNK WCWENWLAICRKLKLDPLTSL
14030	44398	A	14112	3	3349	

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14031	44399	A	14113	294	1107	RRHRLNYPRTAQSPHPRKAL ARSESKRDGGFKNNWSFDHEE ESEGDTDKPEGPLDAPPRP/ESG PRAPGKGL*RRSRSPGSPERGSA ARLTAEPEARNPAASTLLRRGP SSRRARRRCGPWIKKEAAWEE EDGGRQERRLGQDLRTRTLNK SKGGIDSRJISLGQHSHPHTAKL WLDQSLREMEVLKIIGALIMKK KVKEIQIKSRARSTPLHDQIGTT SPRERTIASKRHPYITPKGIRY EQDTLSRTPIITIRSRQRLGPLT ASPPSPFTLAPPTQAIKPSLHLR EGKPTPTPGERSTRPHHPEPPRK EYALSSLYPPTYLLAPTSTDLG NAHPTQEPQFNVDATHPRQNR FIPVAGNSPKRSSQFPVFAPKK NTTPPYLDFAAILGLHRRPPRSR FRTSYPPKEFRSSPPERTAPRN
14032	44400	A	14114	2	297	VQKSVLCSFQAGTMEGVEEKK VPAVPETLKKKRRNFADAIQFL QTVFLAF*YTLKGRQVYWL VEE*HQFYKISYRKKMVQRJRH PQSC TVQKSWWP
14033	44401	A	14115	3	754	GTMEGVEEKKKEVPVPETLK KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRTEIRMARMARKAGNF YVPAEPKLA FVIRIRGINGVSPK VRKVQLQLRLRQIFNGTFVKL NKASINMLRIVEPYIA*EYPNLK SVNELIYKHGYGKINKK*VALT DNTLIARPLGKYGITCMEDL/IH EIYTVGKCFKEANNFLWPFKLS SALSGMK/KKTTHFVEGGDGG NRVDQINTLNRRMN
14034	44402	A	14116	1	388	

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14035	44403	A	14117	1	1145	MTRNYEWLLEAESSQPPIAFQK MEPQPYNSKELNSANNQCLLE KPKLRQLKDKKEYDQGHATAVQ CQSWVYVLTDPDFCQQLILLPS TENFHECSRSDTAGHLRTGHVA SNWLSEHSPQTMPAAMQWDK KMQNTSSWFPQKAPEKVKPMS KLWQTPSQNDTLKAVKALTL SSPERNSINTNKKDVHTETSSK GHQHQRPKVDKSMKMRKNQH KKAENSQNGNASSPPRNHNSP ARERNWSENEFDELTEVVFRR WVITNSSELKEHVLTKQCEAKN LEKRLLELLTRITGLEINQAEERI SETEDQLNEIKHEDKIREKRMK RNEQILQEIWAYVKIRPKLRLIG VPENDRENGKLENTLQDTIQE NFPELAR*ANIQIQ
14036	44404	C	14118	291	551	
14037	44405	B	14119	1	1308	
14038	44406	A	14120	82	367	ITLSSPPHSFIGHKTASGPPQKI PPQPSQ/CKQWGDPTVEAC/CV SCPTQGFIPTRGPPCKHESLV VPLVGTPTRRNQPGGHIQHSQR WAPVLT
14039	44407	A	14121	999	2661	VHLTGCGGPGQPVPPEAPPRGL RSMRC/GP*GFSPGAEA*TEP/C HYGGRRFGPCGPFSLGLATVNSP WLPGRPPPCSPWAGP/CGLCLPLP AAAAERQPALSVPGASPCRLLL PLVVLCGSHLNGGRVLLRPG GSPCGHCHNCAGARRGLGHVL QGGAQARQREQLQR
14040	44408	B	14122	164	1042	
14041	44409	B	14123	320	566	
14042	44410	B	14124	1539	1674	
14043	44411	A	14125	185	780	QKAKKGKLRKSKQNSFPGLKK TVPSQLVQYCPFS*ISWKPMVY QKVPA*PRPPRTPDHHPDPGPA PHPRQHHPPPSPDAP/SPPTPT RRRPPTQPPDPHPRPPHPSKPH PPQQPPTPTATPTTEQQRHTAPP TPRPPTTHPPSTPKHHA/PHTAPP PTKNTKPTPTQRTTQDKGRQKK PRRQPHHSEPNKKS PKAHI
14044	44412	C	14126	1	1128	
14045	44413	A	14127	319	536	
14046	44414	C	14128	231	425	
14047	44415	B	14129	1	1431	
14048	44416	A	14130	75	393	
14049	44417	C	14131	174	371	

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14050	44418	A	14132	79	164	
14051	44419	A	14133	343	775	
14052	44420	A	14134	554	724	SEGPSKEPTHRRMKFSHHDDLIFLDLSN*QPPNSPEPHPPQSP*KPWPQNPSRQM
14053	44421	A	14135	20	242	VSLFMSGSGHCIRSTRGSKMVSWSVIAKIQEI*CEDEKMARES\LAESMSTYVMMNHTYDS*GKTHILIMKK
14054	44422	A	14136	229	366	
14055	44423	A	14137	131	505	
14056	44424	A	14138	1	1317	AGSCSGSRAMAEEQGRERDSVPKPSVLFLHPDLGVGGAERLVLDAALALQARGCSVKIWTATHYDPGHCFAESRELPRVCAGDWLPRGLGWGGRGAAVCAYVRMVFLALYVFLADEEFDVVCDQVSAIPVFRLARRRKKILFYCHFADLLTKRDSFLKRLYRAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHKDPPDLVLP/SLNVTSFDFSCS*KAGMT*SPRGKNSWLLSINRYEREKGIWTLGTGKALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLSFSQKQKISLL/RQLARVCFYTPRQ*GTLGIVPLGRPCYMAVPQFICLIRVGPFSSSI*PQCSQGFCEPDVHFSEAEKFIREPSLKATMGLGWEIPE*REKFSFGSILQEQLYRYVY
14057	44425	A	14139	1	648	MESKEEQGGVADHQKATRGIPTPQPREVVSERATQRGNRAFTKLCNPKTNRKQQQQYQQQKGRKTKLPKGQHPQRSKLDKLTEMRKHQQNTKNPKGQSPSCPPNDCNVSPARVHNWTDMEELTEVGFKKWVRKNCAELKEHVL TQCKEAKNLDKRLEELLTRKTS LERNINDLMELKT/RA*ELCKA YTSINS*IDQAEERISEFEDHLAE

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14058	44426	A	14140	1	1365	MPVKGGTKCIKIVLLFGNFIFW VSEDRCRALLSGPTCSRAPDTG RGRECRQLALPAPGRHRAGRES ALRLPAGSKAGSRAGRDGRDG RIRVGVSGLTFLGTTGLFNQSL AETGFTPYTQKSNDFLVKSLLKJ WHTYFKNFHQEARLYIRTSPGS NWNWFCTLGIESPEQPGVYEG QRPVVTKSFASLTLLKRVGTVL LLAARINADVLYVLQLAGIAVL AIGLWLRFDSTQKSIFEQETNN NNSFFYTGVIILGAGALMMLV GFLGCCGAVQESQCMGLLFFG FLLVIFAIEIAAIWGYSHKDEV IKEVQEFYKDTYNKLLTKDEPQ RETLKAIHYAVCRLGKDTLLRF LRIVSAHRLNCCGLAGGVEQFI SDICPKKDVLETFVTKSCPDAIK EVFDNKFHIIAGVGIGIAVVMPS FRSNHDPHVSYYLLIFGMIFS MILCCAIRRNREMY
14059	44427	B	14141	98	1064	
14060	44428	A	14142	560	964	KRLPRILGIRGKPCPDTSRAGR RVRGAAAAPCREAARGRGQRR FLPPTWRCETGAATMFPSPALT PTPFSVKDILNITVRPRS/LGQAA LTKRLSASLSPQSCARCRRWWS CVILSAVRGN*YAGSRAHRDCT Q
14061	44429	C	14143	189	452	
14062	44430	A	14144	1	647	

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14063	44431	A	14145	890	2905	LRLSLKFPMSPQWTPYNELYTL KVDMMKSEIPSDAPKTQESLKGIL LLHPEPIGAAKSPFAGVEMINSK VGNEFSLHLCDDSKQKEKEMNG NQEQEQESLTVVRKKRKSQQAG PSYVQNCVKENQGLGLRQHL GTPSDFDNDSSFSDDLSPSSSL HFGDSDTVTSDDEDKEVSVRHSQ TILNAKSRSHSARSHKWPRTET ESVSGLLMKRPCLHGSSLRRLP CRKRFRVKNNSQRTQKQKERIL MQRKREVLARRKYALLPSSSS SSENDLSSESSSSSTEGEEDLF VSAENHQNNPAVPSVTYQGP WSKNIKEKTLEINSSQALTAYE CLHSAHVINLISPFYHHFPSSQE RSYLSTLSTLSNKKTGSVWFTR SPKVTQFFPGGALTGLSQRPER EILRPLALPGKGNTPPYFCSPSM GCTHCPTSPNEMNQGISDAA APVRDIYIKPPSPWDRAPGGRG GCGHSFRLKSPYLRAKSAAD FPAQHSSSDKGQAASSSGSLTP VYPVWVTPPSRGRQTPHRGEL WLASDGCPSGRKLPEEGTGSNL CCSAASAGDTQANRDHNSSPA REQTWTENKFDKLTAGLRRW VINSELKEPVLTOCKEAKNLE KRLDESPTRITSSEKNINDLMEL KNTAQELHEEHTSINSQ/DQAE*
14064	44432	A	14146	1	737	LNRGEQRAVRYYSHMKLNMA EEEDYMSGFLH*CPRRYQTRIA NAKANPRSPSKREKQQEANLK NRQKSLKEEEQERRDIGLKNAL GCENKGFALLQKMGYKSGQAL GKSGKSGIGHEASLKRKAEEKL ESYRKKIHMKNQAEKAAEQF RMRLKNKQDEMKGELRLRSQ RACQQLDVQKNIQVPREAWY WLRLSEETEDEEEKEQDEDEY KSEDLSEIKKTYLQIVQDQLLQI MTKIIPNKVET
14065	44433	A	14147	1	1860	
14066	44434	A	14148	1	1203	
14067	44435	B	14149	1	1119	
14068	44436	A	14150	1	1407	

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14069	44437	A	14151	1	1731	ERSSSPATEQSWMENDFDELRE EGFRRSNFSELKEKVRTHHKQD KNLEKRSWFFEKINKIDRPLAR LIKKKREKSQINAIKNDKGDTA DPTEIQTITTEYYKHLYANKLE NLEAMDKFLDTYTLPRINQEEV ESLNR/LNNRL* ^N *GNN* ^L TNQ K/NVQDQMD* ^Q LNSTRGTRRS WY/RFLLLKFQSEKERILPNSFY EGIIILLIPKGRDNTKKDNFKPIS LMNMDAKILNKILANRIQQHIK KLIIHHDQVGFIPGMQGVFNICK SINVIQHINRTKDKNHMIISTDA GKAFFDKIQPFMLKTLNKLIGID GMNLKIIIRAIYDKPTANIIILNRQ KLEAFPLKTGTGQCPLSPLLF NIVLEVLARAIQKEKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLSNFVSKVSGYKISVQ KSQAFLYTNNRQTESQIMSEIPF PIASKRIKYLGIQLTRDVKDLFK ENCKPLLKEIKENTKNWKNIPC SWIERINIVKMAILPKVIYSFNAI PIKHPMTFFTELEKTTLKIWNQ KRARITKSILRQKNKAGGITLPE FKLYYKTTVTKIAWYG
14070	44438	B	14152	1	906	
14071	44439	A	14153	3	553	EHSSSPATEQSWMENDFDELRE EGFRRSNYSELKEEVRTHGKEV KNLEKKLDEWLTRITNAEKSLLK DLMELKTTAREICDECTSLSSR CDQLPRPDGFTAIFYERYKEEM VPFLLKLQFSIEKE/VNPP* ^L TL* GQHHPDTKAWQRHNKKREF* ^T NIPDEH* ^C KNPQ* ^{NTG} KPNPAA HQKAYPP
14072	44440	A	14154	1	909	MKAIEKMFFETNENKDDTTYQN LWDTFKAVCRGKFIADVNHKR KQERSKIDTLTSQLEKEKQEQ THSKASRRQEITKIRAELEIET QNTLQKINASRSWFFERTNKID RPLARLIKKKREKNQIDAIND KGDITDPTEIQTITREYYKHLY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPTGAIEIAINSL PTKSPGPDGFTAIFYERYKEE LECSSSPAMEQSWTENDFDDLRL EEGFRRSNFSELKEEVQTHRKE AKNLEKRLEKWLTRITNVEKS LNYLRELKTMARELC
14073	44441	A	14155	1	969	

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14074	44442	A	14156	377	687	LLEGKLTNRKDIHTKTPSV/SP SSKTKHESSSPAMEQSWMEND FHLEEGFRRSNFSKLKEEVR THRKEVENLEKRLDEWLTRITK VEKALNDLMELKTMARE
14075	44443	A	14157	1	711	
14076	44444	A	14158	1	831	
14077	44445	A	14159	1	744	
14078	44446	B	14160	1	1479	
14079	44447	A	14161	1	810	
14080	44448	A	14162	3	651	
14081	44449	A	14163	2	1067	
14082	44450	A	14164	2	2063	
14083	44451	A	14165	1328	1639	PTNAHETSGRYIAGSSEKRTSA RTCGGTSAAARPAGTSMQTRC RQPPSS*HAVPRVAQSSDGL KATHPQAYQPCGHTPTRLPQES NCIEHERGLGKKKKKKK
14084	44452	A	14166	1	620	MTLGYGQRGANKDLRTGFDPD LCTMDNFAEGDFTVADYALLE DCPHVDDCVFAAEFMSNDYVR VTQLYCDGVNDSFLIGLLRIG CKIENERSSPAMEQSWTENDF DELREEGFRRSNYSLEKEEVR/I NGKEVRNFEKLDDEWITRITNA EKSLKDLMEKLTARELCCKC TNLSNRCDQLEERSVAMEDEM NEMKHEDKFREKE
14085	44453	A	14167	1	514	MGKKQNRKTENSKNQTSSSP KERSSSPAEEQSWMENDFDEL REEGFRRSNFSLEKEEVRTHGK EVKNLEKRLDKWLTRITNTQKS LKDLMEKLTARELHDECTSLT NQFDQLEERINNIEDH*QD**R RKERRIK*MQ*KMIKGISPLIPQ KYKLPSINTINTSMQIN
14086	44454	A	14168	1	366	MDTFLQAERKDYMEAYELIEQ EEQGEREPVAVNNILSTEALMA NAKSTLMFYAVGFLWQPGGGR GHKAAASNPVTRDVGSLSSLT FLRGERSSPAMEQSWTDNDFD ELAREEGFR*SNFS
14087	44455	A	14169	1	1026	
14088	44456	A	14170	1	3906	

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14089	44457	A	14171	1643	2721	IKPTKMGKKQSRKTGNSEKQST SPPPKERSSSPAMEQSWMENDF DELTGAGFRRLVITDFSELKED VQTHHKEAKNLEKRLDKCRTN G*LEWMNG/TRITNAEKS LKDL MELKTKARELHDECTSLRSRFD QLEERVSVMEDQK\MNEMKR EGKFREKRVKRNEQSLQEIWD YVKRPNLRLIGVPESDGENGTK LENTLQDIIQENFPNLRQANV QIQEIQRTPOQYSSRRATPRHIIV RFTKVEMKEKMLRAAREKGQ VTLKGKHIRLTVDSLAE TLQAR REWGPFI N LK EKNFQPRISYPG KLSFISEGEIKYFTDKQMLRDFV TTRPALKELLKEVLNMERNNR YOQLQNHAKM
14090	44458	A	14172	351	898	SGVTPAPWRPNGTLLITAA TASH PVLAI PAHLCSPRCPFLTTVTC SGPQHHAARGRVPFHC/SECGK SFRYRSDLRRHF/ARHTALKPH ACPRCG/KGFKHSFNLANHLRS HTG/ERPYRCSACPKGFRDST/G LLHHQVK TITT*PD/CGGCLVSN IVGSYSRPPWPCTRGPRRPLGSP SPAPGSVCLC
14091	44459	A	14173	1	551	
14092	44460	A	14174	3031	3207	TIHGCWWDPLSSIF*PFWGRGFI SHKICQAQISFRVISGTVLSLDK LLIMFHKAIFASP
14093	44461	A	14175	3555	3957	ENGQKTWTGTQRRTYTGDRM AQIQNPDTKCW*ECKATGTRI CWWECKMVQPLWKS/WQFLT KLSILLPYNLA ILLGNYPNALK MYAHTKGFTCMFIAASFI AKT WKQPRRPSVGEW/INNL*LVQT MEYYSAL
14094	44462	A	14176	3	883	CQPYPRPRPTGTGHCQPPSQ GSAEP*G*CLPTLLRMALKAQP TKVNPRTLDSDDPVC/S*AAHS RVLITSPSRAPWRLPS*RRCPA GTCMPSTATSAR*CSQRPSSW *T*TGSSLSGQACGPSSSTAPPSS SWSACTCGCAAAARCSAASS TRSGPTCGSSPPASSCASSTPAP GTTSPSTLTSWASSPWSTPCPGS AGPSSWSSSSSATPSASASTRTL SPGSPAAP*PWPTALSRLTEQEA VWGAWGISHGNSWDKETKLV RLPHPCSKSPCFRPSLPYRAHR AP

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14095	44463	A	14177	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL/GILLHL ESELAQTRAEQQRQAQEEYAL LNIKVKLEAEIATYRRLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14096	44464	A	14178	2	1044	AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLRLASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALLSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNG/GGLA GMGGIQNEKETMQSLRDLAS YLDRVRGLETENWKLESIQEH LNVTRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRQA YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLSDTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV

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14097	44465	A	14179	1	2040	MPVPQLPPVSRSLAATAAASVT EPGPNEAVRSASAEPEVKEGF PSQNHSGVHSNLIPSGGSVAPSS GRSHYGYASEDGTCSKLRVRPR LAAAPAAPFAFVADLASCOCG LSFFEGILLVRGPYRRLRATVV RDLVAVRMAEEQEFTQLCKLP AQPSHPHCVNNTYRSQAHSQA LLRGLLALRDSGILFDVVLVVE GRHIEAHRILLAASCDYFMSFT TRSTFTNYWSLGSVLATTYGA RLVSSSTARVYAGAGGSGSRISV SRSTSFQGGLESGLAAGMAG GLAGMGGIQNEKETMQSLNDR LASYLDRVRSLETENRRLESKIR EHLEKKGPQVRDWSHYFKIIED LRAQIFANTVDNARIVLQIDNA RLAADDFRVKYETELAMRQSV ENDIHGLRKVIDDTNITRLQLET EIEALK*ELLFMKKTPEEEVKG LQAQIASSGLTVEVDAPKQSD LAKIMADIRIAQYDELARKINRE ELDKYWSQQIEESTTVVTTQSA EVGAAETVLTTELRTVQVFGD STWTSMRNLKANLENLAGEV EARYALQMEQLNGILLHLESQ LGQTPRTEAQRQAQVEYEAALLN IKVKLEAEICHLTRPPSWKIGE DFNLIGDSLDERNSMQTIQKTT TRRISWIGQSGVLRPIDTKVLEA LSQAEASGTLGKQAEANKKFQS
14098	44466	A	14180	275	550	
14099	44467	B	14181	729	909	

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14100	44468	A	14182	1	1415	MGTQCDLLAKSLEDPCPVDEVE DAFQGLGKDEEIEQFSDKTFG SGAIDDDWREAHECLAELVK QPVAVIEQTGNGERDEMDDL DHEENLAERLSKVMVENELEDP AIMRAVQTRPVLQPQPSLNSSI WDGS/VSSSEANPRTTACSGNAY SVCIRICFAEA/SPRVQKMIGTF LNEHYQGGQLHLSLAVLLELS P*APHLNRWLYPASPFRFCVRS LSMFGP/QMPFRYPAPYGERMS PNQLCSVPNSSLLGHPFPSPVPP VLSPLQRAQLLGGALQPGRM SPSQFARVPGFVGSPLAAMNPK SQAPMFRPDTHLHPQHRRLH QRQQQNRSQHRNLNGAGDRGS HRSSHQDHLRKDPYANLMLQ REKDWVSKIQMMQLQSTDPYL DDFYYQNYFEKLEKLSAAEEIQ GDGPKKERTKLITPQVAKLEHA YKPETIICQALCRALHINYLTKA FQQAFEVSASITTYR
14101	44469	A	14183	204	560	QGYWRGCTSSGGDGGCRGCW SPGKRR*GLSRTASGPPAAVAS PGRPRSPPSARTG*S*PGA*ARP CSRTW/PPRCPLRPSSAARASA SRV/APL/GEPAPANTNIYCAAL THRATKSSTREF

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14102	44470	A	14184	59	1695	DMPWVWPVLPWIKDSSPSSELM NPDNTSGLRQKSVEAEPCLW MVHRYTPQSTGEACTMAKAA GPSSPGSCPPRLGADPWPMR LSH*EC*KGTGTTASGYRRHQET APPESSGSPVGLSAGLWLSWA WPVSPACLHPGPPLCP/GPPALG LGPRSPAAS/C/PPLPEAPPACSP FCP*GEISSSGPLEVPVQV*LPGD LSEPLGTSTPLGRAPGLCSLLRA P/RPGAACPPASPSRPAMLLS*E APRRPGPSGETSPSPSLAPSEASP G/PPRHNNGRDSEGAGTRTFGA SGSSKG/LGGQPAHPGPGGR*G GGRYRGSAAGSVHSAAPGCGSP HAPGCA/CDVRG/AKPSHFHSG CQSG*GHQTSGGCPHLGLSPCS TCLCAGQLQQQK/PGSSGNL* GQGHSGLDLSAPPHLVPG/PG PLTAGGHG/SLVGDSEWGSPAP GAVLGQNSSGPDQQRAGR/WLC SRAEKSGCYTAPPLG*LSAQFQ EEKASWVPVPGSGQLEDSDHPDPY TALPLAAPPWGTGTGCPPAWP RL/EPDDCGPRHLSPTCSTLPS WGGCAGS
14103	44471	A	14185	264	643	RCLRPGEGRSRQGRSRTGRGK AEEGGARTQQRRAALLPERS ASQPGPRDSPRWRRRQTTRGR ARPASSGGT*GSSWLTLAWPPR EP*RLRSASAQG/CRRQRLQQR RRGLYQPHRPATCGPRAAD
14104	44472	A	14186	114	1039	QSQRRLPLADTPRRSNRPCSAA GLLFPQSFWSQELSQAFLPPS SPCLHCLPGTAAASRIHQRSPT RPSVQERRETHGLCAHRCEWR AGSPAHP*AHRFVSRAGSPA GP*AHRCISRAGTPARGPYRR* VSEAGSPA/AVVSAPCSLSS*AC VTG/CSPAHS*AHRCASRAASP EHTSREDAEQAP*MQGLCPVH QEQQPSRKSVVTSPIHPETDCR LLPKNPCANKHQPTATGGRAV PPEVQHVPPRSGMTLGLSHQPLA LQFQMQATDAARLGLSPOGQG SPPGPRSTLLGLCLSLFQLSLR

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14105	44473	A	14187	1	1629	MIIVVENPKQSTKCVRAYTFS KVAGHKAIEKRLEKLAVDPHR DRAQMLKVENVQQAQQWIN KLPPARREDEDVKEIRWMIEEL RVSFYAQQQLDHTGVDRGQPGA STWSASLMCSVTQPKLKRKP GFLGLGERNCFSVYGAGRSW GRGLGSCGFWLPPRTRIRAADV CLARWGWRAHRVRVLAGKNS RAESMLWSFHKAIEAARTNII QAQTRVEAAQATERRIAADIDD SELKAPRDGRVQYRVAKPGEV LAAGGRVNLNMVDLSVYMTFF LPTEQAGTLKLGGEARLILDA PDLRIPATISFVASVAQFTPKTV ETSDERLKLMFRVKARIPPELL QQHLEYVKTGLPGVAWSFLYSI NQTICLRLLDSIEAKLQALEATC KSLEEKLDLVTNKHQHSPIQVPM VAGSPLRTTQMCNKVR/CVNP* ATVVPVPVPPPTTQQYQGLDA GATTRVPRSLRSEGQSTQKSP SCGSHSQDNSGGRKAVGARRD RWWLGAGKGPDCRGAKCGLP LSGQKCPDLPYQVVGCTSKTG
14106	44474	A	14188	3	1010	GLQTQLVPLSSPVASLDNFSNL FGADLHVEKGQVPSSDQHLISQ RCHFPKAPPWSVCKALLPRSNP ATSLSGTSKPNSSGDFNSVTKS QPHCELNSFVLTHGSPVWMM SEHDLADVVQIAVEDLSPDHP VQSCGTVVVLENHVVTDDEP ALKRQRLEINCQDPSIKSFLYSI NQTICLRLLDSIEAKLQALEATC KSLEEKLDLVTNKHQHSPIQVPM VAGSPLGATQTCNKVRCVVPQ TTVILNNDQRN/DHCSQDGRPL EQQGTGFPKMSLASQ*HGTNP TFPCHCAESHENKSTLSQGT QHTLHLCGHRVPEGRHRPSSLR SGRAGWAMLNA
14107	44475	A	14189	1	1710	
14108	44476	A	14190	52	457	
14109	44477	C	14191	1	838	
14110	44478	A	14192	92	514	
14111	44479	B	14193	1	531	
14112	44480	A	14194	1628	2008	

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14113	44481	A	14195	2	1616	CPPRRRPRPRAPPHRRPPAAGA RTAAAGDRSRHGPASRVGTGP GQQMRKTYCRNSEPSDLLDQGG GSRGGPRRQSKCVRNWWVLGL TDFKNEAADPHDSGAQLASPSG FRTRAAGGAACQSRAMRYS A1.GWSMGLGAVEQGVV1.VGE AQAAQEPMEWVGSGSMVGCR SRAPPAGRQLRPDKKLSTAPVG RHRWRPSTPSAATGLGAKSLIA RGQQGRLAAPNKTDFKARAVK KDKEGHYIMIKGLVQKESITHNI YAPNTGAPKFTKQLPLDLRNKT DSNTHVGYFSTPLTALNRSSRQ KVNKETMDLNYTLEQMDLTDI YRTFYPTTAEIFYSSEHGTF TDRMIGHKTSLNKFKKIEIIPSTL PDHSGIKLEINSKKNLQNTNT WKLNNLLSDHWVNNEIKMEI LKFFKPNDSDDTYQNLWDTA KAVLTGKFIALNAYIKKSERAQ VDNLRSHLKELEK*EQTKPKPS RRKEIMKIRAELEIKT/QKIQKI NKSQSWFCEKINKIGRPLARLS KKGREKIQISSIRKK
14114	44482	A	14196	1097	1686	APRPLALRFGLPSNSGAQLASP SGSCTGLQVELPANSCTVRWQ VSALGWSMGP/GPGAGGSAD QGGSGGTGAHGGVGRFRHGG AAGPEPCPMGEVAKAPARNRA QRQWAGTAGGPCASS/NSC*PG C*APYCPGWGQPAAPSAGPP SPRPRTTRAGPQAPWAAVPVPAH ASP ¹ PHLPAS*GSLRPGQGSKT YQKSH
14115	44483	A	14197	647	1496	FLNLLSQWNLMLCGLKKRRKQ FKDYEKKVKELNEERDKYRKQ SVYIYTFGKEPTLNKVLDA KFAIDFITPGTYFMGCRWSC LPVLHCALAGLSPWVVDGTRR PGAVGSAGRGGSGGTGAHGGV GRFRHGGQLQVRSPAHEVLRPS EKSSAAQWAGTAGGPCASSTA ADLGAKPLTARGGGPAGPPSA GPPSPRPRTTRAGP/PSTVGS SPPTPLPPLPAS*GSP ¹ SLGQ RKGLPQCSGGLKGWLLKHRQS GCPGRGGAQSERGLRGLPARC

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14116	44484	A	14198	1	560	MAALLLVGASWL/LLLLVGASWLLARVLAW/TYAFYDNCNRLQCFQQ/PPKRNCF*GHLSLCGA/TEEDMRLMEDL/VPLFRDVQLWWLGSFYVPL/SLVHPTFTAPVLQASGG*PGFTTTMGLSFKRAKWQRLA/SEGSVRLEMFEHISLMTLDSLQKCIFSDSHCQMVSPGSCTTSRGPRI GALPTGGARAPENGDPKEIE
14117	44485	A	14199	175	2225	RWSSVSFA SGMPSPACCCWGHPCPSAAQPTGSPWAGCRGLTMPNGQASPAS*VPPGAFPLCIKQPLWENLMTGVGKFSREAAATLEGPTLPTRGVGPQCRQIADLPLERTGWRGDGNPVRGVVRQKRKQLVAGETAASLLPCQASGESCSVP*QARGPPVLF LPQ/WGRRWA KGCASRSCF*PDFRPSHAPGA REGAGLAAAPKRVARLSPAVPPACCGLQGGSSAAQAL*PQLSGPRLPREK*GA/PCWRRGPRCCPQNSAPETLEYVEPRGTGAPGTHTHTGLPSPSQGCRGAEGW/WGLPGLPGPRAGSSPQPRGAWRPRARTPPPASWAAKGRGRPLAAGGLARPRDPGPGSGVAPAGSLRPHSSGRGWGRRRLRARPTGGNRGSEWPR/RPPGYPGARPGAPSVPRPQ/PAA*TRPLPVCGGARPFHPVPATV/VPHAGPP/SGMGRRRGRYRPPASARPAAGRCGAGSAEPGRGTDKGGDGGEGKTKRGGG/LGGGAGAPKAAPGA AEPMGGRGAGAGGGGA/R*GGGGGGGSGTTGSGSSSRPRPRTRAPPETDPA PRPRPGLVRAAGGGAASGSGTGRGAEGCGVRAARGVPASLR AALARGAQARVLVSGPAPGWA EPRPAGGARGVGWGPVLAGPGRGPRGGAGRGPRALSRGCAA*AWTPRGAGQGRGPQSGRGSG

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14118	44486	A	14200	1	2850	MHPQERTAAATNAAIIITDGAA TQMGVSTSPAGHPRDGYQQG KDVSLLAHTHSFKISAAIEAKTT WVGMCRWGCKVALDVTDFVH QKGPEGAGRKNQIPFIQDFPFAL RSEKRPSLPATISGKTLPLNTKT CPQLLQCKREGHSLQCLIWLQ MVPQLGRLAVGGCHSNWFPSP KKAVIWEKFKHNSGLVSDKG GKRTGKGLGECLLMMRKMS ALEALTTFDSSLQHHPRTTFVPS ALEALNPGKPRQLVTPA
14119	44487	A	14201	1	1570	MQSATSDAGSAPKKQKKVMTL QEKSGLAWYFFTAQWPNTPP KLRTCTESMGCLLDCCCTGQ GDWTRVTLYCRYPFILFGTNA WVANFERPRMNANSLASPTG LSPYLRFGLSCLRFYFKLTDL YKKTTLGSLPDAAMAFVNCHG AGGTVAVRTSRGHSRCHFGFG VSGTRYHLLTPQVVWERQQK VDSLLGTQQMLEAQGREF/PGP CIPLPVPTNAPAAKTTQPPSPD L*PPNYLFLCVDGHRPIC*EPKQ NKSDSFTSQA*SQDG*YCGCS/C RAPRPHGTSATIPMSSSCKRFQP SSPF/CKGPYHFRFLEERPLASRP SIHPSGSGSYWLRLGCVAVGRTG /SRLNLQLHSASGLQALSKQR*R YCQSAGAGSPEPPRGGTR*CCR EAAPGCRAGTCPSPAANLPSLR RK/PGTC*PQNPPGRCGSCGASA AVLAETPARIKRSFPRQSCPR TWMAAGAPGSSRRQGTKHVT* *SSTLEKQLDNPTATYFSVPTRK PVH*NQQKDL*VTG*LQIFHL
14120	44488	A	14202	11	356	VSGPPR*APWCPCLAAPTGTS HGSTARDSSTACKVS/GGATCV/ SGCGPGLGVLGRGLSSTRSCCM PAG*CPSSKDTCEKSGGRTPV PPFEWAAQDASLVRRCRILAH PCRGT
14121	44489	C	14204	333	473	

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14122	44490	A	14205	344	1035	QSAAQWFWWPGRSASLGGA GMQPPLASWPHPRISIRCLR AP*QFTNATDPRFRSAPRRSGQ QQPRGSSGPAALASPSRQPNR AGALRTGGAGWATALDTWSC PRTRRRAPMGSL*AAAQQCV TGATWPPPSAIA*QSAAQWFW WPGRSASLGGAAGMGPPLAS WPHPRISIRCLRAPAPCSGPSASS AAVQVACCCSLACCGPSRPASQ GHLDGTPHTSPETCTTSLWSPQR RRAAGPPKVVDIPD*RGSRRLPS GRGAPNTTCIPYGGSPGAKWIE GCPAQ/RPSPPLHPAMRASAL LLMPFLQRRHRSAIRLLRPGS DCTGKK/GKGFLAGPETKRQKR LCPSPKTLGRALGQOEALPANV RC
14123	44491	A	14206	41	292	
14124	44492	C	14207	480	1637	
14125	44493	A	14208	3	410	SPPCGAPPPVFCAPAPRAPAPP RAPPLAEALPGFASAAAGSAPA RSGPAGAG*GSRSRPRARASAS LAPASAGDHLGYPSATAAAAP ASRPWLWRPSLNAARLGDPA GWQASQWAAGSA*RAGSQWA AGEARA
14126	44494	A	14209	1	1274	FFFFHPLRSLLDGLHQSERSA PEIKPGALESTWSQARGAALRL AEAR*RAAPAAGTACSAGGAA SSPR*GSRATRRRRRGPTAPSR ATAPGRGAAASAAPARPART ALMASARGPP/TAASPAQALTR SAPGHLPPMSELGAVTALCESC PVT/AAPRSGGGEAGGTLASEW GRTCRNYG/PAPGIWRPPLSAA RPAAASPPARRIWSPPAPVHSA ASPIGLRVAAPCSSGSAVPLRSR RASPPCGAPPPVFCAPAAPAR APPRAPPLAEALPGFASAAAC RGKRLRALQGGGLGRSGSRQ GPAAGS*LRGKSWSPPPGSA PLPLAQVLQALVEAGSRSPRA RASASLAPASAGDHLGYPSATA AAAPASRPWLWRPSLNAARLG DPACGWQASQWAAGSA*RAGS QWAAAGEARG
14127	44495	A	14210	2	335	

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14128	44496	A	14211	344	1062	TRAEVTQQLSRFASPPVLRLL RSYVSPPAAPTADPRWRPSWST SLRWVVKPNVSAAYRIPPRASN GYRASDWKLDYA*WTGLRLIT SKGKTAYIKLEDKVSSELFAQA PVEQYPGIAVETVTDSSRYFVIL RISDGTGRSAFIGIGFTDRGDAF DFNVSLQDHFKVWKQSEISKE SQEMDARPKLDLGFKEGQTIKL CIGLCSKPGTTAIQLGPVNLGIG RTLRTDLRNKNDLEGTNL
14129	44497	A	14212	573	1017	TDQGVGSPICPRFQCGPPRSPR FQQRSPHSPDSSRG/PPHSPRFQ QGSHPHTPDSSSG/PPYSPDYSSG HPTP/HTSQQGIPI*DGHWLPC GPVFLWSEAPHLNPLGVWVGQ PRAPALPGNSAESKLVPHDRPA RPETPGAGTAWAHQALRV
14130	44498	A	14213	707	836	
14131	44499	A	14214	724	927	SFMDFRFVLLFFHLVNPVK*RP VS/SPGSKLLVPPWVGPKTPVPP HPSPPPPAHGEPGLPPPPPLPH
14132	44500	A	14215	29	157	
14133	44501	A	14216	1	363	
14134	44502	A	14217	770	952	
14135	44503	A	14218	1053	1995	KSSPEPDLSHSFICSPNFPSSSL KRPH/FQSSILACVFCITADSSRA PCVLRVCDGFAGLTRSSAPSSK EKPCGFSLEPFTPLAVSFPQAAL CSLGTVSCLRPRLTPSWECP VLLAGAVCPGLPCAAGCPWA GEEGCPGATSQLDQVSWPSLQE APEVLWPCLDSWGFWFAPSTV IPLMASPRFGFMGRSQQPVLIN HLIKEPKAKFSKNHNSIRCCQG QRKWRRGNAAGMCCQPQIPGK GEVKTEFQPVSNRNVNYGCTM HFQETLWTPRLGLGDGDSNNN NNNNNNNNITANPGKEAEKPE HPHLLVKM
14136	44504	A	14219	482	833	THQGARGCTHARVSVREMRTR RGRWATGMVRPAPCSSVHTTA VQRQQVADQLQTTAELSME/L N/KWDQDPEAFVRKVATSYET WIS*YYPEDKAQSKQWLPRSGS GATLYSATNQYP
14137	44505	A	14220	195	367	

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14138	44506	A	14221	989	2210	LLVSCAILLSVSFLHSSSFVRSRS NRDSPACVDATYRGCSQCGEG VCGEACSCFPDLNPQGVHAG EGVLPCSGWEDTFGKNTCLVS YQQIPNRRRPCTCECGKAFGQ RSHLVQHTSEKLYACQECGCTF SNNSSLVKHWHVHTGEKPYMC GHCCKCFRESSSLAKHQRVHT GEKPYVC/GESTHLVQHW*FHT GEKPFAC/HR/CSKAFADFSALL ACHGTYTGERPYECRVCKAFS PSLSLAEHIRCHTGEKLYACQE CGKAFSHSSSLSKHQVHTECG KAFSQGSYL TQHLKIHSGEKPYI RGEHPYACGKCGKTFHSHKFLT QHEQVRMGKPFMCGDCGRAF MQTSSLALHQRTNNGEKPYKW NECGKSCIQMSHLTEYYQNLPE KGSKDPHTDATVHSPVMD
14139	44507	A	14222	1	245	PPFRKQQAQHRNKTVLVRSQP VPVTVPE/PSA*RTPEGPRRAG CDPRP*PCPAGPELPAQMKVLA IEQLLSLHFKKALLF
14140	44508	A	14223	477	947	LCSSLSPPPPPPPPPPPPPPP PPPPSPVPLPPSPRSPVSPPPH SFQGRSPPELGSSAEPWLRPGT WV*/PPPLTFSQEEAASSAQK*N CPGESVPQVPVTVPERQPDAA NHSLLLPGQCFWCQGPHPY WMGPVDASSGFLSQSFY
14141	44509	B	14224	438	1437	

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14142	44510	A	14225	584	2866	WHFAKLSRNTQDHTRP TLGAA QAVPATGQPAAPG PAGAGPEW VPFLAVYKEQLVRNDSVLKVFF FPPIFYREGWVCCSVVESH LQE GFVWLFSLQL*PPKLRSLFSLSY CLSPSDIEISRQGT PKAVDVL A KEIGLLADEIEIYGKILVSSAGF A*VVWEIL*NSLSPPELRITPTPL GEGKSTVTIGLVQAVSLGLCP S WQLYLVT PALPGQQSETLFLK INK*KDILFL*FNLHLTGDIHVVI SCELSKFM DN*LLCGLIFVLCFF RGILVTLCLFL LKLLTFFLLNH *KLGIN KTDPIRTMPDTHQVAG PYLSTDD*SVLFQ*SPAPCGNG HPTGTVADHYLCLGW/YQAQF DIAVASEIMAVLAL TDSL GREV PRG*PLPG*YFVRNLMFFSHLPQ IDLGFHASVCLLGF*FAFSL*G TPVFVHAGPFAADRDLC PYQFL LCQTHIYKIHVIMAEYFQRYKL MMYAKQTSPLCDLEQAISL SGC VPCRHS HLKNEKFSCTGC*QYL PKLSLPNSDPLTLPFSADYGFKF ESNHANHS GDCQNLPLFLEDNS TYSTCFPTVTEAGFGADIGMEK FFNIKCRDVLSFRSVV*AFLLL AV*LGRFGGRQYTG VVWLLFS FLQNIQLVADGV*MVSLSKT* LNGYRCKTTNIFFTRTDTRAEID LVCELAKRAGAFDAVPCYHWS VGGKGSVDLARAVREAA SKRS
14143	44511	A	14226	3	587	YPASAGLMLQNFVGIVGLRYHF AIHSPAAGGLDGLHAAVAIQG ITKIETTPNHQRA PAHWTLTQ QAHLQPSPLHFNLP LTLCLMHC PTAIPHCFADARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFTRVT VHWGKG NDQTFRGLLDTGSEL TLIPGDP KHHYGPVKVGAYGAQLL

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14144	44512	A	14227	2	1256	CHCGPP/VKVEAYGSQVLKGVLAQVQLTVGPVGRPTHVPVIFPVPECIIGIDMLSSRQNPHTGSLTGRVWTIMVRKAKWKPLELPLRKIVNQKQYHIPEGIVEISATIKDLKDAGVVIPTTSPFNPIWPVQKTDGSRWMTVGYCKLNQVVTPIAAAVPDVVSLLEQINTPPGTWYAAIDLANDFFPIPVHKAHQKQFAFRWQGRQYFTFVLPGRWELNMTKIQGPSTSVKFLGVQWCGACQDIPSKVKDKLLHLVPPTTKK/EAQCLSGFRREIHIPHL/PIYRVSRKAANFEWSPEKEKALQVQVAAVQAAWPLGYPDPADPMVLEVSVADRDAWSCWQASI/GHKVGHAQQHSIIKWKWYIRDWARADPEGTTKGQGRWWQLAE RQDSRDREAAIGERQETA VGK TARDEAVCD
14145	44513	A	14228	155	531	GNLWSVDLRPGTPLRQNFRTIRQHQSRFTKNHCSQTPLLIPIRQTGSGVDLSKLQQTCS*GSCLVCTIDLANAFSPVHKA/HQKQFAFSWQ/YFTFVLPRLTWLQPC*V PNLPAEETNTEPSNGT
14146	44514	A	14229	1	518	MTVDYCKLNQVVIPIAAAVSDVVSLLEQINTSPGTWYAAIDLANAFFSIPVHKAQQKQFAFSWQGGQQYFTFVLPGWYINSPALCHNLIRRDLDLDCFSLPLDITLVHYIDDLMLIGSTIKWVVHSS/DSIIKWKWYVHDWARAGPEGTTNGLAG*SGTCKKHEWKTGDKGIRGRG
14147	44515	A	14230	281	1140	VRVLSPEKEKELKWKNTHKLLSYPTVGAATQLNLAMGVI GSHGARGQVVALNRQGGDLQPFTRVTVHWGKG/NMQIFGGLLDTGSELTLIPGDPKHHCQPPVKVGA YGGQVINGVLAQVQITVGPQTHPVVISPVPECIIGIDILSSWQNPHIGSLTGIMVGKAKWKQLELPLPRKIVNQKPYCIPGGTVEISATIKDLKDAGVVIPTTSLFNSPIWVPQKTDGSRWMTVGYRRLNQVVTPIAAAVPDVVSLLEQINTSPGTWYAAIDMANAFFSIPVH
14148	44516	B	14231	1	1521	
14149	44517	A	14232	3	202	
14150	44518	A	14233	2	367	

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14151	44519	A	14234	1	553	MTVDYCKLNQVVIPIAAVSD VVSLLSEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLQPWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIGPRQLLACY/WALVETEHL TISHQVTMRPELPMNWVLFDP SSHKVGCAQQHSHKWKWYVH DWARAGPEGT
14152	44520	A	14235	3	728	
14153	44521	A	14236	1	635	
14154	44522	A	14237	3	266	
14155	44523	A	14238	1	1245	
14156	44524	A	14239	2	837	CHCGPP/VKVEAYGSQVLKGV LAQVQLTVGPVGRPTHVPVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSRMTVGYCKLNQVVTPI AAAVPDVVSLLSEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPGQRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPPTTK K/EAQCLSGFRREHIPHERL
14157	44525	A	14240	1	533	
14158	44526	A	14241	1	1043	MTVDYHKLNQVVTPIAAAVPD VVSFIEQINTSPGIWYAAIDLAN VFFSIPVHKAHQKQSVFCWQG QEYTFTVLQPVHINCPALCHNPI LRDFDHFSLPDITLVHYIDDI LIGPV*NMMLHLVPPPTTKKETQ HLEVLFGFWRQHIPHERLATPSSP NGPMNKVTMMA/ANVGAWD QKHGLPLTKANLVMGIGESV/ SPAAETNTPEIWHSSGQDSQ VQESKGGNGSGTTHHHP**STS KIFASCSHDITFCWPRGLSSRGR NAATRRHNNNFNIKPEVKIAFWT LWDPPTFKSTG*ERS*SVGW D*HELPR*NQSTTPQGSVSIIPH GQPPHQLFGVAKARTFGIT
14159	44527	A	14242	1	336	
14160	44528	A	14243	3	1885	
14161	44529	B	14244	1	1423	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14162	44530	A	14245	I	1361	MIISIDA EKAFDKIQPFMLKTL SKLEETASPSPVVATYTPQPM PSAFPPLSEENPVL PETTVMAS PEAVTRQDNVDSPQKPPPTPMF ASRPITRLKPRRAPSEEGIQLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAAI.NHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGKAKWKPLEQPP PRKIVIQKYHIPGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSRWMTVNYHKLNVET PIAAAIPDVVSLLLEQINTSPGT WYAAIDLNVFFSIPVYKAHQK QFAFSWQGGQYTFITLPQGYIN SPDITLVHYIDIMLIGSSEQEV ANTLDLLPARVASWGVYPDQL T/GGRED*GLLHRWSCRICRHH PQGSWQES
14163	44531	A	14246	I	1795	MRKCGKPFKLQGTNKANSRI QEELIHSKSLIEQEGEKPVQFSA FHRMWQPADSQCDIIDSADIWA DPLVRHREITGSGGINRRRTRG GRGRGGEAAGGAENCGSREER ERAGVGTAVTQLQNLNTIGIIGS RGGRGQVAANHQRGQGHSHYC KGQKQNSNQNSVTHVELWHI WLNHNSVPRSEIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGK RNDQTFQGLLDGSELMLIFED TKHHCGPPVKVEAYGGQVING VLAQIQLTVGPVSGTHPVIY PVPECIIGIGILSSWQNP HIGSLT SRKTDGSRWMTVHYHKLNMQ VTPIAAAIPDVVSLLLEQVNTSPG SWYAAIDLANAFFIPVHKAHQ KQFAFSWQGGQYTFITVL PQGE TLVNFSLPDITL FHYIDIMQI GSSDQEVANTLDLLPRKSTTPS G/LYGFWRQHS/HLGLLTPY* VTQKAA/SFEWGLEQEKALQQ VQATVQASLPGVYDPADPMV IEM/SLDSPSHKVGCAQQHSII KWKRYVCDQA*ASPEGTS*LY CTSFIMEKEEVC/LSEQLTLTD MGLPILHAMLWHLWIHGLPY PSSWYSTQOCL

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14164	44532	A	14247	55	1241	NRFVRAAPASLKRSAGIGLLCM PDLTVGIVVTQLKLNAMGITG SELTLLIPGDPK*HFGPPVKVGAF GGEIVNKYLAQLGLTDDPVGPR THPVAIFVPPECIIGIDILSSLQNP HIGSLTRVRIMKKGAIMKGY YEGKGKAKWKILELPLPRKIIN QKQYRIPGGIVEMSATIEELKY AGVVIPIPTTFPLNSPIWPVRKT DGCWRMTVDYCELNQVVTPT AATVPDVVSLEQINTSPGTWY ADIDLANA VFSIPVHKAHQKF AFSWQQQQYTFTVLPQGWTV NSPALGHNLIQRDLDRFSFPRDI TLLVHYVDDIMLIGSSEQEVAN ALDLLVFSDDLAIKWMHSSIA SSSGSGICVIRLKKVLKAQPAP MASWGVLYDQLTEEEKIRA
14165	44533	B	14248	1	346	
14166	44534	A	14249	485	717	
14167	44535	A	14250	1	345	
14168	44536	A	14251	300	689	TKRAPCSPAAGSRGRARSLALL TLVYGHYPALPPGPTPAQQPGR GLAEAAEPRGSEGGNGSNPCG RA*DGSRREGRGRLGGWRPC CEPQPWRQAHPAGPDRVDGG ERRAGVLRGQDQDEKKKPK

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14169	44537	A	14252	1	2430	MAVLQPSRHRLRPQLGLEPDN WHSQQDEVSSVATARA VVPSG RGAAWMGPGSNIGGSGLSVSE CGEGTGAAGSTQLQEGMHFCR QSRWAFLTALCEVYTQSLQDT VQWLQLCQWSAQGGDDHTLIE WLMGATWTVVNDAREIPETG TGQDAWLCGSGWVDDQRPVH ELAIHCSPNTNVQVRLALVDTGA DCSLVFGNPVRKPDGTWQMTV DDWELNKVTPPLHAAVPSIMD LTDHLTLMELGQYHFVDYVHSP TICRGLVAMELAAWKCKPGVL LFHYIDDIMLTSDSLADLKVAV PLLWQHAAACGWAINKSKVQ WPGLSAKFLGVWLSKTKAIP AIEKIQAYPRPTTMKQLQTFVG LLEYWRPFVPHLAQMIKPLYGL SKKGATWDWDNEAGTDLAA KWAIQQTQALQVIDQGCPFELD VHVTTDGGFWVLWQRMCEFR TPVGFWSQLWKGAEQLQYSLQ KELAAAYAAQAYETVTDWA TVIVQMSYPIVGTGTATQTTL AKRGAYLEQQSMLTTPLAAE LQEALGPVLMEDKAMGPEAPL DPEPSLLKKGYPLVPDGAWYT DGSSQGA AAAWTA VAIQPI/TD TI*FDTGCGQSTQWAE LR VVE MDILEACQKCPACAQAYLRQR QLPNVTQQVTVGQMP LTRWQI DYAEPLPKLQGYTYALMAADI
14170	44538	A	14253	2	239	
14171	44539	A	14254	3	211	VVYYSPNEVKVVAEGFDSANG INISPD KYGL* NIFILQLWC WPNSLLCFLCQCENSFLDIYGL
14172	44540	B	14255	13	87	
14173	44541	A	14256	42	854	VLVFLTAALFILPTFSNSMMILQ VSGGPWT/VILRRGVLLGVAPP PSLPAL/PENSVYQERQECYAFN GTQRVVDGLIYNREEYVHFD AVGEFLAVMELGRPIGEYFNSQ KDFMERK RADQLPDCRDPLMP D*GVWISPLGQV PNLTAQKTL QHLP SKKEPQQHDDL VYHVT DFYPSIQVRCFLNGQEETAGV VSTNLIRNGDWTQFLEMLEMT PQQDRT*AGVQLLEVTLNLSLF FLEAQSDSVQSKMLTGARGLFI NYLQLNLCTP

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14174	44542	A	14257	3	571	QGRATPENYLFQGRQEYAFN GTQRFLERYIYNREEFARFSD VGEFRAVTELGRPAAEYVNSQ KDILEEKRAVPRMCRHNYEL GGPMTLQRRVQPRVNVSPSKK GPLQHHNLLVCHVTDFYPGSIQ VRWFLNGQEETAGVVSNTNLL NGDWTFQIVVMLEMTPO/QGE DVYTCCQVEHTSLDSPVTEW
14175	44543	A	14258	1	1677	
14176	44544	A	14259	2	430	
14177	44545	A	14260	821	1428	QVTDVQDFPLKCKIQWRRTVR GDLQ/PFTRVTVHWGKGNQDT FQGLDGTSELTLIPGDPKRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQNSHIGSLTGRVRA TMVGAKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT GVIPTSPFNPSI*PMQKTDGWS RMTVDYL
14178	44546	A	14261	507	910	
14179	44547	A	14262	1	2898	
14180	44548	A	14263	1	2580	
14181	44549	B	14264	159	2657	
14182	44550	A	14265	142	377	NHLLRRQQWQTPPPPSWS/SPR SSSDCCGSSENFKPVDSLGLSV GVGPTEPDHLDPLWLPFPQGSE RFCLAGVPGATG
14183	44551	A	14266	363	638	EVWKESSGWHLAGAPLGQSFG RKEQAVIFAVLQPLLVIKQTGS GVDLQQTPAHLQQRGLSGCLQ SLCSLTSS*PQRHPQNSSLVNSC VVS
14184	44552	B	14267	1	2424	
14185	44553	B	14268	446	623	
14186	44554	A	14269	245	690	APSRSTWGSSTAARRNLKTR KLRTPTPPHKKPRNPHHGPPR TPSG*TPRNDHRPPPG/PQVGG PGCWAPSQGPRGWQLGC*RE EVPGGGHAGRHSTPVGG/DFFL QAGPWPPDASLTPNPFVLRGAS TPPHPLSENNKDKFLQK
14187	44555	A	14270	223	365	

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14188	44556	A	14271	1	687	MSEYIRVTEDENDEPIEIPSEDD GTVLLSTVTAQFPAGCLRLCRN PVSQCMRGVRLVEGILHAPDA GWRNPVYVYVYPKDNKRKMV LGLPWKTTTEQDLKEYCSTFGD VLMVRQSQDEPLRSRKVFVGR RTEDMTEDELWEFFSQYGDVM DVFPVKPFRAFAFVPFADDQIA RSLCGEDSMKGISVHISNAEPK RNSNRQ/LRSGRFGGNGPGGFGN QGGFESYQRCERKAV
14189	44557	A	14272	1	833	
14190	44558	A	14273	3	447	RGTAGGQPGNGPALAQSP*WC RLGSGGT*GKSPGTSQQRALPW CSC/SVSTWATAAPGSQQRASP CSWAQPGPLASRLMLPPLR* GHLGHLAWLQLFAAPCPVIHV AVMWSLLGIALRKVHGDWAPL AILSLVVCASNKLNKKKKK
14191	44559	A	14274	988	1803	RAARVPRAPLEAVAHRWASAS EDDGTVLLSTVTAQFPAGCLRL CRNPVSQCMRGVRLVEGILHAP DAGWRNPVYVYVNFQDVLVLR QSQDEPLRSRKVFVGRRTEDM TEDELWEFFSQYGDVMDVFP KPFRAFAFVPFADDQIARSLCG EDSMKGISVHISNAEPKRN Q/LRSGRFGGNGPGRQLQGTRY PAPAPGSPGRAQGLG/AG*SRPS GSWLSGHLQRPEQSVGRAPAA PRHAVRRSLRRLAALCRRTAR CRAQLHVSPQRRRH
14192	44560	A	14275	3	184	
14193	44561	A	14276	1	352	KAAMVRFKHRYLLCELVSDDP RCRLSLDDRVLSSSLVRDIARV IIGTFGAACSIGFAGTIRTCQK FLIQYNRRQLLILQNCTDEGER EAIQKSVTRSCLL*EEEECEEA AKAME
14194	44562	A	14277	1	456	PTRAVEAMVRFMHRYLLCEQ VCDLRCRLSLDDRVLSSSLVRD TIARVHGTFCAIACSIALALARA LNEEGNPEGWRDVAGASAGGR KKGHECPSPCTVFCTLRYPNA YTVIGLLRCKELYQVWWSVL YLMTYLENKGHRYPCCFNTLH
14195	44563	B	14278	34	267	

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14196	44564	A	14279	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSLIGILLHL ESELAQTRAEGQRQAQEYEA LNIKVKLEAEIATYRRLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14197	44565	A	14280	2	1044	SSQMPSPQEGMCGKACTPALS QADSLCPLRLRLASEVEGYWQM ACAEPYVQSEMNDHLSVWSLQ HGSTTLASMSFTTCSAFTNYWS PGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTSFGLA GMGGIQNEKETMQSLRDRLAS YLDVRGLIETENWKLESQIEH LEKNRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAEMTLT ELRHRVQSLEIDLSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV
14198	44566	B	14281	247	857	

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14199	44567	A	14282	1	2104	LRGSELAGGVAAPDPSSRARAP GRGQGSEPPRRS*GRGRAPPRA HTPLDDFPGGRAALSPGRGLSS RRPDPGSAGRPLLLCLRPLHSP PPPRGCQAPAFQSLPSFHLALRL RSSGEEKLWGPRRAAP*SQR RKPDPARPLGAAAAPLRPV*AS D*GAAQVPPPSPLRDGGQPGGR EGVGRRTPHRAAAWLLGE*AA DAAAFHWDGGRPPAAPARLLP GAPHHREDRVHHQPRGHPLQH QSPGDPPTPAGEQHASRH*LCRN PETQKLRH*TSERRDGHREEEH TG TAGVPRSRPATQRP HAVPAG GLQPHRMPLALSSGAASGGEA EHGQLSGRGREEDGPVWPQLP AGLQGHFRGESPRWPPCLGDGS EN*PGPVQAEFSGG*DP AVSESE DNQPRSRQFLRLQREEKAKP/D QRFTYLPANVPPIKTEPTDDYEP APTCG/RGEPGVKSSPKTILQPA ARDATRPQLLPRGLPALSAEK HPDASSPWREPQAPRPFSCR LH QGRQCQGPLSPRTPAAGRRGPR RPG/VPRPVATHPGSPGQPPAL LPQQ*MK*YEMTSPARAPTFC HIGALSSAGVC*LQQT KTFE*IN *THTWYHSEPTD*MPGAEH*Y VQRLALQEGKQGRET TVSP GGEVIS*QKGGGAEHGRPTV QGP/SHGNPHAV*PHAQPFWH PWGSILEVPYLTRPSGHHRIEH
14200	44568	B	14283	41	4224	
14201	44569	B	14284	1	1332	
14202	44570	B	14285	140	215	
14203	44571	A	14286	234	657	VQQPGRGLDLSTDGPGGRSQV GLIWSCCCLH*AASGEPGGRCP GS/GAPGPAGSALEFRARDGVP/ GVGGPSWESHSPAAATPPPAEC RGP GPTSPAPGEAAPEDREDG AAAPGRAEPASIVAPADGSQGG VLATQAGALGA

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14204	44572	A	14287	134	789	PDSQAPSRNSTRPAASTRKSSS PPAARSAGNELGSSRGDADPPP QNPTGPAPQSAEVPKCD/SSSA WASNGSSISPSFFSLRPWPSS/T KVPGAGHHTTPEGAGGASAR/S SSLAPSAGAPVPS/A*RSQLGTW LSVLRPRSL*QSRVRSPPSHVSS PGSMQAPNPSFQPGMNGAWI WWL*THIPLARWPGPPGILVITC PTVTWIKWSFICSFHPT
14205	44573	A	14288	465	1541	GPPKRKLLISNFSKVSQYKINQV KS*AFLYSKK/QTESQIMSELPF TIASKRIKYLGIQLTRDMKDLF KENYKPLLNEIKEDTNIWKNIP CSWIGRINIVKIALPKVIYRFNA IPIKLPMTSFTELEKTTLKFIWN QKRAHIAKSILSQKNKAGGITLP DLNLYYKATVTKTAWYWYQN RDIDQWNRTEPSEIIPHIYNHLIF DKPDKNKQWGNDSLFWKWCW ENWLSICRRLKDPFLTPYKKN SRWIKDLNVRPKTIKLEENLG NTIEDIGMGKDFMTKTPKAMK TKAKIEKWDLIKKSFTAKET TIRSPGSEQKSHTLVRA TRL VSD HSQSFEAWLQFLGDTFRGTQKL RDS
14206	44574	A	14289	1921	3199	GYLAAGQVTSRIHTGRRHFSGP ARCPVSCCRRPGC*PQPAVRP SG*HCRKTA PSHGPSIWQTR**P GSWPNLRPG*GWRWLRAPRG RGIPVGCRSNLQLHPTKPNPGSH *GSGSPWQCPGVLL*ASGRQPG SPSGGCT*SSGKAGLEPQWHPA IPGKCRNKPAAPASWERAPRPR AHALACGWWRYS*SWRS*S SPETPGPAQV*CHRPCAAW/W RCHS**TAQFL*D*FS*FLQTIGE PCICPKPISVPH*PMKQSHRGIG GCLQYSSHPGIESLGMGRGF/D RRDL*TLQIGS*RHPRAGPEGA AL*CLAGESSLRTPSAPCPGSPH TPGSSASGNTSPV**ETGCGSRQ GSARLVLESLLSR**CLSGPSRP SCLLRGISWQCGTAGRLSSSGPP AASGAGADAAPGGFPRLPCLEF GTV
14207	44575	A	14290	3	626	

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14208	44576	A	14291	1	1065	MRGSCERSGEDDEEQKEEAMVA CGRLSGVPEAEQGP EANWDS LETEGTDGLGELVRD TLYLRSC RAHSVVPISCFLRQGS AQELNL RHRGLGPQGARALASSLSSNPY VKRLDLRDNGLCGAGAEALAG AL/QQKQHP*CGPVGEPAGSG RSPGP/RVPPSQ/CNQAMRKM LSGNGLEEQAQHLAELLLAH TDLKSLDLSYNQLNDQAGPAPS LRAFPQANIFLKVLDISYNGFG DPGASAVGEALKANNVLEELN MSNNRISAMGALSGLGLRVN QTLRLVLCVRVSQVSRNPMRS EGCFGLLKSVDNPPASALELDD FSDIQVNAEFDGLASSVRGILPG LGIKDWRLQSGV
14209	44577	A	14292	1	416	
14210	44578	A	14293	2	384	ELWVVTFSFMAYGSAKDLICTH FMDGMNELAIAYILQGV LKAL DYIHHMGYVHR/DLQGYDAKS DIYSVGITACELANGHVFPKDM PATQM LLEK LNGTVPCLLDTST IPA EELTMSPSRSVANSGLMTA
14211	44579	C	14294	142	474	
14212	44580	A	14295	1	1470	
14213	44581	C	14296	91	471	
14214	44582	C	14297	195	480	
14215	44583	A	14298	121	1130	SRSTQYELMSFLTNDASSEIAS FSKQEVMS SFLPEGGWYELLTV IGKGFEDLMTVN LARYKPTGE YVTVRRINLEACSNEMVTF LQG ELHVYKLFNHPNIVPYRATFIA DNELWVVTFSFMAYGSAKDLIC THFMDGMNELAIAYILQGV LK ALDYIHHMGYVHRSVKASHILI SVDGKVYLSGLRSNLSMISHGQ RQRVVHDFPKYSVKVLPWLSP EVLQQNLQGYDAKSDIYSVGIT ACELANGHVFPKDMPATQPM VLVLSPPDAARETERHSALPVG YQHHIPR*GADHEPFALSGQLW PE*QPDHQHPALQR*LALPPLP PNLLPPLPPLC
14216	44584	A	14299	304	412	
14217	44585	A	14300	2	350	
14218	44586	A	14301	191	299	HRPATAVLHVPTSPSPSGSRPS *PPPAALLWTPA

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14219	44587	A	14302	537	5523	LARYYKFMHQDRQGVARNLL CQKEKRR*YTTKCEDNTCHWT GRTSS*PRSV/SNLNSQCQPRLW PPVTIIRQANIKTGEKAH*TSKL LPPVQLKFPARDDTLPPWPGYIP* QLRRPSPR*SILSMLPRKVVPCL *QKP*TVCWKF*EPLSYIIHSLV LKMMIPMPMTLLGA*CLTQAL K*SRMERKKGRAAQRSSLTGC QSPRGSPGGPGPPGPPGAGKQ QNSNVQTSRLLARTLI*SFSSST VKDKELARNTAP
14220	44588	A	14303	2868	3095	PWAGGLFGPSAGMRAWATK PSLTPPAPAGQRCPCQGHRG*SG PGIYAVQPPSVPAWAAHATTQ ARLCHPRSPPLR
14221	44589	A	14304	693	821	SDRQT*RQEKRLTRRQSCCLPC N*SFQPETTLFHGPDTFHDN
14222	44590	A	14305	338	645	
14223	44591	B	14306	181	480	
14224	44592	A	14307	155	543	
14225	44593	B	14308	1	1260	

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14226	44594	A	14309	1	2025	VINIINAAQESSMPMPVTEALDRV LEILRTTELYSPQFGAKDDDPH ANDLVGGLMSDTGLEIHKDGEE EGESRTAQQYPGLSESTRQPWR RSRTPTTTGWGKATEQCCPDF PPPGPHPLELLIFHCEGQGTGQ KHSTSYPTLMSEKRGMLNVPF AKYTGPMARKSSGLTPSLHLHY CADPLHSPKPLFNCPPPTTSKTEI LGCNCNCPSESVRGAEGDQEL LANIKQAEKHEKNHPVETVAM ALTDIDLQLQFSMSQPEALLLL AAGPADHLLQLYSGHLQSAT GIYGEGRASSATLEDLESQYQE LAVALDSSSTIISQLTENINSLVH TLKEEKHEIHQVQKLGRNLFKL KNQTAEPLAEPPEARPSKVEQL QDETNLHRKELESVGRQLQAE VENNQMLSLNRRQEERLQEQ EGWQEEQERLLDKNNENKSAL QLEQQVKELKL\ENLEATSQ*K QQL/TAQLSLMALPGEGDGGG HLDSEQAAPRPMNPINPGDLES EAMVAFFNSAGANAQEEQRVC CQPLAHPVASSQKKPEVAAPAP ETGGESVCGETHQALQGAMEK LQESTSARGQCQRRSTGRGGHR QAGPGPGGDEEMLCTCTQVSS AGRGMGMLTVVLVSLMMLS ASFSTWCMRSISSCHCAYSAHS SISVFWFPREYILASGSEMMNS
14227	44595	A	14310	3	564	SLRVSLKAVVDRAGRSILSYIA GLGVDLFGGGGSRVAGGIADL GRSGGKATRSRRGSRAGGGR LRSRIHEEALQLRETPGGAPE\ PMDQEQYAGPGYDIRDWELRKI HRAAIKGDAAQ/VWSAAMTRR FRDLDAARDKDRTVLHLTCAH GRVEVVTLLSRRQ\DICD/N* NRTPLMKAVHCQEEA
14228	44596	A	14311	515	778	GQAQGTGDREGAVLFTARAPD QCRP*SCSSSRPTASSCPLGHSC SPGPLCTHLPLQGPPQAPTVP ATATCWFSWNQCRCAVSSYP
14229	44597	A	14312	411	608	EAEI**TGLPGHSRPPGPLCTHL PLQGPLGAAAWVPEAGLGQVP TEAAGARAGCSAHKPKWKRKK
14230	44598	A	14313	2	338	
14231	44599	A	14314	1	390	

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14232	44600	A	14315	237	488	PWKTLDSSEAEILRGVSESSAV TLHCMEGQAVGPRQVKRIVHC *ASSA*NPHAMLLQNR*LALC TSVPQGA AVL CGGWD PGN
14233	44601	A	14316	358	616	
14234	44602	A	14317	13	1155	IKLPPPGCRRRGRRHRRHYRG RAEPLAPRRRLPPAPEQPRARP PASRFLKNTMSNGYEDHMAED CRGDI GRTNLIVNYLPQNM TQD ELRSLFSSIGEVESAKLIRD KVP GHS LGYGFVNYVTAKDAERA I NTLNGRLRLQSKTIKVS YARPSS EVIKDANLYISGLPRTMTQKDV EDMFISRFGR IINSRVLVDQTTG LSRGVAFIRFDKRSEAE EAITSF NGHKPPGSSEPI TVKFAANPNQ NKNVALLSQLYHSPARRFGGP VHHQAQRFRFSPMGVDHMSGL SGVNVPGNASSGWCIFIYNLQ DADEGILWQMFGPFGAVTNVK VIRDFNTNKCKGFGFVTMTNY EEAAMAIASLNGYRLGDKILQV SFKTNKSHK

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14235	44603	A	14318	1	2340	MFVWRNVEGHSAAVFSWYSIP FLTTPCSHTRPSNLVPTQWPTR ENNLPWQPLLMSVHQAQSL ALRKEQDSSEKDGSRPNKSDK DHIRWPMSGAHDLQQAAPGPG GAHQGHPNQDNRTVSQMLSER WYTLGPNEMQKYNLAFQNV ARIRYVIVRGNEQGGFRMHHLR GVSSLQLGRRRPGPGTYRLEV DMITIDARYRCSGLRSPDPDH LKSVDLHRNEHFFLQKARWEI LVLQATPSQIQLLHVAFVLAQ PLRCRKQTLFLISVVGTKEN VASEGRNPVRPLRGHRWLPASP AAEHFAGGADRKSRAPR ATATPANEQRAVADVQWAR ARGGRVRAAGRSGSCALRRSR CRRRRRRHRRHRYRGRAEPL PRRAASGQPGKLARRGINCNA SSIPMLQVVRKISIKHCQMAR VAGEGSLPLSHAQLTHCVFGN KQVQRTIAYLPQQQGVQGL KNTMSNGYEDHMAEDCRD RTNLIVNYLPQNMQDELRS SSIGEVESAKLIRDKVAVG LCLCVPIRNVIVASTSWWSL PLAPYVPRGIRRSQPTLMDD LSCRS HQAAPFTASVLLYISGRVKA H TAAQGFNHIPEEGVSQEA GSGWSQAWKDGWLTNVFMF SCTG HSLGYGFVNYVTAKDAER AIN TLNGLR/PPVKNH*GRPLQ LGFL
14236	44604	A	14319	701	1050	LIVHFCLQVGGCGVNTVFPILQ TN/NTNSEYDPSRCFAFVHDL CDEEKSYVPVKSSLDIILIFVLSAI VPDKMQKAINRLSRLLKPGGM VLLRDYGRYDMAQLRFFKKGIL KVLNPNH
14237	44605	A	14320	701	1519	LIVHFCLQVGGCGVNTVFPILQ TNNDPGLFVYCCDFSSTAIELV QTNSEYDPSRCFAFVHDLCD DEEKSYVPVKSSLDIILIFVLSAI VPDKMQKAINRLSRLLKPGGM VLLRDYGRYDMAQLRFFKKG QCLS GNFYVRGDGTRVYLCHTRCNW TRFSPTAGLEKPKPVDRLQ VNRGKTTDNPGLDSVILQAP SVQHQLRGYLLPTRCKPVVVS GLFLKKKIVALGVV/RCL*SQPL RRLRRGGSIE/HQQSNLGKIVRD PVSESNDKIKRI

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14238	44606	A	14321	756	1334	PGKFVLSFLDPQPPTRILEVGC GVGNTVFPIFTNRTMTQDSL VYCCDFSSTAIELVQTINSEYDPSS VFVAFVQGPV**RESVTQCPRAV LDHILIFVLSAIVPDKMQKAINR LSRLLPKPGMMLLRDYGRYD MAQLRFKKEELDITFTAGLEK VQNLVDRRIQVNRGKQLTMY RVWQCKYCKPLLSSTS
14239	44607	A	14322	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
14240	44608	A	14323	1	5796	
14241	44609	A	14324	1	2721	
14242	44610	A	14325	1	3438	
14243	44611	A	14326	1	3306	
14244	44612	A	14327	1	2364	
14245	44613	A	14328	1	2091	
14246	44614	A	14329	1	2334	
14247	44615	A	14330	1	1986	
14248	44616	B	14331	1	2559	
14249	44617	A	14332	1	1671	
14250	44618	A	14333	1	1845	
14251	44619	B	14334	1	2055	
14252	44620	B	14335	1	1554	
14253	44621	A	14336	1	2559	
14254	44622	A	14337	1	1714	
14255	44623	A	14338	1537	2204	

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14256	44624	A	14339	2004	3751	YQSLAETQQQKKNFRPISLMN IDAKILNKILANRIQHHQKLIH HDQEGFIPGMQGWFNHKSINV IQHINRTKDKNHMISVDAEKA FDKVQQHFMLKTLNKLIDIDL EVLARAIRQEKEIKGIQSGKEEV KLSLFADDMIAYLENPIVSAQN LLKLISNFKVSGYKINVQKS/Q AFLYTNNRQTESQIMSELPFTI ASKRIKYLGHKLRGVKDLFRE NYKLPLIKEIREDTNKWKNIPC SWIGRMNIMKMAILPKVNYRF NAPIKLPMTFFIGLGKILLSSY GTTKRAHIAKTILRQKNKAGGI TLPDFKLYYKATVAKTAWYW YQNRDIDQWNRTEPSEIMPHIY NYLIFDKPEKNKQWGKDSLFN KWCWENWLAICRKLKLDPFLT PYRKJNSRWIKDLNVRPKTIKTL EENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLSFCT AKETTIRVNRQPTKWNENFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWVKDMNRHFSKEDIYA AKKYMKKCSSLAIREMQIKTT MRYHLTPVRMAIKKSGNNRC WRGCGEIGTL
14257	44625	A	14340	519	1286	LNLEERAFRHKSSEHLPHLKVH FRHSSCGIKTSLHVSPTTLIF PYPPLWGNPSN*ARPPCSVHSG PYPQGLASIIAHGSPGNVRGVH V*INDEGGISRPSTASHKETPR PPTPARHADLAATRPSLTTPSPS VGAGPRA/PSRAGPSVGGGLRLP SGRAPRAEVALPAGLSPAGLAG PPPSGRSTGALPPAAAPTTSGP/P ASTPPNAPAPGHTLSSRSFHRA ARPPPHCGAEETWGFTMRPSW RISQSFTVKDS
14258	44626	A	14341	482	700	

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14259	44627	A	14342	1368	2416	SSMTQSSCPMTSYLKSKEGPEL MPSYTNPTETGVSKLVNKTQVF TYAHKGPVSIYFDACQAAHLSK LNNIWTISVKI*DKKESASRATK AITEESKKECPDCDNQWTTHEF NQHLTYGRAALFASQEEKIGYT TGTCYPLNLTLKPNMTFWTKG HKGLLTFDQAGALLGLPLVI TKKTQRTQVQLSPIQQFRFYKS FNEHFNSEVSKIQIPPISTENLFV QLAKSIANNLGVTSYVCGGA NMRDQWPWEARELMLQDNFT LPEFVTKFNANPSVWLLRNPIIG KYCIACWGKSFQNIGETTCLG QQYFEESNRTQWRSFIDSSIG HFNPLQFPTLNQSWYQLE
14260	44628	B	14343	1	1071	
14261	44629	C	14344	89	283	
14262	44630	A	14345	244	315	NPKGQKQDREAPLSRSVFVLKIKI KRAFALLHGRF*PSTPAASASP ASKSPRGSGKALASALFYIVQL TK
14263	44631	A	14346	1228	1656	QVYRPSQTPHLALSPERVAPGR RAAGRLAPEARAPRGSP/LPPHR VSEKTIRVVVFHGPARRAGGTP PRAPRGDTGGAPGA\PTYSTPL MSLHRRARLESPTGSSFPADSA KPVPLAVVSLDSR*GQWESRSS IHAIVTN*MTRI
14264	44632	A	14347	2	705	GSWFGLDDGSATRILACPWPGL GDGPAAPKANLPLVRWKPCQCF RGEGL*GSSCFSATLLTGLDLW ACCSSRSASARLSTYPSAFTSG WCSSLGPTEEAPGSWINCLAG ILGAATSPKPSAIPQASPEVSLD AEDTGMKP*DSA/GPPGPARGL CGRGCGLSACMGLRP/PSPPA QSPSTALTSLTPSPFHPPRKKW SPPSAPAPSAPSAPASLTSPAP PAPSPAPTAPAP

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14265	44633	A	14348	367	1174	WVRGQPSQSLDLLACSTPTS* WPPGRAPPPLP/PPPPLP/PTP ASPLLHPRRAPPPVP/SFTP ASPPDPVPRPTKALTGLP/LCP LPCMGR/PFVPLYGLLPLCLGP DFSSL**SPGGWDRPVRPLGISQ IPE/PPLTMGL*MQ*IPP*PRFQG HYAPLPPLQTLICISVKTGRNPR GLPMHKILQPQNPSQPPCELQ AHCPTTPPPKQCP/PAAFSILPVT FADKDPGAAPEGTVKAPMPTQ *EL*PLRPREHRVLSGPTAGQT
14266	44634	A	14349	332	988	RRAGTPASWGHNGARAKTPSR ACACGLYPIHQPTARRAPAAR SHGPGPPALPRKGAAGHGRSVS HHPLRPCSRSSCLAWPCLHHHQ PLHCHPHRHWPKWHPHLAPH PLLGLHPRSRPQTPPWTS CGPSR RLPTPGSWPAPFDRDWP*AR PSALCCPFCQEPQLTPCLHLCPH PHPHRHLPGLSCPHRPPRWSP QSPCPWVLLWWTGQWWQPG
14267	44635	A	14350	190	718	FVLQLPPAPKSGLGRWGSPPPG QFSSSQRTGTVRGRGCAEPRG SLPHPT*GNK*HGNWMGLGS QGLGRQPGEDKH CYQR/IGV GAHLLRPPHQIRSLTSGSGCS HPWSRELGCSDQGRASAPLA LRQAWGEGLAGRNHTIVPFHG DISIAPRLLPCRETLFSAICGGES
14268	44636	A	14351	1	486	MKGEVSCQHQDALQQVLWA MLQDADKQVRAPGPVENENH CDFVKLREMLICTNMEDLREQI HTRHYELRYRCKLEEMGF TDV GPENKFVRVLLFKSLSDSKRVK YDEEWIRLPVE/MKY/MLERKV TQKQP*VPLVFVSWRSR*ESLR REEENQQCHVLEL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
14269	44637	A	14352	1	2380	MMWSVLIQPVVLA AVERQGE ALEFLIGVPESDGENGTKLENT LQDIIQEDFNLARQAHVQIQEI QRTPQRYSLRRATPRHIVRFTK VEMKEKMLRAAREKGRVTLK GKPIRLTADLSAETLQARRDRG PIFNILKEKNFQPRISYPALKSFT SEGEIKYFTDKQMLRDFVTTTRP ALKELLKEALNMERNNRNFFG VTF AFFVGGQSLGKALQETSIPP LREEDLEKTSILETNGDWEAT RGLPEECAGMRERDCQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAAGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNA GRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLPYTDYSGKHGKQS LTTAQVNVSKDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGGH KYLGLIPTYDISSNIYLSKSLCW QANFRLNSALAQSPAITNFQFR GHSLKTLDLLTMKNLDSKVNI PVIKADTVSKTELHKFKIKFM SELVSNQVQIYQFPTDDDTIAK VNAAMNGQLPFAVVGSMDEIK VGKNMVKARQYPWGVVQVEN ENHCDFFVKLREMFICTNMEDL REQTHTRHYELRYRLQLEEMG FTDVAPKNKPASVQETYEAKR HEFHGERQRKEEEMKQMFVQR
14270	44638	A	14353	105	328	
14271	44639	A	14354	107	676	IRPDSLPSASPAQDFYAASNTF PA/DRWSALTKIYEDQTSNINPL SQ/TLIQSKALTLFNSVKA EKDE EAAEEKFEVTRVVHIRGLIDGV VEADIVEALQEFGLISYVMVMS KKRQALVEFEDVLEACNAVNY TADNQIHIAIGHPAFVNYSTSQKI SRPGNSDDPEREQCASLYHPEP HLFDHHGCSLHYR
14272	44640	A	14355	221	648	LDWLRRVVGIPSLRWTCATLV GTRRAARHRCVNVWECGGKKE ITY*SV EGLCRA/EKPKPLALLE ETCKLPERQVVNAKEKFL EELIK SATPVNT*MIRKRNCIITDMEK V*AVWIEDQTSNHLPLSQSLIES RALTLFNYVMA
14273	44641	A	14356	122	317	

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14274	44642	A	14357	338	489	WLGQN*RHGKQPGPGVGHVGT TVWS*PHSPACWAPAPQGPAPT GEEGCHF
14275	44643	A	14358	1	459	RPVWRNSQPPTAAAYRWASGSR MWSTSFSRW/NKTPSGKACSSS DKGPPMAQVPIQQRNVPPPTK/ QPLVLCHGEAPDFSRPPQHRPS LQKHPSGG/PSHSPLPTSA PSSR AGLPLAMTLDLTSGWRLWTPI QPFRLPPGSCREGTILLCSVMD
14276	44644	A	14359	609	2077	GLKAQPSRRGHSRGPACAAA PASRVHLPVTFCEPNSSPCPHC TGGWGGRGQ/PACAGNPTASSP CQIECPALRSCLHALMDLGPQ\ LRGAPRTGVDPRLHLLPQPAL SSPPVLLRGPLLRTCLAAARQ GQSPAPGLLGHPGSHRGLPP AQGGHRLPQPPGPGRRHRA PQP DPRRPGLRAAASGPGLA AWG AVRAAERPGSGGLPGGAGPHH ARAQPGPRAAPAAAAPGVAP AGGGA VPGGHPHRPGGEAALP AHGLPAPAAERTAPR/QPCPAC GLIARSDVHHPPVLP/LSGPAP APGRLVGQLGVRGAPSSPVPH ALHFPRAQ/PPGKGITTTSTQ PAGSPSPCMPPAATPG/ARHPP GSA\GHRAGV*GHTGPCDPHGP GHIHGAQLL*/DQAAVGV RGP GPWALSGMSQPPT/LPTAGHPA PACGVRAFDGTRPPRAKPAL/ LSDKGPPMAQVPIQQRNVPPPT KHPCPGPQSSTWMRQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14277	44645	A	14363	47	1250	EPRPSRSSGGPQLGQGLPRPMK KIPGSSAKTAGPLATRPEVPRAP *SAGRQPFWRPWPWGKRKGRKT *NHGSPGVK/TPGPLNKDKGE KEERPRQDQQRKALLHMFSG KPPEKPLPNGKGSTESSDYLR SVTPGPWSFSPQVASGPMPPVH TTKKPA*APPQVL/EPKERQTGA AADMPQPAVRHQGREPLL VVK PTHSRPEGGCREVPQAA/SQNPR PAPGLQTPGTRQTS/SVTPQPCP PAATHSLGLGSLNLSFGPGAKRP AQAPIQACLNFPKKPRLGPFQIP ESAIQGELGAPENLQPPPAAT ELGPSTSPQMGRRTPAQVPSVD RQPPHSRCLPTAQACTMSHHS AAGHDG/DPASQSALPETGKRT LELQPPGGPLISL*EAGSLSRSE PSCVREV
14278	44646	A	14364	23	714	EAPEIPRQNRMTMKERPVL PHK*IHPNVAKWSRVPVQVQK NPQFQE/PTPEFIPVPGTSPEAAG FWH*GAHDSPGTRDRSEVEPGR GHPHLGPRDSAAADPGEHSPCD CP*ACPEVRRWPA/APVQIQYIIP SVDDFSLEFHAQDGDIDMRRE NVPFSPAEEGKAAPLYQQPLMI PQANHMAGISPS/PTAAEFQHR DVHHRGPGTRDRTHTETGRVC PHPVPTDSPAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,117	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14279	44647	A	14365	3	1869	ITTVAPSRPASSDCESDGS*EQD AGPGSRMGPEK*AGPRPTRRVG RWSQTHSQDDTSGAVVPEYP SDR*YAGGRGPG/PGGPTVHP* KRRS*NPQETKMMARRDPKSW AKRLSPV*PRLAALLTSASPSCP LEPRVLPFRVPPSHGLCEGTSYP NSPGT*RPPCRSSAKTAGPLATR PEVPGAP*SAGRPWFQRPWG KRRG/GKPEPMEAPG*SQPGAL EQG*GREGRETKATRPAAEEGSP PHVFRETREAAAEWKRIHGVF *SSEGHGP*FPFSFPSAGGNRGT PLSCLLGVDRDSTILPGCKRANA GPHNQ*EAARGPCPR*SIAAE MSGRGSVLASLPLRKASLSSSS SLGPKERQTGAAA/AHPSACSQ APGPRASPRGEADTQPPRG*LP RSSPGCLQNPRPAPGRQTPGTR QTS CGDL/SSPARQPHTAWA* APISASGQEPRDLPSSDSGLPEL PQETETGSLDPKRKRHPGR*AG GPGKSPTSASRNRTWTKYVAP DGQEDTGPGAQRRPAASAQQT LPA YCPGLHHVPSLSGQP*WGP ASQS/GSSGDWKTADAGAPASW RPPHFTLLRSREPSLRLMCQR SLRLPVFVSHRASSMRTRFPPPP QRTAILTWS
14280	44648	B	14366	1	1519	
14281	44649	A	14367	312	1326	TTKTGQDKDRLEEFMSQQLSGS KRMSTQPRTELPPNRHTTTTS TTPA TNTTCTATVPQPPQYSYH DINVYSLAGLAPHITLNPHTAH QLKQCVRQAIERAVQELVHPV VDRSIKIAMTTCEQIVRKDFAL DSEESRMRIAAHHMMRNLTAG MAMITCREPILLSISTNLKNSF ASALR/PDGSSAIQL*SNDS*SCS WRPKLYDAFWDLSLRV**PSR PEGEGRVSEGMGESLPFSSSW PRQYQSFLCICWTDAPARNTED R*SHNKVLSSVY*NVC*NQLPC SG*AAQSCCQSHHDPQVLSQ PGCLCSTHCTARETLRGGHQHC HKD*SAEQGL

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14282	44650	A	14368	2	1120	PEPEPGARGGEQLNEDFEG*VA VPTCLHCPALSRQTQRAIQALT VRRGEATIRPPPCDDTKGGHRF LNELIKVVSPKVGAPSPSDDLPC RMWGEERGWTVGLPEEVKIAE AYQMLKKQGEAHRGWGATRA CLPLPHHERPKNVIFEDEEKSK VRLQGGTYGDSEPRWGSVGS! KEMVQF/DSGRAQSTGRRRDG GIELGHNVKLLTEMVMSSHSG GAAAGSSEDLMKVHLPPCLPHS LPTPQPTRTLRMRPTLFLASDT EDNDEALGEPRAGAEVRSPLP PPPAPVRGEEVNGDATAGSIPI EEVAGELGGHPSGWRGTESYP AMPTRPGEQASPEQPSASVSL DDELSLGEGARPGGGRAQQ
14283	44651	A	14369	1	432	GTRQEVTAGVEPAREWQRRLM EVQWGLERAPYCIQHAPR*RRS PARPGTQSCGLGACWIO*GALS SPHCTSISRCHSLAGSTPAVTS CLV
14284	44652	A	14370	16	471	
14285	44653	B	14371	66	206	
14286	44654	B	14372	234	390	
14287	44655	B	14373	207	427	
14288	44656	A	14374	2	572	FLLERAPYGVGFSLLPGLWLGS RAGVGRHHDKRVGLGRAPTWS LEGAVSSM/TPRPQLCVP/WPC WGPSSPGG*QQLGQLSCSYSLV DR*VALLWFWMLVGSPLVKGH CPTPWSRFVDFSVPLATPPGIVY WGLFAVFLFSHLLPARPGEQMS ACCRHLHAPSSPLLTLDSLKVY SCNSQGLVVRVFPFGD
14289	44657	A	14375	175	499	KQNKSMGRKSQGFVASFNGHL YCTASCGMPASSTSTQTWPRVL PLHSQ/ESSHGCSWRGRR*GP RPRPHKTPVPMVMDSTARNRA RRELVLAWCKSPLATALLVSW DK
14290	44658	A	14376	408	625	VFGQEVEFGYMNKFSSGDF*DF GAPITLSSEHCTQCVCVFPYPSAP SFPFPVPKVVHCVIPHSLVPTYE WEHTM

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14291	44659	A	14377	1263	1812	AGDAAPEDPAGRGQEDLYDEE LPGWGLCIPHACLQPCHA*VT KAG/ARVKVILPS*DTQRTKDIL KAGGG/PSSIHFINSAHGKPAVI VRPRGIWVLNITPLSGQWGPVI GVYTAATVDMKSLGSGSLGLQ LALPLAASWLGVLTEAARVFG EQVVFGYMNSFFSGDFWDFGA PITRAVYTVPNV
14292	44660	A	14378	1	693	WDYV/KRPNLRLIGVTSDEGEN GTKLENTLQDILENFPNLRQA NIQIQEIQRTPQRYSSRRATPRIH IVTFAKVEMNEKMLRAAREKG RVTHKGKPIRLADLSAETLQA RREWGPFINILKEKNFQPRISYP AKLSFISEGEIKSFTDKQMLRDF VTTRPALKELLKEALNMERKN RQINETENQGGYPGIELGSAPEG PNPLFCRHLQMSVDGRHLQNSP PQINRIYIFLAPHHTYSKIDHILG SKTLKKCKCRTEITNYLSDHSA IKLELRIKKLTQNCSTTWKLNH LLNDYVWVHNEMKAEMKMFF ETNENKDDTTYQNLWDTFKAVY RGKFLALNAHKRKQERSKMDT LTSQLKELEKQEQTSHKASRRQ EITKIKEELKEIETQKTLQINES KSWFFERINKIDRPLARLTKKK REKNQIDAIGN
14293	44661	A	14379	2	1299	
14294	44662	A	14380	2	383	
14295	44663	A	14381	1	1536	
14296	44664	A	14382	2	1118	REHLAEGMAVGTSADLNISA CWLRRQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFORK EQAAIFA VLPPLVIPRKTTGSGV DLEQTPADLQKRGTLVTRKTN KQKAIAISTSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSPAR EQNWTENEFDELTEVGFRRWV ITNSSKLKEHVLQCKETKKLD KRLEELLTIITSLEKNINDLMEL KNTAGELRDAYTSINS*IDQAE RISEIGDQLNEIKCEDKMREKAR MKRNEQSLQEIWDYVKRPNLR LIGVPESDGENGTKLENTLQDII QENFPNLRQANIQIQEIQRTPQ RYSSRRATPRIHIVRFTKV

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14297	44665	A	14383	1	1154	MLPILGSRHPSSLGQARKLDYR PSKSQCLEPGTPRACLV.YTLV AKLIYNDYFIHYFAPRGLPPME KNVVFVIDISGFMGTKMKQD HNFSLARQNWITENEFDKLME VDFRRVITNNSSELKEHVLTOC KEANNLEKRLDELLTRITSVEK NINDLMELKNTAGELREAYTSF NSCNDQAEKISEIEDQLNEIKP NLRIGVPESDGENGTKLENTL QDIQENFNSLAKQANVQIQEI QRTQRYSSRRATPRTHIIVRF TKVGNGREKMFKGQPGGKGR VTLKGKPIITLADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKYFTDKQMLRDF VTTRPALQELLKEALNMERNN RYQPLQNHAKM
14298	44666	B	14384	1	1554	
14299	44667	A	14385	1	909	
14300	44668	A	14386	2	207	DIMSCILQNYNRPPVMALAIPIA VKFLHRGNKELCRNMSNYLSL AAITKADLLADHTEVIVKSILQ
14301	44669	A	14387	496	1207	PLITGTHDSGSVESQLIKLILTM HQLFRLVLGQKDLRAGDLFS *NNSEIEDSLTEALEQIKIHSSSD YQTNNNDQAVVEICITRITTAIR ETESIEKHAKALVGLWDSCLEH NLRPFKDEDTPHAKIASDIMS CILPELQPTFQSMALAIPIAVKF LHRGNKELCRNMSNYLSLAAIT KADLLADHTEVIVKSILQGMVR KLSLGTCTFGRYLKVFSSSIYGL WEARPRVLEAN
14302	44670	A	14388	219	448	VSLELCLKTTGPDCCGQTSQTP PAAAYHHHLPAGAGLPCGRLPA LCCSCPMGARPL*HHKR/DPSRF QEKTHLYLPSSH
14303	44671	A	14389	542	1365	GTEGVMANRSQEGNGGGSWR AKQVVVTVPF*EQSLVIMLWR RGGNT*QRPSEGTSSSHCSFH MSRHQ*CKCLLKEP/VSAEAR DALDTKTHTFLAMIPSYLLNG NIGELPEGPAGGCAQNPGLWAS /RGPARR*RSQASSSPEVRWPPG QCGLRGRPKCKE\PRPHWPSP CASPYRGAGGQRLRACSAAG RKTPDRRLPEPTRGPVSQRAV LGKLRAAAGHRIPIGDLGDGLS LGAPPAGRHLHTVPLRREFSP CEDALGIGEQQGKKRV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14304	44672	A	14390	3	723	PVLRGGIQEFAYIKALYERKFL VPKPIDYNRHAVDMELINGVPL C*IIHHVEDPASVYDEAMELIVE LANHGLIHGDFNEFNLIILDESD HITMIDFPQMDSHTSPNAEWYF DRDVKCIIDFFMKRFSYSESELFP TFKDIRREDTLDVEVSASGYTK EMQADDELLHPLGPD DKNIETK EGSEFSFSDGEVAEKA E VY GSE NESERNCL E ESEGCYSDHLETL NK*RKTVYQKRVLMHGV LK
14305	44673	A	14391	I	1889	MGSKVKEVEDDSQMSDLVRG MNAFSKTGSGGVEQGR TGQGG TNGHIKKAKARDRRRFFKTP QRKVGNDNLQLPLRWTEQHAE THIMNFC SKNYNRNIPGKPRESI DTLNEAACRGRLSKTARKLWS EAQDQRSFQATEMQAFLFSAK RIAAEKKTIIRRRDLCSIWGKLL PRPGSQSVPAQIPENLQEQEERA KWLNLGRSKFFPQTSTLKGVT SNKTGVKEPELESRQPNLLKVE MGMKNH EIVPGSLIASIASLKH GGCNKVLREL VKHKLI AWERT KTVQGYRLTNAGYDY LALKTL SSRQVVESVGNQMVGKIESYI YIVANE EGQFQALKHLRLGRTS FRNLKNR DYHKHRHNVSWL YLSRLSAMKEFAYMKFRTL EIR DYFYWVKINVLTPGCS PKRGSS GEFVPCLLQLLLGFGDCWHSFG LWHITPVSVSMLTLLPSLLLVK QKKPTLDSRMGQDFVVELQL YLCVLEREVIREYPPDGQIFGRY FDRDVKCIKDFFMKRFSYSESEL FPITFKDIRREDTLDVEVSASGY TKEMQADDELLHPLGPD DKNIE TKEGSEFSFSDGEVPEKA E VY G SENESE RNCL E ESEGCYSDHLE TLNK*RKTVYQKRVLMHGV LK

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14306	44674	A	14392	150	1910	STPPGGPSVLM*STEEPGAGRS QPLCDDLSTRPLSCLGAGCCLW PAKRISAKEEPWYSSRSKDKKE KNYSSPETTTSGGCHSPGDSQY QELAVALESSVTINQLNENIES LKQKKQVEHQLEEAAKTNNE IHKAQMEQLETINILTLKADL KTTLYHTKRAARHFEEESKDLA GRLQYSLQRIQELERALCAVST QQQEEDRGHCLSSPDQNFSLFTI QSSSCREAVLHRLQQTIKERA LLNAHVTVTIESLKQVQLERD EYAKHIKGERARWQERMWKM SVEARTLKEEKKRDIHQELER SLSELKNQMAEPPSLAPPAVTS VVEQLQDEAKHLRQEVEGLEG KLQSQVENNQALSLSKEQKQ RLQEQEEMLRQEQAQRVREQE RLCEQNERLREQQKMLQEQGE RLRKQEQRLRKQEERLRKEER LTKAGKEAVGPGGEAVEEGGE ATKAGGEARALPEPQARQAAG RATVQLRGSEQREKERTAVGA ASKGAAGEARRGEGDAVHGHL SAADL*EGGAAQAVTAADPVR GPAAAAGSLGQSGAPRSCQPPE PTARDPAKPRGSPWRRRWRTT
14307	44675	B	14393	463	3755	
14308	44676	B	14394	175	1835	
14309	44677	A	14395	102	465	RAYCWAYIRLSCLTVILIAWCS QESALSEEEEDTTRPLETVTFKD VAVDLTQEEWEQMKPAQRNL YRDVMLENYSNLVTGCVTK PDVSSWSKKRSPG*WRKKCL GGTVQNPEERTAV
14310	44678	A	14396	1	330	
14311	44679	A	14397	1	531	MLLNIPQIHTRQSPRAKNYLAQ NVNSVKA WCSQESALSEEEED TTRPLVRLKHLFVSCILQCSYV LLPLTPEYQLNKFLYVVTMPN FDDFKLISIMFLQETVTFKDVA VDLTQEEWEQMKPAQRNLVR DVMLENYSNLVTGCVTKPD VSSWSKKRSPG*WRKKCLGG

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14312	44680	A	14398	1	539	MPTTTTREMTONSSETIKNKNG KKQRKQRKNSKKNRKQKDE DKTRRQNKRRHKKNDINPEEE RTAVRLKDGGAAPQAVQEHD AGICASGGAQETYILVEGKGE ASTSPGQSKGSREGGVGANETC SKKLYRDVMLENYSNLVT/VG CQVTKPDVYSSWSKKRSPG*W RKKFWEALSR
14313	44681	A	14399	322	1227	FDLKMSKCRKTPQLQLASPASF SPDILADIFELFAKNFSYWKPL NNEWQLPDSEIFTCDHTEFNA FPWI*RTP*NEVKKPTGVIRTW DEWHEHTCFH**SGE/ISFPHGR KSVNAELWTQAWCKFHEILCS FPLIPQEAQNGKLNLSHLCEAP GAFIASLNHYLKSHRFPCHWSW VANTLNPYHEANDDLMMIMD DRLIANTLHWYFPGDNTGDI MTLKLFTGLQNFISSMGTVHLV TANGSFDCQ*NPAGDQRMVKG HCYFSPWNWLHLSKHTQCGNE FIFMTKKKQSLTAKSLPDTFS
14314	44682	A	14400	3	183	KRKEITNSLDAASRGTVPAAL AGVQYLEPRAGAAGRLGGAG WGRVPRPGSS/SSLVLGR*GW CPV/LRTQGRCCRPPGGCWVGA RPKAWELLSLVLGR
14315	44683	A	14401	21	399	IWNSAPTASRRPWSLAPGSPRS TWCVASTPPCAPGKAREPRDRS EVPPATAPAVLQSHWPCPRSSR SGSAGNCVGPSPHWSAPGHSQH LTPGPGHGGPRGP/CWHLLMQT AWPALTPPGAMPGEAEGQ
14316	44684	A	14402	59	478	RCSQPWHCPAALAGVQYLEPR AGAAAGRLGGAGWGRVPRPREL LSLSLVGR*GWRPQEQDQLFPH LRRPVGTRSESTWGNRAGAAT W/RAATPSPWRT*NGTKSKQW TASGLWQKGDGWD*GSGKPPL PLSPVAGQRLVPVC
14317	44685	A	14403	1150	1319	PRRLPTACTP*RS/CSRYWMVP KSPRMTMMMWTKLARMGAQ W*PRKSNACLSRAASS
14318	44686	A	14404	34	304	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPRRAPPPAPRRVPST TQ/EARRSAASLLSPAPRAHRD GTNNSRRATLRAVTLTARVRG F

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14319	44687	A	14405	1	360	SSLSYLPAGQGS GPAARHA*ASHPLHGLLCGSPSPNEHRPLIQGAQSH*PPKG*GVRAHGVGLA GRSTCSP/ECGIH*VKPAGLLSFLGPRCFYEL*QSPRRSAAASLLSP ARSRAHRE
14320	44688	B	14406	80	1166	
14321	44689	C	14407	1	543	
14322	44690	B	14408	1	930	
14323	44691	B	14409	1	1473	
14324	44692	A	14410	388	606	
14325	44693	A	14411	1	798	
14326	44694	A	14412	687	832	
14327	44695	B	14413	1	1218	
14328	44696	B	14414	1	642	
14329	44697	B	14415	1	807	
14330	44698	A	14416	554	724	
14331	44699	A	14417	216	494	
14332	44700	A	14418	1	3408	
14333	44701	A	14419	330	858	VPSLDGQRGLELDTECLRVVYLQ SLS*T*RFSTSSPEQLDTECLRV HSQTLCT*QGADWCYKP*VGL QVELPASPAP/WLAFSPWVVN GTGRHGAGGGARRGGSGCTGA HGVGGRLRHGRLQVSPSPAPWE GSCLSPSPIGPPFKRAHSVLQKG SSTLMVGTCASSPKVVPFHLLS
14334	44702	B	14420	182	1513	
14335	44703	B	14421	1	1608	
14336	44704	C	14422	1	1830	
14337	44705	A	14423	167	433	LPSRGAGLGTCSPPCLSLPPTPW APVRSEPPRRAPP/GSTVPSPIN HPRAEECERMARDWQAAPPA PVRDPLGEASWAEFFGSMPL
14338	44706	B	14424	32	352	
14339	44707	B	14425	103	451	
14340	44708	A	14426	158	921	LPSRWAGLGTCSPPCLSLPPTP WAPVRSEPPRRAPSPAPRPVP/ RPPKG*GVPAHGA GLAGSSTCS PDICRVC RSEGTPEKPL.YH*CVCTGSIKFIHQECYSPDMPSRLPIQ DIFAGLVTSIGTAIRYWFHYTLV AFAWLGVVPLTA WHQLLDLGS TLNPGCSHLVILKLTITSTKTLFP NKATFILVVLSDQKTLMEDPR MEDKWKEDRFSFNFSEALEITL GERHRPQTASVIPWFCSSRHVL NLGKINFEVD

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14341	44709	A	14427	242	515	IQSVHWCIIHKP*ARHRVLIGVFT IPELDIKVLHVPTRLRNPAFTH WILHRDCRCSCMPVLRHAPALL SPWVVNGTGRSRAGDSTHRGG SG
14342	44710	A	14428	759	988	TWPRKPLFPPRPLGL*WEGMLQ RSLTCPGDIFPILVISIWL LVY ANFGSWL*FLPRKWVFFIPVP NKFLIFI
14343	44711	A	14429	130	788	VLQLIKAVWTPTQEPSWLPV NPARELQVELPASAPCARTPQ LLGGRWDWAPWSRGWRSGFE ARAAQKPMEGVGGSGMAGCR SRALPHGKAAKARRAIEHSTGG LALLGDPVHSPQPLARVLSPLP RASRAGWLLRVRGPPSPRPGT PAGRQAPHAAPVPARASPTTP/ CRAERVGSSPGQPRKGLPQCRG EAEGLLKCHQSGSPGRGEELW HSR
14344	44712	A	14430	108	1686	ANRCPLPHPGTGAGRCGLGASA GRAEEAGV*GPLHEGLGYRPA GLFLRADTGHRTPGWGGGGGG AGGRGGAAPGPGVATRRFAG RRGCARHGAAVPAAVR/CCERL VLNVAGLRFETRARTLGRFPDT LLGDPARRGRFYDDARREYFFD RHRPSFDAVLYYYQSGGLRRLRP AHVPLDVLEEVAFYGLGAAA LARLREDEGCPVPPERPLPRRAF ARQLWLLFEFPESQAARVLAV VSVLVILVSIVVFCLETLPDFRD DRDGTGLAAAAAGPFPAPLN GSSQMPGNPPRLPFNDPFFVVE TLCICWFSELLVRLVCPKAI FFKNVMNLIDFVAILPYFVALG TELARQRGVGGQAMSLAILRVI RLVRVFRIFKLSRHSKGLQLGQ TLRASMRELGLLIFFLFIGVVLF SSAVYFAEVDVDSHFTSIPESF WWAVVTMTTVGYGDMAPVT VGKIVGSLCAIAGVLTISLPVP VIVSNFSFYHRETEGEEAGMF SHVDMQPCGPLEGKANGGLVD
14345	44713	A	14431	1	427	
14346	44714	B	14432	8	323	

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14347	44715	A	14433	20	1050	FNLVYMSHVSDEGALSSESASAT AASWPPHGFQLHFVPGRPQVPI CLYLLGQKGTG*HMAPLLRQVT GSPIPPKTIPGRGIRNMKRNEKR RYKTLMADGWELHQELSLGRT SSLPPYKGPWPSPGFQKVSKG ANPVEIKRGVMLAVDAVIAEL KKQSKPVTKEEIAQVATISAN GDKEIGNIISDAMKKCGRKGIIT KISSVQSIVTALEIANAYCKPLV IIAGDIDGEALTILILNRLKVGL QVVAVKAPGFGDNRKNQLKDT VIATGGEVGEVTVIKDYAMLL KGKGNKSIIEKCVQEIIDQSDV TTSEYEKEKLSIEKLSDGVAVL KSHPWSECTKIYPLT
14348	44716	A	14434	3	764	TTATVLARSIAKEGFEEKSKGA NPVEIRRGVMLAVDAVIAELKK QSKPVTTPEEIAQVATISANGD KEIGNIISDAMKKVGRKGVITV KDGKTLNDELEIHIEGMMKFDGR YISHPFINTSKQKCGISRDAYV LLSEKKIS/SIQSIVPA/LEIAHAH RKPLVIIAEDVDGEALSTLVLN RLKVGLQVVAVKA/PGFGDNR KNQLKDMAIATGGAVFGEEGL TLNLEDVQPHDLGKVGEVIVTK DDAMLLKGKGDK
14349	44717	A	14435	1	3288	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRTRLRAEDVFPPI GVAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWVVDLHIIHAEDTLLPF YLGEKDDVTYA/KPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGITNVVC
14350	44718	A	14436	2	422	

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14351	44719	A	14437	529	2484	WGINIIKKNKKAAPRAFGVRL ECQPATENQRWQDLNVISLLK SFFRKLPEPLFTDEELPLAPSCF EEENGGRGGGSPRYRLEPMDT IFVKNVKEDGPAHRAGLRTGD RLVKVNGESVIGKTYSQVIALI QNSDDTLSELSIMPKDEDILQLPA ERESGGEASEPPRVVRPEPSTRA LEPPAEDRGDEVVLRQKPPPTGR KVQLTPARQMNLGFGDESPEPE ASGRGERLGRKVAPLATTEDSL ASIPFIDICVRPCAWLHALLDW MAQQRVLDMQGSIGMGVSW DRELEEKSEKGYDEPTSPSIDL QAKHVPASAVVSSAMNSAPVL GTPSSPTFTTLGRHYSDQCST SAHLNIFAGIFDISNDHLQVSTL ESNFTRIHLTHYTGGNFAWLA WDAVPFSSDLLNLGVHVLETG AGTPFLGSACSSDGIASQMNTA GLPQIRDLPGHYETLKLFLVGHV LKTIAHSEKKNMEPRNLALV FGPTLVRTSEDNMTDMVTPHA *PLTRSWETLIQALQTGSSVTKR YKKGKENCGLTRSLRQCPTLST FLPNIWQDSAPWRPGVSGPVGD LKDSTTCSSAKSKGSWAPKKEP YAREMLAISFISAVKPAQEA GDAGAGQQHRRRLGAGGAQS LGRGPQRRGHQERS
14352	44720	B	14438	1	1473	
14353	44721	A	14439	5	694	VPDKWGWCLFMSRYLETAIRT AACAAAPRYLNPGRCSAARGPS SQSPRPWPWSGHKKRTASPGWG GQSAASPMPSPSRWPASVGGPE FRLSETPSRPFRTLGMK*GWQV HSWAPALFCSVMSFSPDTCCLC K*AHSQPCSPSPSTVILLRETSSN WDWQPEDLGAPKASASPPSTT RITRLRSSELQLRRLNPSDSCHR GFCFSFRCLLTPEHVLKPTVLRI QPGCKVA
14354	44722	A	14440	303	757	MAWKVSLRGRKVAGRAPSQLR WASPPSSGQSVKSLLLPPARRL CPGPGVPARCHHRI*GLPGRG WRGEWRRDTPNWEPPQPRSPS/ G/PNCA WSDGCPGAPRRPRAL *AGAAARAAAPARI*VPWRGSAG GCSNRRLLQVPAHE*TPTFIRYL

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14355	44723	A	14441	1	534	RHEDHSEPTFLISPSLLCFLLP PPLPRLTPAALLVPAVQRME PVLFLPAPGAAACRVWHPALPP PRQAAVSSSRPCYPCVARSAPA GRVRAAGVPAPPPSSPRLGRV GGRSRSPNVVFRVGAAPGPG L*ISPWTP/LNEAS*RQRCGPAS FAVYGGQEWPPQWPGRP
14356	44724	B	14442	157	2143	
14357	44725	A	14443	258	4089	QLITCLSRPETGGKFEVDTRP VCPPSRARAASAAA TLTPPTMDSFDLALLQEWDL LCVYEPDRNALRRKERERNQ ETQDDGTFNSSYSLFSEPKT NKGDELSNRJQNTLGNVDEMK DFLTDRTNQSHLVGVKPGVPQ TPVKNIDEHFVADSRAQNQPSI CSTTTSPAAPVPQSKRGTMG WQKAGHPSPDGGQQRATQGS RLLGDGVGRQQ/HSGQTSVQC GGGSPDGEATCHGQ
14358	44726	B	14444	1	1326	
14359	44727	A	14445	453	710	SQHFGKPRQVDHLRPGV* DQPGHGETPSLLKIQKLTGRGGAC LW/QSQLLRRLRQENRLNLGGG GCSEPGSCHCPPAWATERDSVS
14360	44728	B	14446	32	290	
14361	44729	A	14447	244	426	
14362	44730	A	14448	69	221	QWRFCGIERGERWGKD*EIGW LPCLCGKK*IWETFLFCTKKN SSALGSC
14363	44731	A	14449	27	220	AVILTAKICSFTPEPSKTTSPPGG TNNRRATLRAVTLTVKVCST P*GSAASFLKSVRPRTHQ
14364	44732	A	14450	115	732	EPETRIDPLSWNSSQLPVAALH LPGMSSVAGQAICNLCLGDL VSPSSLPALERTGPPWNRGPK GRGRLPSL/TVSQPSLVIPPTG KSEVNADRSPRAYCSNLGRYS GPGPPSLVIPPTGKSEVNADRS GPPAYCSNHFPSPALP**RSSMRS LSLQQTSAWTCRHFTSLKSR WRFPNLNSCLCTCRPNITWKP CLGACTL
14365	44733	A	14451	528	875	EHGYFGQTLGQKGCKSGKPPG GTLKTLVTLREPGRLQSP* TSLWVSERLP*YP*GDTGENCPKLS FHLRLGPS*AG*RERPPQGG LYLPPQAYRLMQGSFAFWPLFGY APSPQR

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14366	44734	A	14452	2788	3414	ACFSYIAFWRIINTSTANLSKES LTSTTSRSWVINVIVICTDWL FYKWLKFNFIYFYMIFFPNQIT FHSMGSCAARASPTSTPCSTA PSPIDHPRAEESSTRRTGRQL HLQPAKICSFTPEPSKTTSPGG TNNISALP*EL*HSPRRSAAL QFRTR*YPYRYSQSGPGSHF*L PLPLPSSIIHDHF*LFHLQHTFQS HALLP
14367	44735	A	14453	662	1338	VLQLIKAVWTQRPLGGRWDW APWSRRWCSGRLRPHRNQWS GWEAQAWGLQVPEPCAPGRQL RPGEKSSTA PVCTSCCRTRSTA GPTGCPSTRDPTLSASPS*TST TSLATATASASMWAGSCTSIST RGSASLVHQALTWPGSGPASPR KRVTGSHFVA*AGVRWRAHRS LPQTPGLK*SSHFLPSGWNRYR HSNHPISQSFPHLSPLSQNH CHHGPFMS
14368	44736	A	14454	3	415	DFLLFSEILPASQASAILPALPA SHRCPCLLDVPLPPEVPGPARLP VAAASVWRPVQHLSSLGRWA GPT*DRTESRETNAEVEADLPP LYAHGRLEPTAGPSGASAVLST SSEYCPGPHPKMGHRRVTSCLS TCQS
14369	44737	A	14455	659	818	
14370	44738	A	14456	2	710	
14371	44739	A	14457	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGGLHDLKIVVL
14372	44740	B	14458	1	1338	
14373	44741	A	14459	83	426	
14374	44742	A	14460	93	345	APALCLQILLDCXSVNRNRSR RPREVGIIQYKKGGAAGKGG TGNA PGFLLFKDS*KDPTPLPP PLLL*GQRDH*IQLHQE
14375	44743	A	14461	1	1302	
14376	44744	A	14462	1	1174	
14377	44745	A	14463	274	1428	
14378	44746	A	14464	411	627	HCLSHFQNTGPRGDVDFQQLA FPVLMADIRKEERSHLCSR RSTWILDKS*IQGSRLLSKEQGW GWGTSRK
14379	44747	B	14465	1	1553	
14380	44748	A	14466	226	449	SLQPDPI*CSGLRGSLLLV*PKSD
14381	44749	B	14467	1	2061	
14382	44750	B	14468	10	1099	

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14383	44751	A	14469	34	406	GGGFISLDTGSHHKSHPGGG*H ALGWVRPHLTNSPSPSQQPGNC GNPAWEC*GPHG/APSRWSCST PCRPSHPKVPAVRVAGPAGGCT PYRT/PTRRTPR*RPGPCAACDR PLHPHCGRPGGAYPR
14384	44752	A	14470	623	1671	VLRSSVSWLPTSMAMTVLAPM LRAMSAGRLLM*PPMSRCP SLGSHSGGR*PDS/GHAGAHVPPQ GAIFVDSHG*GGDICGHVEVRQ P/QGPQSAYPGRPDGCGG* RQTQ*TWRLGT*GPTQVPAPKSCS WPTPGPAASCGWRCAPPRTTLR *KSQWTCRPPGPRGPPPLMPL VLRCASSPWPRLAQGWCS P*APSPSGRSRCA GPRAWRKPS RRAHAAWQCGGAKRGGADSA GAGAPSTSCAYLATPRCAWGP HPPLGGAGLAA*GRAQPCSPAS APAGRG*APGPPGPQ*GCSR PVAGSARSASARRPSGRVRYGV HPPAGPATLTAGTLGCYPVRRP PGVPG
14385	44753	A	14471	32	972	QSGTFSTKNEGRFTTRDYYDGR GPRVGRCGTCVYVRYVHDRPH APPHERRNDGNTQRTGNAR PGTAMPTATTDQPKGRSTRHK ETKRGRRTARNKGQNNPRK/RP RKDKRKQGSAGEGERGAGGKE KGQPRDTEAKGDRRTDFPPPNG /P*GQSKRGANIGGWFPPLGT PNPPLPGQSAQVSGP*TPQM WMPGTGTGCCGGSQSGSPPPWCV SP*PVAEALFHSST/PAPRHPSP SSSPKHSHQSTPPP*ISLGQGPC RPPKRRPAPDQPPVRCPEPSC AYLATPRPTMRMQSACRGSAR SRASARRPSG
14386	44754	A	14472	1	3128	
14387	44755	B	14473	239	5474	
14388	44756	A	14474	542	781	PASIIIMTGSISHITILTRVNR LNASIKRHLRTDQWQIR/KS QDLSVCIYQETHFTCKDP HKLKIKGWRKIYQVN* KQKKK

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14389	44757	A	14475	724	1340	QLTLQGRRVAPR*PSRVALEQE/ CGYNALLRYEGFENDSGLDFW CNICGSDIHPVGWCAASGKPLV PPRTIQHKYTNWKAFLVKRLTG AKTLPPDFSQKVSESMQYPFKP CMRVEVVDKRHLCTRVAVVE SVIGGRLRLVYEESEDRTDDFW CHMHSPLHHIGWSRIGHRFK RSDITKKQDGHFDTPHLFAKV RSFYKNPHL
14390	44758	A	14476	1822	2226	KRLFTNRTTRITPFVAINSHHHHH HHITINTIITTTTINSHHHHHY YHHHHHHHHHHQHHTTTTNTTT TNTTTTNNNTTTTITTTTNTTT TTSINSHHHHHNQCHHHHHH HHHH/HHHHHYHHHHH*HYQ \HHHHHHYYHHHHHHHHHHQ/ HHHHHQHHHNQHHHHQQQH DHHHHYHHHQHHHHQHYYQ/H HHHHHNQCHHHHHHHHHHHQH HHDPHHHHQH*HSHQH
14391	44759	A	14477	232	625	EGCCCIAMVQKYSQPVRYVK YPFELIMALRKRYPRCCVTC* TGGAQQVGRFRLDPLSLCTP* CLWRTSSNF*KAAGCSGSR QSHHFGILPQPTAPKPWSSPLHI TKPQTLGQRDPGPRTRKRSK
14392	44760	A	14478	1	808	MPKTTACNVHTVTWASCENAD SDSTGLRHHDSCEDPASPGRS LCLVPHPTPAVRGGRPAGGRC PAVPAEGPWRLHQQAQEGKKR LAGGLERLENPVRRALPQGA QGHRAEPTEARPHAPEIRRAG AAAEARLESQPVGASAAAA SAASARIPYLVAVPAAGPPRHR CRRHRRGPGTSSGPR TALIRPAT ARARAGIVSEPTAPGATRAR WRQGSHPVAPSAP*LLRGPSIP WQIRPMCPCTISHQTCSERRPSG RWQMPGSACRRSLETSSAGAG RAQEAGGRLGETSGESG/RAGL YLKELRAIVLNQQLRVTRQQS IDELERRLNELSA*NRSLWEHP QLPQAQPPPGFLT*PSPLPALL GTAAATAAGAEHLQDHDGQRS SARPLPAPELASFQNEQLLAQ PEPDPGGRAHTTQSPHQHPGL GVKANKEKKGPPGCCAAPGTP LQESPAAPSARES

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14393	44761	A	14479	1	831	MIRYFGDYWTQALLTLIPGDPK HPRGPPVKVGYYGGQGYINSL ALCHNFIWRELNRFSLLQDVPL VRYIDNIMLIGSIKFLGVQWCG ACRDIPSKDPADPMVLEVSAD RDAVWSIWQALIDESQQRPLGF WSKSLPSSADNYSPPERQLLAY YWALVETERSTMGHQVTMLPE LPVMNWVLSDPSSHK/ANGLA GWSGTGKKHDWKIGDKIEWRR GMWMDLSEWSK/D/VKIFVSHV SAHQRVTSAAEEFNQVDRMT RSMDDTQPLYPTTPVIAQWAHE
14394	44762	B	14480	56	3476	
14395	44763	A	14481	3	591	DPADPMVLEVSEADRDA/VPI ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLM GHQVTMRPELPINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEKSSQW
14396	44764	A	14482	1	1275	MEKNDIDQSRRRKVVEMNENV QLVRYGEQASDLKATKFKSPS EVKHIRFIQAFIGSKLLMRPW TTVTQILSLKSAKIALSESLIPC RKRAEFVEKQTQAFIMQVSD QQKVHAQPSQVSTVKVKALIG KEWDPATWNGDVWEGPDEAG DTEFVNSDEAFLPEATAFPSPEV GNDQTVWGLDGTSELMLIPG DPKYRGRPPVKVGAYGGQVIN RGLAQIQLSMDPVGHRTRPVVS SPLPECIIGTDILSSRNPHIGSLT DITLVHYIDDIMLIGSSEQEVIT LDLLVQAVQAALPVGPYDPA DPMELKVSVADRDAVWSLWQ APIVTMRPERPIMNWVLSDPSS HKVGCAQQHSIIKWKWYIRDW ARSGPEGTNHSRRVCS/LPQVQ APSA*ATARRGGQAASGCCLF WSTCFNSFDV
14397	44765	A	14483	604	1760	NSWCRWFNFRY*YPTFYWES* NT*IPLEWFG*NHDASCP*TL SKSFSFETRTGSPCSSSLQTAYC GTLWIVQGV
14398	44766	A	14484	2710	3060	
14399	44767	A	14485	3	227	
14400	44768	A	14486	3	266	
14401	44769	A	14487	2	564	

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14402	44770	A	14488	2	503	FFFFLPIGFWRQHPRLSVLLQHI Y*VT*NAASFEWGPEQEKAL*Q VQAVVQVALPLGPYPADPML LEVSVADKDAGCTRLAQAPIGE SQWRSLGFRSKALRSSAENYSS FERQLLACYWALVETECLTLG HQVTI*PELPIMNWVLSDPSSHK VGHEQQHSIIKWK
14403	44771	A	14489	2	469	
14404	44772	A	14490	1	633	MTVDYRKFNQVVTPTMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFSIPVHEAHQKQFAFLPQ GYINFALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTDLLIHKRSKEAHTAASRI VSCLPEQKSHEQTL.PWEQVPSS GDIKEYFPNAFVLLTTASLQGG DNTSQLTLTWKAPEDIKMSKT DADADEEIEALRG
14405	44773	A	14491	1	518	MTVDYCKLNQVVIPIAAVSD VVSLLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQVTFTVLPPQWYINSPALCHNL IRRLDLCFSLPLDITLVHYIDD MLIGSTIKWVVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKH EWKTGDKGIRGRG
14406	44774	C	14492	33	932	
14407	44775	B	14493	27	2457	

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14408	44776	A	14494	332	2158	RGYVFCSWKKTGDS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQQQQYTF TVLPQWYINSPALCHNLIRDDL DCFSLPLDITLVHYIDDIMLIGP RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVFLFDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTTPVISQWPHEQCGHG GRDGGYAWAQCRLLPLTKAD LNTATAKRPICQQQRPTLSQY GTIPQGDQPATWWVVDYMG LPSWKGQRVLTGIDTYSYG AYPACNASAKTAICGLTECLIH HHDIPIHSI ASDQGTFFMAKEVR QWAHDHGIHWSYHVSHHPEA AGLIEWWNGLLKSQLCQLGD NTWQGWGKVLQKVYALNQH PIYGTVSPIAKIHRSRNOGLEVA PLTITPRDPLAKFLPPFATLQS AGLEVLVPEEGTLPFGDTMPL NWKRLRPPRHFGLLPLNQQA KKGVTVLAVTDLDYKDEITL LLHNGGKEEYAWNTGDPLGLL LILPCPMIKVNGKLQQLKPEAL VPKGVVFPFGDTTMLSLSWKL RLPSGHVGLLMPLSQVQKGV
14409	44777	A	14495	1	3187	MAEGKEEQVLSYTDGSRQREN EEDAKAETPKTIRSHETYSLPR EWYEGNRPHDSITSQWVPPTTR GNYGSTIQDEI WVDHSGHYVRP VPVPRSLNSDISYFVGVGKQAV FFVQGSARMISKPADSQDVHEL VLSKEDFEKKEKNKEIYSGYI RNRKDDYDNHTGIDLVGTHIATI KGSNEEDTDPLFIGKVRTLEFP FVNGSAEIMLMPNSQQHKTE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP
14410	44778	A	14496	266	467	
14411	44779	B	14497	152	1245	

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14412	44780	A	14498	1	1445	MLRAAAGGQGLAAAGMGLCA RPAGGSQPLPRERMKGNRACLP LPPAVALTKGREKPDAGHQGR STQMMRESERGPCTHWTEERP GRQLKILLKQOMRQNTLMAFQ VSWDGRNKEIGRTFPHTAPHT QQLIFAMKIKRTGTVPEPWGLF ETGQRIRPIQAAGL*LSSSSTTC VALAPLLTMHVKSALLSAP/Q MGALSTITSITTRRQIPAESHF PAARFHLAPHSPITLPPCCGP SESAVTLCFAKGKTAQDAAV PTTSLTAAGHLAPRS*SSWSRM PVKVRRAADSLPETSAAHPLT H*SWLPASWGPASRALPGSEW VLKPVWQ/AITGPVSQITSSPGIP KPIGPLQA*GSAHPQALGFSVL QIPLSNSPTSPMTPLPRPKISNS SLPSQ/PPQALFPNRWNTSSSPV HVITSAAQ/PRTPREWPAVSFYR TTATTASLPHLWAPPQEN*QTS PAQNGSTLPCMSQA TFHFPS
14413	44781	A	14499	44	455	HLNRNR/PSQITPHIYNHLIFDK /PLFNIWWENWLAICRKLKLD PFLTPTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/TGKDFM TKTPKAMATKAKIDIWLIKLL SFCTAKEITIRVNRLPT*WEKIF AIYP
14414	44782	A	14500	1	346	
14415	44783	A	14501	1926	2448	DFIAVITTRKQLTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAACKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRCRRGCCGIGTLLH CWWDCKLVPCLCKSMWRFLR DL/DPAILLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP

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14416	44784	A	14502	1	2142	MHILDAEKAFDQIQPFMLKTL NKLGDGTLYKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFIATIKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRGRINIMKMAILPKVIYRFN DPIKLPMTFFTELEKTTLKEIW NQKRAIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSIYHN LIFYKPKDNKKWGNDSLFNKW CWENWLAIKRLKLDPLTPYT KIHSRWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVILKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELQIYRKKTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTMM
14417	44785	A	14503	209	3816	QGRPTFRFKYREHHKDTFREE QLQDT*SSDSPKLK*RKCC*GQ PERKVKLPTKGSQSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKREKNQIDTIKNDKGD ITTDPTIEQITIREYYKHLVANK LENLEEMDKFLDTYTLPLNLQGE EVESVNRPTGSEIEAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLKLFLQPIEKELPNSFYEASII LIPKPGRDTTKGNFRPISLMNI DAKIL

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14418	44786	A	14504	1	2877	MENDFDELREEGFRQSNYSRLR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERVSAAME DEMNMKGEGKFREKRIKRNE QSLQEIWYVVRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPRQYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTITSEYYKHLVTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPIGAE
14419	44787	A	14505	1	2347	MELKTKARELHDECTSLSSRF QLEERVSVMEDEMNMNLPK KSPGPDGFTAIFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKENFRPISLMNI NAKILNKMLANQIQQHKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIIISDAEKAF DKIQQHFLMLKTLNKLVLVLA RAIRQEKEIKGLQKEEVKVS FADDMIVYLENPTVSAQNLLKL IGNFSKVSQYKINVQKSQAFLY TNNRQTERQIMSELPFTIAKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGDLSLFNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAACKHMKKC SSSLAIREMQIKTTMRVHLTPV RMAIHKSGNNRKIQ/GGIWCD RIL*R*TTCTRVAKIEQSL*RR/W KRLQRTLSIPVLDAV*PPMF*AS
14420	44788	B	14506	1	2265	
14421	44789	A	14507	1	2832	
14422	44790	A	14508	1	2109	
14423	44791	A	14509	1	2757	
14424	44792	A	14510	1	2304	

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14425	44793	A	14511	I	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRKLNLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHLNANKLENLEEM DKFLDITYLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAIFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFTELEKKTTLNFIWNQK IRAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSKFSTAKE TTNRVNRQPTKWEKIFATYSSD
14426	44794	B	14512	I	2337	

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14427	44795	A	14513	1	1544	HINRAKDKNHMIIISIDAFAFD KIQQHFMLKTLNKLGDGTYFR KSINVIQHINRAKDKNHMIIISID AEKAFDKIQQHFMLKTLNKLGI DGTYFRKSIN/DNPAYKQSQRQ KPLIISIDAFAFDKIQQPFMLK TLNKLONHIVYLENPIVSAPNLL KLISNFSKVSQYKINVKQSQA LYTNNSQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTKKWNIPCSWVG RINIVKMAILRKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA PVAKAILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI GQWNRTEPSEITPHVYNYLIFD KPEKTKQWGWKDSL FNKWCWE NWLAI CRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKLEENLGI TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTWEKTFATYSSDKG LISRIYNELKLIYKKTNPIK WAKDMNRHFSKEDIYAAKKH MKKCSSLAIREMQIKTTVRYH LTPVRMAIHKSGNN
14428	44796	B	14514	110	2153	
14429	44797	A	14515	1	3210	MVKGSIQEEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTROKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDLTLSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
14430	44798	A	14516	3	2820	ENKDDTTYQNLWDFAKAVCRG KFIALNAHKRKQERSKIDLTLS QLKELEKQEQTHSKASRRQEIT KIRAELEIETQKSLQKINESRS WFFERINNDRPLARLIKKKREK NQIDTIKNDKGDITDPTIEQTTI REYYKHLIYANKLKNLEEMDKF LDYTYLPRLNQEEVESLNRPIG SEIVTIINSLPTKSPGPDGFTAE FYQRYKEELVPFLKLFQSIEKE GILPNSFYEASILPKFGRDITK KENFR

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14431	44799	A	14517	687	2274	LRDCKRINQHPVKTDQSAFCM/APIMQDVVLEVLAIRARQEK EIKGIQLGKEEVKLSLFADDMI VYLENPVSAQNLLKLSNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRIINIVKMAIL PKVIYRFNAIPIKLPMFTFFTELE KTTLFKIWNQKRARMASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNYLIFDKPDKNKQW GKDSL FNK GWENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKLEENLDITQDIGMGK DFMSKTPKAMATAKIDKWDL IKLKSFCIAKETTRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKRCSSSLAIRE IQIKTTMRYLTPVRMAIHKSG NNR/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMQRKNKTLI
14432	44800	B	14518	1	3192	
14433	44801	A	14519	1	2814	
14434	44802	A	14520	1	3144	MGDFNTPLSTLDRSSQKVNK DTQELNSTLHHADLIDYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRICKLTQNRSTTWKLN NLLNDYVWHNKMKAIEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKKQKQCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK

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14435	44803	A	14521	1	2616	TTYQNLWDAFKA VCRGKFIAL NVHKKQERSKIDTLTSQKLEL EKQEQTTHSKASRRQEITKIRAEI KEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDAI KNDKGDITTNPTIEIQTITIREYYK HLYANKLENLEEMHKFLDTYT LPRLNQEEVESLNRPIITGAEIVA IINSLPTKKSPGPDGFTGEFYQR YKEELVPFL/KLFLQSIKEGIM NIDAKILNKILANRIQQHIKKLI HHIDQVGFIPGRQGWENICKSIN VIQHINRAKDKNHHISIDA EKA FDKIQLFMLKTLNKLIGDGT FKIIRAIYDKPTANILNGKKLEA FPLKTGTROGCPLSPLFNIVLE VLARAIQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFFTELEKTTLKFIVNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTA WYWYQNRD IDQWNRTPQSEITPHIYNILFD KPDKNQWGWGSLFNKWCWE NWLAI CRKLKLDPLTPYTKIN SRWIKDLNVRPKTTKLEENLG ITI QDIGMGMDFM SKTPKAMAT KDKIDKWDLIKLSFCTAKETT

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14436	44804	A	14522	782	3024	SKTVPTGNSLEPTQNCWLQQW LPQDIEIEKQEQT/HSKASRRQEI TKIGAELEEIEETQKTLQKINESR SWFFEKINKSDRPLARLIKKKR EKNQIDAINKNDKGDITTDPTIEQ TTIREYCKHLYANKLENLEEMN KFLDTYTLPRLNQEEVESLNRPI TGSEIAIINSLPTKKSPGPDGFT AEFYQRYKEELHINRTKDKNH MIISIDAEKAFDKIQRFMLKTL NKLVLVLEVLARAIQKEIKEIGVQ LGKEEVKLSLFADDMIVYLENP IVSAQNLLNLISNFSKVSQYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNERKEDTNKWK NIPCSWVERINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIKASILSQKNKAG GITLPDFKLYYKATVTKTAWYS YQNRDIDQWRNTEPSEILPRIYN YLIFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDPFLKP YTKIKSGWKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLSKFC TAKETTIRVNRQPTEREKIFATY SSDKGLISRIYKELQIYKKRTN NLIKKWVKDMNRHFSKEDVYA AKKHKMKCCSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRITI VLLPGSLIVRSFHVTLNAILLHP
14437	44805	A	14523	1	1701	
14438	44806	A	14524	1	4434	
14439	44807	A	14525	1	2913	MGGPAALCIAVVPGLDVLVALC LEEGLSGSIATWACSPWRISQ THLTFRSSLAVAAIPEGLPIVVM VTLVLGVLRLMAKKRIVVKKLPI VETLGCCSVLCSDKTGLTANE MTVTQLVTSGLRAEVSGVG DGQGTVCLLPSKEVKEFSNVS VGKLVEAGCVANNAVIRKNAV MGQPTEGALMALAKDQEDY FMKGALVEEVIRYCTMYNNGGIP LPLTPQQRGAGPDTALPSAAS AFARMSAAERNDAFQG

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14440	44808	A	14526	1	3009	MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDGS AIKLELRKIKNLTONRSTTWKLN NLLNDYVWPNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14441	44809	A	14527	1	4800	MGDFNTPLSTLDRSTROKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRKIKNLQSRSTTWKLN NLLNDYVWNEMKAEIKMFF ETKENKDDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14442	44810	B	14528	1	2901	
14443	44811	A	14529	569	3443	RKH*TWKRTSSTSHHKNNPN* LEKQEQTHSKASRRQEITKIRAE LKEIETQKTVQKINESRSWFFER SNKIYRPLSLIKKKREKNQIDT IKNDKGDITTDPTETIQTIREYY KHLANKLENLEEMDKFLDTY TLPRNLQEEIESLNRPIGTETIVT IINSLPTKKSPGPDGTAEFYQR YKEELVPFLKLFQSEKEGILP NSFYEASIIIAKPGRDTTKKN FRPISLMNIDAKILNKILAKRIQ
14444	44812	A	14530	3591	8157	TGTSQKKTfMQPKKHMKKCST ITGHQSNANQNHNIPSHTKLE WRSLKRSGNNRDVGNVVEAM YGDLPPIIMLIGHSMGGAIAVH TASSNLVPSLLGLCMIDVVEGT AMDALNSMQNFLRGRPKTFKS LENAIEWRNKIDLSWADSIKNV AAASLACISGALPASAVTTSPD NKRMRNVLYKIERLLAESPNH VVAEAVIQRPNIPLQTRDTYE GLCQTLGSQPTLYQIPSLYCSYE TNSNAYLLQPIRKEVI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, v=-possible nucleotide insertion)
14445	44813	A	14531	172	328	AVKTEPEMSQATKLSVVHEK KSQEGKPKHEPEKSLPKQASD TGSNDAHNIKAVSR*SHRQPSC LWFMKKNPKKESRKNTQSQKA YPSRHQIQEVTMLTI
14446	44814	A	14532	3	660	TSPDCWEGRSVDWPRPGPALS LHNCKLDLGIEGGTLPPTPSF* PTGTRAV/PTRRRSRQETQLNSE RTVSPGSR**EKRTSRAW/RSP QGPGPGHAGQVAGGTGPRIGS TRGD/TLQKCGKIQSVPLNCELI PI*/PSILKPKVLPSCPGIGASS) CPSD*VFFCTS*PWPVLLSYPLS MNFYRYHDHILKLLVQYTLVYL LLQFLQVLLKYLLSHPKQHS
14447	44815	A	14533	1	1086	MVDNDVPWPLVVAQEKQPD LCLSSKGYRPLALVQLDFHQVS VTSKIFILSGALRSLTGAATAD WTCRVLVIYPHDIMADSECNLS LVPSTRKIMKHLASEKIKTQ NFNYNVDECVSLLYHHKANKL EAAEARQECCELLRVASVSRHC W/RDPAHPHSCWPRC*APHCLG PARAPNARPAKPATTWNLRSSR APCAAPVPTQSWAGAPSGTAG AEPS*ECRPPENQARTAGSGVH AEACAPATCAPCGPGPCSGLP SSGRALFLL/CATLAIPC*V*LC FLATPPPCR*HVTAPSAGKCIW* PDA*VTK/PRDLCPVQVARDN GPRQVAQKKESSVVSWFGTFI SRVGDSPPPRAATL
14448	44816	A	14534	23	506	PDIDNIFEFGAKSKPYLTVDQ MMDFINLKQRPRLNEILYPPL KQEQQVQLIEKYEPNNSLARKG QISVDGFMRYLSGEEGVVSPE KLDLNEDMSHPLSHYFINSSH TYLTGMNVLVLCYFSQSHQISP TSTFCSEAEV/WFSSISCVEVPLR TLGFHH

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14449	44817	A	14535	341	1248	KNAFTSFLTSFPFGQISVDGFMR YLSGEENGVSPEKLDLNEDM SQPLCFMGIWGLFCWCFIAGQL AGNSSVEMYRQVLLSGCRCVE LDCWKGRATAEEEPVKILAY* IYMCSHF*EVIEAIAECAFKTL SLPTFLLLFLFSLSPKQQA KMAEYCRLLIGSSIFKEYAFHFY* LESGVPLPSPMDLMYKILV KNKKSHKSESGSGKKKLE SEQASNTYC*NGDMMICY* NLTGADTESDADSGNV/CLFY SYFQGTAGSEAMATEEMS NLVNFLLTPFFVLLLNSE RNKSFEMSSFVETKGL
14450	44818	A	14536	574	647	C*PGNM/HISGQHLVAGEKEAE SEDEEEEDMKLLGTPEGGSKFT QKKVKLADEDDDD/DDDADDD DDDDDDDDFDEETEEKAPV
14451	44819	A	14537	3	630	PGATHASAPPGVRLKCGSGPV HIIGQHLVAVEEDAQSQDEEEE DVKLLSISGKRSAPGGGSKVPQ KKVKLADEDDDDDDDEEDDD EDDDDDDDFDEEAEQQA PVKKSNRDTPAKNAQKSNQNGK DSKPSSTPRSKGGQESFKKQEK TPKTPKGPSSVEDIKAKMQASI/ EKKGGSLLPKVEAKFINVYVKNC SRMTDQEAHQDLWRWRRSL
14452	44820	A	14538	1	1971	
14453	44821	A	14539	316	1169	RVGGQSHGTQRISLCRHSVCSP LARQSPSNMK*VRTIEIQMAVS CYLKRWQYVDSGGLPKQGLR LPQTAEEELANLTVHRESHCAD IVSAVPCQAEPOQYEVQFGR LRNFLIDSDSPHSHEVMPLLYPL FVCLHLSLVQNSPKSTVESFYSR FHGMFLQKASKGQVIEQLQTT QTIQDILSNFKLRAFLDNNYVV HLQEDSYNLIHLQSDSYTAL CKMFILLIHLDVQPAKTTD*QL YASGSSSRSENLYEAPDMPSPI LQNDAALEVLQERIKQVKDGC PSLTTVCFYNT*QLLNTAEISPD SKLLAAGFDNSCIKLWSLQSRK LKSESCQVDMRSIHLACDILEE
14454	44822	A	14540	1	297	

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14455	44823	A	14541	2	1089	APLLGECRSGRGLASSRSRRRT TMTQSVVVQGKLRAGRDLVA AESSGHVSLMSYSLSFLSSGRS RLALREHAAVNQVPARRREPPR LSARSSSPSYFHLQSE*L*KKIH* LYFIFLSQAVLIDMEEGVVNEIL L*IRTNQIKK*MQGIFKIHILIFR AVGHKVFGLYQDQILEKFQIL HNYILNHLCL*FLKTL*SSGTGSG LGTFLKLVLEDFPEVYRFVTSI YPSGEDDVITSPLVEYHLHPLF LIA SLPMFFPQKSLFDIISKIDLM VNSGKV/GGTTVKPKSL\VTSSS GALKIELHLKCIILKLIKFSF*C* LFSSARFEGSLNMDLNEISMNL VPFPSS*EIVSLKYVLYFN
14456	44824	A	14542	129	461	TCISGWHLFRASVTCPGIQTSPH NWHISDNSSLPNNIFVCWNLL GMTRNYIIFIEQPLKMNWLKIA TSKIRGKAFSDGISGNPQCNT FHVVEKRTGQLLPGRYYSKPF
14457	44825	A	14543	1	522	
14458	44826	A	14544	1	927	MEDLLTEARSPYWGRARAKIQ DSCWSVTSDPNAGSVLDILAPLL LPSPSSYLPNFTCTSVVVTSHLH EAFDLDFGRGTGGSNCKTSRQV QLNNQKRKKKKSKSLPFHMSL QIQNYKTQEEPFAKPSQQHQH SEHESIQTCLVFRSSMTYMHIL KLIREKGSIMLSSTQGECPNSTC RWPAEEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNWLKIA TSKIRGKAFSD GISWEPQCNTFRHVVEKRTGQT T*INPDKISIQKHDIHAYIEAD KRKRKHNAVIHTG*M/YQI/GTC RWPAEEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNWLKIA TSKIRGKAFSD GISWEPQCNTFRHVVEKRTGQT LNVKTMRMKTFMMIYYHLMN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v/-possible nucleotide insertion)
14459	44827	A	14545	1	882	MAEILTQVDPDDLKKKTPRVK SVWRSQRGSCTPLIGTTTLD TSHMSIRNMDRSHINVHTVRKP SADLPYFRTHEWAHTGGKPYD CEECGKSFISRSSIRRHIMHSG DGPYKCNFCGKALMCLSLYLIH KRTHTGEKPYECKQCGKAFSH SGSLRIHERTHTGEKPYECSECG KAFHSSTCLHAHKITHTGEKPY ECKQCGKAFVSFNSVRYHERT HTGEKPYECKQCGKAFRSASH LRTHGRTHTGEKPYECKQCGK AF*PRFQMT*RRKLPE*NQCG EVSVGHVHSLNRHHRADTGHKP YEQYEGQKPYKCTYCKKAFS YLPYFRTHEWAHTGGKPYDCE ECGKSFISRSSIRRHIMHSGDG PYKCNFCGKALMCLSLYLIHHR THTGEKPYECKQCGKAFSHSGS LRIHERTHTGEKPYECSECGKA FHSSTCLHAHKITHTGEKPYEC KQCGKAFVSFNSVRYHERTHT GEKPYECKQCGKAFRSASHLRT HGRTHTGEKPYECKQCGKAFG CASSVKIHERTHTGEKPCSSNTS
14460	44828	A	14546	3	395	SAEVGAAETTLTELRTTVQSL DLDSMRNLKASLENSLGILLHL ESELATRAEGQRQAQYEAL LNKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14461	44829	A	14547	2	1044	AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLLRASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALLSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNGVGLA GMGGIQNEKETMQSLRDRLAS YLDVRVRGLETENWKLESQIEH LNVTRL*LETEIEALKKELLFM KKNNEEFAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRQA YDKLARKNREELDKYWSQIE ESTRVVTTQSAKVGAAMTLT ELRHRVQSLDLDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV

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14462	44830	A	14548	1	1212	GP GTGIAGGLAGMGGIQNEKET MQSLNDR LASYLDVRSL ETE NRRLESKIREHLEKKGPQVRD WSHYFKIIEDLRAQIFANTVDN ARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKYDD TNITRLQLETEIEAL K*ELLFMK KTPEEEVKGLQAQIASSGLTVE VDAPKSDI AKIMADIRVAQY DELARKINRELDKYWSQQIEE STTVTTQSAEVGAAETITLTEL RRTVQVFGDSTWTSMRNLKA NLENSLGEVEARYALQMEQLA NGILLHLESQLGQTPRTEAQRQ AQEYEA LLNLIKVKLAEIICHL TRPPSWKIGDFNLGDSLDER NSMQTIQKTTTTRISWIGQSGV LRPIDTKVLEALSQQEASGTL LKQEANKKFQSFK
14463	44831	A	14549	1	2382	
14464	44832	A	14550	2	173	
14465	44833	C	14551	1	732	
14466	44834	A	14552	455	682	AWKRAVALGKSRPMGAVAFK RRMQPVAGPRAMQEKFPSSSS SLSIIPAF*YRLALSLAEPSSRW RARTGALMQL
14467	44835	A	14553	158	368	
14468	44836	A	14554	87	251	
14469	44837	A	14555	1	1026	
14470	44838	A	14556	201	578	
14471	44839	A	14557	336	767	AFVRAGSRFGGTPGARPDPA TRAPNPVGQSRHLRAASSRGRL FLRRTRDRKFPRRPLSRLLG A1/GCRWNQPRAEKFSAGAV LDFSPGLSCLPAVQSGPAARH A*ASHPLHGLCCPSIPDEHHPL LHGAQSHRPPKG
14472	44840	A	14558	6	535	ARHRVLIGVFTIPELDILSTSPD SGAQLASPSDPAAGLQVELPAS PARCARIPQLGGRWDWAQTQ EPSWLHLVEPAPGLQVELPASP TPCACIPQLGDRWDWAPWSR GWCSLGR LGPHRSPWGWEEAE AWRAAGPEPCPTGRQLRLGEK SSAAPVGWHCWGTQYTLRSH WPGC
14473	44841	A	14559	375	638	
14474	44842	A	14560	92	514	

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14475	44843	A	14561	54	380	SCHHYCRIHRRCARFLAGP*LPS RGARLGTCSPPCVSLPPAPWAP VRPEPPRRAPPPAPQRPVPSITTQ GLRSAGARRGTGRQLHLQLRG SAASFLKSVRPRTHTQFRTHT
14476	44844	A	14562	531	773	
14477	44845	B	14563	92	1774	
14478	44846	A	14564	1	390	LHDLQLSKPLSDDTALTDGG/Q PLPARWWAQPGRLQRCARFLA GP*LPSR/WGRARDLQAMPEP PTPSVGSCAAQASPTSAAPCSM APSPIDHPRAWPVLCSCMLLS LFVASISSCSQHQPMPQVGTMC L
14479	44847	A	14565	165	545	SLHSKLCWWLQQLWVYDTCP CSVQDCRQRWASAGNQS*RLL VDPAPGLQVELPANPVPCARIP QPLGGRWD*APWSRGWCSSGR LGLHRSFWSGWEAQWRAAG PEPRPAGRQLGAMSKVETGT
14480	44848	A	14566	1	309	SACLACRPIRGPRDLQAM PEPTPTSMGSCAARASPTSATPC STAPSPIHHSRAEECGHTALG/H GRQLHLQPRNLPQTINWRTTYS SFPATLNRLDGGG
14481	44849	B	14567	1	843	
14482	44850	A	14568	143	535	
14483	44851	A	14569	375	571	
14484	44852	B	14570	289	972	
14485	44853	A	14571	27	363	
14486	44854	A	14572	2	490	
14487	44855	A	14573	574	961	RLTLPDLRGSPPDTHQAQQITW ALI.PQGFADSPHYFSQAQISSSS ITYLGIHLHENTRALPADHV*LIS QTPISSTKQQLLSFLGMVRYFC LWIPSFITLTKPLY*FTKANLAD PTDPKSFHSSFSRL
14488	44856	B	14574	182	1513	
14489	44857	A	14575	894	1305	QTQEPSWLHLVDPALGLQVELP ASPVPCARIPQLGG*WDWAP WSRGWCSSGRLGPHRSPWSGW EAQAWRAAGPEPCPAGRQLRP GQHPL/RHMNKSQALSLLIAQP LGINLLSWWPPKYNRPVPLIGL SGLLIPATF
14490	44858	A	14576	531	801	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
14491	44859	A	14577	441	783	RAPPPAPWRPVSTTQGLRSAG EQRGTGRQLHLASAAPVRDPRG EAIWAPESGRSAASILKPARPPA HREERTTPDAPP*EL*HSPRKS ASLREDPWLHS*SQ*DQEP TNSGHTVSQDQSYYS*LEVSETKNP PIPDTL
14492	44860	A	14578	344	1632	FLAGPYLPSHGAGLGTCSLPCL SLPPTPWAPVRPEP/PPMSTTPCS TAPSPIDHPRAECERTAQDWQ AAPPAAPVWDPLGEASWAPES GTNISITPGNATFVTRVQQQAW FASCITGHDMSCLKTSSVVVLR RQSEALLPANLTCNWQDSSAL ATLESALSQVRHKRFTFTLMVF TGSADIMATVSIADVVSITESVQ TTAFVDNLAKNICDELLQDM DEAGNQHSQQNNTRTENQTPH VLTHKWELNNENIRIQGGEHYI LGPVGGRDEKTLRLRTYCLKSQ EGADTKCRNKHNKETQKQSKS LVYSSTLNPEKLLVCKRLSLEL TRPENTLRCNTNIGKLKAVAGG MSAASGIYLETDTQPYPLKQEL KEIKECVGKNSVVVVFLVRKK LSVSQYAFARCLDAKHSTSENV EIAGKLRIQSFEVKGQL

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14493	44861	A	14579	3	2233	NWLPSVSRCEQETHKIAANQSLT QRQMPLTSLYCDVVILPVSVGL ESLQSPYYRTSPCDPVSQFCLIK ISASSLPVLSLWTKLNKNAQSVQ RDYRHDNKAHYFQKLVMTQE NLYVLLCDEELDAVSLEAVHQ QKMKNRQAHSSGCCQKVAN APRNEESSGQFRVIGNEKFEKG PCGVRQQIFEKVLLPNRTCEV TPRFNRNFDLIKDLKAAETLID FLVYEPKNQRRLVNRFRLPCKL LHNLGHPLKTDAAQSPRKPPGP SWMPSPGSKPPSHPLVSPHLNP QVWDTSPPSLATEHASLTISLKP NHPPYPAQSQYSIPQHALKGSKP VITRLLEHGLLKPINSPYNSPILP VQKLDKSYRLVQHLCLIQIVL PIHPMVPNPYTLSSIPFTTHYS VLDLKHAFITILYPSSQPLFAF TWTDPDTHQAQQITLAVLPQCF IDSPHYFSQAQISSSVTYLGIIL MKTHIGLGAVEQGVVLVGEAR AAQEPMEWVGSGM/CGLQVP SPAPWEGS*GPARNRAQ/PVTIV PVLDFNPAPFHIPDTTPDHHDCI SLIHLTFTFPFHISFFVPVPLEHT WFIDGSSTRPNCHSPAKEYAI VSSTSIIEATALPRSTTSQQAKLI AYTDSKCAFHILHHHAVIWEER NFLTMQGASINAFLIKTLKDI LLPKEAGVIHCKGHQKASDPIT QDNAYADKVAKQLAFQLLSL
14494	44862	A	14580	1	642	SGTVPTTFVRTVIQAQGARTVI QQSLIGSLYIFRHCVRCOGIESV FVIIIWSRVGYDEKGFCLFTSVL GVWGHVTRKPCLLITWRTLKS RSGLE*PAGFSSSPGTSPQIRKQ KRGVPQHPVCDLPGRFRPRAGT PLAAQIQVPLPPCGHQE*NRR WAGSSALCPPLYLCARAGTGAV CRACEPAGV/AGWAWAWWAP HSEHAASAPGRQWGT
14495	44863	B	14581	393	549	
14496	44864	B	14582	1	591	
14497	44865	C	14583	226	828	
14498	44866	A	14584	1	1362	

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14499	44867	A	14585	1	585	MANVHQTMPLRLRLPDSFKP PEPKSNSQRVSTEAGTAGALTP QHVRHSSPASLQLGAVSPGTL TPTGVVSGPAATPTAQHFQSS FEIPDDVPLPAAREMAKTSSGQ RYFLNHIDQKTTQDDPRKTM SQMNVIANPPVQQNMMNS/PQS PQGGV/MGGSNSNQQRMRPQ QLQMEERLQLKQQ*LLQQLA LR
14500	44868	A	14586	345	1053	RWRLQNLSCSSCSGSGSEGAT CFARGRQSNLQSKIFPSNTD SRSTGYNSFDRQPNICFYKRQE TPHTGPPIPVPEGRPYMPG*CG A*SPGPFASRN*SEKN*SYKCSL HTAFNVIFSSVI**RYCTRQWHI VKCLDSFCDPFLISDELRRASTD AGTAGALTPQHVRHSSPASLQ LGAVSPGTLTPTGVVSGPAATP TAQHLRQSSFEIPDDVPLPTSW GEAKTSSGSKIPIF
14501	44869	B	14587	607	1185	

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14502	44870	A	14588	1	2142	MIILDAEKAFDKIQPFMLKTL NKLIGDGYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGGP LSPLLFNIVLEVLAAQIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTLSSKNAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTASEVTSHIYNH LIFYKPKDNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKLTLEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVILKKSFCTA KETTRVSRQPTIEWEKIFAIPPS DKGLISRIYKELQIYRKKVTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
14503	44871	B	14589	1	1647	
14504	44872	B	14590	1	2025	
14505	44873	B	14591	4	2121	
14506	44874	A	14592	2	1879	
14507	44875	A	14593	1	2130	
14508	44876	A	14594	1	3018	
14509	44877	B	14595	1	3171	

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14510	44878	A	14596	1	2700	MEKKQSRKKTGNSKNQASPPPP KECSSLQATEHSWMENDFDEL REQGFRRSNYSELKEEVRTHGK EVKNLEKRLDEWLTRITNAEKS LKDLMEKKTMARELLDECINLS SQFDQLEERVSVSMENQMNEMK PNLRLIGVPESDGENGTKLNT LQDIIQENFPNLARQANIQIEIQ RMSQRYSSRAIPRHIIVRFTKV EMKEKMLRAAREKGRVTLKG KPIRLKADLSVETLQARREWGP IFNILEKNFQPRTSYPGKLSFIS EGEMKSFTDKQKLRVYVTTTRP ALKELLKEALNMERNNRYQPL EKQIQTITIREYYKHLVANELEN LEEMDKFFDITYTLPRLNQEEVE SLNRPITGFEIEAIINSLP/TKKSP EPGGFTAEFYQRIEKEGILPNSF YEASIIILMLKPGRDTTKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHQDQVGFIPGMQGWFNIR KSINIIQHINRTNDKNHIIISIDA EKAFYKIQQPFMLKTLNKLGD GSYLKIIRAIYDKPTANIILNGQ KLEAFPLKTGTGRQCPLSPLLF NLVLEVLARAIHQEKEIKGIQLG KEEVKLSLFADDIMIVYLENPIA SAQNLLKLKGNFSKVSQYKINV QKSQAFLYTKNRQTESQIMSEL PFTIASKRIKYLGIQLTRDMKDL FKENYKPLLNEIKEDTNKWKNI PCSWEGRISILQMAILPEVIYRF
14511	44879	A	14597	1	2310	
14512	44880	A	14598	1	1305	
14513	44881	A	14599	1	2148	
14514	44882	B	14600	1	777	
14515	44883	A	14601	2	2971	
14516	44884	A	14602	1	3810	

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14517	44885	A	14603	1	1773	MNIGAKIINKILANQIQGHIRKLI HHQVGFIPGMQGWFNICKSIN VIQHINRTKDKNHMIIISDAEKA CDKIQRFMLKTLNKLGDGKY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKDIQLGKEEV KLSLCADKMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLQIHQTRDVKDLFKEN YKPLLKEIKEDTNKINIPSCVG RINIVKMAILP/KELEKTTLKFIW NQKRARITKSILSQKNKAGSIM LPDFNLYYKATVSKTAWYWY QNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNQWGDLSLFNK WCWENWLAICRKLKLDPLTL YTKINSRWIKDLNVSPKTIKTLE ENLDITIQDIGMGKDFMSKTAK AMAAKAMSTKAKFGKWDLIK LKSFACTAKETTIRVNRISYASS STSLQAFSRKILNCSKRFFKIAQ MCKLVELRPQDMIHTRSGSGNC SEARTLLCDFSAGRTSVNHGRI WRQIREAGAADPEIGLEVCNKN PTSFTLFYFLSYTTG
14518	44886	B	14604	1	2070	
14519	44887	B	14605	1	3190	
14520	44888	A	14606	1	3370	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14521	44889	A	14607	569	3030	RKH*TWKRTSSTSHHKNMNP* LEKQEQTTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKREKNQI DTIKNDEGDITTHPTIHTIIREY YKHLANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLK1.FQSIEKEGILPNSF YEASIIIPKPGRDITTKENFRPI SLLNINAKILNKILANRIQHHK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIISID AEKAFDKIQPFMLKTLNKLGI DGTYYHKIIRANYDKPTANIILNG QKLEAFPLKTGTQGCPLSPLL FNIVLEVLAIRQEKETEGIQLL GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKIN VQKSQVFLYTDNRQTESQIISEL PFTIASKRIKYLGIQLTRYVVDL FKER/YNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIVNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPKDNKQWGNDSLFNKC WENWLAICKKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLLEN LGNNIQDIGMGKDFTSKTPKA MATKDKIDKWDLMLKLSFCTA
14522	44890	A	14608	1	2742	
14523	44891	A	14609	1	3828	
14524	44892	A	14610	1	2667	
14525	44893	A	14611	1	2325	
14526	44894	A	14612	1	3057	

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14527	44895	A	14613	603	2973	DNTARGETIRQQHLLFTNIRCSA ASAADTQANRVWSGPPANSNR PAAARVLTVRRKTNKQKGPH QNPICTSPSSKTKETQTTIREYY KHLIYANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRTESDIE AIINSLPTKKSPGPDGFTAIFYQ RYKEELVPFLKLFQSIEKEGIL PNSFYEAIIIPKLRDRTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKHHGGVGFIPGMQGW FNIRKSINVIQIHINRTNDKNHMI VSIDAEKAFDKIQQPFMLKTLN KLGDGPYLKIIIRAIYDKLTANII LNGQKLEAFPLKTGTROGCLLS PLLFNIVLEVLARAIQEKEIKGI QLGKEEVKLCLEFADDMIVYLE NPVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTGDV KDFFKENYKPLLNEIKEDTDKW KNIPCSRVRINIMKMAILPKVI YRFNAIPKLPMTFFTELEKTTL KFIWNQKRARIKASILSQKNKA GGITLPDFKLYYKATVTKTACH RVGRAQQHSISKWKWYIHDWS QVGPEGTNDSARYPDTTQKWT AAALQPLSRTSLKDSHEGKSSQ WAELEAVHLVLRFAWKEKWP DVQLYTDSWAVASGLAGWSG TWWKHDWKIGDKEIWGRATPV IAQWAHEQQRGHGGRDGDYAW
14528	44896	B	14614	1	3105	
14529	44897	A	14615	1	3654	

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14530	44898	A	14616	735	2839	RSFPRSFPFLLSRYLRHIMV FSVLPFGLQNP KYLLSGSLQEK FRTPGINSHKTLDPNRV IIVRR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITDATEIQTITREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPI TGSEIAIINSL PTKRSPGPDGFTA EFYQTYKEE LVPFPLKLFQSTEKEGILPNSFY EASIIIPKGRDRTTKKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHQDQVGFIPGMQGWFNKRK SINVQHINRTNDKNHMIISIDAE KAFDKIQQPFMLKTLNKL GIDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCP LSPLLFNI VLEVLA RVRQEKEIEGIGLQK EEVKLSLFADDMIVYLENPIVS AQNLKKLISNFSK VSGYKINI QK SQAFLYTNNRQTESQIMSELPFT TASKKIKYLG IQLTRDVKDLFK ENYKPLLNEIKEDTNKWNIPC SWVGRINIMKMAILPKVICRFN AIPKLPMPFFTELETTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWY WYQN RDIDQWNRTEPSEITPHIYNYLI FDKPEKMSIIDTGGWYEA PVSS FFKEGLCRTGTENQVNRQPPAA SPFKVYVVSCTGSLHPRPHYFLE
14531	44899	A	14617	1	2250	
14532	44900	A	14618	1	2870	MKAIEKVFFETNENKDDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDLTSLKLEKEQEQT HSKASRRQEITKIRAELEIQTQ KTLQKINESRSWFFERINKIDRS LARLIKKREKNQIDTIKNDKG DITTDPTIQTITREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPI TGAEIVAIINSLPT KKSPGPDGFTA EFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK

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14533	44901	A	14619	248	2623	RQWAGVVGRCSHLASVWSSNT SETGAIRSSTEVDAPDDSMMLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAIFYQRCKEELVPFL KLFQSI/EKEGILPNLFDEASILI PKRGRDITTKENFRPISLMNID AKILNKILANRNQQHKKLIHH DQVGFIPIGMQGWFNICKSINVI QHINRTKDKNHMIISIDAFAKAF DKIQQPFMLKTLNKLGDGTYL KIIIRAIYDKPTANIILNGQKLEAF PLKTGTROGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKWKINPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIVNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWYWYQNRDIDQ WNRTEPSEITPHIYNLYLFDKPE KNKQWKGKDSL FNKCWENWL AICRKLKLDPFLTPYTKIHPRWI KDLNVRPKTIKLEENLGNTIQ DIGMGKDFMSKTPKAMAACA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKKTNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPLAIREMQIKTTMRYHL
14534	44902	A	14620	1	3253	MGDFNTPLSLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFPSAPHITYSKIDHIV GSKALLSKWKRTIHTNYLSDH SAIKLELRILNLTQSRSTTWKLN NLLNDYVWHNEMKAIEIKMFF ETNENKDDTTYQNLWDAFKA VC RGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQIDTIKNDK
14535	44903	B	14621	1	2758	
14536	44904	A	14622	1	5178	

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14537	44905	A	14623	1	3382	MGDFNTPLSTLDRSTRQKVNK DTQEFNSALYQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCERTEIITNLYSDHS AMKLELRKIKNTQNCSTTWKL NNLLNDYVWHNEMKAEIKM FFETNENKDTTNQNLWDAFKA VCRGKFIALNAHKRKQERSKID TLTSQLEKELEKQEQTHSKASRR QEITKIRAELEKIEETQKTLQKIN ESRSWFFERINKIDRPLARLIKK KREKNQIDTIKNDK
14538	44906	A	14624	965	4091	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEYTFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKIKNLNQRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKELEKQEQTHSKA SRRQEITKIRAELEKIEETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID
14539	44907	A	14625	3	3229	
14540	44908	B	14626	1	2791	
14541	44909	A	14627	1	3158	MVKGSIQEQELTILNIYAPNTG APRFIKQLSDLRDLDSHTLIM GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNLYSDHSAI KLELRKIKNTQSRSTTWKLNNL LLNDYWRKQERSKDTTLTSQLE KELEKQEQTHSKASRRQEITKIR AELEKIEETQKTLQKINESRSWFF ERINKIDRPLARLIKKKEKNQID TIKNDKGD
14542	44910	B	14628	1	7849	
14543	44911	A	14629	1	3985	MENDFDELREEGFRSSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRSLRSRCDQLEERSAM EDEMNMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLARQANVQIQIRMPQRYSS RRATPRHIIVRFTKVEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDYRTLHPKSTEYTF FSAPHHTYSKID

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14544	44912	B	14630	64	5735	
14545	44913	B	14631	891	6894	
14546	44914	A	14632	33	476	
14547	44915	A	14633	1	360	GQGEPKQLGRHPGVLRPHVVS AKTGDACITWQVRNLFPERPK VQWKEGCA\IQSGNSQESVTEQ GSKVSA\YLSPLTLKADYEK HKLYACEVTHQGLSSPVTKSFN RGEIIEGEVPPCI
14548	44916	A	14634	40	508	LPGECHRAQQGQRLQPQLLG LLMLWVPGSGGEIVMTQTPLSS SVTLGQPASISCRSSQSLVHSDG NTYLTWLQRRPGQPPRLIYHV FKRFSGVDPDRFSGSGAGDTFL E/ISGRVEA*\DVGVYYCMQGT QFPCSFGQGTKLETKRTVAAPS
14549	44917	A	14635	3	652	AWWNSETPAQLLFLLLWLPHY TSGEIVLTQAPGTLSLSPGERAT LSCRASQTIGSTYLA\WYQQRPG QAPRFLIYGASSRATGIPDSSSSS SSSSSSSSSSSSSSSSSSSSSQ YNNWPPGGTFGP\GTKVEIKRT VGCTHLFFIPAHLM\SQLKIWE LPSACVPVCNNFY\PREVQSYSG KVDN/VPSNRVTPRESVTEQDAS KDSTLQPSAATLDA
14550	44918	A	14636	3	440	
14551	44919	A	14637	457	1270	SRRVSFPPSA*QAVSDPSRQQLP SLRLRWGPEGRSFP\AENLGRGV RWVGGRDPLAA\LP*SSGPLNA GRLFARPQESGAPRIGNVRDVP RAREDVGTQAGREREFPRLFG PA\AVVGCERHLSPFPRAAGAG GRAGAAGRRSAPPGLGSCRSC RISAGPHGNDVPTLGGRGW/PL *NSGAEKL*EQ*G*/TGTGWSL AA\ILGGVPREP\GFRGAGRETIG PRGWL\VMLSRAVLLHSVLLCT CHSSWVLLHSDLACHADNNPD IQSCLFPMISKY
14552	44920	C	14638	90	465	
14553	44921	A	14639	116	439	
14554	44922	C	14640	278	364	

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14555	44923	A	14641	116	687	EIKDAALQLPLWRAQDRERAM KERREKRREREKERDREKKRK EKMFCRKRSCHTIMEPTPELSCV LPCLAPJVLAPPPLPLPVLPLPY ATR*LPQQNRQSTLTEAHGLATR GPITLANRCMPSTTRDRRLT PPSTLPNTTNLSWGVREGPNQD PEPSLSPCVPHDPFDYNAESLFS YWLVSVPMTAHTP
14556	44924	A	14642	474	1166	HPNRQGLRAPATAPGHGPREQ ALCEAPQGPQKCGPPRAQEA Q/GTEPRRRASRAAGACRHHWP QVAIRPGAGAPAGAARLGGV*E PGRAA/APRLPLPSQCCHR*GTS PAHLSASRSSSATCPWRRTAGR SGPSPCMTLAKQRQGHPRDGWI RAPSCDVTNRGLSSLLNLGGSA QQLLLASRPLGSGSGALEALEH GKSRAPWEPWLHGTHNPVHGK DPAGSTSHWPRPPAPRT
14557	44925	A	14643	283	806	PRGSFSTGRTRNAAGSTSNCSL RSLSARIEERKVSRCVGVPNHR HLRLGALTTRTPSWNGAIPTLA KLPAKRC*RRSGRRSKTWSFPG ST*LGNF AEEMICAASARPAGV PGPALPTPLRAPLPGVPWTSSR GRMCARLSCC/HAGRPVPARPG AARARRAAAGERHRPPALRV
14558	44926	A	14644	1	338	
14559	44927	A	14645	1	1091	MSNDGRSRNRDRRYDEVPSDL PYQDITIRHTPLHDSERAVSA DPLPPPLPLQPPFGPDFYSSDT EEPAIAPDLKPVRRFVPDSWKN FFRGKKDDEWDPVSDIRYIS DGVESPPASPARPNHRSPLNS CKDPYGGSEGTFSRKEADAVF PRDPYGS�DRHTQTVRTYSEKV EEYNLRYSYMKS WAGLLRILG VVELLGAGVFACTYA IYHKDS EWYNI.FGYSQPYGMGGVGGL GSMYGGYYYTGPKTFVLVVA GLAWITTHIILVLGMSMYRTIL LDSNWWPLTEFGINVALFILYM AAAIISM*MIPTRGGLCYYP LF NTPVNA/GSAG*KEDR*LQ*SSC LSP**FISLVLWFA

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14560	44928	A	14646	398	1107	SPGLVCGLLIFCKVTVPCAGPY RCPFGGLRH*SAR*QPPSGLREN GARPPGGEWLCP*FPP*PLNSR WKLPPRLVT*GEPWAAGEKFP RLGAGTGPAAGEGLPRARDWE PGRAGPERWAPGRGPAGTPAK TAAVKRSAPLPGSGDYANGER KPPSPFCQVKSGLN*VLCG*RL SLPAA*KPKKA*RRGRQSPGK TGYQVQQRPKNDPKSSIGPSP KNRQSLCLQPLWSFLIQ
14561	44929	A	14647	1	540	MGVRDPLEEAVCALAEQLHCA GRFAALFRASQERLSLLKLCPL QLPLPPRALSQGYKPLIGLLAF FQRCTAQRGGI*RGSLATVTLIS CGGLCPV*TSQRCLPVRGKLP TQASVMANAPPRTLRQLHRSTS DCCAGSENFKPVLSLLGSVGV GSTELDHLAPWLQPAFQGEW FYLTIF
14562	44930	A	14648	169	487	EVCYYPSETYFCQFVKLLICPV LFPCWQGVVQPKLSCMRCLST LLRGVSQ*GYMGVRDPLEEAV CPLAELEHCAGRSALFRAGRQ ERLSLLKLRPQLPLSPSA
14563	44931	A	14649	1	210	
14564	44932	B	14650	1	1683	
14565	44933	A	14651	1	529	MDSEVQADDEVSDENGELIGN WGKGMGVSDDPLEEAVCPLEAE LERSAGRSALFRASQECLESL LKLTLTAAPSPRGTAFRSPFKS PAQRSSIIC*Q/LYSCKTFRSTVA PMPRLCLPQASGKVQ*EN*SWA IPA*QGTSPMCSLCSGAPHQPG APLVLPPLPPVNRRLRELQCWL
14566	44934	C	14652	295	430	
14567	44935	A	14653	452	637	
14568	44936	A	14654	151	446	MVLSHWHSRCHWGMKKNYLQ LARCLPKWLPSFVFETQGPCDV STQGTLLVYGLQRPWEKHSI*A R*HHPSQHGPSQLPLARGSSP TPCASRMQRHPT
14569	44937	A	14655	2	335	EDRSAFRRPQPTHPLHPLHARS APKSPTPSPSPDTQLGLSGPTS GPESAPTA/PGNPSWRSSRWGSS SPCAASST*KSPYP*/CSPT/CAFP SPRLPFCRSAYQPAAGAGRGK
14570	44938	B	14656	373	502	

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14571	44939	A	14657	1	400	GSPAPAAAMDEERALYIVRAGE AGAIERVLRDYSDKVKSPGPGR AVSHPRAAALRACTSHPSPPSPFR GCALPPPKTFPAWACVFVPPAF SIHAS/SHPTTPTVAPTPLIPGPA A*PPVLLSSVQVTPPESVDVHL
14572	44940	A	14658	659	1177	ARKGSALLRLYSNAWCVCVK VLRIFSTASAYITRRDSSLGPVW TFLNFSFGSPGEIPTPFFFFPVFP LPLVAWFCPASFCPLPQCPLVPS EPSPPPHSGDAHCSPPKTFPAW ACVFVPPAFSIHAS/SHPTTPTV APTPLIPGPA*PPVLLSSVQVTP PPESVDVHLCPVPHS
14573	44941	B	14659	1	318	
14574	44942	A	14660	2	131	
14575	44943	A	14661	354	762	CPEIRPPS*THGTHK/SHFPPTASG THSVLEAL/PDTRQSPSRVHQ DPSPAI/PALLPSHEHGQPHLL QLPSHRCHPDPAFNCDAVKAC PGHATAALEHPYLSGRQSPSP THLPKLPAGRGYTVCALPKPGG ERSAV
14576	44944	A	14662	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDAIPLL
14577	44945	A	14663	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL/DPAIPLLGIVPKDYKSCCYK DICTRMFIAALFTIAKTWNQP
14578	44946	A	14664	1	1584	
14579	44947	A	14665	1	4729	
14580	44948	A	14666	1	1566	
14581	44949	A	14667	1	1424	
14582	44950	A	14668	1	576	
14583	44951	A	14669	1	3325	
14584	44952	A	14670	1	2195	
14585	44953	A	14671	1	3162	
14586	44954	B	14672	287	2018	
14587	44955	A	14673	1	1073	

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14588	44956	A	14674	1	3335	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLELEKQEQTSHKASRRQE ITKIRAELEKIEIQ
14589	44957	A	14675	1	1838	MIIPIDAEKAFDKIQPFLMLKTL NKLGIHGMYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTTRQGPC LPPLLFNIVLEILARAIHQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGDLSF NKWCWENWLAICGKLKLPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNIELKSFC TAKETTISVNRQPTWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPIKKWAKDMNRHFSKEDIY AANRHMKKCSSLAIREMPIKT TMRYHLTPVRMAIIKSGNNRC WRGCGEIGTLSHCWDCNLVQ PLWKAVWRFLKDLELEIPDPA ISLLG/TPYKDYKSCCYKDTCTQ STFTCRQHLPL

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14590	44958	A	14676	1	2354	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFPSAPHRITYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRICKLTQNHSTTQQLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKTSRRQEITKIRAELEI ETQKTLQKINECRSWFFFEKINKI DRPLARLIKKREKNQIDAIAK DKGDIITDPTEIQTITREYKHL YGNKLENLEEMDKFLDTYTLPL RLNQEEVESLNRPIGTGSEIAIIN SLPTKKSPGPDGFTAIFYQRYK EELRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTLTKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYQYN RDTDQWNRTEPSEIMLHIYNHL IFDKPDKNKQWGKDSL FNKWC WENWLAICRKLKLDPLIPYTK INSRWIKDLNVRPKTIKSLEEDL GNTIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWEKFFAIYSSDK GLISRRYNELKQIYKKKTNSPIK KWTKDMNRHFSKEDIYAAKRH MKKCSSLAIREMCIQTMMRYH
14591	44959	A	14677	1	3144	
14592	44960	A	14678	1	2745	
14593	44961	A	14679	1	2742	
14594	44962	A	14680	1	3264	
14595	44963	A	14681	1	2982	
14596	44964	A	14682	1	3102	
14597	44965	A	14683	1	1443	
14598	44966	A	14684	1	3723	
14599	44967	A	14685	2	1841	
14600	44968	A	14686	572	744	DLLTTIRMPDVKKCSSLAIRE MQIKTTM*YHILTPVRMPIIKKS GNNRCWRGCGEI
14601	44969	A	14687	1	3588	
14602	44970	A	14688	1	5569	
14603	44971	A	14689	1	3992	

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14604	44972	A	14690	755	2415	QELRVSGWSPASAPANT*CPPA QPCPTRRSGGQRAPARTSRPG SRPRTASALPRPAAQKAASRSA RASRTNPYTAPKPLPSVESALQ EAAIGEHAHQQRVSCCTAAPA APPSPAWPWSAARSAAPPPRT* ASAPA*SPL/PVRLKKSPGSSNC EARGEGWKT/PALPVQLGAHGF PQPAAVPCASPGSGAGPRWRSR ARRTPRGCLQQRGTWVSPDPGR EATPSGTQWPQKTRGSLPGS*C APETPCSA*SSGTSPPRGAGGC CPGTVPALAEHGN*PQRWGS AGRVEITRAEGPQCQQAAGC SLGVGGQRGPPGLPIPVPLGC* TCRSS*MEAATGSVEKCKRMA SLMQASRWFLRVAPVSGQVK YTPGTARWAEPSSLGSDTTLV GAS/RAPADGGFGLKFLSHLV DGVLRGCGPRPGTASAPAGLR AAAA/PSVPSLVGPWRGGLGAG WLGFSLWAFSPTDLSF*PGPA LLNLSMALNS*KNFFMVAARS CGGGTRGRGGTGPSRGRRRR PATGRK*KKKKKKKKFTSPPEV PPSPGLPRDNL
14605	44973	B	14691	1	822	
14606	44974	A	14692	1	2789	MAAVRKQLPRGVLYGGGSGAL LSTAAADTSLLLGSLQERKSAS AGPGYLRSVAAWGLWLTGA SEAHSVVLACFSRKDVEASLV GLPVHPDASCARRLDAADGVA GGSPRLPQSTDGWRLTAHSLPQ STDGWRLTAHSLPPPTDGWRL TAHSLPQSTDGWRLTAHSLPPP TDGWRLTTHSLPQSTDGWRLT AHSLPQSTDGWRLTAHSLPQST DGWRLTIHSLPQSTDGWRLTA HSLPQPMDGWSCRSAQWCV
14607	44975	A	14693	176	440	
14608	44976	A	14694	114	253	

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14609	44977	A	14695	124	890	GSRAWDRPRLVAAATTTLFY GYGFVSAELKKASKRMTCHKR YKIQK\KAPEHHRKIRGEAKKR GHNKPRKDPGVPNSAPFKEAL LUREAELRKQRLEELKQQQKLD RQKELEKKRKLET*SWIFKPSN VDPMEKVEFGLCKTENKAIRSG KQNSKKLYCQELKKVIEASDV VLEVLDARDPLGCRCPQVEEA VQSGQKKLVLYLNKSDLVP KEDL\ESWLKLF*RKDLPSNGCF RASTKTQRVKGKITKVSFIS
14610	44978	A	14696	553	997	EVTACWSSQPSLTLGASSAW APTLAALIEPFSPLLHCGSPFLG WPRLEPAPSAPPWAPVPRPEPP QGPPSAPGRPIPTTQGLRSADA GRRTGTQLHRQPAKVCFS/IS*S QRDHEPTRRNEQLQTRRLKSCN THREDLQLHSRRKKL
14611	44979	A	14697	1410	2036	
14612	44980	A	14698	3	630	RYKGSRPHQTQEPSWLHLVDP APGLQVELPASPAPCARIQPL GGRWDWAPWSRGWCSSGRLG QHRSPWSGWEAQAWRAAGPK PCPAGRQLRPGKSSTAPVGRH CWGIQYTLRSHWPGC*VPHSSG PAGLAGCSGTPAGPQAPHAAP VPARA/CSLHTSLQAEGVGSSL GQPRKGLPQCRWGLKGSSNAA KVGAQAGEVQARALRTAS
14613	44981	A	14699	190	383	ASHPLRGLRSGRSLPDERHRL HSAQSHRPPKG*GVRAGAGL T/WQLHL*PQCGIHWVKPAGLL
14614	44982	A	14700	1	1095	
14615	44983	A	14701	1	777	
14616	44984	A	14702	1	933	
14617	44985	B	14703	1	996	
14618	44986	A	14704	978	1207	ASLPLRGLLCCPSLPEERRPLLH GAQSHRPPKG*GVRAGAGLA/ WQLHLRPRCGIHWVKPAGLLS LGPHQSSKSA
14619	44987	A	14705	111	558	

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14620	44988	A	14706	1	1103	MKPWALKVSVTALKVARLEFV PPDVRMCSEFLPCGVKLQTFAY SVTALKAAARLELFVSPGGLVVS LASGVKLQTFPVSVTAHKSSVD PRSEQQDLLQRAKEQTFHTVE GDRSGSPDSSGAQLASPSGSR RAAGGAACQSRALRPHSSALG WSMGLGAVEQGAVALIREARAA HEPMERVGGSGMAGCRSRALP REKAAKARRETEGSAAVSGWL SGIAQWPKIDHEGFRAVKMPQ AAWLLKAVTFIDLTTLSGDDTS SNIQRLCYKAKYPIREDLLKAL NMHDKVAAGFPAGQTHLKTRL EEIRLAVEDGATEIDVVINRSLV LTGQWEG/LYSPVVYSALPCNI* HSRLFLPSGNALLWLWCLHS
14621	44989	A	14707	2	2300	
14622	44990	A	14708	2	1058	ARSNIRMVTAFRSLPAGSSGAA RA\MSAHNRGTDLWSISKIQ VNHPAVL\RRAEQIQAARTVVK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGITTAAVCVYP ARVCD\AVKGTSPAG/CVNIPV GISRAAGFPAGQTHLKTRLEE IRLAVEDGSLQKIDV\VINRSLG A*QAQWEALYDEIRQFRKAC GEA\HLKTILA\TGELGTLTNVY KASMIAMMAGSDFIKTSTGKE TVNATFPVAIVMLRAIRDFFWK TGNKIGFIPAGGIRSAKDSLAW LSLVKEELGDEW/LKPELFRIGA STLLSDIERQIYHHVTGRYAAY HDLPMs
14623	44991	A	14709	576	998	VLQFLKAACPEFVPSGVPMCE YLPsGGFVSLASGVKLQTFPV SVTALNALRLELFVPPGGLMVS LASG/GSCRSSR*VLQLIKAVWT QRPLGGRWDWAPWSRGRRSFG EARAAQKPMEGVGGSGMAGC RSRSPAPREGS
14624	44992	A	14710	2	589	RHHPRHVAQARFPFAPGLAGA QRGSGAE*RGPGGS/PGPAGLS GGESL/PGETDRGADKEERGRQ RWQRALGRLSAGADPLPAELR GRRQRGR*AGQRAAQEAACE APIQSGSARNGRRG*GRRL*GC YQ*V*FPGLTRGWGRGSRPSAV HCGWEPP*AGKPSGQTPRHSG* PAGVVDGLPPKVTGPPPGTPQPR

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14625	44993	A	14711	1	1596	MRLTRCQAALAAAITLNLVLF YVSWLQHQPNRSRARGPRRAS AAGPRVSLPPHPLTCVWRCSR AMDRPPAASRPETTVATEFVAL VLDGARAEAHALLERMVEALR AVSARLVAAVPVATANPARCLA LNVSLREWTRYGAAPAPRC DALDGDVAVLLRARDLNL PLARPVGTSFLQTLRGWAV QLDLTLFAAARQPPLATAHAR WKAEREGRARRSALLRALGIRI VSWEGGRLEWFAACNKKNQRC
14626	44994	A	14712	225	980	VPSRTWAEYRTRFVPHSLGQPR SSHIPQSPQTDQTAQQQALAP PAGRSGQ*GRPGRRLGPGER HS*APPPLSQLLQTFPHLQALP SAHARPSGQPHADRHSRSPSG /DLSTSSVLKVVVPQAGGPKQA RCPQAGRVCHCPRGGRRGPE/Q Q/GG*RPEAPQASPEKGSTGLRP SAKDSKNQGTGIFLRQCVAPRP EALCCPPPRGADTPVSPCLWVA GAGIPLQPPEGAEGAVLGSCLT LCPGSPDSPPTS
14627	44995	B	14713	405	893	
14628	44996	A	14714	178	499	
14629	44997	A	14715	231	436	
14630	44998	A	14716	141	393	
14631	44999	C	14717	97	351	
14632	45000	A	14718	119	358	
14633	45001	A	14719	21	614	PPCTSLRPLHAFSGKMTLNRG TLSLDLSQLHNLIALQMTCFKD VEIPNFFWEPSTPSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGGGYLSSDVSSSP RKAASVASVMYTVITSMNLNFIY SLRNRDIKGVL RQPHGSTVQFQ YLLICSIPIFVVVWKKGSKVK
14634	45002	B	14720	162	1263	

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14635	45003	A	14721	696	1791	VWIALKSENITCELLLFKMQTQ CQVLVYLFPFQPSFLGKRCPIS TDPQNLTDVSIFLLLEVSGDPEL QPSPCWA VPCCAWVTVLGNL LIILAISPDSHLHTPMYFFLSNLS LA/DIGFTSTTVPK/MIVDI/QSHS RVISYAGCLTQMSLFAIFGME EDMLLSVMAYDWFVAICHPL YHSAIMNLCVGFVLVLSFFFFA LSLSDSQLHNLIALQMTCKDV EIPNFFWEPSQLSHLACCDFTN NIIMYFPTAIFGLPISGTLFSYY KIVSSILRVSSGGKYKAFSTCG SHLSVVC*FYGRGVGGYLSDD VSSSPRKGAVASVMYTVVTPM LNPFYISLRNRDIKSVLRPTEH CLISKK
14636	45004	A	14722	1	1971	MTRKVTLLLRRTWRGGCGRLA MGMEATPQGS LHPLFQEHWIR AEDFGLSPMHPNSVQGVDDM IRLGDLEAGMVHNLIRYQQ HKIYVSLSPVSTGEPLTGANLL DREKMMHHRGHCPIALTEGVS GPDNPEGRARAKAKAKARAE PLPGAEGTDHLLPSQTYTGILV AVNPFQVLPPLYTLEQVQLYYSR HMGELPPHVFAIANNCYFSMK RNKRQDQCCIHSPQNRVGAQTDT VLKVFQHLLISLICKTTLQACCI PSHPYLSAPGPPPLTTQCRSYS DSLGPQLFGDVVCYNCSHVIEG DGEALCSLPHTCSGAWVLQL VSPLNKA WCVSCFSCSTCNSKL TLKNKFVEFDMKPVCKRCYEK FPLELKKRLKKLSELTSRKAQP KATDLNSAEGPLAQLGAVGA/V TGITHEPHIPQVENGSQLDDV PALGVENWRIFMAERMEAQ GQRLLLSTMHEEYEFVSPSSVAI AELVALFLEGLKERSIFAMALQ DRKATEGGPVGLTKKQGLLAS ENWTLGQNDRTGKTGLVPWH CLYTIHTVTKHSDSCCTA VPTL LEASSGCIFMSYKKHITLTPKSA DSNKRPS TLGSQFKQSLDQLMK ILTNCQPYFIRCIPNEYKKPLG FSDSFMLIKLIRIDK VQYDSFSYI

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14637	45005	A	14723	1	1197	MNMNKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTVAEYNGYH V VFALAGSRKTLMTHQSTCPKH RASRVGPSNLSQNKQTVKKGD QTSVRRKRNDLKVEERHKNNH LARELTSSAAAAAPTGHAAATA QAPQRHVEVGRAAAPAGDLGE GIVGEQVLGAERLVGPDSRAR ALCVLGDREAGHTAEMTAAP PAQVPGPGGPTALRRPSSYLGL GVDEQNPMSSVDGEDDVRVQ HQELRDCLIKHTILIRGEFVTRS LNIAQAADRRDAFVKGIYGALF LWIVKKINAIFTPPAQDPKNV RRAI/GLLDIFGFENFENRIIRT LCWRYREARC
14638	45006	C	14724	1	1032	
14639	45007	A	14725	1	4960	MSTTSIFQQLNLLSHSHKQKQ QIQLPNGRSRYSLMAAFRMQ YFLSLPMKSLILVGFERLQAIAR SQPLARQYQAMRQRTVQLQAL CRGYLVRQQVQAKRRRAVVVIQ AHGQGMARRNFQQRKANAP LVIPAEGQKSQGALPAKKRRSI YDVTVDTEMVEKVFGFLPAMI GGQEGQASPHFEDLESKTQKLL EVDLDTVPMAEPEEDVDGLA EYTFPKFAVTVFQKSASHTHIR RPLRYPLLYHEDDTCCLAA
14640	45008	A	14726	86	370	RTWMTHVWRRRRVQAAPTAY SSFRPGTSPCPAQPRAGARA*TR SGTSIMPTGFSSHTSCLTVPAFFT ASSAGQHRQRHRKTTAAGHPT TTGAASF
14641	45009	A	14727	3	455	MQSVLPAAHGVSSSTRASSVTL SSPSTSTNCRGRKSSRVTLSPVG SGPGGGGGGPGSGRFGIDPPRK FAAAGSFSTGAPSSVMVVRVSG MPSLSW*QYP*SCSTLGCRRSS STISLSSLWA/VQPIAAPYPPELA TQLPISCR*SPSPCAPS

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14642	45010	A	14728	338	1782	NQLSK*KAHSIRT* TALQSSGR SQICIVQSSADALPSSRCTNPSSST FTPTPLPPRPHRTCTSLGCRSR SSSTISLSSLWAASR*QPLRTPN SRTQLPRSWPLKSTALSPPPPGQ ATRLCWWMVSSK*RTWMTHV WRRRRVQAAPTAYSSFRPGTSP CPAQPRAGARA*TRSGTSIMPT GFSSHTSCLTVPRLHCVCWTA SSTPQESSPGGWTRPWPSWRRRC CTCTGAGRYLQNSTAS/T/VPVS TSVSQTAPSPKEDYRCWPSYHH GSLPPFSVQPG*GCGMSVRAMP SVGPLWSPTPPGQIKRQNYLL NYWSCWKMTLLAGIIPSS/TS RPADLDYFLGSSQCPRDERTLK GHVSCDPTSSISITGEKLKQKLE S/SSTLADTKSAFLQDSWT/SSLP TLGASAIURTSAS*TDQCPPAP GPLHVSE/SLNSTYPSRLCSSTCS TVDSFQIIMPN*MPFSTCGAFC WCLWFSAITALYFVM
14643	45011	A	14729	148	1040	WCTGSGFSKGTWEILLRKKPSL GNVGALPCVATACLTTVEKRA PRGHPLAPVLGDIKPCVGSMS STSEL/CTWGNFEFWGRNKYNH WF*WGWALLHQFKMGKGAQG LQEASFYRKDTY*A/TMP*NPIG ISEFGTLALPGCKNVFERFMS RFELPGKAAAMTDNTNVNYVR YKGDYYLCTETNFMNKVDIET LEKTEKMWKPRFRGICPOLQG CSVTEQGFESDDAKSWALQH PKRPAQQDWAMSRGNQGWAN LGLKIIRGEAVTTAKEVSVVL KVLEVTDGKVVAREKKLRDSR
14644	45012	A	14730	189	507	AAGADTSQGGGGPPPSQSR PKSPSAGRKGSQLSPOQPKKGL PSPQGRKSPASSKATPQASEPV TTQLLGQPPQTQEEGSKAQGM PPQRLGASTQQQTNQEAA
14645	45013	A	14731	2	356	DGVSLSCHPGWSAVALRSQLTAT SASWAVCWQCGCETGILLPCW WECEKVQPLWKQYGRSLCEDH LNS*VQVILTTQPILPKWLHL FTFPPTGQKDSSTFTLPTHCPG GRGCELSRHRCTPAWVTE

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14646	45014	A	14732	1	408	FFFFFYTTFFLFFYFYFFEMESH SVTQAGVQWYNLSSLPQPPPRF RRFCLSLSPSS*DYRCPPHPAN FLCF**RQGFLLAKMVSIS*PH DPPTSASQSAGHVLTSKWELNI EYTWVIKMGTDATGEHKNKEG WE
14647	45015	C	14733	262	536	
14648	45016	A	14734	179	745	TDCLHNRCHRSPRSPPPGPPG*R SRADWRRGRGWGSWCASSR RVC*RCAPASAFSCCRSPRGRQ GRTFPPSPCAPD*TQ/PVSPGDS TRPCPPSPSPAHRAT/GCCGRR RLPGNASYLASPGKEAGEFPAS QGDS*PGQYGYIGDSSS/RPTRG TWMKASTPRHPIAPQICGA*G FGEHQEVVPREK
14649	45017	B	14735	1	1164	
14650	45018	A	14736	35	542	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGA PLDVTFTFY/KDYDGKLNMLSE KYKLDKESYPVFYLFDRDGFEN PVPYTGAVKVGAIQRLWKQGG VYLGMPGCLPVYDALPGEFIR ASGVEARQALLKQGQDN
14651	45019	A	14737	11	908	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGA LPLDVTFTFYKVIPKSKFVLVKF DTQYPYGEKQDEFKRLAENSA SSDDLLVAEVGISDYGDKLNLM NELSEKYKLDKESYPVFYLF EGDF/EEPSHYTGGS*RLGAIQ RWLKGKGVYLDGDLVCT V*LTPWSGFIRA/SGVKARQAL LKQGQDNLSSVKETQKKWAEQ YKIMGKILDQGEDFPAEMTR IARLIEKNKMSDGKKEELQKSL NILTAFQKKGA/EKEEL
14652	45020	A	14738	3	227	
14653	45021	A	14739	1	424	
14654	45022	A	14740	1	207	
14655	45023	A	14741	2	352	
14656	45024	A	14742	1	441	

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14657	45025	A	14743	1	461	MTVDYRKFNQVVTPTMAA/AVP DAVSLLLEQINTFPGTWYAAIDL ANAFSPVPVHEAHQKQFAFLPQ GYINFPALCHNLIRRELDFFLL QDITLVHYIDDILLIGSSEQEVV NTDLLLHKRSKEAEHTAASRIR VSCLPEQKSHEQTLTPWEQVP
14658	45026	A	14744	1	928	
14659	45027	A	14745	283	1074	
14660	45028	A	14746	450	1970	VRVLSVPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLAMGVI GSHGARGQVVALNRQRQGD QPFTRTVHVWGKGYDRFTWGL LDTGSELTLPDGPKHHCPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHTGSLTGIMVGKAKWKQ LELPLPRKIVNQKPYCIPGGTVE ISATIKDLKDAGVVIITSLFNS PIWPVQKTDGSRMTVGYRRL NQVVTPTTAAAPDV/VVSLLE QINTSPGTWYAAIDLANAFSIP VHKPHQKQFAFSWQQQYAF VLPQGYINNPALCHNLIRNLD HFPLLQDITLVHYLNDIVLIGSA IKWVMHSS/DSIIKWKWHVHDR AQADPEGTS*PGYGHFWCPIC QQQRPTLSSQYDTIPWAISQLPG DRLIIGPLPLWKGGKFVFTGIDT YSGYGFAYPACNASAKTTIMES QNTLSTLMVFHTALPLTKALTS WLKKCSSGLMLMEFTGLTMFSI

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14661	45029	A	14747	1	2589	MGPPYKPPTTWPPQTLTSHSTT PVKLQSLSLPPTAARGATEPCH LQAPASSVQOMTPPAPGLKHL GGKSQMCLEQDGRSGSVRGSP CHAGHWVAGAGFGKGTTTRTW GHVNLIVPPNCPATSSAARDS APNQPLLGVVTAQIVPPTCPA MTVQELIAPLTLPPAAGCRRGV RPFQTRVWLLAQLLRLRGGP GEGVVTCHSWRLERVAPRLAS LWWALAAETAARLDWAACKRP SAWGSIKAAEFSSKATPRLEGA SSRTLWVSYIAKETTTGKNGP VEPSHLWEAYCRATAPHPA VH SPSAEVTYTCGIVNLLQLGLVP KSHLEHTGCHVVVELIICSVV LPLISRLSDPDWIHLVLMVIFSK ARDPTPCASGPEQPSVPTSLPL IAEVQQLPEGRAPSPVAAPGFLS KQIQDALCALEGSQALEPKGGE GSEGVAEAGPGTETETVLPVST LNFCEPIQIDIAKEIEQGEVTT VTALLLEGLEKTCSSRPSCLEKD LTNDVTYLDPTIFSEPLSSPDG PVVIQNLHITGTITAQELSGTGL QPCTRYTVKCETSLDGENSSLQ QLAYHTVNHRVWEFLNLQ/SH QEKKPDL*KFIKNIEKMVVSAL VDNLKTAFCSESQGPTEELSE AETESKSQTEGKKARKSRLRFS SSKISPALSVTEAQDTILYCLQE GNVESKTLSSMGMESFIEKQTK
14662	45030	A	14748	478	3507	SKILRAVIWGSHLVRSAMKTET VPFQETPAGSSCHLNNLLSSR KLMAVGVLLGWLLVIHLLVNV WLLCLLSALLVVLGGWLGSSL AGVASGRLLHLERFIPLATCPPP EAERQLEREINRTIQMIJDFVL SWYRSVSQEPAFEEEMEAAMK GLVQELRRRRMSVMDSHAVAQS VLTLCGCHLQSYIAKEATAAGK NGPVPSHLWEAYCRATAPHP AVHSPSAEVTYTRGVVNLQ GLVPKPHLETRTGRHV
14663	45031	A	14749	1	417	
14664	45032	A	14750	34	350	RERGQEGGVAGRVEMDVSVVE RGAYADQIWGRPKGGESRGEK RKGRWVQRVRLARVTPAGL GECKWGRGRGD*VRRVKPRAL REKWDGSTVSDSTPMKPGLE

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14665	45033	A	14751	1	1604	MASKRCIRDFRSRGGKLSFQL YATFRKEGCGPVLANGNPGGG RGQEVSA TQDLRRGWGIASSAS RFPWRQSWPGRPRLGNYDSGA PGEAKMPKSGKDKKKGKSKGK DTKKLIKTDSEVVDRAKANASL WEARLEVTELSRIKYRDTSRIL AKSNEDLKKKQCKMEKDIMS LSYLKKQDQEKDNMIEKIKQQ LNETKEKAQEEKDKLEQKYTR QINELEGGFHQKAKEIGMIHTE LKAVRQFQKRKIQVERELDDEI NDLLVKEKIMQLVQQRSQIQT QKKVVNLETALSYMTKEFESE VLKLQQHAMIENQAGQVEIDK LQHLLQMKDREMNRVKKLAK NILDERTEVERFFLDALHQQVKQ QILSRKHYKQIAQA AFNLKMR EHVQEEQNIPKSEHLMAESTAP V*IRIFWRPKNGHILKEMWILEI *PGSRKKYCDCLQK*MAVLL GNTTQSSRPSSSRMTLFLDSGET KEFGDESKLDKIFITQQAISD VFW*SGATHYSKRTSGV*HSGK SESLQPRGQRLI
14666	45034	A	14752	95	473	
14667	45035	A	14753	168	449	

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14668	45036	A	14754	1	2000	MAFEQAKQVVKLALDLWPGD GPVELQVTVLDQHANWSLRQE QHKGKRGPLQFTDVAIEFSLLEW HCLDTAQRNLYRNVMLENYRH LVFLGIVLSKPELITCLEQGKKP LTVKRHEMIKPPGQKNWEKQ ALPLTGCLTKYPSWAKNIDHVT CSHFARDLWPEQSIKDSFQKVT LRRYENYGHDLQFKKGCEV DECKVHKRGYNGLNQYLTTTQ SKIFQCDKYVKVIHKFNSNRH KIRHTGKKPFKCECGKAFNQS STLTHKKIHTGEKPFKCECG KAFNWSSHLTTHKRIHTGEKRY KCEDCGKAFSRFSYLAHKIIHS GEKPYKCEECGKAFKRSSLTT HKIHTGEKPYKCEECGKAFKR SSILTAHKIIHSGEKPYKCEECG KAFKHPSVLTHKRIHTGEKPY KCEECGRAFKYFSSLTTHKIIHS GEKPYKCEECGKAFNWSSHLT THKRIHTGEKPYKCEECG/KGF KYSSSLTTHKIIHTGQQPFKCEE CGKAFKCFSLTTHKRIHTGEKP YKCEECGKAFNWSSSLTAHKRI HTGEKPYKCERCCKAFKRSFIL TRHKRIHTGEKPYKCEECGKGF KCPSTLTTHKTLIEIHAGKKPNK *E/ECSKAFKDTALTRHKIIRTG EKPCEFDECRKAFNQLSTFTKY
14669	45037	B	14755	269	1131	
14670	45038	A	14756	2	149	ALFRAGRQECLSLKLCPPQPL SPTCFVPGR*GFYLHFFQRCAA QRGGI
14671	45039	A	14757	2	175	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14672	45040	A	14758	1523	2667	PLLVIHRQTGSGEDIQQTPADL QQRDLERKLTNRNE*HQHQQ KRHPLKNPTQMSP/CIKDQRYIN PRSTIKLELGIKKLTENCCTTTWK LNNLLNDCWEKQERSKTDLT TSQLKELEKPEKTSKASRRQEI TKIRAEKKEIGTRKTLQKINKCG SWFFEKINKIDRSARLKKKKRE KNQIDTIKNDEADITTDPMIEQT TNREYKHYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TSSEIEAVINSLPT/KKRSFGSDR FTAEFYQRYKEELVPFLLKLFQ TIEKEGLLPNSFYEDSIIILPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHNNQIDFIP GMQGWFNHKSINVIRHLNR
14673	45041	A	14759	640	1771	APVARMATA/PLFYTALLVFSAL GNILALCLTCQ/KRRKINCTGIY LVHLAVSDLLFTVALPGRVVC YVLGSSWPFGKGLCRLTAFLV YTDYGGVYLMACVSVVDHYPT VVCAHWGPCLRTAGRARLVC VAIWTLVLLQTMPLLLMPMTK PLVGKLACMEYSSMESVLGLPL MVLVAFAIGFCGPVGIILSCYM KITWKLCASTAGRTQ*PAGKDTT GGASPGGSPSDQPEKTPPAGAAQ EDPVTPTRETPPAGQPERTQ*PA GKDATGGTAREDPVTSRKGRH WRGCLLTLLMLVAVVVCFSFY HLNIKQFMARGMLHLPSCAER RAFLSLQATVALMNMNCGI/D PIHYFFASTHYRKWLLGILKLKG SSSSSSSSSTLY
14674	45042	A	14760	1	401	MVLVQWLTAITSAFWETQNK SLQFEDK WDFMRPIVLKLLRQE SVTKQQWFDLFLSGATLQDSSG PLLTGKLKKKRRKVSGETKY/IEAS SATSLKATTDTHLLLYNPFWI PLTLI*HLCWLQRFA*SCDTPDP P
14675	45043	A	14761	184	2720	
14676	45044	A	14762	34	251	
14677	45045	A	14763	2	452	LQIEII*ALEELAAKEKANEDAV PVCLAADFSPAGMGSSCDGQE DELDIKSRAAYNVTLL/NFMDP PKIPHLKEKPYFGMRKMAVRW HHAENLVDRPQEESEDDSHLE GRDLDTWHVGVKISWDVKTTPG LATPQGDYCFMLGNLWRTKIL

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14678	45046	A	14764	1	1701	MPFKCKKQHTFNKTSPEGAII FTHGCLCTSPFNSELSHGLNL KLSSWEHLHRRSQQTLSVRLH VPTQPQVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPLWQL KYPKLILREASSVSEELHKEVQ EAFLLTHKHGCLFRDLVRIQGG DLLTPVSRILIGNPGCTYKYLNT QLFTGPFVPKGSNIKHTA*IA AVCETFLKLNLDYLIQETIQAEE LAAKEKANEDAVPLCMSADFP RVGMGSSYNGQDEVDIKSRAA YNVTLNLFMDPQKMPYLKEEP YFGMGKMAVSWHHDENLVD RIQLQLWDPVDGTTASSAVPKQ GRDKRREVPNTLSQPNSEQGLI SAFHSRCVHAVFYKLTSAPKTT SLPDVPSDLLAEGLAASRAGQA LWRCDDKSLTLVRKJNLQKG RDGGRSATNQSQPHLDNTGL ERQLEQKVGRCRSPWRGLGHL EGNAQKGHLLHGVNKNQGHLL LRRHGV SIRAGRAPHLAAADT APGRISCLGHSEALKPRIQAGGL GAESIWWQLWEGGSNSSVFCCR HDEEPAALPLPGKQASGGHMH
14679	45047	B	14765	16	1462	
14680	45048	A	14766	89	566	MEQGSIIQAWREDALVLTQK GLVSKISSPKRPHVCHILK\APFC CSCTQHVGQSSSPR*ANPHIRRE STPIAMSDQLQRLQYQFYQIPG TCLLPEVTEKNQGRICMVTDL ETLVHSSFKPISNADCLVPVELE GTMHQIHVLMRPMYMEFLT*M EEMF
14681	45049	A	14767	1	305	LSGLEMFQAGAGAPSSPGY*GS CWAISWSGPPDKHSNRGASCG LETWAGAAATDTAGPHPAAGR C*A*AGSGGDQGTGSTAPLPAT P*PLQSLV*AAALPA

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14682	45050	A	14768	1070	2653	SLKPCMACL*HS*EKTLSDDSG RSWICAVSPGSPGPAAPLPEL SFPLRPGYTKLLPHATEEVSPFG SGAGRKLGPMLPSTAELCPGTR ARWSEGYRDLGRQAQDLQAG RKS VVTWALEGHPREEERAAA KVQQCQRMWEGCSDPQELIPR PGRNPDVPDSAVALLPWGPSR VPDLGPDSEHR/PAHSRVQYWL HKAPAPPSPPQLAEPATPPTRP SSPGSRSPSSWHRLRSWSLNAD PWRPRPADLPPGNPAPPSRGGA HGTWGGKDVRLGRGSRFSV CGRREVQRAARRV GTTGPWGR APGREERAASR*QPPGTG/PASP MGRASSSGSRVSPGPIRRAPW EGCSCRSRHHWGKGLGPPDGE PG/PGSS*VAQPTVGGRRSLGPG GAAPARDAAAATPPGDAAARE GSGRHLRAPASRPQHQRSPRS HPPASATTASLQKFRSASSEPPS EDRPFDFTPTAPPQCPRVAPSAG AR*/AGGRLPE/PR/RPGPWGG GSRTNLTIPSTLHGPTAAARTS PHRKS
14683	45051	A	14769	748	1073	SQHFGPRWVDRLRSGVRDQP GQHDKTFSLLEMQKIAGRAGG CL*SQLLRRLRQENPLNPGGGG CSELRSGLCTSVWATGRDSI*K KKKKKKKKRPWSLLSLIVLVQF
14684	45052	B	14770	59	466	
14685	45053	A	14771	2	3184	HRTGIPGSTISSPGGETVPE/MTA AMRERFDRFLHEKNCMSDLA KLEAKTGVNRSFIAL/GVIGLVA LVLVVGYGASLPLQLLGFY PAIYISIKAI/SPNKEDDTQW/ V*TYWVYGVFSIAE/FFSDIF LSW/FPF*LHG*KCGFLVGWGN GPEAPSKWGLKLL*QAASSGPF LSLEATKSQIGQVLVKDALKDQ GPKETADAIH*KPKKSLP*ILL G*KKKK
14686	45054	A	14772	14	455	PQFPCRRFRALSEEELDNEDYY SLLNVRREASSEELKAAYRRLC MLYHPDKHRVPELKSQAERLF NLVHQAYEIVVERRTPAEIRE EFERLQREEREERLQQRTPNPKG TISVGVDATDLFDREYDEEDV SGSSFPQIEINKMHISQ
14687	45055	A	14773	328	479	

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14688	45056	A	14774	15	1095	KVAKMATALEEELDNEDYYSLNVRREASSEELKAA YRRLCMLYHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKRGLEMEGW EVVERRRTPA\ EIREEFERLLREREERRLQQRTPKGTISVGVDATDLFDYDEEYEDVSGSSFPQIEINKMHISQSIEA PLTATDTAILSGSLSTQNGNGGGSINFALRRVTSAGWGELEFGAGDLQGPLFGLKLFRLNLTPRCFVTTNCALQFSSRGIRPGLTTVLARNLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPESFRPFLHVPTWDAECSGARTPSTAWTSAVKLREACLSGPGSGSHQLLLTPRSKRRTGGG
14689	45057	B	14775	508	1765	
14690	45058	A	14776	2	639	GRRRHRRRRHDCSRGDCYLPTGTNTQQPLPPPREPLPELPARTPLDSMQNSEGGADSPASVALRPSAAAPPVPASPORVLVQAASSNPKGAQMQPISLPRVQQVPQQVQPVQHVYPAQVQYVEGGDAVYTNGAIRTAYTYNPEPQMYAPSS TASYFEAPGGAQVTVAAS/SPF AVPFHSMVGITMDVGGSPIVFSAGAYLIHGGMDRPELLANL

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14691	45059	A	14777	1	2091	MKPPDNDSTQNEGGQSFEEHRE TLQRVKFRGGPKTAPGRKLIAT LGQMNSGTSGGQVRVPGEEELM AGGATCLPNTAEHQPIRMKNL HTPAFRLCPLTLQDNEADAFW HQAIFVDWGMPTGKKPQTLGLT YKTHDLSMQNS/EGGADSPAS VALRPSAA/APPVPASPQMLPLE LVILGVV/PLDKCIPAQWSKEG QTNSTYTNPEPQMYAPSS/AS YFEAPGGAQ/MVGITMDV/GGS PIVSSAGAYLIHGG/MDSTRHSL AHTSRSSPARSFRNSKAPSSRK FCC*LPTLSSKTL/SLFSKNLLRK LPLGKIISPDSVQWPWYIGLLV AGSESLASLLFPKASSSETLGF ATGQLAGESRLPSLLAFILVPID VAVGKEQLVTQTTVYRVQGS GQHLNKAWEPAALVNICGMGE KVDVQVGLCQHRAHLDGWNS SRAASVWPGETLTHHQDQCQA NLPGIETISILGTGARYYSPQE QGGGRVWLERLDPRG/AVSGT DL*CLPQSDVPPGRA*SGGTGD KSISTHDKSGRGNISKYHY/YGIR LKPDSPLNRLQED/TQYMAMR QQPMHQKPRWCRAELGGAGSP L/GMEDVSHVPEFPAPD/LGSF LLQDGVTLHDVKAL/QLVYRR HC/EDVV/MNLQFHYIEKLWLS FWN/SKASSSDGPTSLPASDED EGA/VL/KDKLISLCQCDPILRW
14692	45060	A	14778	94	3006	RTRSLTRKAMAEHAPRRCCGL WDFSTQVKKVAVDAELNVFY EESVHFDRDLPEFGHVLVDVHG VHVHKDGLTVTSPVLMWVQA LDHLEKMKASGFESQVLALSG AGQQHGSYWKAGAAQALTS SPDLRLHQLQDCFSISDCPVW MDSSTTAQCRQLEAAVGAQA LSCLTGSRAYEFNLVCDRKHLK DTTQSVFMAGLLVGLTLMFGPL CDRIGRKATILAQLLLTLIGLA TAFVPSFELYMALRFA/GL

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14693	45061	A	14779	1	710	MGPAAGAPTSRASRGPRAPALR AAVGRRCPRPEMPCQCHPLAR CGLDPAWTQLPQETAGAPRQD PRCTNQLICEHLPLEGLGFVYL GNKDSLRLHVKVVAVDALNVF YEESVHFDRDLPEFGGLASSAV TQSSS/DDLQQVP*SLQSLHAA* SLQTNASPFTFEHSFLGKRHPK GAGQKRAESPTRPPLRLQEAAAP GELQRPLPYGTQVPAGLCPSVS GLRLRARALLPYRTHSLSV
14694	45062	B	14780	1	252	
14695	45063	A	14781	73	198	
14696	45064	A	14782	762	1080	AGRAEMQQRRESHEEAKDPSP LSPREGSQKQQQNVNTSTPSHC PR/PPLRMPPPAPRRPV/CDHPR AECECKAQHWQAAPAAPVR DPLGEASWAPESGGDVESLYI
14697	45065	A	14783	1	309	MTKTEREQNEQLDGGGYGERL GEYSLFLLCVPELNLQNGKCEV SSYFGMNLGGVLLKLPFPPTRE SWPPPHFTGTPHNHHGGVNSG ALGCAQRCSLHHATNAGGWER GGVNSNRLFFLLSASFSDAKIK PAPSPIDHLRAEEC*/PPPLSQPP ALVAVCREHLWAHPKAPLLTP
14698	45066	B	14784	1	471	
14699	45067	B	14785	1	1143	
14700	45068	A	14786	1992	2205	WRSMGLRKRQLASQISYCP WS/CP*EESHCRRVSPAPLA*LL SPCPAPQQRSHDTPPPFFKHFP LPFSG
14701	45069	B	14787	389	973	
14702	45070	A	14788	287	525	TNPFNLLQH*KKP*CYTYISITD PTDACHKNKAFSSPAVSQLT/CI FSSTAGSFFVLGSHSCGHVAFS LWPRSPQLPGTR
14703	45071	A	14789	475	616	
14704	45072	A	14790	1	704	MTKWKSNPQHIMELQRTLSNP NNLEKSNVKTYYKAKIFDDNLI QLTFQQHRQDRDTEQEKKEE EREKRKQQQEPLRKKAKMQTV RPGFDLTQGPNCILTPHGKTWSR LPPKNHRRPYSRPEGPRVKA* NHGPEGRRGTRLPPAAKRAQ AEEAAQ*WPTSTRLRELVTPRA MPPSPSEDPVAVGHPAPPRGP RSDS/APLRPQLRPRLSLASE PAAAGNARGHRSVLALY

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14705	45073	A	14791	200	408	SPHLMISINLITFANFLFPCERNS QFLKS/SIFVMWMIHNGMKCRQ LDTCHCRHGTCKDSICPGLEES PLP
14706	45074	A	14792	240	771	GRGMQSPAQVDPAAKRGNIAG HTAHLWPKGGTLP LCF/YHLII MQIREQP*SSLEYPTF/RILSLVS GTKLNKILANRIRQHIKKLIHHN QVGFIPGMQGGLP TPGSEQGHL RVSPSSPSTVTLKLFNFMEPFE NLNL SKGKASVHTITQENTDSL KVQSGQFSQGHEKRTLDLKV S
14707	45075	B	14793	1	1557	
14708	45076	A	14794	150	1668	ESDARQGGPFPLENT RPHPSCMQ NHGICRSLHPGLCGCPPTARDA APATAGGVPA Y/GPLTGAPPG* LPGAGIGSKQSSTMGPSGAGSC LGL*APSQPAD/PGSIQGVLVIA DTE*PLVGGDGGLEAEHQWQ* EAGP/GGLIPKHMNPQSRQQSLF GRRGYRDSSLRSVLGRTGQQT* HAELGAGVMGPGNGR*GH/G PRGLPCLVQRRRGPVAAVAA GVSVAVPSGMLSENGPGCSK/P HSGDAGQRRGLREN L*GVRALI WGAASSFLLTEQDLQELADCL HSGRKTCCFFYFQGRGDVAPGPV APAHHRLAGISTVVP EGPGLCV GEDRQLPG/GNQRAEPPP*LVRS VSSLTGLPALGPRQMPNAGAG NGSGK*RGVRGSGPDWDCTGT HGGAGTGKLLWAGLSLFFPLSG KSEAHQRAAGHGYGRGLGSP GRPPRSRKGRVLGSESA PA*GSP QPLRSARQPESSCPRQQQPVG RGPAGPLEAGHCSFPRPLGP AR SLHPDFPQGLQA
14709	45077	A	14795	3	374	RRPPSWG*RGCSQLPECAADGS LEDHGLPPMVSCFSRHPAGRF LRVFPPSPLLA VDCCWHNNSYV VAVDCCSATCSLLLYPSQEFPP HKFLVYLVLSWHQLLGGLELIC TQQPVNPVVS DG

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14710	45078	A	14796	73	890	MSLVRTDGKVSFPHSRAASSPP PRFAGSLPWTPKKGHGFTSFPR EGYCP/REGPSDWGRNSFRVSS WAWRPSQGVSHHTPGQGP/PSP GNRDK*VATRKSPGQPGSSPEP GWSLQSTSSPGATRTKGNLNTL KG*KQVVD*WVGVTGWEGS GAPQSPQPSREWLSRPGVGVV KETWSPSPWSGR*APPCGQPQG QQTHMERGGR*G*QVGACGLG P*GQWSSVTNGKDTAPWSPPP RQRNGRWPAPPPFTFHYYYYY YYYYYYYYFFFFGE
14711	45079	A	14797	273	678	TEESTSVLSVPNQTGAGAAIRGI VSLRLCGLYVTSPRAARMHIR PHGPWPGGSHHENGEGAPES/E GAPASASGRGAPEGQAWPPRD AVLSSLMLALFRTKSARHLVLG TRQTAASPFFFSQPSWYCSLG VDGG
14712	45080	A	14798	551	743	PTRITRSAGSSSWGSCRPRAPAP FSWSRPLCQGPGR*CRGLHSRF YAAP*VQGHVPVHILPYSKFRRG RAALRPRGQWGLDSVLGTAVC GCGP/RSESDICSGR*GPE/WYIS PPVPPHVHRGFQQLNCARQVG KGGGGPGCPMLGNHSSQVGL GLGGQDQDSLESPGRVSSPSGP SAASDPGG*GFQGNPDVHPAP APPDW

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14713	45081	A	14799	705	2299	KREWRPRHHPLGPPPRCAGRSA PLSGPASPPS*WLPFGHGPCGR MCSRAARGGDVTYRTHNTRAP SCPSLHWVGERG*DAHTRTPSC PSLHWVGERG*DAHTRTPSCPS LHWVGERG*/GCPHSLQLSFP PRSAGCCKALFEAEKSKGDTGL GKRGWAGGGAGGAARPCICNP TVPCPQSTQSPPV/PPGTR*QLG SSASHSRAASSPPRFAGSLPWT PKGHGFTSFPR/RGBVLPFPEGP SDWGRNSFR/GPAGPSMW*PAP PSDAQVGHGPRAGLQRCRGR GGHTPFVAAAAIDSAYFS*/D P*VFGSNFPHLSCFPG/GCGEGN Q*ARRRPLAGAAALPGPNLES WVCELSVAGPAVWDPVPSP/GD PTTGPEP/RNSAGACGAQGS R*T*GTPATWSL/GPPPELPGSR HQRQCECGPAHVQREMPGW ACMLKSVAQRGFQRR*QLSKA QAAA*WRV/PGGR/GAGKD*GW RRWGVSRGGGGLCCARGGGGS SVRRGEVEGS/GCARGGGGCAG WRALSPSSLPSGAQELGS
14714	45082	A	14800	1	267	CSAGGPWRAPQPRRFHRRRP AQLPPLPLPPLPASPRIHNRFT PRPSQRTPPPAALGCPPEGS/RS QGRGHARPPGSGEGDPTVSSPG
14715	45083	A	14801	218	430	
14716	45084	A	14802	9	201	
14717	45085	A	14803	1453	1936	EVEKHLCCQ*ELLRAQH*AA ACRRPRPAPGPQCSAGGPMAR APAPQVPPPPPPCSA/PPPLPLP LPAS/HAHPQPHFRHGRSALLP RPPWAVRSRGALAGPRTRAA GLRGGAGAAPAPADARFPASSP AE*PKFPQNSARALTGFPRCTD PTVSSPGY
14718	45086	A	14804	1	580	TSGCSHSLHKPAGVSTRPTVA SICAPRPTSPLRRGLTLWPF GGHLTLLET*/GFDSCPEEVEGP RFSTFKTS*ARGRRQRCA RREVGPSSAAESGRARGEP RLLCRGK/DQPRAGEGAAAA GTPEGSRAAGSSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR CWVGEPPGRRTRLFPDE

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14719	45087	A	14805	279	1148	ALHEFAMSRSLHASLH*S**STC P*QQPAPAPAGEPRARFPKGSSS ASSGPG/WPRNHGKQLHLPAPQ Q/QQGRISPRVAGSGCTGRA LLLAAGLQNSTRSLNPRDPPTIL SHRPLQGM/PDAP/RGCSHSLHK P/SRS/TPLSGQL*PPSAPHAPQ APSVAGPLPCGLSPGDT*RYWR LLRFDSCPEEVEGPRSTFKTS* ARGGWQRQSRVWASARGASTL QASVQGR*NQPRAGEGEEAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR FLGGCLL
14720	45088	A	14806	765	4270	SQDTPGDLQCHGDDL*DGAVLS EAPGGERVPRDD*GGVCEGVP HVSLRLDSVAEALQPRGEAGG DQVPEAHARPPSAQR*PAGAGL RLHPPAAGGVPGQSGGHLPKIQ DDLTSKS*TNSTKTLFPNKVTL SDSGRA*ILEGHRSTQGSLGLEA DPGTVSHHQPCPPNAAATHFF HRTARPGVQQGPGPASVQQPES DGDGALLRSPCSLLPQGADEV LQPDGDKQGGPRGDSSESD*G YSERR*AQDEYQGH
14721	45089	B	14807	133	2943	
14722	45090	A	14808	1	814	MEEELLRELLYSENWWSIPYND TIQELCCWAVLKRTFINGNTSR KPGMKMVTGLKKQERRSKQW GCEKEAKFVPMWVILEVGR EERGIDGKRWGKSCSVESQSVW AFQNPWSKAQTLNLSMK/AYE KGKEGVEEKFEARRSWFMRKK AISHLHNMEMQGEAASADVEA AVSYPEDLAKIHDESDYTKQWIS NVDKTVFYWKMPSTRFIATE EKSMPGFKASKDSLTPLLGTNA AGGF*LKPLTTYHSQTSRALKN YAKLTLLMLYKWNK
14723	45091	A	14809	123	515	PKQSAKTIWTSARPEDVVTCS FKEEFLPGNTHHDFSINKRSDPE LEVSRPLARPENFPANRSHSLL L/RPCRGRWAHWTGCSLLD ASSAPRTDQPSLWRNLPASLG GPWSHNQPGIVFQNTYLMKP

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14724	45092	A	14810	279	1136	VDDVLCACVRGLLSCDEFLSW LALNRTVLATPALPSCLSQMAS SLPGLCARTRRGERADSQRGTC AFFSPARTASQAPLVASSVRKQ RVWAPNPLNCHTLPPSRGSQRG GYIGEEGVFGSRVVGIVVPGPN GSPWPLGVQR/PECVLLGVGSG S/SSHELFEADFISRLLAAPSPSP APAS/MGNAIEFEAPELGPLGRV FVDDFHYDYNFIHLHEDLCYGP LEGPDLDLAGTGDRTPPLHSRP RASLSPSALRCP*ALGF/WTLA WGSPNSSSRVPEAQPPAPSLAE
14725	45093	A	14811	1	1597	GGRKAAVGVETRPQGSQAQPTW LPVHGDTCITLLPCRAWWRL GGLPWAASVVGAKCVWTPPER GLLMLHKPMFGWSSGYRVVLP AVAFFRLRAQVTKLGEVSLRF LKREAKLCGFLQKSFLEAKR MKASESSRLKLEGSRLGELES WEKLRGLMEERLALQGQHEE SHLLEQCQGLDAAVAQLTKFV QQNQASLNRVLLAEKAWDA KGRLEESRAGELAAVQENLE AAQLAGELARQEMHGELVLLR
14726	45094	A	14812	150	1625	CLGKAFSCRELNAYLRLPTFFIV FSLRQPSLRMHSAWVVKTCGA MPCSCCRRHCSSVTDMAVRSL ALLQLVNRTPLRRRQISAACQR MSTFLFFRACTF*PRNRSSGRH /DLTARPRQAILRQNFK/RAQS RNLTA PNSPR**LLVKTYRQTS RPVSAAH*CPR*RGRAALAAAC HSGSPGARQTAGPAEGPAR*T RRDFL**RAACLRRRWKWP*L *RSRSSP*SQGSCPPALPAPRR CSAGSRTGPAARWCRAGAGSR RHAGSSA***SRR*GRSASGRR PRHGGTAGSGRWLWWARCPA *AGIPWSPWCHSSWP/PQSVRV VSSG*RASLHSPGLDSSGGGLQ SFLLVQLPAQKKTSSQP/RHAA APSAACPHAE*CTLGSCPRSA TLSPTPPRASPPAG/RSVSPCPP GHEGVLVISKHLLLSRSRGRG LGGNVVRPCSVQPMDGVGQEL AVADRDQLPCLVCQDGECPLK ASGRPVLGCP

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14727	45095	A	14813	921	1446	ACCISHGNLWHHLDDQKHGLQS *GEKSRLFSRPNLQVPVHTGLD HRARYLTGPRKQGHLLWPTGPS SVFDNENFCKLSVGM*TRGRASA RQQIQSPFAESGKAFFDICSVSL RLCVLPHPWNSRLRSPALRNSL KYSVTSSAAARRKLLPLASGPL RLGPRSLPTRLQVLRWEKVASA
14728	45096	A	14814	1	675	
14729	45097	A	14815	1	2341	MASDLVNRCEACDLPGQPISVH QFPRLSNEVTTTVGRNSESPNQ RSVSGPWTPEVRRGVAAAH GFSGQNAKWAAHIPATAMSF LPYSLVHSPHALTTPLNPGDA VTMPSTSTVSAANASKGRSFS QCFQSTEEGQERRRPRTSQAKV QQGSTAGKYNELITLAGHIKSQ APHGKRKPPRDSHVICSMLRK RKPDETPSPSDDAQFSGMLAVA VSSLLCPRSSPSQWCHCSPSTT ILGSSDVSDTSFQPSTKLGPVHG FPPQSRDCILDFELIRKVTGAWS SLTAGSWETKIQEFSEEDILAPH RITPGPHSSKSPVHFLASLWGR KTKLYHHTIQDKEPRSVPEAGS SGRRDGGGAHSMCLMAPEPD HPGSPNCRSPATLHADADGN LQREAAKCGDGTQVSTHVDH TSAPRQAETGPA TGENEK MESH GRSKRGLVGADQCPAETLDSY TLLVGHKKRDKDRQTPGPAPQ VNSFVPENYLLRGLAPLGSALS MKTAGAVHIRPSGDLGRAPAP AVRPRPRPRPRRLLPGPAHL GAPRPPAPAPLSRRAARQSPAA AAAPPPGCE/RRG/PAGPASGAG PPAPAHGARPGGKPAANPPRAP QP*P/RRRRSRRAQPRPGPAPL SRMRAEGPARALRPPPHYQPEL GPPSETVGPVTELLAPIPTARFP TRSHYPVVTASPARSS*TSGLD*
14730	45098	A	14816	44	455	HLNRNR/PSQ/TPHIYNHLIFDK /PLFINIWWENWLAICRKLKLD PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNITQHLG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP

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14731	45099	A	14817	1	279	IQDIGMGKDFMTKTPKAMATK AFIDKWDLIQLKSFCTLKEITIR VNRQTTENYPSPDKGLISRMLP NF*RLFPAS*KKPPLFDIGKTEK TNY
14732	45100	B	14818	1	2025	
14733	45101	B	14819	1	3570	
14734	45102	B	14820	1	1380	
14735	45103	A	14821	1391	2742	KKRESSLTHVMRPASF*YQSQA ETQKKRILDQYP**TLMQKSSI K/YLAKRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHMIIISIDAEKAFDKIQQPF MLKTLNKLLEETTVMKFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSL FNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIFTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYA AKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAI IKKSGNNRHAPFSIH THIMFGSLYLQIKDLSILGFW YPRGILEPT

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14736	45104	A	14822	1	1698	MEDEMNMKQEGKFREKRIKR NEQSLQEIWDDYVKRPNRLIGV PESDGENGTKLENTLQDIQENF PNLARQTNIQIEIQRMPPQYSS RRATPRHIIVRFTKVMKEKMS RAAREKEIQTTIREYYKHL YAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAIFYQRQSESI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTIFFTELEKTI FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDLP FLTPYTKINSRWIKDLNIRPKTIE TLEENLGITIQDIGMGKDFMSK TSKAMSTKAKIDKWDLIKLSKF CTAKETTIVNRPQTKWEKIFA TYSSDKGLISRIYNELKQIYKKK YTNNPIKKWVKDMNRHFSKEDI YAAKRHMKKCSSLAIREMQIK TTMRYHLTPV
14737	45105	B	14823	91	1596	
14738	45106	A	14824	1	2757	

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14739	45107	A	14825	1	2677	MGKKQSGKGTGNSKKQSA PPP KEHSSSPAMEQSWMENDFDEI NKIDRLRLARLIKKGKKNQIDT TKNDIGDITTPTEIQTITREYY KHLTYTNKLENLEEMDKFLDTY TLPTINQEEIESLNRTITGSEILAI INSLPTKKSPGPDGFTAIFYQRY KEELVPFLLKLFSQIEKEGILLN SFYEASIIIPKPGRDITTKENFR PISLMNIDAKIFNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIR KSINVIQHVNRNTRKDKNRMIISID AEKAFDKIQQPFMLKTLNKLGI DGYTLKIIIRAIYDKHTANIIILNG QKLEAFPLKTGTGQCPLSPLL FNIVLEVLARAIQEKEIKGIQL GKEEVKLSLFADDMIIYLENPV SAQNLLKLISNFSKVSRYKISVQ IPQAFLYTNNRQTESQIMSELPF TIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTKKWKNI SWAGRINIVKMAILPKNWKKT TLKFIWNQKRARIKSIKSNQKN KAGGITLPDFKLYYKATATKTA WYWYQNRDLQWNRTEPSEIT PHIYNYLIFDKPDKNKQWGKDS LFNKWCWENWLAICRKLKLD FLTPYTKINSRWIKDLNIRPKTI KLEENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIKQE SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYSELKQIYKK
14740	45108	B	14826	1	1186	
14741	45109	A	14827	1	2304	
14742	45110	B	14828	1	2995	
14743	45111	A	14829	1	3095	
14744	45112	A	14830	1	3654	
14745	45113	A	14831	1	3189	
14746	45114	A	14832	1	2064	
14747	45115	B	14833	1	3031	
14748	45116	A	14834	1	3192	

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14749	45117	A	14835	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSAAPHHTYSKIDHIVGSK ALLSKCKRTEIHTNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYVWHNEMKAIEKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQETKIR AELKEIETQ
14750	45118	A	14836	1	3144	
14751	45119	A	14837	113	1336	PTLAGTGNETSHLGFNAIPIKL RMTFFTEL/EKTTLKFIWNQKR ARITKSILSQKNKAGGITLPDFK LYYKAIVTKTVWYVYQNRDID QWNRTEPSEIMPHIYNYLIFDKP DKNKKWGKDSLFNKWCWEN WLAIRKRLKLDPLTSYTKINS RWIKDLNVRPKTIKLTLEENLGN TIQDIGMGKDFMSKTPKAMAT KDKIDKWDI.IELKSFCTAKETI RVNRQPTWEKIFATYSSDKGL ISRIYNELQIYKKKTNNPIKKW VKDMNRHFSKEDIYAAKRHMK KRSSSLAIREMQIKATMRYHILT PVRMAIHKSGNSSRSNIVHSVT QANALESSWIPFLIPHQYISKP QASSFKMYHVTDPILPPSSQHL DQAAIINLCLQWPLLWFECMCP SKIHMLKLTPQ
14752	45120	B	14838	1	3127	
14753	45121	A	14839	1	2742	
14754	45122	A	14840	1	1998	
14755	45123	A	14841	1	3030	
14756	45124	B	14842	1	2558	
14757	45125	A	14843	1	3828	
14758	45126	A	14844	1	4134	MRKKQSRKTGNSKKQSTSPPPK ERSSSPAMEQSWTENDFDELRE EGFRRSNYSKLQEEIETKQGEV ENLEKNLDKCITRITNIEKCLKE LMELKAKARELHEECRSLRSRC DQLEERVSVMEDEMNEKMQE GKFRERIKRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLAQANIQI QEIQRMQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSQ
14759	45127	B	14845	1	3555	

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14760	45128	A	14846	1	3345	
14761	45129	A	14847	1	3451	HTKNPSVHHHRQRPKVDKTTK MGKKQNRKTGKSKTQSAFPPP KERSSSPAMEQSWMENDFDEL REEGFRRSNYSELREDIQTGKG EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRN WIKSQDPSLCIQETHLMCRDT HRLKIKGRRKIYQANGKQKKA GVAILVSDKTDFFKPTIKRDK GHYIMVKGSIQQUEELTILKIYAP NTGSPRFMKQVLSLDLQRLDLS HTLMGDFNTPLSTLD
14762	45130	A	14848	1	2606	MVASRSSRVGVFYGGQNSVDG VSRSSDGLNELCLYRPPTGAY LAYDTLDVLPSSGQFTVNTPID VNGKSLALLWEHTSLLTSMG GGRWAMQPLGLGLEHLGD RRDQVLDGRSRRLLDAAQHL RHRPDRRQGMVGVLTNQKEP RTRWIHSRLPEVQGGTGVTPSE TIPIDRKEGILPNLFDEASIIIPK RGRDRTTKENFRPISLMNIDAKI LNKILANRNQQHIKKLIHHDQV GFIPGMQGWFNICKSINVQHIN RTKDKNHMIIISIDAFAFDKIQ QPFMLKTLNKLIGDGTYLKIIRA IYDKPTANILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLR AIRQEKIKGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSAKYKINVQKSQAFLYTN NRQTESQIMSVFPFTIASKRIKY LGQLARNAKDLFKENYKPLL EIKEDTKKWKNI PCSWVGRNI VKMAILPKVIYRFNAIPKLPMT FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLHY KITVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNLYIFDKPEK NKQWGKDSL FKNWCWENWLA ICRKLKLDPLTPYTKJHPRWIK DLNVRPKTIKLTLEENLGNTIQDI GMGKDFMSKTPKAMA AKAKI DKWDLIQLKS FCTAKETTIRVN
14763	45131	A	14849	1	2862	

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14764	45132	A	14850	1	3724	MGKKQNRKTGNSKTQASPPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSADEDEMNMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIQENFPNLRANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14765	45133	A	14851	2	2375	
14766	45134	A	14852	1	2376	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQAIDLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIL GSKALLSKCKGREIITNCLSDHS AIKLELRKIKNLQNRSTTWKLS NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKIEIETQKTLQKINESR SWFFERINKIDRPLTRLIKKKRE TNQIDAINKDKGDIADPTDRQ TTIREYYKHLNANKLENLEEM DIFLDYTYLPLNLQEEFESLNRP ITRSEIVAIHNSLPTKSPGPDGF TAEFYQRYKEELRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWSVGRINIVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARIKSLSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWYRTEP LEITPHIYNLIFDKPEKNKQW GKDSLFLNWCWENWLAICRKL KLDPLFTPYTKINSRWIKDLNV RPKTIKTEENLGIITQDIGMGK DFMSKTPKAMATKDKIDKWDL IKLKSFCTAKETTIRVNRQPTK WEKIFTTYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAACKHMKKCSSSLAI REMQIKTTMRYHLTPVRMAIHK

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14767	45135	A	14853	1	1576	MDKFLDITYLPRLNQEEVESLN RPITGAEIVAINSLPTKKSPGPD GFTAEFYQRLISNFSKVSQYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKFIWNQKRARIKASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNILIFDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFLTPYTRINSRWIKDLHV RRKTIKLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYA AAKKHKMKCSSLA IREMQIKTTMRYHLTPVRMAII KKSGNN/R/CAPGTPERQNHLS WKG S*SQEPGLAQWIPLWSP AS*DPLA*NSCCQHSCLKSTWD AQACARKLRTLIGYRNCQLE
14768	45136	B	14854	328	1467	
14769	45137	A	14855	3	3412	
14770	45138	A	14856	1	2907	MDKFLNTNTLPRLNQEEVDSL NRPTGSEIVAINVSLPTKKSPGP DGFTAEFYQRYKEELRIKYLGI QLTKDVKDLFKENYKPLLKEIK EDKNKWKNI PCSWVGRINIMK MAILPKVIYRFNAIPKLPMTFFI ELEKTTLKFIWNQKRALIAKSL SQMNRAGGIMLPDFKLYYMAT VTKTAWYWYQNRDIDQWNRT EPSEITPHIYNILIFDKPEKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLTPYTKI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14771	45139	A	14857	1402	3004	TEPKTKTT*LSA*MQKGPLTKF NNPSC*KLLIN/IVLEV/LAIRQ EKEIKGIQVGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNILCSWVGRINIVK MAILPKVIYRFNAIPIKLPMPFFT ELEETTLKFIWNQKRARIAKAIL SQKKKAGGITLPDFKLYYKATV TKTAWYWYQNTDIEQWNRTEP SEIMLHIYNLYIFDQPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEENLGITIQDISMGK DFMSKTPKAKATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELK QIYKIKTNNPIEKWVKDMNRHF SKEDIYAAKKHMKCSSLAIR EMQIKTTMRYHLTA VRMAIHKK SGNNSLIVGASMDTSLSGPIPY DIQHDFRFGSVTVRRGCAIEFY

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14772	45140	A	14858	884	2925	GIKYLGIQLTRDVKDLFKERS/Y EPLLNEIKEDTNKWKNI PCSWV GRINIVKMAILPKVIYRFNAIPK LPMFTFFTELEKTTLKFIWNQKR ALIAKSILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI DQWNRTEPSEITLHIYNLYIFDK PEKNKQWGKDSL FNKWCWEN WLAICRKLKLDPF LTPYTKINSR WIKDLNVRPKTIKLEENLGITI QDIGMGKDYMSKTPKAMATK AKIDKWDLIKLSFKTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYA AAKKHM KKCSPSLAIREMQIKTTMRYHL TPVRMAIHKSGNNSPTCVSQD WKLTA VGLWSAEAEAPKSAQ RRPLAEGHRAAVQRDGSGLQL LCTVKLQVLPCHIAQNGGRKA TSSLEAELTSWRPLCLEDGTGF RGEDTLETVNAEGRENRRKAG HRAAGSSASRRCRNTGRSVQRL RPQKTQAFPTHCHFCLILVVK TQLNPKSRVRKVPFAPMKHKG ALAGPWANICAGKSSNEIRTC RHGCGQYSAQRQSRPHQGV LCSAGSTVYAPFTGMIVGQKEP YQNKNAINNGVRISGRGFCVK MFYIKPIKYKGPIKKGEKLGTL PLQKVYPGIQSHVHIENCDS SSDP
14773	45141	A	14859	1	2577	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
14774	45142	A	14860	3019	5574	RÉTRGEVKNKSNQSTAPPKDC SSLADPKKIQTITREYYKHLYPN KLENQEEMDKFLDTYTLPRLN QEEVESLNRPIGTGEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL VPFLKLLFQSIEKEGILPNSFYE ASIIIPKLGDRDTTKENFRPISV MNIDVKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFIHHSI NVIQHINRTKDNHMHIIHAEK AFDKIQQHFMKLTLNKLGDGT YLKIIIRAIYDKPTANIILNGQKL EAFPLKIGTRQGCPLSPLLFNIV LEVLAIRAIQEKEIKGIQLGKEV VKLSLFADDMIVYLENPIVSAQ NLLKLISNFGKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLEIKEDTNKWKINPCS WVGRINIVKMAVLPKLPMTFFT ELEKVTLLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLKYKAT ATKTAWYWYQNRDLQWNRRT EPSEITPHIYNLIFDKPDKNKQ WGKDSL FNKWCWENWLAICR KLKLDPLFTPYTKINSRWIKDL NIRPKTIKLEENLGITIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKQESFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYSEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAANKHMKKCPSSLA
14775	45143	A	14861	1895	6140	
14776	45144	A	14862	1	2875	MKAIEIKVFETNENKDDITYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDTLTSQLKELEKEQEQT HSKASRRQEITKIRAELEKEIQTO KTLQKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITTDPTIEIQTITREYYKHL YAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPIGTGEIVAIINSLP KKSPGPDGFTAIFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
14777	45145	A	14863	2843	4460	HQHQQKPHPHRNPIQKSPTSST KVLVLAIRAIQKQSGIQIGS QEVKLSLIEDDMIVHLENPIISA KNLLQLISNFTKVSQYKINVQK SQAFPTYNTKTQIENQIMSELPFT IATKRIKYLGIKLTROVDLDFK NNYKPLFKIEIREDTNKWKNIPC SWVGRINIVKMAILPKVVIYRFN AIPKLPMTFFTELEETTLKFIW NQKRARIASLSQKNKAGGIT LPDFKLYYKATVTKTAWYVY QNRDRDQWNRTPESEIMPHIYN YLIFDKPEKNKQWGKDSILFNK WC*ENWLTICKRLKLDPLTPY TKINSRWIKDLNVRPKTIKTLLE NLGITIQDIGIGKDFMCKTPKA MATKAKIDKWDLIKLSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHKMKCSSSLAIREMQIKTT MRHYLTPVRMAIKKSGNNRC WRRCGEIGTLLHCWWDCKPVQ PLWKSVMRFLDLLEIIPDPPI PLLGIIYKPGYKSC
14778	45146	A	14864	1	8335	MGKKQNRKTGNKMQSASPPP KERSSSPATDQSWMENDFDEL REEGRFRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSADEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDIQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIRTLHPKSIETFFS APHHTYSKIDHIVGS
14779	45147	A	14865	1	3166	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDISRTLHP KSTETVFFSAPHHTYSKIDHIVG SKALISKCKRTEHTNYLSDHSA IKLELRKLNLTQSRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYQNLWDAFKAVCR EKFIALNAYKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAEKKEIETQ
14780	45148	A	14866	1	3912	
14781	45149	B	14867	1	2832	

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14782	45150	A	14868	1944	3531	LRDCKRINQHPVKTDQSAFCM/AP/ MQDVVLEVLARAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPVISAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRIINVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARMASILSQ KNAAGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNLYLFDKPDKNQW GKDSL FNK WGWENWLAI CRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKLEENLDITIQDIGMGK DFMSTPKAMATKAKIDKWDL IKLSKFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYA AKKHMKRCSSSLAIRE IQIKTTMRYHLTPVRMAIHKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCCMRKNKTLI
14783	45151	A	14869	1182	3891	KMIKGISTDLTEIQTIREYYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIGTAEIVA IINSLPTKRSAGPDGFTAIFYQR YKEELVPFLKLFQSEIEGILP NSFCEASIIIPKGRDITTKKENF RPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFN IRKSNVIOQHINRAKDKNHMISI DAEKAFDKIQQHFMKLKTLNRL GIDGTYFKIIRAIYDKPTANIILN GQKL
14784	45152	A	14870	997	1161	CTSTVIMSICTKLQNKEHVJEA LRRAKFKFPGHPKMHHSKK*DFT KFNADFED
14785	45153	A	14871	1	1458	
14786	45154	B	14872	53	1468	
14787	45155	A	14873	1819	2235	

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14788	45156	A	14874	707	1613	VRARAGERARVVRENGKAELP VALVLPRLSHSTFTCTDLKVQ FHQRLRLQEKSGKFGSNMSQE SDNNKRLVALVPMPSPDPFNTR RAYTSEDAWKSYLENPLTAA TKAMMSINGDEDSAAA/HRPAL *LLQENQSEPIPREGVGWG*GE ER/ERMTEEEQEGEGGGGRRGG GEGEEEEEEEDVEEEEEEEEEE EKEEEEKGGKEEENEKEKQKQ EGRRGKETSNQGMVRPRLLP HQEHSRNYLVFIMDSNMIEICF REASISPKAQAYVLIPDFKNCIY GWEDSIEILWGLPGSHVL
14789	45157	A	14875	3	346	QRSKCKVPLGKPLTLPPKPE KVPQGQKDRRPTGFKP*N*RRRR SEKSLRFFPPGS/PQAVPIPVGFS FDTNL*HFL*KPLIFIMGTVSL PHPRSPSAPPPTPQRPMTFCHLK Q
14790	45158	A	14876	1868	2666	GLLLSPFQGLQGVAPRKTRSNL HPGSLAHLSHQPPAPWPPRGLW PPGQETSCHCASGRALGTGSPR PPHAPWLHLEPQRAHSGAPSP GSSPSAPLHIPVAPENQLSLGHR SPPNPSPGDCYPSPSGP/PPSSLD SPGLQTAPGAMFLSPRSVGQSA CPTPRSLDLRNSPASTPDQSVCP TPLSLA WLWPPPSPTSAKSLIFT LTSEVQSFSPPTIPPGSSDPPLSK QP/SGSCLSSSGHLTSPSVPRHSP WPRSSPQNPHSWTLPS
14791	45159	A	14877	762	1528	AIPGGAA WPFRAEGAQGFGKR LTFKPLGAQRQSVSGSEVPPL PLHLKMAPEMPVAL*SPGTGV HPSLLPPT/GPKVPPGRIDRGVPV TLAPQVGTAPIQWHCRGSRCP G/SRPPGGWR/RPCQAPAPPLGQ HLPRLLPPTPGQGPRLTPSEP PPWSCWLPASPPAGPSRRVGG GPGTCQGLLRS*GLLLSPFQGL QGVAPRKTRSNLHPGSLAHLSH QPPAPWPPRGLWPPGQETSCHC ASGRAVGTGSRPRRA

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14792	45160	A	14878	1	963	MARKDCCSPGDSSPGRLPLVL PAQCLVLLRLQITAFSSIHVAAN DMMSFFLMAKQDSIAKYRIFF IHSSVDGHARPLSPSLVVENG GKQVLLCSDNASPEVSTVALA SCPGTFPRHCGAAESTHICATG LGELTPQGGHGHIPNKLACCAT GLEELVPRDHGKLGISWFGFIA GAYLNLARVVGECQGSYGYS LHHYCYHYHYHYCHYHYHAA TY*NHYHYHYH/HNNNSYHHH SYHYHYHYHYHYHYNCYHHH YHCRHYHHPDYYHYHA/RHY SLYYCIYLCYYYRYCHDHSS HQHNHHECL*VRHSAEHLQY
14793	45161	A	14879	105	1448	CHQPPASPFSRREFGGSEKPPER GCPAWEPAAGPVQPLGEDGP RLCQPPPPSPDHALG/PYGHQRS GRPTLPGRPK/PAKKRGR*PSS TGQ*SHRPITGTGGQAGGSG* VTAGGQ*PPQNL*AKISCEMP GPSPGMQQGVKHPSLFSHTV AKGFTTRWNCRQVCPHRGERK WISSVRPCGGALAPSCA/DGLR GRRTLSGSQPLW/PPAAVSAVG QLQPPCHTLTPHPLQNSTQHAE PQRGSVYSL*EGTSP/LAAVPFA PHIEKRFSTFPAGDA*PSEAH/A PGPACCHSPGLEGVPSRAGPG TSAGR/PGNGRERAWPPHSGPS TPPDTSCG/SPGPQLARAGSRRA NGSTLPPTRQGF/LPGRKDSAGA CGQP/*AEGAAAGPSRPAER AVLPLPR/GRRKCRGGGPGVET GVSGARRGGDRSGCSPAALDA EAPASLAGVSIRES
14794	45162	A	14880	1	2421	

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14795	45163	A	14881	1080	2571	VHCRFWILALCQMSRLQKSPILL FNIVLEVLAKAIKQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI V/SAQNLLNLISNFSRVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTKKWK NIPCSWVGGRINIMKMAILPKVI YRFNAIPIKLPLTFFTDLERTTL NFCNQKRAPTLQVQSLSIQKN KAGGITLDPFKLYLQGLQ*PK TAWYWYQNRDIDQWNRTEPS EIMPHIYNLYLFDKPWEK/HKQ WGKDSL FNKWCWE/NWLAICR KLKLDPFLTPYTKINSRWINDL NVR/PKTIK/TLEENLGITIQD/IG MGKDFMSNKTPKA/MAVTKAKI DKWDL/KLKS/CTAKETTIRV NR/QPTKWKIIFTYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSTSLAIREMQIKTTMRHYLT PVRMAIHKSENSRCWR
14796	45164	A	14882	136	420	RESRNLSRGEESDPAEPS/RNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPSPAPPETHTGSPRPPSGRSR IRAYLH
14797	45165	B	14883	1	1197	
14798	45166	A	14884	3	538	GAGTDGGRTPAPRAFDPDLGEA RTSAPTGPARPGGSASAARPA VRPAEPAAEETQEOPRAGKRAI HEYRYVYVQQRKTDPPQAVA VFGIPADGD*VSR TAYHAHQPL AWSGR/E*MCLSMAMWNT*ST MKK*ISIRVISRCSGPVHRTN*QI PEPVRAWRFLICRCICFSPGRWI KT

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14799	45167	A	14885	1208	2765	KMAPTWDKMVSSAQMGFNILQ ALLSQLSQDELKSKFYLIITFSL AHELQKIPHKEVDKADGKQLV EILTTHCDSYWVEMASLQVFEK MHRMDLSERAKDEVREAALKS FNKRKPLSLGITRKRERPLDVDE MLERFKTEAQAFETETKGNVICL GKEVFVGKKPKDNRCRYLK TKFREMWKS WPGDSKEV/RGY G*EIQDADPIQQPGASRALVPY TVVLYGPAGLGKTTLAQKLMML DWAEDNLHKKFYAFYLSCREL SRLGPCSFAELVFRDWPELQDD IPHILAQARKILFVIDGFDELGA APGALIEDICGDWEKKKPVVPL LGSLLNRVPLCIENKLGVGGED WGDQLRVYWWNPSKREGGSG WSHGSEDANQSLKHLRLSANV LLDEGAMLLYKTMTRPKHFLQ MLSPWETTTLAQIIMLDWAEETS SDKLKYAFYCSCRELSRLCPCN FEELVFRDWPELQDDIPHILAQ ARKILFVIDGFDPLGGRTLWTL TRGHLRELGNRRKRCPSWGV
14800	45168	A	14886	213	625	EPGIDTSCLCAGRCSRPGKGRA CGGSSPCSWPGQPPAPPAAAV PACPSGGRGAGPIQSGTCCSR ADSRCSTWTAW/WPPGLGAAT VQTVMS*TV/WPMPHVPAQGW LALGQGA AAAKHPLTSATTRS WCLGVGPGPVM
14801	45169	A	14887	1	375	MCNAQVLEYMGKSSLLTSDL QLVRDALRSLRNSFGHDPQHH TIDSLQGISSLMERLHVMEQ KKQERKPPVIPRQT/VVWSGP PANSNRPAEGPDC*KEN*RDA LRSLRNSFGHDPQHHTIDSLQ GISSLMERLHVMEQKKQERK PLVIPRQTGSGVDLQQTPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL

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14802	45170	A	14888	1	750	MGELNQGSWRQGHLP.DAAN GIAIRVPRRRKDESRRKNPTRKPH SWKPTKNFEDDVEVMKRSMSI RIEDTHSGPSAAGVLEFAGGPL QTLFAWVSPAEEAEQORLLPVP /CLWKLCPRGAPARCQRQNSPSK LPSTGFVYTVRGKLPQTQASVVVD APPATKLECPRTSDCCAGSKN FKPVDLSLLASVGPVRVNLQQES SHYGKISVTVAGHCPTHTATGRI LGKQALRWSPMCSMFIGRALG LVPEVGGLLQIA
14803	45171	A	14889	81	164	VGKQGLEWTFPANSRRPAE GPDCKEN
14804	45172	A	14890	1	674	MVVYACSPSYLEAEVGGSLSE VEATNPKNSSKKFLDLISEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFYFGI YLTKEEERLKPSRKKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNAADGTPPLVIPRQ T/VVWSGPPANSNRPAE GPDCKEN*QTERNSINIKKDIHTKT PLCI
14805	45173	A	14891	619	931	YLLMDFLLHSWLVS LGDKVP HEFWRGCPSCSFGPRFWVAGV LVL*APKL*LRQVRSAGKRCGQ KW*IK*/SDRLCVD*NK/WSDS LKPATSCSLIVTCHSLLGF
14806	45174	B	14892	1	658	
14807	45175	A	14893	48	288	LCSIKKPEKSLLCW*Y PGRNVW SGPPAKSNRPAAEGPDC* KEN*QTERNSININKDIHTKT PSEGH QHQRPKTKPGRI
14808	45176	A	14894	801	1157	QSGPSAAGLLDFAGGPLQTLFA RVSPAEEAEQORLLPFSSGKL RPRGAPARCQPELSCMR CR*SL LGGVVSQSGYMGVRDPFEEAAC PLSELECSAGRSALLRMVRQ GHLGLLKLRP

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14809	45177	A	14895	1	1891	MPVWVTVVKSWNTQIGRPGH VSALGFELTKNPWPLTYESGDG RSLGKPGA VSRGRGRHGPHPQ QAECDLPAGRIAGPCERGLERQ EKLPPAPQGGAWHLRLSRERFK SEDAPKIHVALGGSFLNLAF LVNVGSGSKGSDAACWARGA VFHYFLLCFTWMGLEAFHLY LLAVRVFNTYFGHYFLKLSLVG WGLPALMVIGTGSANSYGLYTI RDRENRTSLELCWFREGTTMY ALYITVHG YFLITLFGMVLA LVVWKIFTLSRATAVKERGKN RKKVLTLLGLSSLVGVTWGLAI FTPLGLSTVYIFALFNSLQAHKQ LKDRKVGPHFMQGA VFLEKGF WGVDIASFEPQEQFWWTNLGK EDEDKSFDMPHSWVEQIEISPEE EAMGSAQMVRGVSGPERGSKK RPQLTVSTAFETRCPNGKKVIQ YKRAKLEKWAPYLNNSGLVSR LTTYEDLQCTNILEIKWYQNR EDMLELKHINKTTDLKTDYFKP GHPQALRVHSYKSMQPEMDRV IEFYETARVDGLMKREETPRMT TEYYQGRPDFLSYRHASFG/RPS QEAHSEQCRVKPPAHCAKPAE DDV/RKSACFWSRRSASSCATT AVRTTSRPPSASSCGAPRWAK
14810	45178	A	14897	1	425	HVQQTETISRTVSTGSPILSCSVP VTLPNGPVLWFKGN/AGPNRKL IYNFKQGNFPRVKEIGDTTKPG NTDFSTRIREISLADAGTYVCV KFIKGRAIKEYQSGRGTVFVT VSYSSRSQKSEICISGLKSRHQQ NCSFWRF
14811	45179	A	14898	1	393	RQGNFPRAKQIGDITKPGNTDF STRIREISLADVGTYYCVKFIK RAIKEYQ/SGRGTVFVTEQNP RPPKNRPAGRAGSRAHHDHT CLSALPERNSTNYFVQPCCLLR LLGLTGFAVKIIQTGKERTSK

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14812	45180	A	14899	1	753	MGSSLSPVLVYALPVRQPLI.RS VVEERSTKMRVSGPGFQAKFRF YSQGLSWSARGEGLVPFAFWL QPYPRPLNFKAEEMTEQKENQT YVDGGFRPYIHRRKNL.TEGHK AEKEMEPWDGFSDESCRTHCQ VHDYAKGHGEVQRERVDEQK EHLGRRRQDCQQHLNRRL.HC /TVSGEAPSEASGSVRGHGRAH GLAGSERHGHDAAPEHQLLQ SVDADHVVPVAVYQFWDDEG RGLSPGDHFKPDRRGAALY
14813	45181	A	14900	6	726	VEGISRTGIQAEQAPGFTTMP VSNPGDVLTLACNMSALSPE GPVLWFKSIGPGQQLIFSCNGS HFPRVTPVENTMVDQTDYSIILS CSVPNTLPNGPVLWFKGTGPNR KLIYNFKQGNFPRVKEIGDTTK PGNTDFSTRIREISLADAGTYYC VKFIKGRAIKEYQSGRGQTQFV TGEYVSYTPYPLVYNS/PLWDE ASRGRSRQSQLFCSLHW*YPR KQDEWTSSKLQQTCCRVA
14814	45182	A	14901	760	978	KKLLLLLLCGIEWHGFSSDSGS GGWVPEG*K*GCEHELLPEDVP SCFGWAECWLVRRTLPLFHYV ELCYSFHG
14815	45183	B	14902	772	1165	
14816	45184	A	14903	1	2133	
14817	45185	A	14904	1	1311	MATTPGRALGSLLPITLLGLTA GQPFISLTGPSHRTSPGDSVPFN CTAVPFNSQDFSRDFNVTWLK DSDEHPASAQRLVPDNGGNDFI TSKAWVTLTRQDVSSEITCEVT HRAIAEPLKTTMNLSSQATRNP DGTYSLEHTWQAEATLEEREF ACWVVHDEQPLKANVTLQQAQ VRRQGGKQSVQPYKLQGPLQR SEPGTRIRLTASSGFSTHQVTV TWLKNKHELPNPQTSVQYSGH TYNVTSSVLVPLMDDDDVFSHV VCHVEHKLTFWFQKTTGLDQY L/QG/DP*QLCGGHLTLPSSPRAP PQLPGLQHP/VVFHSQVLLFSC VAVTCLVQRFYPQNVHLAWLE DCHTLKGTEQPTLKKNNDRSY TLEKLLLVNASVQGPVRLTC MMEHEGQPPKRANLVLSTAHH TAYKPIGSTESIMVTMIITISQM

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14818	45186	A	14905	3	341	RRATRPGN*GGRHNAGRSSARL ETGRPAMAPQGRPRPLGCRTPQ HPGHWPSAPGLLPPAPGPVAG MTQAQRWCPEPDAHFLQYTLTY FVRHIPQLPKQTPHHYIATRLPC ATQ
14819	45187	A	14906	154	679	GVCCPLLGGVSS*ATWGS GTT* GGNTHLI
14820	45188	B	14907	1	2554	
14821	45189	A	14908	387	826	ARAACLPRGSARGTAGAGEEPP DPAPLHLRGEGPAP/HRPRSFRG MGWPAAPSTRSPST*RRCLPP RPRWSP*SHPGPRASARRLP*LS *RASRSSEAPSGSLGSAAGQD CSRTGTGFSPPAFSDGQQTTPP APSSVPTLNSLG
14822	45190	A	14909	86	2223	GQEPQVREQKACHHLGSSPPPS WEL*EQRPAGP*N**PSTLTGT GSTTT*QIRMKVN*MGN/DSPQ GKNTPKMYSGEFSPPVRVHVFFS LSDLKQIKIDLKGFSDDPDGYID VLQGEDILAKAGAIRHLNIGEG THVCCPLLEEGINPEVWATEGK YGRAKNAHPQVVKLDSASFY QRQYPLRPEAQGLQKIVKDL KAQGLVKPCSSPCNTPILGVOQK PNGQWRLVQDLRIINEAIVPLY PAVPPNYTPLSQILEAEWFTVL DLRDAFFCIPVHPDSQFLAFED PLNPMSQLTWTVLPQGFDRDSPY LFGQALAQDLSQFSYLDTHVL WYMDDLLAARSETLCHQATQ ALLNFLATCGYKVSQKPAQLC LQQVKHLRLKLSKGRALSEER IQPISAYPHPKTLKQLRMFLGIT GFCQIWINRYGKIARPLYTLIKE TQKANTHLVRRTSLOPVA YLS KETGTSLQPVA YLSKEIDV VAK RWPCHLRVVAAIAVLVSKAVK MIQGRALTVWTHD VNSILTAK GDLWLSDNHNEEKIEHNWQQV IAQTYAAQGD LLEVPLTDPDLN LYTDGSSFEKGLRKAAYAVFS DNGILESNLTPGTSTQLAELIA VTQALELEGKREPNADNASY SCEPLEDLRLFRQPIEA VKLQ MVLQMEPQMOSMTKIYRGPLD WPASPCSNVDDIEGTPPKEISTA

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14823	45191	A	14910	929	1324	RRYQVQRPSEGLTVYLFWPV*/ PVVGVDWPLPTGPD\YSLLVPIPP PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPSPCTPMFHS PCSAMTAVTPSLARP*THGSP KAQGAQGVKGPSSGLEAPPW A
14824	45192	A	14911	2	286	
14825	45193	A	14912	220	249	P*N**PSTLTGTGTTT*QIRM KVN*MGN/DSQGNTPKMY GEFSPVRVHVPFSLDLKQIKID LGKFSDDPDGYIDVLQ
14826	45194	A	14913	1	163	EPENPADNASYSCPELDRLL FRQPIEAVKLQMVLMPEPQM QSMTKIYRGPLDWPASPCS*DF LGRGAFNVINIGAWASRPVQGS AVDLSHGLHLGLHLKNNHL
14827	45195	A	14914	1	287	
14828	45196	A	14915	2498	2788	
14829	45197	A	14916	112	333	
14830	45198	A	14917	329	1666	
14831	45199	A	14918	1	756	
14832	45200	A	14919	1256	1651	RRYQVQRPSEGLTVYLFWPV*/ PVVGVDWPLPTGPD\YSLLVPIPP PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPSPCTPMFHS PCSAMTAVTPSLARP*THGSP KAQGAQGVKGPSSGLEAPPW A
14833	45201	A	14920	1	987	MLVLGYNRKNTTEGTQKQKGT NASDFHFLSQVLEQVSPKGS EAQCCVLRHLGCESESAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLKGER QREGERRERKREKREKRESQR KERKREKGGKREKREKDRSDL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLTVWRDMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQA VP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPIN*SMIST ITQKKEENPTAFLERLREALRKH
14834	45202	A	14921	473	1015	
14835	45203	A	14922	3	937	
14836	45204	A	14923	530	612	LQAKVFFLLRWPAILRG*NYGP RGVPH
14837	45205	A	14924	101	430	

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14838	45206	A	14925	1	1587	MAALTLRGVRELLKRVDLATV PRRHRYKKKWAATEPKFPAVR LALQNFDMTYSVQFGDLWPSIR VSLLEQKYGALVNNFAAWDH PGDIVLDLCAAPGGKTLALLQT GCCLTWSRKCAALSMFSRPA RCLCRARTTAPRAVRRPDQRR ATAAATKQARATPEAPGSAA HSSYCTMIPSAACCI.PRLKPPH AQPARSAAKPLDQPGSHARL RGRGGEARQSLAIRGGPSGIA PSDIPLPAKPSRRVIAQTYAARG NLLEVPLTDPDLNLYIDGSSFVE KRLRKAGIKAVKLQIVLQMEPQ MQPMTKIYCGPLDQPASPRSNV DDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLLTWRDIMLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAAP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKRKKPIN*SMISTI TQKKEENPTAFLERLREALRKH
14839	45207	B	14926	1	939	
14840	45208	A	14927	1	4317	MQSMTKMYCGFLDQPASPCSN VDDIEVKLEIMLLTERDDGKEV LDVGEERRYEIEEYDSK WTRK YNCLAVLRVHSGSQITTMKIL WYLVVALWCFKDGKIAASRS GGFSYGSSSGDLDRKKPLFSL EFGSPGETEDKSRQRQDAGSPK SEDTAGGFFNSSSSGSDSRTK PFFSLGLGAPGKAEDKSGDSQD AGGSKSEDTPPGGFFYGSSSSG DSDKKKPLFSFEFGATGEDEDK SRERWDAGNRSSEDS
14841	45209	B	14928	110	269	
14842	45210	A	14929	1	561	EVFPACSQLVYWGKPIITTYPLCE NNVYMLSPNASVCLYSPLAEQ FSHQFPSHDLPSVLAKFSLPVSL SEFRNPLAPAVQETQLIQMVV WMLQRRLLIQLHTYVCLMASP SEEEPRPREDDVPFTARVGGRS LSTPNALSGSPITSSDDMTLTSP SMDNNSAELLPSGDSPLNQRMT ENLLASLSEH

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14843	45211	A	14930	1891	2522	GLSNQNOQPGRCIPDAHPVQDI. VQDLVHTWCRVPCTSYVPCV* VPGAYLVHTRCIPGAGPGAYPV HTWCRTWCIPGAGFPAL/RPYH ALLLLSDEKSLLGELPIDCSPAL VRVIKTTSAVKNLQQLAQDAD LALLQAMGSAVALVMWAWP RATGPKLYCLRVGAGGACGWR PRLVAVSRALLVWRGSPWG PALAWQKSPEYSTKVLKQ
14844	45212	C	14931	113	274	
14845	45213	A	14932	1	1634	MEIPAVILTVAPILHLTSCGFV TGDGLKQAEKCAPEEWNPTK FIKLTNDQACFAGLWPLSEIQ RRTSRTVTIISRISALREKGNR KPTSISGSVNEMRQVLVKDQVS MPRVLPTHIFVPDEAGFSAGAV WPCAAPLWGSSWTPKVENCS FYIRLSFAISVGGDELKIAKLVS AFPERAYDLVGHQHQRPKVDK TTKMGRNQSRKAENSKQNMS SPPKEHNSSPAREQNWMENEF DELREVGFRRSVITNFSELKEH VLTHHIKEAKNLEKRLDEWLTR INSVEKSLNDLMELKTTLREL EAYISFNSQFDQAEERVSVIDQ ISEIKQEVKFREKRVKRNEQSL QEIWDYVKRP/NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANIQ/QGKLQRTPTKVASSRT ATPRHISVGSPLNMKEKILR AAQRERSGLPTKGKPFRLTAAD LSAETSTSQKTEWGPIFNILKEK NF/QPRVUSYPAKLSFISEGEIKYF TDQAKCLRDFVTTAFSCLP*K STRPALKELLKGST

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14846	45214	A	14933	1	1429	MVLAAGDPVEKGITWARENAG IYISCTMMKLSMIPIGDQSYRNL IPLKFVACILIEGNAKCWPLPEF DPSQIRLIVYQDCERRGRNVLF DSSVKRRNEDISVSRIKYLGIQL TRDVKDLFKENYKPLLNEIKED TNKWKNI PCSWIERINIVKIALIP KKLGSDAQVKVFGKCCQLKPG GDSSSLDSSVTSSSDIKDQCLK YQRTVDLSAQLSSSGKGQTTSS SGSLTPMTPHWEIPPSGGQOTS HTGELRLASGRGSSGMKLP EEG TDRNLCCSAASSGDTQANRDW SGPPANTS RPAEAGPDCDRENG TKL.ENTLKDIIHENFPNIRQAN IKIQEIQRTRQRYCSRRAATPRHII VRFTKVEMKEKMLRAAGEKH WVIHKGKSIRLTVDLAETLQA RREWGPIFNVLKEKNFQLRISY PAKLSFISEGEMKSFPEQMLR DFVTIRLALQELLKEALNMARE /NR*QPLQKHM
14847	45215	A	14934	2320	2811	ESKLTRGVKDLFRENKYPLLNE IKRGHKQMEEHSMLMGRKNQ YREKWPYLPKVNL*IQCHPHQA TND CFHRIGKKLL*SSYGTKKE PALPSQS*DKRTKLEASHYLT NYTTRLQ*PKQHRYWYQNRDI DQWNRTEASEIMPHIYTILILWT NLRKTSMGERHP
14848	45216	A	14935	2	872	
14849	45217	A	14936	769	828	
14850	45218	B	14937	1	669	
14851	45219	A	14938	1	807	
14852	45220	B	14939	35	212	
14853	45221	A	14940	235	837	QQAHKTPQRRHSAFTEYVRNN RLPETVIRVKQPALAIFSPDIAPL FVHFRADDDVTARVIAIIMIF WCDRVEKRVSDAVACFTLESEI AEVGVLCRTHIRQ*RVQVTPARM *ALSRLHACRS E D V R H N R P P Y P VIRVKQPA/RRDLAPT*PHCSSIS AQTTITSLPGCMREVTELRPEFF K*RKTVLRPTPIMRARAERRCK
14854	45222	C	14941	1	1755	
14855	45223	A	14942	1	747	
14856	45224	B	14943	1	2466	

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14857	45225	A	14944	1	333	LNLVLFQQRAELMIS*PQ*FSRA LLVIFPLLQTELQQLFLLHVN AAVEAPPSPVIGLYSENVRRNR LPETVIRVQKQALARFSPDIAPL FVHFRADDDVTARRVEKRCK
14858	45226	B	14945	1	1794	
14859	45227	A	14946	1183	1899	LNRRDSYVEYLADKVADREED AEEYLEAIMEARVTVAGMGLV MEVQDYDFDGEADRLAKAWLA EYTPQIKSLKDERKEAYRQIVE MSTEPQDQDLVVRPANKFEMTR VREGEKEADLPVWKHHL/SV*R KRELSGSVEPLGNQVFEIETKRE NS*EL**KSLKDERKEAYRQIVE MSTEPQDQDLVVRPANKFEMTR VREGEKEADLPVWKHHLCD SGNYPALLNHWETRFRLSKPN VKIHRSSDKSPTYVFFISQYDL PAFYPIHGHLFVERVVKVRIVFI EEFADHHHLAIFQFNRLQRHA FVVTLANVTNQPFSSVVVVNL
14860	45228	B	14947	1	3099	
14861	45229	A	14948	1174	1545	
14862	45230	A	14949	1	945	
14863	45231	A	14950	62	576	
14864	45232	A	14951	1	1642	MLANIGFYNSNVIHRSKGAIGE GPPDPRGIVEQNLGGDISIPCYN GPPRRRSQAQKTTGLPNQPRIPS AQCAGAFPRVAAAGAGGGGG GGSGGSGFCLGWRLRRRRQRR RRWRRGEGEGDGDAGHMRPR PAGRAEARRRRRLRGNPPPGAR LPNREGNGSGVSWAAEVSGDG RGARTEAARTRRRPGGADNYP GAVPPVQLLTGWCVTAKAPPDI SAISALTAVKHGNCSSLTPLLNP PGSDVIVCAEMDEQWGYVGAK SRQWLFYAYDSLRTTVVAHV FGERTMATLGRMLSLSPFDVV IWMTDGWPLYESRLKGLHVI SKRYTQRIERHNLNRQHLARL GRKSLSFSSKVELHDKEELAAL FSELKQEQKKVDELIKLVKNR TRIVNESDVFSSWVIRREFQELR HPVDEEKARCLEGGGHTGLV ASLDMQLEQAQGTRERLAQAE LCWNSSEMRTTSSSSGSTPWP PVSRRRPWTERRLGSGVRGDLR ERSRPAVNRTPRMSRVPSGAPR GTPSRRWMMKCDWHQMRG LVEEEVG

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14865	45233	A	14952	1	1513	MIILQKESLMSLQAQLDKALQ KEKHYLQTTITKEAYDALSRKS AACQDDLQALEKRTGRDWNW PPFRTQQRGSKSLTAIRPLCLFR KLNHVTSETKSLQQSLLTQTQEK KAQLEEEIIAYEERMKKLNTEL RKLRGFHQSELEVLIEEEMG NHNENTGEKLHLAQEQIALAG DKITSLERSLNYRDKYQSSLS NIELLECQVKMLQGLGGIMG QLSKTSSDLSKM/RCY/TTW*M WTKLQFIHSILTSVIFHLLSFSSM GSI*KWIMALSGSSFLDAHYSIS QFGPRQLPSVCAEPEKEKATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQFAGQ*RHRL RGIMDEQWGYVGAKSRQRWLF YAYDSLRTTVVAHREQGSIK CKLEEDLQEATKLEEDKREQLK KSKEHEKLMEGELEALRQEFK KKDKTLKENSRLKEENENLR AELQCCSTQLESSLNKYNTSSQ VIQDLNKSMPMEIRFQLYIFPDQ
14866	45234	A	14953	125	363	INVSVWSQPFPGG*QPEKGLKE HPADARPGSCPPAGRVPQGRA EVASAAAPRGSSPAAAPGQSH PSCLRAPLYWSFSR
14867	45235	A	14954	306	583	TCSTRRRKNDLSVKYVSVWSQ PFPGG*QPEKGLKEHPADARPG SCPPAGRVPQGRAEVASAAAP RGSSPAAAPGQSHPPSCLRAPL YWSFSS
14868	45236	A	14955	225	407	LRGMVTFSPFSSILNGQFENSG CPL/CPVCWVCLREPGDPEKL EFLQKDNISVHYFCLVS
14869	45237	A	14956	484	722	NTCRCGHNRSPVNSRRGGLRS JPRMPDAGSCS/PPAGRPSAGPG RRSPPLLPRGSSPAAAPGQSH PSSSQGAIVLEL

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14870	45238	A	14957	434	1790	GNFFRKTIACIIISVLSYLVSCLR GASPTASMDFLKTSKREAR ASRKICFVCKKKGAAINCQKDQ CLRNHFLPCGQGERGLPFTIFWR VQIIL*QTSPEHRTSNMGHVGE ESCILCCEDLSPTCLRTFQSPC CSQAIYHRKCIQ/TNMPHQSK HFFKCPQCNNRKEFPQEM/REN GNSYSRQRCCLGTRARGFLRLI SALSAL*CPHLVCMNKAETALR MKGGGASFCVLHADPTEPTGT APLLDLTVRNGSVRSVHL/PA TDYIPENSGDIPCCSSTFHPEEHF CRDNTLEENPGLSWTDWPEPSL LEKPESSRGRRS/VLLEVQGCQ NH*QLQKIQVTPSE*LLVPHNR V*TCAPPSGLGREHSGTVRQGS RASSETMS/LSKEKSQWSMRRE QSRCCQGNAFMATRVPLLSPL LPPRILPP*SCFHMPLLTSPMFV VMQIKVFSPPKKKK
14871	45239	A	14958	146	484	
14872	45240	A	14959	228	353	
14873	45241	A	14960	214	722	TARELPGRVLKEMYIQK*EGA ALGRPTRPGRQGQVRRAECR RLFRGVLRPCNRC
14874	45242	B	14961	1	951	
14875	45243	A	14962	241	517	QSCGQRLPTVLR/PLRTPWILPM YPQPLPAGGPTCLRSRPYINITI LKGDKGDPGPMGLPGYMGRE GPQGEPP*GSKGDKGEMGRP RRPVP
14876	45244	A	14963	748	1055	DRKQTSFGDAYHTIPGSLSSSD HVLSEPD*GEGSHL**SVQHD VPPTA**RLQYRAVVLFTATL PAILIM*GMRCLVPRNCSRTW TAQIRAYIEVQQT

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14877	45245	A	14964	1	832	MPHVCAQRRLPVAAVLPPDGA QNCILLAGLSAGTFCHHGGVHI LLSNPVATSLLVADRVGQIPIPP PPPPALPYDCCPPPSRHTEDRE HVPILPHWKLMVNRWFLPVPT EWIATLSNSSRSRTCMSQGLSF LDSQVHLKAMIEDLRGNVSKES SPCLADNADVGQFPMEGGQKD PKQRIIPFCQGVTNLSGPHGPGA VCGGSHYQKQESSEISLSVGQV WTSSRRMSQVGGSSHCRGARL GPCNVPRRPDGVQDEFSLQPEE DAG*QTSVDPMVLEQYVVVA/ NYQKQESSEISLSVGQ/VVDIIE KNESGWVWFV/STAEQGWVPA TCLEQMGCRMSFLCSLKKML DWIQRVSL
14878	45246	A	14965	1	346	
14879	45247	A	14966	157	413	ALVCS/SSLAIEMQIKTTMRYH LTPVRMAIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDAIPLL
14880	45248	A	14967	1930	5781	RAKSPANIIMTGSNSHITLTN VNLNSPIKRIHLASWIKSQDP SVCCIQETHLMCRDTHRLKIG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYKIDHILGSEA LLSKCKRTEIITNYSLSHSAIKL ELRIKNLTQSR
14881	45249	A	14968	1	2235	
14882	45250	A	14969	1	2148	
14883	45251	A	14970	1	1821	
14884	45252	A	14971	1	1248	
14885	45253	B	14972	4	2121	
14886	45254	A	14973	1	1137	

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14887	45255	A	14974	1	1240	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGFNICKSI NVIQHINRAKDKNHHIISDAEK AFDKIQQPFMLKTLNKLIGDGM YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLFSIVL EVLARAIRQEKEIKGIQLGKKE VKLSLFADDIMIVYLENPIVSAQ NLLKLSNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRLKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMPFFTELEKTTLKFIWNE KRARIAKSIPSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEITPHIYNLYIF DKPEKNKQIQKAFILHAKEPWV MWNMGTNVR
14888	45256	A	14975	1	2241	
14889	45257	A	14976	1	2802	MYGTGYRDVAGKWAIDPDSK REFLDVTQEQIGGCDPSGTCRQ TSLILTOPLRQWGLEGIKKPN WIIEESVSNGGPPLIPRQTAS GVDLQQTPTDQLRLVTVRRK TNKQKGIASSTKRTSTPKPHL YVTIHKDSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWVYKRPDLRLIGVPD SDGENGTRLENTLQDI
14890	45258	A	14977	1	2739	
14891	45259	A	14978	1	2478	
14892	45260	A	14979	590	727	
14893	45261	A	14980	1	3255	
14894	45262	A	14981	1	3810	
14895	45263	B	14982	1	3127	
14896	45264	A	14983	1	3325	
14897	45265	B	14984	1	1734	

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14898	45266	A	14985	1	2067	MELKTKARELREECRLRSRCD QLEERVSADEMEDEMNMKREG KFKREKRIKRNEQSLQEIWVYVK RPNLHLIGVVPETDGENGTLEN TLQDIIQENFPNLRQANVQIQE IQRTTPQRYSSRRATPRHIVRFT KVEMKEKMLRAAREKEIQTIR EYYKHLHANKLENLEFMDKFL DYYTLPRLNQEKVESLNRPTG AEIVAIIN/SLPTKSPGPDGFTA EFYQRGILPNSFYEAIIPLKLG RDTAKKENFRPISLMNIDAKILN KILAKRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHVNR KDKNHMIIISIDEKAFDKIQPP MLKTLNKLGDGMYFIIRAIYD KPTAHILNGKKLEAFPLKTGM RQGCPLSPLFNIVFKVLARAIR QEKEIKGILGKEEFKLSLFADD MIVYLENPVSAQNLLKLISNFS KVSQYKINVQKSQTFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPKVPMTFF TELEKTTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKATWYWYQNRDIDQWNRT EPSEITPHIYNLYIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLDPFLLPYTKINSRWKD
14899	45267	A	14986	1	1293	
14900	45268	A	14987	1	3229	
14901	45269	A	14988	1	3352	
14902	45270	A	14989	1	1419	

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14903	45271	A	14990	1	1716	MKAIEIKMFFETNENKDDTTYQN LWDTFKAVCRGKFIALNAHNR KQERSKIDTLTSQLEKEKQEQ TYSKASRRQEITKIRAELEIET QKTLQKINESRSWFFERINKIDR PLARLIKKRQKNQMDTIKND KGDITDPTETIQTTVREYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEVESLNRPTGAIEIVAIINS LPTKKSPGPDGFTAIFYQRYKE ELPGRDPTKEENFRPISLMNIDA KILNKILANQIQHIKKIHHDQ VGFIPGMQGWFNIRKSNINVIQHI NRAKDKNHMIMSIDAFAFDKI QQPFMLKTLNKLVLVLAARAI REKEIKGIQLGKEEVKLSLAD HMIYVLENPIVSAQNLLKLISNF SKVSGYKINVQKSAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFRENYKPLLKEIK EDTNKWKNI PCSWVGRINIVKV AILPKVIYSFNAIPKIPMPFTEL EKTTLKFIWNQKRARIKSLISQ KNKAGAITLPDFKLYYKPTVTK TAWYSYQNRDMDQWNRTEPSE ITPHIYNLYIF
14904	45272	A	14991	1	702	

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14905	45273	A	14992	473	2385	HSFLSFIVLMYLTMDLTRSQKH GWASSPSHGTSPWPVRLRTSLA KPKCWQVSLCWVLSASPGSSF SLVRSLLIIVPHAESVSRRLPSLL SRVGLFPARY*HRVWQSRSPSQ TRDHLIKRNPQDV*RRQQPRG TRVSNKCSLHTSALGGRQPSC DATL*GQQGLP/VK*KRQQPAP/ MSQQQTGAALVLAIRAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPTVSAQNLLKLSNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRITYLGIQ LTRDAKDLFKENYKPLLEKEKE DTNKWKNIPCSWVGRIIVKM AIPKEPGWARSLVFGARGLQG QGRCGQSRGGGSCGGGGST ENWQHREPSARKTGSTENRRH REPAAPRTGSTENQHREPAAPR TGTENRHREPSARKTGSTENRR HREPAAPRTGSTENQHREPAAP RTGSTENRHQEPAPRTGGTENR QHREPAAPRTGSTENRHREPAAP RTGSTENRHREPAAPRTGSTEN RQHRESAAPRTGSTENRHQEP APRTGSTENRHREPSAPRTVGT NRRHRELVAAPRTGGTENPREP PAGTRPRHTPMRGGSEGALFH QRRFLEPTPDREQLGIRYPPVA

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14906	45274	A	14993	687	2274	LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNI PCSWVGGRINIVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARMASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNYLIFDKPDKNKQW GKDSL FNK GWENWLAICRKL KLDPLTPYTRINSRWIKDLNV RPKTIKLEENLDITIQDIGMGK DFMSKTPKAMATAKIDKWDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYA AKKHHMKRCSLSLAIRE IQIKTTMRYLHPTVPRMAIHKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMRKNKTK TLI
14907	45275	A	14994	1	3189	
14908	45276	A	14995	1	3351	MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSAMEDEMNMK QEGKIKRKDEGHYIMVKGSIQQ EEL.TILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIYRTLHPKSIETYFFS APIHTYSKIDHIVGS
14909	45277	A	14996	1	3192	
14910	45278	A	14997	1	2742	
14911	45279	B	14998	1	2313	
14912	45280	A	14999	1	1542	
14913	45281	A	15000	1	3300	
14914	45282	A	15001	1	1824	
14915	45283	A	15002	1	2982	

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14916	45284	A	15003	1	2375	MSGFLISPKHKHGTNSGIVSWA DVQSQLRHIEAFAFDQEA AAVL MARLGVFRAESEEQPDVLRWL DRQLIRLHSLTTLDIVPAGKGE VVKGPMSISQAKGCKFGQY NKEDPTSFRLSDFSLSYPQFMF HLRRSPFLQVFNNSPDESSYYR HHFARQDLTQSLIMIQPILYSYS FHGPPPEVLDDSSILADRILM DTFFQIVIYLGETIAQWRKAGY QDMPEYENFKHLLQAPLDDAQ EILQARFPMPRYINTEHGGSQK KREKNQIDAINKDKGDITTEPTE IQTITREYYKHL YANKLESLEE MNKFLDTYTLPRLNQEEVESLN RQITGSEIEAIIINSLPTKKSPGPD RFTAKFYQRTNDQKHMISIDA EKAFDKIQPFMLKTLNKLGDID GTYFKIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSLLLF NIMLEVLAIRAIQKEIKGIQFG KEEVKLSLFADDMIVYLENPIV LAQNLLKLISNFSKVSQYKINV QKSQAFLYTSNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRF NAIPKLSMTFFTELEKTTLEFI WNQKRARITKSILSQKNKAEGI TLPDFKLQYKATVTKTAWYSY QNRDIDQWNRTEPSEIVPCIYN YLIFDKPDKNKKWGKDSL FNK
14917	45285	A	15004	1	1428	
14918	45286	A	15005	2	1975	

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14919	45287	A	15006	1	3891	MKPEIKMFFETNENKDDTYQNL WDTFKAVCRGKFIALNAHKRK QERSKINTLTSQFKELEKQEQT NSKASRRQETIKIRAELEKIEITQ KPLQKINESRSWFFKINKIDRP LARLIKKKREKNQIDAINKDKG DITTDPTETIQTIREYYKHLN KLENLEEMDKFLDMYTLPLN QEEVESLNRPTGSEIAHNSLP TKKSPGPDGFTAEFYQRYKEEL VSFLKLKLFQSIKKEGILLNLFYE DSIILKPKPGRDTTKKENFRPISL MNIDAKILIKILANRIQQHIKKLI HHQVGFIPGMQGWFNIRKSN VIQHINRTKDKNHMIIISIDAEKA FDKIQQPFMLKTLNKLGIHGT LKIIIRIYDKPTANILNGQKLK AFPLKTGTRQGCPLSPLVFNIVL EVLAWAIRQEKEIKGIGLKEE VKLSLFADDMTVVYLENPIISAQ NLLKLISNFSK VSGYKINVQKS QAFLYTNNGQTESLIMSELPFTI ASKRIKYLGLQLTRDVKDLFKE NYKPLLNEIKEDITNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTDLEKTLNFIWNQ KRARITKSILSQKNKAGGITLPD FKLYYTATVTKTAWYVYQNS MVLVVPKQRYRSEMQNRLRN NAACLQLSDL
14920	45288	A	15007	1	4215	MHSCLPDATEGELYNSLGLST WSFLSMIGVLLWVDFSGDSIDL CSPLWNRTNLEALQKKLEEL DEQQRKRLEAFLTQKQKVGEL KDDDFEKISELGAGNGGVVFK VSHKPSGLVMAKLIHLEIKPAI RNQIIRELQVLHECNSPYIVGFY GAFYSDEISICMEHMYVLQER PCPGFLWMENSDYGLLLPLDLL LCLSFSSKVLSDLVSDLIHGM KARNRSIHGDVVVVELLPKNE WKGRTVALCENDC
14921	45289	A	15008	1	2823	

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14922	45290	A	15009	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKWKRTEITNYSLSH SAIKLELRRIKNTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQLEKEKQEQTHSKASRRQE ITKIRAELEKETQTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNK
14923	45291	A	15010	1	2816	MEDEMNMKREGKFKREKRIK NEQSLQEIWDYVVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIEIQRTPQYRS SRRATPRHIIVRFTKVEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFFTCICDDAEDLQSPSTA GPWFGVLYTKGGPYQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPQCH IGEVLDDGFTAIFYRRYKEELV PFLKLQFSIEKEG
14924	45292	A	15011	1	3347	MGDFNIPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTEYTFSSAPHHTYSKIDHILG SKALLSKCKRTEITNYSLSHSA IKLELRRIKNTQNCSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRQERSKIDTLT SQLKELEKQEQTHSKASRRQE TKIRAELEKETQTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDAIKNDK
14925	45293	A	15012	1	3855	MGGKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRSSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLSR CDQLEERVSADEMNMKRE GKFKREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQ QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14926	45294	A	15013	1	2559	
14927	45295	A	15014	1	2956	

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14928	45296	A	15015	1	1853	MGRNQSRKAENSKNQSSAPP KDCSSSPAMEQSWTENDFDELT EVGFRRSVITNFSELKEHVETNL KEAKHLEKRLDKWLTRIKSVE KILNDLMELKTMAQELHDTCTCR SFNSQFNQVEERVSVIDQINE MNIDGTYLKIIIRAIYDKIPPRNII LNQQKLEAFPLKTGTGRQCPLS PLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNRRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIASILSQKNKS GGITLPDFKLYYKATVTKTA/W L/YHTPLSCLPP*WNRTEPSEIIP HIMAVAQIQVKLLLLQGQHA SSRLQPTSSTKCGGWTAASSAP RSMGLSSWKGNLASAIHYFPCK PLTLPSRISTSSSSWGCRQAHAV LEVLRWPPGLGWPGWIHLTL HVPPVRITKSNGPRACTRASAS HARHHQYNQFPLSPLHSPLPP PEQVLVSTAERTEDRSYHRTL RHSPYFKNEAADLRGEGYSS
14929	45297	B	15016	1	3276	
14930	45298	A	15017	1	2274	
14931	45299	B	15018	440	3383	
14932	45300	A	15019	1	2646	

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14933	45301	A	15020	1	2229	MGKKQNRKTGNSKTQASAPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRLSR CDQLEERSAMEDEMNMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLRQANVQI QEIQRTPQRYSSRRATPRHIIV FTKVEMKEKMLRAAREKEIQ TIREYYKHLVANKLENLEEMD TFLDTYTLPRNLQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGT AEFYQRYKEELVPFLKLFQSI KEGILPNSFYEAIIIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDKIQPFML KTLNLGLIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTQR GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLIISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKIGKTTLKFIWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWYWYQNRDIDQWNR
14934	45302	A	15021	1	960	
14935	45303	A	15022	1	2928	MEDEMNMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLRQANVQIQEIQRMPQRY SSRRATPRHIIVRFTKVEMKEKM LRAAREKDRSMRQKVNKDQTE LNSALHQADLIDYRTLHPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEITNYLSDHSAIKLE LRKLNLTQNRSTTWKLNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDAP
14936	45304	A	15023	1	1782	
14937	45305	A	15024	1	4881	
14938	45306	B	15025	1	5962	

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14939	45307	A	15026	1	2053	MKAIEIKMFFETNKNKDDTTYQN LWDAFKAVCRGKFIALNAHKKR KQERSKIDLTLSQLKELEKQE THSKASRRQEITKIRAELEKEIET QKTLQKINESRSWFERINKIDR PLARLLKKKREKNQIDAINKDK GDITTDPTIEQTITIREYYKHLYA NKLLENLEEMDKFLDTYTLPRLN QEEVESLNRPIITGAETVAIINSLP TKKSPGPDGFTAELYQRYKEG AVLEVLAIRQEKEIKGIQLG KEEVKLSLFGDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYGF NAIPKLPMTFFTELEK/TT*KFI WNQKRARIK*ILSQKNKAGGI TLPDFKLYYKATVTKTAWYV YQNRDIDQWSRTEPSEIMPHIY NYLIFDKPDKNKKWGKDSLNF KWCRENWLAICRKLKLDPLFT YTKINSRWIKDLNVRPKTITILE EKLSTNIQDIGMGKDSMSKTPK AMATNVKIQKWDLIKLSFCT AKETTIRVNRQPTTWEKIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKVVKDMNRHFSKEDIYA AKKHKMKCPSLAIREMQIKTT MRYHLTPVRMAIIKSGNNRC
14940	45308	A	15027	3	3229	
14941	45309	A	15028	1	3907	MGDFNTPLSTLDRATRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFPSAPHHTYSKIDHIL GSKALLSKCKRTEITNYLSDHS AIKLELRKLNLTQNRSTWKLNS LLNDYVWHNEMKADIKMFFE TNENKDDTTYQNLWDTFKAVCR GKFLALNAHKKKQERSKIDTLT SQLKELEKQE/THSKASRRQE TKIGAELKEIETQKTLQKINESR SWFFERINKIDKPLARLIKKRE KNQIDAINKDK
14942	45310	A	15029	1	4005	
14943	45311	A	15030	287	2708	
14944	45312	A	15031	1	4602	
14945	45313	A	15032	1	4806	

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14946	45314	A	15033	965	5928	TWKGTTSTRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKLNQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQKLEKQEQTHSKA SRRQEITKIRAELEKEIETQKTLQ KINESRSWFFERINKIDRPLRLI KKKREENQID
14947	45315	A	15034	383	8708	
14948	45316	A	15035	2	3257	WRKIYQANGKQKKAGVAILV/S DKTDFKPTKIRDKEGHYIMVK GSIQQUELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLSTLDRLMRQKVNKDTQEL NSALHQVDLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRKLNLTQSRSTTWKLNNLLN DYVWHNEMKAEIKMFFETNEN KDTTYQNLWDAFKAVCRGKFI ALNAYKRRKQERS
14949	45317	A	15036	1	3508	MELKTKARELREECRSLRSPCN QLEERVSAEMEDEMNMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTLEN TLQDIQENFPNLAQANQIQEI QRTQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSHSAIKLELRKLNLTQNHST TWKLNSLLNDYVWHNEMKA EIKMFFETNENKDTTYQNLWD TFKAVCRGKFIALN
14950	45318	B	15037	1	4760	
14951	45319	A	15038	1	3110	
14952	45320	A	15039	1	5546	MELKTKARELREECRSLRSTRN QLEERVSAEMEDEMNMKREG KFREKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDAENGTKLEN TLQDIQEDFPNLAQANVQIQE IQRTQRYSSRRATPRHIIVRFTK VEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQUEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE

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14953	45321	B	15040	1	4534	
14954	45322	B	15041	1	1826	
14955	45323	B	15042	1	1626	
14956	45324	A	15043	248	1212	NSKHYSRGQKKKLPTLPRAAN SRWRSLLK/GFTVSFDETLKPFV RDVSGSRLKDLPKPNKSDDETR ANDAVNRYKLLKKDARTIAAQ QVARLESAMCLRRRWLENFQ LFLVEHPLVRHLTRRLIWGVYS AENQLLACFRVAEDNSSSTADD DLFTLPEGDISIGTPHVLISPTD AAALLFADYELLPPFRQLDRNS YALTEAERNASELTRWAGRKC PSGRVMGLANKGWIKGEPQDG GWIGWMIKPLGRWSLIMEIDEG FAVGMSPAELSAEQLLSKLWL WEGKAERYGWSNSTQEAQFS VIDAITASELINDIEALFE
14957	45325	A	15044	1	1788	
14958	45326	A	15045	1	3048	
14959	45327	A	15046	1	3546	
14960	45328	A	15047	969	1205	SPVRCCISA VHRTYHRRTSALL RLAELHRLLEKCSARQWMYEN I*SPFRQIA*CLPYS DHKNQRLH GLDSIFLARLLW
14961	45329	A	15048	877	1248	WPLTVPYCGVGYAS*A*VADN HRAVGYLSRWAGRKCPSGRV MG/LANKGWIKGEPQDGGWI/G WMIKPLGRWSLIMEI/DEGFAV GMSPAELSAEQ/LLSKLWLWEG KAERYG/WGSNSTQEAQFSVID
14962	45330	A	15049	854	1313	DHGVASAAATCVYTNHGRQSY VRVCEYASRTRVSHHCSV*RVL RCEAIRIVSPDRSC*RDPEFSYL ALPENYNRLFLPNSTNQTNRI KTLNSIAIGKLLAAGGVYNGNI EGFRDTAEKLDGRTIDGYDQIL NEKTAVIAKATA/SILLTKRS
14963	45331	A	15050	1010	1396	KPFGKLYKLFEGHAWLVKAE KVRVG YRILGR LTYPFDIRFPAL PFGLVL*KGAHFTVPRIWAGHA C*LMPMALPMFRWKVTGLLFIP ICLVKPSFLTLTHIAIRRISTSTN CRKTPKQPSRWCKPR

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14964	45332	A	15051	361	837	DGQQLIALHRLALREIQQAVH AGLPQQAQKILFDGGSEIGKIPSEI YFCQLVKLILCPVLFPWCRRVA ILWRRRDVLFSGSFSFSAIVSPH LCG/SYLPFVFDVGDRL*LSVG WSKEIWPCK*GFGHLMVSLNT PMKSLVEGFKHFPLAGFGYEYL SFFCR
14965	45333	A	15052	1563	1652	
14966	45334	A	15053	2756	2995	AMRSAHRCVTFSAALLNCWQITP HLTPSVMICGQLLTLYNRC*PSS TIFSIPLSKQVARMFRSAMSPL NRARCWKVPCN
14967	45335	A	15054	762	2184	WRAPSEPISEILKADTEKYVY L*NSSSAQYSGSCTRAYYLDQ HPTPRLCLIFGGKDSGLMLHLT AELARQMGKKICVLFIDWEAQ FSCTINYVQSLRELYTDVIEEFY WDALPLTTQNSLSQYQPEWQC WEPDVEWVRQPPQDAITDPDF CFYQPGMTFEQFVREFAEWFSQ KRPAAMMIGIRADESYNRFVAI ASLNKQRFADDPWTTAAPGG HSWYIPIYDWKVADIWTWYA NHQSLCNLYNLMYQAGVPLR HMRICEPFGPEQRQGLWLYHVI EPDRWAAIGSPADREDAEEYL EAIMEARVTVAGMGLVMEVQ DYFDGEADRLAKAWLAEYTPQ IKSLKDERKEAYRQIVEMSTEP QDVDLVRPANKFEMTRVREG KEADLPVWKHLLCDESGNYP ALLNHWETKVFEIETKREGFAF WYRNPOYTQSSSLGIAYVEAE QYKIVRPDLFFAEQDGKMOVV
14968	45336	A	15055	2069	2586	PWLENLPVGCWSAVKMGGT RSLVSL/AVTLVSPQLMAYL LGQQLPEVWDFGMFSIAKVG YQAQVIALYLVVVVPCSLILAV FLAHALIGPFRMIGDGVAFV RHLMTGSFAPIGAALFGFLYAP LVITGVHQTTLAIDLQMIQSIGC TPVLPVNALSNDLWHISILV

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14969	45337	A	15056	356	1205	APASMTFEQVRFVA/VMVFTK RPAAMMIGIRADESYTVLSPSP V*INNVLPTITWTFPQTITDFLW LIGEAIF/YLPVGICWSAVKKM GGTRSLVSL/AVTLVSPQ/MN AYLLGQQLPEVWDFG/VCSLIL/ AVFLAHLALIGPFGRM/GDGVA FAVRHLMTGSA/PIGAALFGFL YAPLVIT/GVHQTTLAIDLMM QSMGGTPVPWPLIALSNIAQGS VIGIISSRKHNREIPGEVFPRT GVGKGLSLG*PLH*LQPYRQHL GAGSYSQTLKKQIAESAVRLSIP
14970	45338	B	15057	1	435	
14971	45339	A	15058	2	1785	WLLYRAHVKG/STEALLPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLGDKVIPATIL GIQSDRVIRGHRFMGEPTIDN ADQYPEILRDSGKVIADYEERK AKIKADAEAAARKIGGNADLSE TLLEEVASLVWPPV/LTAKF/E EKF/LAISRTALVPYASADNMYQ LVNDVQSYPPQLPGCTGSRILES TPGQMTAAVDVSKAGISKFTTT RNQLTSNQSLMNLVDGPFKKL IGGWKFPLPSQEAACRIEFHLD FTNKLIELAFGRVFKELAAANMV QAFTVRAKEVYSASMRYYIVIV YISYRPPNLLDSHIGFSSITTHC AVTSHHYNCDMTMTIHSYVT PYISVRVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDTRHIHTI ESRCRVCGAHDSDAERLDRF AQTADRIADRGFSSRPECIRS LAFGEADYIVRVHWRGLRWLT AEGMRDFMMGLRGLDCALIS KTRLLSENRRKGRVVQAETLE AAGHVLLLTSLPEDEYSAEQVA DCYRLRWQIELAFKRLKSLHL DALRAKEPELAKVGIFANLLAA FLIDDIIQPSLDFPPRSAGSEKKN
14972	45340	A	15059	1	993	

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14973	45341	A	15060	1	5621	MSEKTFLEIGTEELPPKALRSL AESFAANFTAELDNAGLAHGT VQWFAAPRRLALKVANLAEAG PDREIEKRGPAIAQAFDAEGKPS KAAEGWARGCGITVDQAERLT TDKGEWLLYRAHVKGIEGTEA LLPNMVASSVAKLPIPKLMRW GASDVHFVRPVHTVTLLGDK VIPATILGIQSDRVIRGHRFMGE PEFTIDNADQYPEILRERGKVIA DYEERKAKIKADAEEAARKIGA KAWGTNVEFHVQNPQ
14974	45342	A	15061	82	732	
14975	45343	A	15062	1	3849	MDLGANGWQTFRYVVLPLNLS ALLAGMGLAFALSFDEIIVTFT AEQVDAAVRAADAFAEWGQ TTPKVRAECLLKADVIEENGQ VFAELESSNNTAFARASSNGDL PTKADLQAQLDSLKNQKDLA QDKLVQQDLTDTLATLKDIDRI KEETVQLRQKVAAPEKMRQA TAALTALSDVDNDEETRKLST LSLRQLETRVAQALDDLQNAQ NDLASYNLSVLSTQTPERVQ NAMYNASQQQLQIRSRDLG
14976	45344	A	15063	219	1186	PPKLGKRKGIFLPSHSNPNTNRI CPNCCMNGVSTANTTSKSSLVI CAWTKHALLNAILQPEQLWKS GSRWRINLALPRGYRESLLQPW QAERLTDDKGEWLLY/RAHVK GESTEALLPNMV/ATSLAKLPI KLMRWG/ASDVHFVRPVHTVT LL/LGDKVIPATILGIQSDRVIAA TGKAKIKADAEEAAR/KIGGNA DLSESLLEEV/ASLVEVPVVLN AKFDEK/FLAVPAEALVYTMKG DQ/KYFPVYANDGK/LLPNFI/ VANIESKDPQ/QIISGNEKSFVR LADAEFF/NTT*KRLFLPHQKL PPSQILHQQTRNYASFCHRRHD NWTSA

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14977	45345	A	15064	1	1496	SGGCAGLHGGILCSKEPFQASV QQGVAGHACAPAAALQVPVCGT LSDCGSRAASLCENPFSISLYGR LVATSLAKLPIPKLMRWGASD VHFVRPVHTVTLALGDKVIPAT ILGIQSDRVIRGHRFMGEPEFTI DNADQYPEILRERGVADIYEE RKAKIKADAEAAARKIGGNAD AKFEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIFVA NIESKDPQI/DRIQALAGWIAE QNGADVNHATRAGLLSKCDLM TNMVFEFTDQGVMMGMHYAR HDGEAEDVAVALNEQYQPRFA GDDLPSNPVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRIIVEKNLNLDLQTLT EEAVRLYGDKLTANVVDVVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPTRPADFDWHAALG RAGTGDVVVGVRGLAIVPLT DGLDEAGHSTGVLQGEVPQRL ERAFTVPGVTLQPALQARGL
14978	45346	A	15065	134	384	VTPTGWRKRRIRQWCSADAGCG VNALSLGRFHSALFSAAMFI LGVVSGITMSISP*ILSCVRSKNP LLVSGSGPLSCNSTIH
14979	45347	A	15066	1	723	TKSPKIARSRHPLCHFIFERRPI MTNSNRKLTWISFLSYALTGA LVIVPGMV MENIADYFNLVSS MSNTFTFLNAGILISIFLNAWLM EIVPLKTQLRFGFLMLVLPVAG LMFHSLSALFSAAMFILGVVSGI TMSIGTFLVTQMYEGRQGYR LFLAASLFSMAGMIFPMIAAFL LAPSS*W*WVYACGLAYVTIF IMTFGCEFPALGKHAPKSYAPV EKVKWGILGGASSFRAV
14980	45348	A	15067	422	1045	LLEGKLTNRKQ*HQH*QKARPC KKPIQSAQN/WNREEDDELTEV GRRVWIITNSFELKEHVLQWK EAKNLDKRLQEGLTRITSLEKKI NDLMVLKNTARELHEAYTSINS RIDQAEERISEIEDQLNEIKLED KIRGKRJK/RQTNKQSL*KMWD YVKRPNLRLIGVPESDEENVTE LENTLQDIHQENFPNLRQANIQ IQEIQTLLR
14981	45349	A	15068	1	1131	

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14982	45350	A	15069	383	756	LNPSNKLALINPAASPIIKGVDL TANQ/PCIIDIPLYDADVQQE* CFPATVEALGEQIRQADGVVIV TPEYNYSVPGGLKNAIYWLRL RQILVFLDAMVMNKPPEFMGGV IQNKVDPQTGKVIDH
14983	45351	A	15070	343	924	
14984	45352	A	15071	223	308	
14985	45353	A	15072	57	5546	NKMARKKFGSLEISLIVLFVIVT IIAIALIVVLATKTPAVDEISDST STPATTRYTTNPSDSGKCPNVL NDPVNVRINCIPEQFPTEGICAQ RGCCWRPWNDSLIPWCFVVDN HGYNVQDMITTSIGVEAKLNRI PSPITLFGNDINSVLFITQNTQPN RFRFKITDPNNRRYEVPHQYVK EFTGPTVSDTLVDVKVAQNPFIS IQVIRKSNKTLFDTSIGPLVYS DQYLQISARLPSDIYIGIGEVH KRFRHDL
14986	45354	C	15073	1	1818	
14987	45355	A	15074	493	576	
14988	45356	A	15075	381	498	
14989	45357	A	15076	48	514	LLLFLLLQSYDWSSESGKRQSAL HGRQKGLPKSPTAARGGSDPW PSCRHP*GPNRKRRKS/R*PMET APRRPSVSPALTPARPPGLTATP RLHPRPP/RSPNPSANLLRRPTP DT*AHATFGPGRSRHHFPGQLS TE/RRRSAEGGRSRNEASRRE GGE
14990	45358	B	15077	1	1116	
14991	45359	C	15078	249	332	
14992	45360	A	15079	710	1326	RAAGNCFPEPGFVKQLSAAAA VVAPAAAAATEGSIPTDGKSPSSI SHWPNPQKNVICKRRGRVEQE QAWKGR*RVVFGI*KSMRCP VDLLPQSCLCQRFHQ/GKWIL TKDYIIHSAKSGRWLDATTYE WGYKIEKDSRYSPQMQSAPKR WREELKRTGAPGAFHRWKVVL LVRTDKRSDSLRFSDNFGDCDI RMEEKTFRTLMES

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14993	45361	A	15080	602	1257	FGKRGRTITLCILAVGMLCCRK GHTKPRRRPGASPISTHLHSSPPI STHLHTSPPPHREEAR\SGQ*R QSCGAAAR*PWW\NCDGWG PKCQRFKSH*DIAQPDEVSWGQ *PWAVALAGPIH\PQASEGPL GCTPASICGSTRKPSKPLSKKPP QAARTSSSRIVFTPISTRPPTQG QPEKAKSATPTNDLEGPSAKVK FVNFLMDETFPEPSFFI
14994	45362	C	15081	140	175	
14995	45363	A	15082	2295	3089	NLLGYQINPPLQIFWDKLLAV SERDSSVKEESGDVESDDTML* MLPCP*ETTEFSS*PFRJSS*LSS* STAQIPAECTCFAGGWYSIFCPQ RIEQETMCLL*SWQSEVAVSCE SPWPTALHHSHPNRAPPPCY/S KSTSSLSPPLENSG*QNRPPSLL ITSVLPLRITCLP*VSFIPPIMQLG GSFLSNDRL*QSFLPKNVSLF VSFPLI*GAVSKPAISFNTSVSPL LVSDIFFALSLLP*GLGTWLIPSS SLLLVVRF
14996	45364	B	15083	143	1727	
14997	45365	B	15084	307	1017	
14998	45366	A	15085	1	959	MSRMGLLGFGERKELPNHPAV SEWPLTLVTGSSGTVAEGEGN LTTSGLFSIVLHPDGVAAQGR HSSLPRWGSQAEALLTSQTVDG QAEMLLTPQTMGGQEEMLLTS QTTGEDFITRSTESGTHSKSHKG DEGEPRWMLGWMLWVCDIAE PLVKAKLLDCKHTCCSVCLQQ TRTSQKDVRCWPWCSGVTKLPPD FSVSQLLDDPEVLAVITIPHASE HMPVFIRLPGSGCY\SCPCPSPRS TRCCPEI*AATCCPGTGRSPSL/C DHPCWTAASARQGSPPGGGGG AGQAGHGKLVVGVGVHCHL GGLRLGLPPQHRAP
14999	45367	B	15086	112	672	
15000	45368	A	15087	2	530	SGRSAALLSARVNRSSQSFAGVL GSHERGPRSPFVSPGPPRKP ALSRVSRMFSVAHPAAKVPQPE RLDLVYTALKRGPDLGAVH QQEQEKLQGIRESKRNS/RLG EWREGFLYDLDKQVKSIERFLR RLEFHASKIDELYE\AYCVQRR LR\DGALHMGRA\YTTGSPGSR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
15001	45369	A	15088	216	1369	EPVLRRRPQPRAGAQGFPVFS PPGPPRKPALSRVSRMFVAH PAAKVPQPERLDLVYALKRG L/QAYLEVHQEQ/DKLQGOIR ESKRNSRLVMAGGVLTWTVV*E RGAVTSLASAGVLLIPPKYLPL LPTPAGLALYDLQKVKSIERFL/ RRLEFHASKVRVQHVCRWD/D ELYEAYCVQRRLRDGAYNMV RAYTTGSPGSRARDSLAEATR GHREYTE/DEGWGPMRQHRHS MCLLES/ELEAQLGEFHLRMKG CAVDINDLGTIKLSLEVTGAAS SVNKASTVTKRSPPIARAHRT PHFGNSFLSTRKPNTYTANHRR RPIEQHPDMRTPPPPHRARTNT GRKDKVRAHEGEKATPTTRTG APHGKAQRLRLPLYQYVTIATLS
15002	45370	A	15089	1	940	MSYNSKNYVETITTMNSVKFG ETTPRNRTHYLSTNEKIFLSGV FSNAYPAGLSRGWDSPPWGSTP WVRHFCYLSSTQLCDQNCSSL SLLPAGPSVCNRLLASAWQKSS SSASSEASETCQSVSECSPTSD WSKVGSHEQPSGATLQRRKDR VE/PCETQSPGPASGGTLGPSGE EAPRPRMSPATIAAKHGEVSP AASDLAMVLTIRGMSL*HQKSS RDSLQYSSGYSTQTTTPSCSED TIPSQGRPAGLGPTKPVSIESTYL QSPQRLKQEWATEGKIQLPPQ IQVVNFQVDSSPSLPLIMVPEH MHVS
15003	45371	B	15090	1	777	
15004	45372	A	15091	26	336	KISPMINVCSESSPSGERRGA* TPPSPQSPGCGPKPS/PPSCSPSR NYFLLFQGLCAEHPALAAPAAS VGTCPSPASGTHAAAPSGPWGR RCVHSGPGGRLW
15005	45373	C	15092	46	423	
15006	45374	A	15093	1773	2219	ELDYLYCSNSSAQCPGALLPSL ALPGPAGSARQAQSPARRLCAP VQPSGRWPAPGGPGFPGSSCPA SPTRQ*LLTSGSGCPRPCHHPSG PPQ*QSTQAWDWVILGPAHG PSGQRCERCLPSRPSGPQTHSG VGSEPRAVRGPVSVF
15007	45375	B	15094	1	7916	

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15008	45376	A	15095	16	545	GLPWRQHVRRVEECGRS/PLRPC SPGTPSPS*PLPAATRGPATCQS LSGLQPEKTT/SPS/CAAVAHER PPGPVPQCPAQGTGLIF*EGWT QPQIQRGPHPAHE/CAHDLQ QAAPGPGGAHQG/PSQPG*PDR QPDRAERAVVHPGAQ*DAEIQPG LPGEGLPLATRTERSPAQRPS QARG
15009	45377	A	15096	320	1167	MDLKTAVFNPARDGKLRLLTK *WASKSKEEVSSISEKTNGAT PLLMAARYGHLDMEVFLLEQC SASIEVGGSVNFDGETIEGAPPL WAASAAGHLKVVQSLNHHGAS VNNTTLTNSTPLRAACFDGHLE IVKYLVEHKADLEVSNRHGHT CLMISCYKKGHEIAQYLLVKG ADVNRSKSVKGNALHDCAESG SLDIMKMLLMYCAKMEKDG GMTPLLSASVTGHTNIVDFLTH HAQTSKTERINALELLGATLFT QKEISCDSESGRTRDLSPPRKPPH
15010	45378	A	15097	187	623	KLKTKNNIGPOACNSQLASVS TRSPPTLSVPIIMTDDSQASQL LLAAVTIRKLWSRMAPMLALP TGQSGQTGAEGQGKEGERGQS PCWKPRLDPKLC/EPQPAQLL* ADVCTGP/CGVRGCPADCRLLP LSPSSAQPKAESRSA
15011	45379	A	15098	789	1041	
15012	45380	A	15099	707	1373	SAWPSCHCHLDILSR/PGDDA CSVQILVPGLKGDAEGKDGK APGRPGRVPGTGEKGEKGDG DIGPPGPNGEPLPCECSQLRK AIGEMDNQVSQLTSELKFIKNA VAGVRETESKIYLLVKEEPYA DPPLSWQGRGGTSLMAQDEAV HGLKGAYLQGARLGRGFIGIHR PWKRRAPLLLF*TLSPRSF*KG DGGGNTQKGRKKRELAGQIW GPCIRR
15013	45381	A	15100	79	420	WRRFLFLGLVFRGYLGCLRSRS VLGRKLVSDMRIFFFACGCGHL STLPSWPLRPSLWRL*EEQELP SLSVSPSSGRSASRL*LGWRGF GPSRPLRLTVQFSGGRRAGQPS
15014	45382	A	15101	3	284	
15015	45383	C	15102	83	112	

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15016	45384	A	15103	84	303	EEQELPSLSVPSCLWGPCPRAG WLHSLHWPVSHSFSASTTFGM AIWT*SLASGIKPSQSSKVSRRQ VPPTM
15017	45385	B	15104	112	462	
15018	45386	A	15105	326	1323	DRKAINLQVKLEGAVAL*KPVG EAQLEFGKALGLFQ/STLGHFF VNNKEKILGDF/QEATLQAATK LTRGRSLVMENMEQLLSMRME DQSQRNMLPSVVLIREKAHSPF ENRKQEQGEGASPENFRAR/QG *FLAFKAAPPA*AASGPAAQER SVQEPSVNAPG*IPEGGLHTLA GVHHE*ALAWCSPLNKPFLW KRLP/SRTFHFPPVEDESAAGSKP SGDLLTLLGGNAAGDFKLK/P CLVYPSENPCFLKGSFKPNLPL VWCSSHKKA/WVQPG*QSETPFQ KKKKKKKKA/WVTMSLFQEW LHFCSTVE/ARCTQYDLQYKGL PILDSTPGHPCG
15019	45387	A	15106	3	375	HASAHASGLQSSYQAVKESS EALFEMKRDLTFTQVVOHDT ACTIAATASVVEKELATEGSSG ATEKMKKGLSDFLGVISDTFAP SPDKT/STAMSSPYDGTKARLY SLQSDPATYCNEDPGPP
15020	45388	A	15107	184	377	YCTNNQKVN*KTEIITKRKTSPR QKKDASAFSPSHPLTEGLK/WND LTLVSLSLTHDGFVWRRGKGV
15021	45389	A	15108	3	816	SWEDVGWWRSLWQQSYQAVK EKSSSEALEFMKRDLTFTQVVO HDTACTIAATASVVEKELAI CSRGAFLCPFSIQTEGSSGATE KMKKGLSDFLGVISDTFAPSPD KTIDCDVITLMTGPSGAEPYD GTKARLYSLQSDPATYCNEDPG PPELFDAWLSQFCLEKKGEISE LLVGSPSIRALYTKMPAAVSH SE/TFWHR/YFYKVHOLEQEQA RRDALKQRA/VSGDSCT*SGVL TNE*KGSWVRDTERVRSLLPQT FSEGVGWREC
15022	45390	A	15109	1	281	

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15023	45391	A	15110	1	1194	MGFLHLGQAGLEFLTSGSSDTI SEDWEKDFDLDMTEEEVQMAL SKVDASGEPPFCWKGYPGGEL ETLIRLLQKLFFLKTDPAFVLSP STLVKLHLWGNEGLQESLES LHDAALVILVPNLEKKGEISELL VGSPSIRALYTKMVPAAVSHSE FWHRYFYKVHGLEQEQAARRIA RLKQRAEQSISEEPGWEEEEEE LMGISPISPEAKVPVAKISTFPE GRTLAPQSPCEENLVTSVEPPA EVTPESESESIKSPPLTRALGTD
15024	45392	A	15111	213	1031	AGNKPDPWAGNRNRTAVLPDVS VFHREDVGVWRSWLQQSYQA VKEKSSALEFMKRDLTFTQV VQHDTVCTIAATASVVKELA TEGSSGATEMKKGLSDFLGV SDTFAPSPDKTI*RDVITLMGTP SGTAEPYDGTAKARLYSLQADP ATLLY*PDGPPFLFDWLSQFC LEEKKEISELLVGSPSIRALYT KMVPAAVSHSEFWHRYFYKVH GLEQEQA*RDALKQRAEQSIFE EPGWEEEEELMGILPIFPKEAK FPLAKISYIP
15025	45393	C	15112	414	557	
15026	45394	A	15113	98	467	
15027	45395	A	15114	1	155	
15028	45396	A	15115	16	94	RCPIASEASWTITD*RCPIASEAS WTITDALGNSYSGGMAF
15029	45397	A	15116	95	115	IIRHLCDN*TPREGCLSP*PAW SDTFETWVNNQASLQ
15030	45398	A	15117	3	282	LKPVITCLLQLGLLKPINSPYNS PTLPVQKPDPRYSKPNSLP*LNP SLLQRNYTSIFLLTLNMPISICT TMLLYGQKEISSLHKGPSSLMP
15031	45399	A	15118	548	1401	SCTPCWHLTGRLWGITA VRQK RHVLSVDPKLRHQSRGTGKAAPF WCLIIAGTPL*LYTHVSRVSDH AGMPALVHLPLQQVPLFWGRG NTL*KD*SLLSLAC/VQHGLLKP INSPYNSPILPVVVKPDKPYKLQV NLRLINQIVLPIHPVGEAPVPLE TGGKSGKDCILWFECHLSHNTI EHQVSSSTFRIVVATGVLVSLH PQLYMAQNREHAECLEGESKG REQESLSGNPENSRSLLTSRRY LYKSTRTIVLLGLAGPLKQKKL RSQHPSLYKYLQSRNKDSYR

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15032	45400	A	15119	144	298	WQVPLFWQPFPEPELEWPKA/HLTDSFPDLLGLAAED*RCPIASEAPCTQVI
15033	45401	A	15120	449	667	
15034	45402	A	15121	2	111	
15035	45403	A	15122	323	401	LLGLAAED*RCWIASEAL*TITDAK
15036	45404	A	15123	2	593	CTLPSH*NLITLPLNANIPSHGML*KD*SLLSLACYSTAF*GL*TPLTIPPFYLFKNQTRLTG*FRICPLSTKFLCSTPWCQTHILSYPPQYLPPQPIFLFWISNMLSLFLCTLYPSSLSSLGLTLTPIRLSKLPGPYCRKPSQTAPTSNHPSSFSGSWYSVETSYPSSSIFRKGRDTSWSLKDTPHQAQPPT
15037	45405	A	15124	354	630	
15038	45406	A	15125	29	354	RFLVSLMLPPAVVMLNHCYSLIFTNALVKRLFAWNMLSELATCAGNLATGPRNARSPGFLSCVP SVRDPTGNQTVQLTWQPLPEPLELWPKA/HLTDSFPDLLGLAAED
15039	45407	C	15126	1	576	
15040	45408	A	15127	377	624	RDQLQCLQLWDAGACYTCWK SATGPRNAHSTVFLLSHVPSVW DPTENRTVHLTWQPLPEPLELWPKA/HLTDSFPDLLGLAAED
15041	45409	C	15128	1	462	
15042	45410	A	15129	44	340	PCQTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHP*RQVPLF WGRGNHISGTQELPNT**TAV/VQAF/LPEPPPTG/CLLHVPEIWLPGQMPAGQDSS
15043	45411	A	15130	242	522	RLVWPATQRAWWSQSEAAAAK TVDLALSARNATSATGPRNACSPG FLLSCAPSVWDFTGNRVTQLTRL QPLPEPLELWPKA/HLTDSFPDLLGLVTEDE
15044	45412	B	15131	1	1080	
15045	45413	A	15132	1	642	

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15046	45414	A	15133	245	1033	TALLLTQSLFGGLFTQTRMKFG AVTRIGGPPLGDQSPVLLFFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPI/ ASHSML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRFTG* FRICALSTKLFCCLSTPWCQTHIL SYPQYLPQSIILFWISNVLSLLF LCTLHPSLSSSLGLTLTPFRLS KLPGLYCRKASQTAPITSVKPK FLPYLLPISA
15047	45415	B	15134	146	556	
15048	45416	A	15135	1	555	LTSFLHCLLSHHYHGAQIHPRH FLHLICRCHCHQYCHHAYLDPC PQDSHHHLHWCWQPLPEPELELRP KA/HLTDSFPDLLGLAAED*HCP IASEAALPPCFPRPDMITSRLQL QRRRQTALGVRYRNATYRTRT ASTNSLRPRGSPFPPLALVTNDR QVRSQALALWKRDRLLQLSPINR AISESSFT
15049	45417	B	15136	1	555	
15050	45418	B	15137	499	769	
15051	45419	A	15138	752	1111	MQPTIGNSQSVSRPTA*MPLAE SHPITQLVGTVTTPRVTPLSIRH PWRCRSANAGAMILTMKQLAI VMRVYQHQRVRRMRPGRNGA RSGMSAVGAYYSSCIRVM TAL QSCTGDDEAVLL
15052	45420	C	15139	1	632	
15053	45421	A	15140	1	375	PGVRGAQGGPSIPRQCEESAIGP KFAWIISSFFHWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGFIWQPLPEPELELPKA/HLTD SFPDLLGLAAED*HCP IASEAPA LVYTAGLHCFKPSQ

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15054	45422	A	15141	1	1340	CSEYEDSSPAPVPATDLSSTLSS SVPQPDGTGTSQQHLPLDPWHE LLRAQELQGATNHKGYSAAEH EHAGLG VQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWVFSGFQAFSDRLKA ALSASLLRFGSDSWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTL QKRKKGMPPHAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTD AHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTDQPKHLTNFKSKTKET GFIHGPKTPAPVTDWEGSLPLV FNHSGTPL*LFTHVSRVSDHAG MPALVLHP*RVQVPLFWRGKI* LTSPSRCTIIEKSCNSLPPL*DKP QPHLQHTRTSKCLNRSGQAF/L PEPPPTG/CLLHVPEIWPLGQGM PAARDSS

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15055	45423	A	15142	2	2107	IDMIFTGPPSTPKHKKSQKGS AFTFSPQQSPRNEPYVARPSTSEI EDQSMGMGKFKVERQVQDMG KKLDFLVDMMHQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSCLKTIICNYSETGPPPEPPYSF HQVTIDKVSYPYGFADHPVNL RGGPSSGKVQATPPSSATTYVE RPTVLPLTLDSRVSCHSQADL QGPYSDRISPRQRSITRSDTP LSLMSVNHEELERSPGFSISQD RDDYVFGPNGSSWMREKRYL AEGETDTDTPFTPSGSMPLSST GDGISDSTVPLFLSSEILKQVVG QSITSMGLFSLRSGPSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFSLSVTSYS SFAFHKFSVAVYNISNLKTVD AKFPTRYCYCLNNTDLSDF ALLVDIGNSTSYLTFKSTSL SVNQSNESDCIFCVMTGKSGR NLSDFWEIEEKYPINIYFTSGL SGVLALLLTQSLFGLFTRTRM KFGAVTRIGGPPPLGNQSPSSCSL LHEKDPPTTSGPQTDPKKHLT NFKSAARPTFLGQGQVPLNPF FTLS/EQVLLS*AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPLLCVSSLFSLASFTM GAFTHGTQTPTSPTKATAPRYPQ TGDLSAEWFTTAGEEPVLVPRP
15056	45424	B	15143	1	930	
15057	45425	B	15144	401	1093	
15058	45426	C	15145	1	843	
15059	45427	A	15146	1	498	
15060	45428	A	15147	112	669	SLQGRSLSDYTPTFQGCQTQGC LPWSFTLCSKSRFSGEGTRFKR IKACYHSPATAWPFKAYKLSLQ FPHFTRCKTRQALQVSSSEAPY QPNCFAYPFRGAEPHSPILNTS LHNPLFCSGSQTCFLY/SLCTL HPSLSLSLGLTLPIRLSKPLPGL YCLKSSQTAITSVKPKFLPHLL PISA
15061	45429	A	15148	957	1100	

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15062	45430	A	15149	303	2028	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKHELTNFKSD KGD MFYPWTQN/YQCRSRTGK AAFPWCLITAGTPL*LYTHVSR VSDHAGMPALVLHP*RQVPLF WGRGKLLLRPS*VPILPQPLLL HPIIFLSPPLTPGPAYSFVL*LA LPHLPSNLLKRWLEPKA*SSM/ TLKGLKPVITRLQHGLLKPTN SPYNSPILPVLPDKPYKL VQD LRLINQIVLPHPVLGIHGLTSSV RRDAGQDLKRDRAEFLGDEV HHPHRRRIAEARRLLQGHEFDP LHRLIGQVLEGEARYAPPVEQ HHRLAPARRTGQRLHPLEQFG QAGRAQRNRNLGIEHRDLDRP DDGAGNALAGDGDFFRGCLFA GIGIRPRYCRYRQSQDDRRPSH AAPRPRALPIHPRPATPIADV VMFSVAIMSQRLRLVLRHIDGIS RWPPAVVFITDVKIWLVPSPDD CRIRSNDRDDMQGEAPAMSMN AAARVGDPIGHISFSQGLFGEAL DGLFFARRSEVDMRAGNLGRLI ARGLSGGRWTPADGQLTLGSR DVFIGPPATMTIRSTGQCRCQH
15063	45431	A	15150	653	1076	RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCPTPYFHDPTFPPLFW KELATSARNLATRPNACSPGF LLSCVPSVRDPTGNRTVQLTW QPLPEPLELWPKA/HLTDSFPDL LGAAED*CCPIASESP*TSDIIG RDTLLALKVQTVVLQTACGE GHVAGNCGRPLETEGSLQLTAT KKLRDSVLQPKSPEFCQQFTRA WNRITQVPDETEAPAGTYAAQS GDLPWEINPLSSCSLLHEKDPTT ASGPQTDQPKHELTNFKSGFRG VRPRRDACLGPSPLAASPAFLG KGQVPQPLLSVSLPLLRLSGGQ ETPNPFSFTLSGKSAFLEEQVPQ PRISVPQSLISTRPLISVAQSLIS APQPLISLCPNPLFPCPDLLSLHP NPLFPRPNPFAFLGACYKCQ KSGHQAKECLQGIIPKLRPICA GPHWKSDDCPHLLAATPRAPGT LAQGSLLTDSFPDILGLAAED
15064	45432	C	15151	234	449	

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15065	45433	A	15152	2095	2663	LGLGDLPEWINPPSSCLLREKD PPTTSGPQTYQPKKHLTNFKSA CFERIKACYHSPAKAWPFKAYK LSLQFPHTCLKTRHAI/PS*FSD LCLINQIVLPIHPMVNPNPYTLCC SIPPYTMHYSVLQIRAFFTIPLH P*PSLY*VSLGLTLTPIRLSKLP GLHCRKASQTPITSVKPKFHP HLLPIST
15066	45434	A	15153	678	1189	LGSGLDPEWINPLSSCLLCEKH PPTTSGPQTDQPKKHLTNFKSE TKETCFIHEPKTLAPVTD*GRQP SLGV*SLQGRPL*SFHSIRVSD HAGMPALVLHP*RVPLFWGR GKYPNPFSPCLLPLLCFSGDRG KYPNPFSPCLYSFAFLGTGQVP QPLLSLSLPLLCF
15067	45435	A	15154	649	1428	QCISELQFLLASTVRQTPATSPA HKNFQTPELQRPGVPPEPPTG ACYTCRKS GHWAKECPQGIIP KA/HLTDSFPDLLSLAA/ED*HC PIASEAPETITDAELPVTLTVEA HLHPGEINSHVAHTKPVWWSL HRDAHEIWCCDSRGTSLRRPI PCPPALCSVTKIHLRPQVLRPTS PRNISPSINPAAPHQAE LGPNPS/ SSLCSSLT*SFYHLPSSHLVWLT VSFRD
15068	45436	A	15155	240	1208	LRSGDLPEWINPLSSCLLREKD PPTTSGPQTHQPKHLTNFKSC KQ/DLFLSSPSTLTIPQLSPFN LGATLQSLPSLNFNSFHLVETK ETRFIRGPKTPAPVT/VLGRQPS LGV*SLQRCLSDYTPTFQGCQT TQGRPLPWSFTLSGK/CPLFWGR GNTL*KD*SLLSLACYSMGLLN PINSPPFSSHFTCPKTRQAVTS* VQDLRLINHIVLPIHPGGAQPH TLFCPQYRPVVLPIILFVYVKHA FFTIPLQPLIPSLSLPSRLTLTPI RLNKLPLGCCCKAFRDSPHYLN QAQISSSVTYLGIILIKAHVLSL PIVSDW
15069	45437	A	15156	1174	1623	KFGLVQLTLGKPLPEPELWPK A/HLTDSFPDLLGLAAED*HCPI ASEAPYTTTDAELRVTLTVEGK SVPFLNTEATHSTLPSFQGPLSL ASITVVIGIDGQASKPLKTPQLW CQLRQYSFKHSFLVIPTCPVPLL G*DTLTKLASLTIP

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15070	45438	A	15157	1	1610	MGLGKSLCILKDAVLALREIKG ISFYAPNITNRLWGYRQAKQT QHLSGISTLDCPQRYNGDDTGS VWALEPSCMLWACPLVFPSEIY YFISEDVWKHLDAQEKFAAVM GPSRRTSVRAVWKGNVGLEPP HRVPTGALPRVAVKRGLSSRP QNGRSTYGLHCLKDTPQEDW LVSVLPEGSRVGVDP LIPTALG HGRITFLKVLDFQGPAPCPAA MGVRLMAGPQCVSDDYWKKM AKVLRSAAGHLIPVKENLVDKI WTRDRPERPCKPLLTGLDYG SWKDKVADLRLKMAERNVM WAFVVTALDEIAWLFNLRGSD VEHNPFVFSYA IIRD*ETFMLFI DGDVRIDAPSVKEHLLDLGLE AEYRIQVHPYKSILSELKALCA DLSPREKVWVSDKASYA/V*SE TIPKDHRCMPYTPICIAKA/VK NSA/ESGMRISDEKSAGNLTED PFYVIDRTLITGVVCNSTEKSS LMSVASADTAENLWHLFFHILP SERALTRKLRVLKLGPNVYSVQ NPTAQLHQQGGPHLGVA
15071	45439	A	15158	1	756	
15072	45440	A	15159	1	1677	
15073	45441	A	15160	1220	2620	GPTEPHTGELWLESGGCPSGK LPEEGTGSNLCCSTASAGDTQA NRVCSGPPTNHSRPAADRVPVR KINKQKTATSTSTKRTSTORPH PKVTNDHSSSPAREQNWMEIE FDELTEVGFRRWVITNSSELKK HVLTCCKEAKNLEKRHSLGK EPAALKGRQYVWDSSPADLR PWLCA TLKQYKPTVFSHSTVA VHPRAGFLNLSTVDQHPVLDEP IAEAVCIADTNKWSVQVATSQ RKVPHNLKLGQDVLVSSQVSSL LQSILQLYKLHLPA DFGVDILLD NNLKCVFQLGSILPVTFRSHDP YDGEPTDELRTAACSPDTEQLA RQSGTYPVSLGQATVLEDSKA ALPGLGPTLMAVTVTTEAAV DMVVGDRGEERGGLVAPGTR GLTEIWFVPVSPSRWSSHPV VAFITLAKYGPTSSPVFHHGPN IIRHGAQGAASAGDSGSSSRCD RLPCRQNA

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15074	45442	A	15161	666	1536	FSSAGDTQANRVCSVPPTNHSR PAADRPVRRKVNKQKTATSTS TKRTSTQRPHPKVTNDHSSSPA REQNWMEFEDELTEVGFRR WVITNSSELKKHVLTCQKEAK NLEKRVVNCLTRIT*P*RRTI KTLMEKNTARE/LHEAYTSINS WINQAEERLSEIEDQLNFIKRED KITEKMKNSTTVRVAASMQSK LLQGVAAEEGPLRLTRSAFSAEI SMCHQWLFSTFGNGKSRNRYH CEKAHIEGNQLVEETGRAFKSR HRYGTGPLHKFEIHEYTELHHV LMLQGGK
15075	45443	C	15162	104	364	
15076	45444	A	15163	162	467	
15077	45445	B	15164	1	1122	
15078	45446	A	15165	188	456	
15079	45447	A	15166	485	1580	GEGYKADLAAATVECPICQQQ RLTSPQYSHIPQGDQFITW*Q VDCIGPLLKGQRFVLTGIDTYS GYVFAYPVCNASAKTIISGLTE CLIHCHGIPHSIASDQGHFMA KEVWQWAHVHGIH*SYHVAD YPEAAGLIEGWNGLLKSQQLQC QLGDNTLQGWGKVLQKPMYA LNQHLYGTVSPATIHTHGSRNQD WNGSSRLGWFTILFTAPRREP GTYIASDQRTHFMAKEVWQW AHAHGIHWSYHVADYPEAAGL IEGWNGLLKSQQLCQLGDNTL QGWGKVLQKPMYALNQHLY GTVSPATIHTHGSRNQGMVEVA PLTITPGDPQAKFLLPVPMTLCS AGLEVLVPEGGTLPPGHITPLN
15080	45448	B	15167	10	2352	
15081	45449	A	15168	2	497	WKPIAMRKSRRRQEKLLPVQK EGQPKEGEREEGGPVQAQKVP NRLHLHWT/HLPSPFQLPLLLD SLWRALKFVVLAEIVKMIRFNG VLGKCEAIRAQLHEGGPPLPL AVFHNRLQIVACRSISARLRGS PPPKSNNEQSSSLDRLTDSQRL PPLSRNAQQKG
15082	45450	B	15169	1	1911	

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15083	45451	A	15170	1	1569	MPIGKVGEYYIKGTLRATKESE QQSSALELSSDRVLYLNEKEPGD QPWNAAFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPS TLNPSNWSLTLIIQCKQEGFYS PSMRPRVVPKRGSA PKVRAEEN AALPSRCPPGGLPVAQPRGLLM GAHVSSAPAVGVGAASCHRLC PGFPDRPRPTLRSCIMNAVVG CDLRGQVYDPTGGWANEGTR DL SAVQGVPNHPGGRPCPTPOS SRQLPVVSRPPVVRPGGEAPPP LDILPAALALHQSLTPQDPRE DRPSPADLWAQDSWVGQPQEL PVGSRVVRTGTEPDTHSGSVCTS RQKKGSGPLARESSVRVILQG PSSAWMMFPEYTPGPRARAGT AVVGAMARQTVNVCLTKVRL QHPEGIPGGGRGPLVPKPVCTC/ IVDVKGSRVVWHVHICMSMGC RHVCLCGRSVGSRMCTAGQT PKLARQASIELPSMAASSTKSW WETGEVQAQSAKTSPSCKDIV AGDMSKKSLWEQKGSKTSST IKMDSVTT
15084	45452	A	15171	328	641	LLMRWSLPSAPRGFSCSCLQP QYPCRTESWPQTEPVSPVSHR LLVLATAMLGSSME/RLAG*LG GPASGLDGLGVLFQPLINLGDG QVWLGFLHTVTLLYGAV
15085	45453	B	15172	120	1458	
15086	45454	A	15173	1	440	IQQDSQAPLYSIKETQRANTYL VEWEPGAETAFKTLKQALVQA PALSLPTGQNFSLYITERAGIAF GVLTQTRGTTQPPVVYLKDGEP IEHDYQQIIAQTYATQDDLLEV PLANPDNLNLYTDGSSFVNGIR RAGYAIVSNVTVLE
15087	45455	A	15174	288	376	NHWLLLTMDPRIQQDSQAPLY SUKETQRA

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15088	45456	A	15175	777	1548	SKIQRDSQAPLYSVEETQRANT HLVEGEPEAEIAFKTLKQALVQ APALSLPTGQNFFLYITERAGIA LGILTQTRRETPQPVAYLSKEV DVVAKVWLHCLRDGEPKHDHC QQHVIQYAADDDLLEVPLANP DLNLYIDGSSSFVENGIRRAGYAI VSDVTVLENSLAAVTLQNRQG LDLLTAEKGGICTFSGKECCFY TNQSGIISPLEDTTITAGPFLHPI QQEVARAIIGQFPTAFGVSCLE GRLRGEASWTSWVE
15089	45457	A	15176	1	1359	MGPEPKNTHPGSCTCLACSSS HKGFEC LAVEQGSYTPVASPIV GVKENQEILDLELKYNQTRSA VTRCVLGAASTARIKQAEEGGR SRLAESSGLRPFVLELPALEHQ TPSSSGFELDLHQRLATWSQA FNYRLKDTLLASLLRFWDSD WLPCCSSVCSWPVGLHLVIIERN YSYQQGTETTVSSWATGVSAA ASVSATIPINRYQGHCGFLGKR CFYCCIGECNHSDHQGPQTVAG SWARGVSATASQIQVDLGKFS DDPDRYIDVHLHTWRDVMLLL DQTLAFNENNVAAAAQEFGD TWYHRPVNDRMTAEQRDKFPT DIKTAAGIPWNHWWLLTMDPQ TQRDSQAPLYS\I*ETQRANTYL VEWEPEAE/TSFKTLKQALVQA PALSILTGQNFSLYVTERARLAL GVLTQTCGTTPLYQDELRRKKT LRRHDSSEGSFGNLEASAD
15090	45458	A	15177	368	5192	AAPAPQLGLGPCKLASHLLSQS HLSQSVRSEAEQKAGASPASSI QREPLFKDQLKAPLEQKRRSL LTVPLLTFRQKCGPGSPVVAR GGATDSWLVSSEFRLSDSTAPP TELRGQEATGITKPPASLHPQPH AWDWARGRDPRRHLLGTPELQ EHSEKTTTETLPADMGLRTW ERKEATAGQAAEGAAGGIHFE ATSLLRPSYVPQTQGALSTTY KEAKMDRDLHLTPILAAQQRAR GPRIHSFSPDEMIEPS

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15091	45459	A	15178	76	969	KKSTALVIDNGSCMKAGFAG DDAPQAMFPSTVGFPGHQGV VDMGQKDSYVGNEAQSKRSIL TLKYPIKHGIITNWDNMEKIWH HFYNELHGAPE*QPVLLEDPL NPKDNREKMTQIMFETNTPA MYVAIRDVLSLYAFGRITGIVM DCGHRVTHTVPIYEGYSLPHAI LHLDLTGWDLTEYPCILFSEK SYELPDGQVITIGNEWFWCPEV LFQPSFPCMESCRHQTINSIKK CDVDIRKDNVTLSSGTTMYPG IADRMQKEITALAPSTMKIKIIA PPERKFSVWIGCS
15092	45460	A	15179	1	451	
15093	45461	A	15180	130	227	LMKMKVVM*RA*KEEERTTP AEDDFEKDLEWLINENEKSDAS IIEVYIANSIHNNYITKCFAIL
15094	45462	A	15181	104	1715	KEEERTTPAIVIPAAAFYTAY FLHKQKMENKDTDSKKEEY EDDFEKDLEWLINENEKSDASII EMACEKEENINQDLKENETVM EHTKRHSDPDKSLQDEVSPRRN DIISVPGIQPLDPISDSSENSFQ ESKLESQKDLEEEDEEVRRYI MEKIVQANKLLQNQEPVNDKR ERLLKFKDQLVDLEVPLEDIT TSKNYFENERNMFGKLSQLCIS NDFGQEDVLLSLTNGSCEENKD RTILVERDGGFELLNLQDIASQ GFLPPINNANSTENDPQQLPRS SNSSVSGTKKEDSTAKIHAVTH SSTGEPLAYIAQPPLNRKTCPS AVNSDRSKGNGKSNHRTQSAH ISPTSTYCLSPRQKELQKQLEE KREKLKREEERRKIEEEKEKKR ENDIVFKAWLQKKREQVLEMR RIQRAKEIEDMNSRENRPQQA FRLWLKKHHEEQMKERQTEEL RKQEECLFFLKGTEGRERAFKQ WLRKRMEKMAEQQAVRERT RQLRLEAKRSKQLQHLYMSE AKPFRFTDHYN

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15095	45463	A	15182	881	2040	MKAGWRQTQHLHDAGQLLHLI LPGEQGVARVQLRRDAAQAPH VNGHVVGVAQDHFVGSVEPA LDVRVYCGGKTGGKQREEREG RCGVEILMVGERKMENKETD SKESEYKDESEKDLEGLTNEN EKSDASIIEMACEKEENINQDLK ENETVIEHSKQLSDPKSLQDE VSPRRNDPISVPSIQPLDPISDS SENSFQESKLESQKDLSEEDDEE VLPSSNSCVSGIKKEDSAAKID VVTHSSTGEPLAYI/ASTYKLAY IPPLNRKTCFSSAAISDRSKNG KSN/HGQSAHISVTSTYCLSP* QKEL/QKREQKREKLKREEEQ KIEEEEEKKRENGIVFKAWLQK KREQVLEMRRIQRAKIEIDMNS RYSKTSLNKFIQI
15096	45464	A	15183	873	4292	MVVS LGRVSSLSEDSPTGRVG R*VDCKVDRSIWAGVWISEDAP SEA*EIGGLGRK*MLSGGPSPS KHVHIL*DQDSSSIPPMGPPCP PHAPGKEPGTSCSIDTDGKLSG VSGDDS*T/GTDGGESEIILLPQ *QLPVTLPSP.LP.G*VRYTSR SRSRSTRDPGRKSRPISGLRGLC GDGATS/PLTPRHAPARDVQ/P VSMFAFGADR/GDGRRGGASQ/ PAPPGPAVPRPCAQYSARAMPA SGRRRES
15097	45465	B	15184	1	2214	
15098	45466	A	15185	3	361	
15099	45467	A	15186	1	1035	MKIHKSGGLKATPQLYASQFSG VAILATWGPHRPRNSSTSFSTQS KLRRPDESSVDFQKMLCKEAT KKSKEKEPGMAFPQGHIFSDV AIKFSVEEWKCLNPEQRALYRE MMLENYRNLES/VG*LFKIHHDG VLINRARQYRSVPHRDIGKT*FL LPRNQERYSL*VSVARN*KK WP*STHNRNQRVN*VHTGEKP QKCNCGKTFSSQSYLQCHHR LHTGQKPYK*E*CDKVYSCRSQ LKTHRIHTGEKAYKCKVCEK AFWDNSCLSCQKRVHIGKPYT ALVMHKAHTGEKPYTCNECG KAFSRKANLALYHRLHTGEKP YKCECDKVYSRRSHLERHK
15100	45468	B	15187	1	1347	

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15101	45469	A	15188	1	1446	MWRETKRYAAVLLI.TPHYSAS LLPDW/PNLYLHQSGHHVPGVY LKFGSSNPIYPCVDSAKTVFPN APLHDRVQSVRRMGPFKGVFR KVFSNLGFEYSLSTWATMGSPG SLGVSPFGKTLFVESASGSLDA LWPTVEKEISSHKNYQKHSEKQ IYDVRIELTGLNALPNISLNFYK NSVSKLLNRKKGLIHLQPFILR LCVSLHKNREENLGITIQDVAM RLSALPNIVCRLYKKTASEVLK EWSTRWDEYTHHKEVVSQKALP TL SVKIYKKNICQLLNQNNGNP SEMNALITKKS VKSASGYLESI AALVEKEISSYKNYTEAFYNLL CDVYSHVTEMKLSSEIQIGNTL FVESASGVWRALRPRGKEVNDI FIDQIANSVLVDSSKDICKRFEA CGAMVKKENLHIKTRQKISEKL HWPFGAPRLTSLTQPEKTGKGE HPGAKARGELSGAPPLJHTRKL SLMSNVETLLEKLQGYTGAH
15102	45470	A	15189	1	966	
15103	45471	A	15190	157	531	GDHTTFLCLLMVNAEFKYNFK TIIS*DLLKKDGGQYGHFTIFFRS MSIGCFSIYLCIFNFFHQCFAYF LVEIFTFLVKCIPQVDSIEDTTFG HPEEATPHPFSFFMRLEQFSHIF SSWPVSFTAH
15104	45472	A	15191	9	494	PTDRPRPRALAGARGPPGRAPR VPPAGGPRPSQYGHGGRPNPR HGWHDAFCPNNTPYR/ERPLDS RYLTPGPLDMRGDSGFRTGRGS DVGSLKPTDTRRNGKIYLNGS/ NVFYYQQLRHPVHRGDGARRG FSGRCTCLHRMVC*YEQTGHQS DQT*KARSAYG
15105	45473	A	15192	1361	2038	
15106	45474	A	15193	1376	1906	LAFPDGMASLIMMSLPAMRTL AWAMAVSGNCIPEGQFSALSC ADFGISPKLIL*SSSAPNLYLAMG ISCPRADDLPEAGTAETDRACR SIPQYGTDLGWYPATAAGPQSE SVQGAV*PHRYEAG*ST/VWKP LKKK*KPLPRR*LARWQMRFR KPSPLTTSCLKTCA WRFLDFRW LE

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15107	45475	A	15194	1	1388	MIEHPRRRDNYRQSGPPVADKP TTKGEPLISDIVSDAQANLLIP VDETPPVINDEQSTSTPLTTAQT MALAAVADKNTTKDEKADDL NEDVTASLSALFAMLPGFDNTP KVDTPSTVLPTEKPTLFTKLTS EQLTTAQDDAPGTPAQPLTPL VAEAQSKAEVISTPSPSISGVT RSKMRQREWLVLPEDSLVIRR SNKTSQLPAFNVPLSAKAAAS KPWRASNTACRNSRPSKVCSAE GEQWFSASGRGEIHSQSPARDM AQMCKLAAEGHFAEARVINQR LMPHLNKLFEVNPPIPVKWACK ELGLVATDTRLRLPMTPTDSGR ETVSGDETYLEAAPLAELHAPA GMILPVTSGDYAIPVTNGSGAV GSYSAITEPGAGSDVGSLKTTY TRRNGKIYLNIGS/NVFYQQRLL HPVHRGDGARRGFSGQTCLEHR MVC*YEQTGHQSDQT*KARSA YG
15108	45476	C	15195	1	1905	
15109	45477	A	15196	285	1706	YARVHSGRSSIRRSIPVSCIRSSI RGCVPVHHCIRSSIRRSIPVDHL YQIHTKKHTRCFVSDHPYEE APDYSASLLPDWLPVPSKVVVI TYPGFTSICGYTTSSKACFSVF AWCFTSDVPGRFSEDEDDSE MWSLTALMGVMGGWKTARS EVSILCSTSSKVIHSSYPYADRA FQVWSLDARFAHINKPFGVDRF SGAEPSRAITMYGVKVLNRPA TGTARHLVPPDVPVHPHGGESN KPRVQTTVSSGISRLSIPISASAL QNVDPKTHDISNITDTVYHCPL SQSSRWYWRFPVPRSPLSNGQ TAVRPGGRAGAAGGPLSEYS GSGFGVMKWTKDQLTVTVKV HHLPEVVEFLYYKQGGWLSVL FGNDERKLNHYAVVYVLSRE KGTKCWI/TDSMDYRQR/PAPT NDAETYEFINELGARKTTVPPI GPLHVT/DEPGHLRLFVDGENI IEEANNE*IHRTQC
15110	45478	A	15197	3	1396	
15111	45479	B	15198	1	1399	

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15112	45480	A	15199	283	796	FVGVKSAGNRLKTI DELANESR SSVGLTQAALKTLESSGAIRIER RGRNGSYL VEMDNKALLTHVD INNVCAMPLPYTRL YEGLASG LKAQFDGIPFYAHMRGADIRV ECLNGVYDMAVVSRLAESY LPQKGLCLAL*LGPPPYVGE\YQ L*QVKAKSEYVKRVGHV
15113	45481	A	15200	48	3376	
15114	45482	A	15201	49	681	DPGADRRGSVWGLSDLRNTYN ALYLTHSGRLSECP TPANEEKE PTNHNRTLNTQTQKEKKKTRT KDCTTRNKSTRPGSGIAGPSY YTVAGPPSAIDPRWLRPTPPAL DPQ*MPHTSKRGKRADQSQPN ANKPNTEREKKDKNEGLHHKE QEQQRPQSGIAGPSYYTVAGP PSAIDPRWLRPTPPALDPQTEPL IFQQLEIDHYVAGLTHEVMSLS HLTLVMRWGSVSAHLAHWA RCRWISTELTPNSITSTSSPLKD CSSSPAMEQSWLENDFDELTD KKTCLCDH
15115	45483	A	15202	3	587	
15116	45484	A	15203	3	774	MVLMAGFTAGNEKGELVVLG RNGSDYSAAVLAACLRADCCEI WTDVDGVYTCDPQVDPDARLL KMSYSQAEMLSYFGAKVLHP RTITPIAQFQIPCLIKNTGNPQAP GTLIGASRDEDEL PVKGISNLN NMAMFSVSGPGMKGMVGMA ARVFAAMSRARISVVLITQSSSE YSISFCVPQSDCVRAERAMREE FYLELEESLLEPLAVTERLPIS VGSDGNPPPCGGISPKFFAALA PRPISKFVALCSGIPF

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15117	45485	A	15204	1474	1511	HS*VPANLYMELKACFTGA/NE KGELVVLGHNLA VSYFIALAAS LRADCCETWTDV DGVYTC DPR QVPDARLLKSM SYQEAMELSY FGAKVLHPR TITPIAQFQIPCLIK NTGNPQAPGT LIGASRDEDELP VKGISNLNNMAMF SVSGPGMK GMVGM AARVFAAMS RARISV GLITQSSEYSISFCVPQSDCVR AERAMQEEFY LELKEGLLEPL AVTERLAHISVVG DGMRTL RGIS AKFFAALARANINIVAIAQGSSE RSISVVVNDDATTGVRVTHQ MLFNTDQVIEVFVIGVGGVGG ALLEQLKRQQSWLKNKHIDLR VCGVANSKALLTNVHGLNLEN WQEELAQAKEP FNLRGLRLVK EYHLLNPVIV DCTSSQAVADQY ADFLREGFHV VTPNKKANTSS MDYYHQLRYAAEKSRRKFLYE HNTFVSPHIRPLIERRGRSSTRD KWCARPSTERQQDNSAARILSC QQGNTSFEHTSSIRVGT TNSLN
15118	45486	A	15205	198	462	

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15119	45487	A	15206	31	1981	RWLMRGMGIALPAAMASTVSP STIAETPEPPPLSDW/LRASG/DV VVHLLGLDPHLSLLLSICLFSR SLIWIF*LQP*SV/ALAFQMGAS LFASNIGVIEGEGPQAKPL*CLT VSYFEMLNLLNAQGPCKGLSP CQCLSLQVMTMPPEYLKKRWTL GQRSQWPQMHSVFS*LPF*A DIFAGAIKQPSGEGKYMRT G*NALVLFLLSGGLEVVHINIG CLRFQ*DISFYSDAFLAFNEVGG YESFTEKYVNATPSVVEGDNLT ISASCYTPRADSFHIFRDAVTGK GR*LPLKSSPGLFHECVTFSRQV IVQRCL/CGKDMSHVKAACIMF LFV*WLLVLPWASLDSLLNSSP DMVACVVPSECVISTLSGLARQ CPATNQCLYPPAPGLRGLMLS VMLASLMSSLTSlFNSASTRTK AQWK*L*CFCLMFKLCCFLRLI FVLLLTVVSVVWVPLVQVSQNG QLIHYTEI***LT*ISFYFLNLI FFLLLLQGAFWGLMVGLAMGL IRMITEFAYGTGSC LAPSNCPKII CGVHYI.YFSIKVPFYYTIANICL LLMHFCMVPVQLYRLCWVLR NTTLTRISSFVI*IFCNHLLIFVP DYPEKSRGCLCKAYDLFCGLQ KGPKLTKEEEEALSKKLTDTSE
15120	45488	B	15207	1	1392	
15121	45489	A	15208	57	1523	
15122	45490	A	15209	473	589	LPRQLALSCVVHCQTLVPAIRCI DWGWLF*W*SVTPVM

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15123	45491	A	15210	1	1297	MGKIMSSYQHVDLIVDCDFEA YHRQPSSGTSVVTGPSAQUALI TEKIVTYHWDQHVGDVVLNI YCVINVL DHTVKAVIDDRFMG GITTINLQLMAIIVRYFFASGSA YIVAMLPVFAMLANVSGAPLM LTALALLFSNSYGGMVTHYGG AAGPVIFGVGYNDIKSLCFDER TRIDVADTYASNWRSRCNQITF NGECPNTRQHIAAVRRGIDTLL MNDYLKQIIDI STRIAGTANN GDFGTGWITAANTVNFQIVAGT HNCHQYFIALRLFILKYIQDR AREGLKQRDLAEALSTSPQTVN NWIKRDALSREAAQQISEKFGY SLDWLLNGEGSPKKDLESNIPP ESEWGTVDADWKNTPLPDDEV EVPFLKDIEFACGDRVHDEH NGFKLRFSKVVQPRVGC*QG* G*LLYLDV**GDPLEST
15124	45492	A	15211	62	301	SWMSSPRAFFSSCTLETAAPTR MATALTSAACRLPPAAGSGSP WAPAPYRWRARRRTGPMSSDR Q*RTSQPCPEAAASR
15125	45493	A	15212	1	1665	MQDSAHLRLRPPAASRRVWLA LGSCPLPLESSPAHRA YERPSVA HQPAVPGARRSLEVPSEVPLTV PALTPPRIPAMLTAVCGSLGSQ HTEAPHASPPRLDLQPLQTYQG HTSPEAGDYPSLPQGEQLSLPL GPEVDFSQGYELPGASSRVTC DLESDSLAPGPFSLKLLQPDMS HHYESWFRPTPGAEDGSWWDD LHPGTSWMDLPHQTGALTSFG HPGALQAGLGGYVGDHQLCAP PPHFAHLLPAAGGQHLLGPP DGAKALEVAAPESQGLDSSL GAARPKGSRSSVPRSSQTVCR CPNCLEAERLGA PCGPDGGKK KHLHNCHIPGCGKAYAKTSHL KAHLRWHSGDRPFVCNWLFCG KRFTSRDELQRHLQTHGTCKKF PCAVCSRVMRSDHLAKHMKT HEGAKEEAAGAASGEGKAGGA VEPPGGKGKREAE GSSMASSPD SPCSCDCFSVPPASAI PAIVIFA HELGP TPRGAGGGVCPRRHS HSWEPAPGL*AVGGGGGASGQ AGDRGCHA*EAGRS/SCSRGS GL*RA GTS*ISASS

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15126	45494	A	15213	3	471	GRPSSPGVHGSSQTPTAHVGSF PGCGPIPPD/ACRRSKIRPGGW GGVGG/CRDGRNSR/DLRNLPC PFLFLPGP*AAAPSPWPAAAGA APCGQCLDGWPHSYSHGHSSA AGRGGICRSPLLAGELRPPGIQ YNGRTEVRGILSGSPCPPFSGAG
15127	45495	A	15214	3	449	PHQDLEEA MVLL*PPSP/PAWPT MRTRKRPSSKVSSTSRPLKXSIM TTYAVPSRAPTPA*PSASKPTNA FS/HMVGSEPRSHAHLDDGRHRD SR*RKPRPLSGPRTLGGKSLRGS AGAGRGGVPRPRPLPENLDAPL WNSPGNSAGAAVQLA
15128	45496	A	15215	26	1126	EGPSSEAAHPGGTPREQDGAM DPARKAGAQAAMIWTAGWLLL LLLRRGAQALECYSCVQKADD GCSPNMKMTVKCAPGV DVCT EAVVAVETIHGQFSLAVR/GCG SGLPGKNDRGLDLHGLLAFIQL QQCAQDRCAKLNLT SRALDP AGNESAYPPNGVECYSCVGLSR EACQGTSPVVSCYNASDHVY KGCDFGNVTLTAANVTVSLPV RGCQVQDEFCTRDGVGTGPFTLS GSCCQGSRCNSDLRNKTYFSPR IPPLVRLPPPEPTTVASTTSVTTS TSAPVRPTSTTKPMPAPTSQTTPR QGVEHEASRDEEPRLTGGAAG HQDRSNSGQYPAKGGPQQPHN KGCVAPTAGLAALLLAVAAGV
15129	45497	A	15216	1401	1983	AQRAQALECYSCVQKAD/DGC SPNMKMTVKCAPG/VDVCTEA VGAVE/SHPFWIWPRPFNAAPP LSAWPGPYDTALQARPLY*QL QARGAES*ELVH/GQFSLAVRG CGSGLPGK/NDRGLDLHGLLAF IQLQ/QCAQDRCAKLNLT SRG LDPAGTSPVVSCYNASDHVY/ KGCDFGNVTLTAEPPTVASTTS VTTTSPQ

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15130	45498	A	15217	1	964	MNVKGD TQGNTRVRVDNIGG VGAQTVNGIELIEVGGNSAGNF ALTTGTVEAGAYVYTLAKGKG NDEKNPSVYRPEAGSYISNIA AANSLFSHRLHDRHSC LQPLKI LVTGGAGFIGSAVVRHIINTQ DSVVNVDKLT YAGNRESLADV SDSERYVFEHADICDAPAMARI FAQHQPDV MHLAAESHVD RS ITGPAAFIETNIVGT YVLLAAR NYWSALDSDKKN SFRHHISTD EVYGDLPHPDEVNTEELPLFT ETTAYAPSSPY SASKASSDHLV RAWKRTYGLPTIVTNCNNY G PYHFEKLIPLVILNALE
15131	45499	B	15218	44	405	
15132	45500	A	15222	1	498	MTRSLLSVFEE DAGTLTDYTNQ LLQAMQVRVYGAQLNLLHTELA KQLAETQWFYLSYNSEKRISQTL SAMWRGRAAAQ/TQGHVWVG MVEAVCSKVSTLKD LFLGLASN EHDLSMAKYSRLPKK KENEKL AAFGQPTWCDPAERYVGFLPV GPDPGAKSAPSPRDRASTL
15133	45501	A	15223	1	1224	
15134	45502	A	15224	1	1353	
15135	45503	A	15225	1	2580	
15136	45504	A	15226	1	3117	
15137	45505	A	15227	1	1260	
15138	45506	A	15228	1	2142	
15139	45507	A	15229	1	1413	
15140	45508	A	15230	1	4049	
15141	45509	A	15231	1	381	MLMLNIGFKNFQFEHLKCSHGS YSEDIGFPNAGALSGAMFLEE KHLLFGLKEERLRASIRRESQ QRRMRKQHQRLSAS YWNLI DTMRRRKARSP/YSLAAIKNRY KGGIRDQKPSYDSLNL CMT
15142	45510	A	15232	1	467	DHSSSPAREQNW MENEFDEL T EVGFRRWVITNSSELK KHVLTQ CKEAKNLEKRLGELLTRITSLE KNINDL MELKN TARELHEAYTS INSWINQAERLSEIEDQLNEIK REDKITEKMKNSTTVRVAASM QSKLLQGVAE EGPLRLTRTSASF
15143	45511	A	15233	1	1140	
15144	45512	A	15234	1	2640	
15145	45513	A	15235	1	714	
15146	45514	B	15236	1	546	
15147	45515	B	15237	1	735	
15148	45516	B	15238	50	1603	

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15149	45517	A	15239	1374	2220	QAENSHININKKDVHSETPSEG HQRKRPKDHSSSPAREQNWME N\EFDELTEVGFRRWVITNSSEL KKHVL TQCKEAKNLEKRLGEL LTRITSLKNNINDLMELKNTAR ELHEAYTSINSWINQAEERLSEI EDQLNEIKREDKITEKMKNSTT VLVSTWGSQLEQNNLPHIISPLF HSTHDLNISFYGGCLLQACSSK LLQGLAEGGPLRLTRSAFFAA KLCLTKHFLPTMILIKSRKTTP DTQPRRLYLLQGVVDQTSRKG PTALNIRQKTFAAAPPHR
15150	45518	B	15240	1	1311	
15151	45519	B	15241	46	212	
15152	45520	A	15242	3	371	EPLPPEPPAVPSEVELQHLRKEL ERVAGELQSQVKNNQHISLLNR RQEERIREQEERLRKQEERLQE QHEKLRQLAKPQSVELKISQEV QSLQQQPDHFLGHLQQYVIAT LSAARWAAQQLD
15153	45521	A	15243	392	558	
15154	45522	B	15244	52	689	
15155	45523	B	15245	400	603	
15156	45524	A	15246	5	1158	RKFWRWMVVMMAAQHSQAAQ GQRR**VSKGP**PGPMGGPVL GHWWHSGGISLAVPSLPPGKS SVFLFLFSASFSDMKLNPGTVSP RLIFGSYDDGFLVETVVKFDFQ LWQKTPLHRAAGERRRAEQRG KLSFVMP

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15157	45525	A	15247	1	1808	MAEETQHNLAAAKKKSATGF HREGPTSSATLKDLESPCQERA VVLDSSTVKISRLKNTIKSLKQQ KKQVEHQLEEVTPDNLPVWV GLSWGIGGILGACLLCHLCLP LEKKANNERQKAERELEVQIQT LIHQKEELNTDLYHMERSLRYFE EESKDLAVRLQHSIQCKGEI.FS ALSAVIATEKKKANQLSSRSKA RTEWKLEQSMREEALLKQVLT QLKESFQQVQLERDEYSEHLKG ERARWQQMRKMSQEICTLKK EKQQDMRRVEELERSLSKLKN QMAEPLPPEPPAVPSEVELQHL RKELERVAGELQSQVKNNQHIS LLNRRQEERIREERLRKQEE RLQEHEKLRLQAKPHCAFSSRS *TMRTRAHLQLEQQVKELQE/Q ALARVFLQVELKSQEAQSLQQ QPDHYLGHPAAEHLEAASQQN QQLTAQLSLMALPGEGHGEH LDSEGEAPRPMPSPVEDLES EAMVAFKKSAGASAQEKQAL QEQVKEQRVCCQRLAHPVASA QKFEPAARPGAPGPGGESSF MDHLKEKADLSE/PGEKRTLH P/PTG/GDRRHQKTHHLLSEPGG CAK/DAALGPQHHQAGAQQGGD
15158	45526	A	15248	2085	2700	YPGKRGLEWT*ANSNRPAAG PDE/SSSLPATEQSWMENDFE LRKEGFRRSVITNFSKLEEDVQ THRKEAKNLEKGLDEWLTRINS IEKTLNDLMMEMKTMA*ELHDT CTSFSSRVQVEERLSVI*QDM NEMK*EEKFREKRVKRNEQSL QEIWNYVKRPNLHIGVSEIDR ENGTKLENTLQDIFQENFTYLA RQANIQIEI

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15159	45527	A	15249	378	1744	QTERNSININKKDIHTKTPSVRH HHQRPKLHKTTKMGKKHSRKA ENSKNQSGLPPKECSSPAVE QSWTENEFDEFT EEGFRRIESQ MNEIKGEEKFREKRVKRNEQSL QEIWDYVVKRPDLRLIGVPDSDG ENGTRLENTLQDIIRENFPNLAR QASIQEIQTPTQRYSSRRATP RHIIVRFTKVEMKEKMLRAARE KELKIKKLTQNCLETTWKLNNLL LNDYVWHNEMKGEIKMFFETN ENIDTTYQNLWHTFKAVCRGK FIALNAHKRQERSKIDTLASQ LKEIEKQEQTSHKASRRQEITKI RVELKEIETQKSLQKINESRSWF FEKINKIDRPLRLIKKKREKNQ IDTIKNDKGDITTNPTIEQTSRE YYKHL YANKLENLEEMDKFLD TYTSLGLENKEEVSLENTSITGSE VEAIINSIPTKKKSRTRWIHSRIL PEVQGGAA
15160	45528	A	15250	935	1269	LIEGKLTERNININKKDIHTKT PSVG/PPSSKTKDRSSLP AIEQS WMENDFDELTEVGFRRSVITNL SKLKEDVRIPHKEATNLEKRLD EWLTRINSIEKTLDDLMEKMTM
15161	45529	A	15251	401	497	KTFSPFYFS*RRRTVRDINGFTE Y*EPEKLLG
15162	45530	B	15252	220	940	
15163	45531	A	15253	1	1476	

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15164	45532	A	15254	1	2423	MNGKNTNIYQEPTVCQALHW TLARIGKEEPRRGQRGEGLLCS RERQPRGLSSPGTAAPAAPAP TPPALPGHRTSRGSPGEPILR RGGSADAPGRVKTWVNRPAF VGKCLDGSDTACDQAMKG QRGSNRKRKTSLSLTFPTSSDM HAGGLSAAHPCAHSRAPPPASP SPYKGLGTRTDGLTDSRADSA ASGARALGVDDGPQPSPPRRAP PRPVGADGSSRGPGQRRRVER RGPATQPGDSRALPEPRGVPAV HPAGSGSEWERPPAAPSPPEHR DKMLPGLRRLQLQASARRPQPP EAAARWWVWSPCFSSGTLCPSPFQ ERPLLPFGGASFPQTTLHQRCLP VAALHSGSGKGQKWQSQSHCYA AAVMEPPAPGRSSLSLQGPLS WAGGAPASACLLMLLALPLA APSCPMLCTCYSSPPTVSCQAN NFSSVPLSLPPSTQRLFLQNNLI RTLGARHLWVQPAHPVALLQQ PLHHLPGHFPP/LQALEELDGLD NRHLRSLEPDTFQGLERLQSLH LYRCQLSSLPGNIFRGLVSLQYL YLQENSLHLQDDLFADLANLE PTSLHGNRLRLTEHVFRGLG SLDRLLHGNRLQGVHRAAFR GLSRLTILYLFNNLSASLPGEAL ADLPSLEFLRLNANPWACDCR ARPLWAWFQARVSSSDVTCA TPPERQGRDLRALREADFQACP
15165	45533	B	15255	47	482	
15166	45534	A	15256	1	636	MRDPNTKRSRGFGVTCATVE EVDAAAMNARCKVVGRTVEPK RAVSRSDSQRPEDTEELHLRDY FEQYQKIEVIEIMTDQSGKKR GFAVTFDNDHSDMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQGRSGSGNFGGGRGGGF GGNDNFGRGGNFGHGGFGGS HGGGGYGGSGDGYNGFGNDG GGGSYNDFVYNNQSSHFPGM

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15167	45535	A	15257	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDLSLRSHFEQWGLTDCVV MRDPNTKRSRGFGVYATVE EVDAAAMNARPHKVDGRVVEP KRAVSRSDSQRPDYFEQYGKIE VIEIMTDRSGKKRGFAVTFD DHDSVDKTVIQYHTVNGHNC EVRKALSKQEMASASSSQGRS GSGNFGGGRGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSYGSGRRF
15168	45536	A	15258	1	286	
15169	45537	A	15259	1	1674	
15170	45538	A	15260	235	1370	KREGEGRLADTFVSLLSARGR RRRSIVKVSHPAVMSKSESPK EPEQLRKLFIGGLSFEITDES LSRSHFEQWGLTDCVVMRDPNT KRSRGFGFVYATVEEVDAAAM NARPHKVDGRVVEPKRAVSR EDSQRPGAHLTVKKIFVGWH* RKTTFWGGKKRAKHHHLRD YFEQYGKIEVIEIH*LDR/GQWP RKRGFVFTDDPDSVDKIV/ QKYHTVNGHNCEVRKALSKQ EMASASSSQGRSGSGNFGG GRGGFGGNDNFGRGGNFS/ GRGGFGGTGGGGYGG/SVG DGYNGFGNDGSNFGGGGSYN DFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRN/ QGGYGGSSSSSYGSGRRF
15171	45539	B	15261	1	660	
15172	45540	A	15262	2	486	KMRQREARQGGK/VAPAPAVV K/KQEAKKVNNPFEKRPKNFG IGQDIQPKRDLTRFVKWPRYIR LQRQRAILYKRLKVPAINQFT QALDRQTATQLLKLAKYRP/G DKGALAKLVEAIRTNYNDRYD EIRRHWWGNNVLGPKSVARIAKL EKAKAKELATKLG

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15173	45541	A	15263	3	845	PPKMPKGGKKAKGKKVAPAPAV VKKQEAKKVVNPLFEKRPKNF GIGQDIQPKRDLTRFVKWPRYI RLQRQRAILYKRLKVPPAINQF TQALDRQTATQLLK/LVAHKYR PTEKQEKQRLALARA/EKKAA WQKGTSPTKRPPVLR/AGS*HP VTTLVENKKASAGW/WIAHRR GFPSSLVVFLPALCREKWGSPY ICIIKGKARLGRLVTRKCTTV AFITQVNLGRQALLKLVEAI RTNYNDRYDEIRRHGGNVLG PKSVARIAKLEKAKAK/ELATK
15174	45542	A	15264	1	5796	MPRVEKNIPGRNRNSKGFEDPLE VTQDVTREWAKKVVWVWREKA SKINGAYFCEGRVGEAIRIRT MKMRQQATLTMTVDKGDNVN ISFKKVLKEEDAVIYKNGSFIH SVPRHEVPDILEVHLPHAQPD AGVYSARYIGGNLFTSAFTRLI VRILPPQENIKISNITHSSAVIS WTILDGYSISSITIRYKVQKGNE DQHV DVKIKNATITQYQLKGLE PETAYQV DIFAENNIGSSNPAFS HELVTLPESQAPADLGGGKML LIAILGSAGMTCLTVLLAFLIILQ LKRANVQRRMAQAFQNVREEP AVQFNSGTLALNRKVKNPDP TIYPVLDWNDIKFQDVI GEGNF GQVLKARJJKDGLRMDAAIKR MKEYASKDDHDFAGELEVLC KLGHHPNIINLLGACEHRERGD RRHLENQVPTLILRFSNLSKR HTRRLYPEPGSEGPTPTPEPSLL AQQSEIKLHGGSEPLLIFRQTG SGVDLQQTPTNLQLRVLTVRR KTDKRKGHPHQKPICSSPSSKT KEGFRRSNYSKLEEVQTHGK EVKNLEKKLDKWLTRITNAEK SLKDLMEKTKARELCDECASL TSQFDQLDKRVSVMEDQMNE MKQEEKFREKRIKRNESLQEI WDYVKRPNCLIGAPESDGEN GTKLENTLQDIQENFPNITRQA NIQIQEIQRTPQRYSSRRATPRHI
15175	45543	A	15265	1	2212	

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15176	45544	A	15266	1	743	PPLLIFRQTGSGVDLQQTPTNLQ LRVLTVRRKTDKRGHPHQKPI CSSPSSKTKEGFRSSNYSKLKEE VQTHGKEVKNEKKLDKWLTR ITNAEKSLKDLMEKLTARELC DECASTLSQFDQDKRVSVME DQMNEMKQEEKFREKRIKRN QSLQEIWDYVVRPNLCLIGAPE SDGENTKLENTLQDIQENFPN ITRQANIQEIQRTPQRYSSRR ATPRHIIVRFTKVEMKEK/MLR AAREK
15177	45545	A	15267	1	618	EVSRRNTRTKTSYKQDMNTSK GF*KDTST*PVT/KERSSSPATEQ CWTENDFDELREEGFRSSNYSE LKEEVRTNGKEVKNEKKLDE WLTRITNAEKSLKDLMEKTM ARELCDETSLSRRCDQLEERV SVMEDEMNM
15178	45546	A	15268	200	618	
15179	45547	A	15269	158	594	SGSSICCSPISTVLQPPLLTQRQT GSGATSSK/SPTDLQLRECS SSP AKEQSWMENDFDELREGFRSS NYSLEKEEVQTHGKEVENLEK KIDEWLTRITNAEKSLKDLME KTMAREQCDECTLSRRDQLE ERSVIEDQINEMK
15180	45548	A	15270	3	1453	LSDLELAQSIIFAGYETTSSV LSFTLYELATHPDVQQKLQKEI DAVLPNKERSSSPATEQSWTEN DFDELREEGFRSSNYPELKEEV RTHGKEVRNLEKKIRQM/VTRI NAEKSLKDLMEKLTARELRD ECTLSQFNQLEERVSVMEQ MNMKKEEKFRKRIRKKEQS LQEIWDYVVRPNLRLIGVPESD GENRTKLENTLQDIQENFPNLA RQANIQEIQRTPQRYSSRRAT PRHIIVRFTKVEMKEKMLRAAR EKEIQTIREYYKHYANKLEN LEEMDKFLDTYTLRLNQEEVE TLNRPITGSEIAIINSLPTKKS PDPGFTAIFYQRYKEDLVPFPL KLFQSIKEGILPNSFYEASIIIP KPGRDTTKENFRPISLMNSDT KILNKILANRIQHIKKLIHHDQ VGFIPGMQGWFNIRKSINIQH NRTNDKTHMISIDAFAFNKIQ QPFMLKTLNKL
15181	45549	C	15271	111	269	

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15182	45550	A	15272	94	4505	YLDMMSFVQKGSWLLALLHP THLAQQEA VEGGCSHLGQSYA DRDVKPEPCQICVCDGSGVLC DDIICDDQELDCPNPEIPFGGCC AVCPQPTATPRPPNGQGQGP KGDPPGPIGRNGDPGIPGQP GSPGSPGPGICESCTGPGQNY PQYDSYDVKSGVA VGGLAGYP GPAGPPGPPGPGTSGHPGSPGS PGYQGPGEQAGPSGPPGPP GAIGPSGPAKDGESGRPRGP ERLGPPIKIG
15183	45551	A	15273	1628	1832	RRRRKARERRRLAAEQGRMK EQCKDGFSE/QASGALKLMGSN EGEFKAEGNSKFTYTVLEDGCT KHTG
15184	45552	A	15274	1	362	
15185	45553	A	15275	1076	1240	LRQLL*LCPSWRLCLLGGWQL HLFF*RHFFVHLVSQRCSIAM SPSRRCFSLHL
15186	45554	B	15276	480	1167	
15187	45555	A	15277	3	379	
15188	45556	B	15278	13	369	
15189	45557	A	15279	112	1112	WPPASPSASVIRTVKEFALTNP KSSTKETERKETKAEELDAEV LEVFFHPTHEWQALQPGQACPC RNPTYGLNLQTGEREAKLQYE DKFRNNLKGRLDINTNTYTSQ DLKSALAKFKEGAEMESSKED KARQAEVKRLFRPIELKKDFD ELNVVIETDMQIMVRLINKFNS SSSSLEEKIAALFDLEYVHQ DNAQDLLSFGGLQVVINGLNT EPLVKEYAAFLVGAFFSNPKV Q/EWEAIEGGALQKLLVILATE QPLTAKKKVFLALCSLLRHFPY AQRQFLKLGGLQVLRITLAGE GHGGARRARGHTALRCPCHREK CSPRRRLS
15190	45558	B	15280	54	385	
15191	45559	B	15281	274	776	

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15192	45560	A	15282	362	1323	HQLGRSALLDTRTVSMQKAKN GDAVTEPQVA/ENEANGKDTA EVDLLTKELEDFEMKKATARA VTGILASHPCSTDVHIINLSLTF HGQELPSDTKLELSVVRHYGLI GLNGTENSMLLSAVGKHGVP EHIDIYHLTREMPSPDKTPLHSL VTVSSPRQRDDMSDGHLCAR RHTDIRDDRSPDAPDTARSLAR STITTRRIFALATPSRTLQVCS ALAYTSHPAARTQLASTALTR RYMLPSPQLPSLRDHRRTNPLH SAVATIPHTTTGEADVSLLCIGL STLHYALVYHVSVLTAALSAQS MSATDASIIFFPKR
15193	45561	A	15283	3	537	
15194	45562	A	15284	1	455	MPRPEKLGKTQVPLAECLTKD SFLGQKQASLGLPTFRDVTIEFS LEEWCQLDVTQQNLYRDVMLE NYRNLVFLVISS/HFTQDFWPD QSIKDSF/QRIILRTYARCGHKN LRLEKIVKVS MRKHQIIHTGKK PYKCECAKLLSPQLENMR
15195	45563	A	15285	1	397	FAVLMAHYDVQEEDPVLTVIT YMGLSVSLLCLLAALTFLLC KAIQNTSTSLHLQLSLCLFLAHL LFLVAIDQTGHKVLCSIIAGTLH YLYLATLTWMLLEALYLFLLTA RNLTVVNYSSINRFMKMLMFPV
15196	45564	A	15286	191	1332	AJETQAITDNCSEERKTFNLSV QMNSMDIRCSDIQGDTCQGPSVI AFISYSSLGNIINATFFEEMDKK DQVYVLSQVVSAAIGPKRNVSL SKSVTLTFQHVKMTPTKKVFC VYWKSTGAG/CSQWSRDGCFLL HVNKSHMTMCNCSHLSFVAVLM ALTSQEEDPVLTVITYVGLSVSL LCLLLAALTFLLCCKAIRNTSTSL HLQLSLCLFLAHLFLVIGDRTE PKVLCSSIIAGALHYLYLAFTW MLLEGVHLFLTARNLTVVNYS SINRLMKWIMFPVGYGVPVAVT VAISAASWPHLYGTADRLAF KATAQLFILGCTWCLGLLQVGP AAQVMAYLFTIINSLGFFIFLV YCLLSQQAHHKFTPMEVPRQN HRCLOQN
15197	45565	A	15287	263	397	GRPPAPAAVSGPASVSAG*KR VSAGSVGVRSMRRGSALLPPN F

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15198	45566	A	15288	1	278	MKFDHGRGQMOPKPSAEAVNS APQREPEGSILRAADPLVWAAK AMSASR/RGS/CGGSSADPRHTE RTPTPEPDADTRFQPAETLAGPK TRAAGAG
15199	45567	A	15289	5	545	SFMTEAKSSPNPAQQRLSTQRP SESRRKVPSSSELQTLSCGLQRPC HPGRPGDPYYASASTRTRSPS ARHAVWGRRGCYPEA/AVRAR EGPHPTLAPASTYGLASPPRAD SAHRPRHRSLSRLLPNRKLGG SADPRHTERTPTPEPDADTRFQ PAETLAGPKTRAAGAGGQPWD S ANASPP
15200	45568	B	15290	121	822	
15201	45569	A	15291	1	1308	MLRMVIGIEISNGQWSTPPCQVL HLEGNDIYNPKEQGLGNTCRW GWMAAGTRRNLCWAPFPFLNP VASLVLHSTIQIALQESKDRVL GTLINSLPVTSTDKANWSRLA LEVGDGGGLVGLSPQVVGSA MSRCPNCTRKLGSGISPTSSL AEEQGSVVKTHSHQGGARCSK EKGWQIL.LILVAGLCQLVVVV QNVGVRKIPRKYLAALRVAIGH ALAIERRRIRVDVADQAQDTDR DDRSFGRDRNRDSKTDTDWR ARSATSDSDDDYPPRRGDDRF GDKYRDYDSQYGRGYWYER DGPCTDMDRYGGSGRRAFG SGY/RRDNDYRGGRDRYEDRY NRWDGSGSSRDSDRSDDCRY NDRRPPQRPKLNLPKHPNTPKGD DSSASTSQSSRASVFGGAKPV DRAARETKVEEVLQEQDKLQ HQLDEAKLE
15202	45570	A	15292	2	293	
15203	45571	C	15293	56	298	
15204	45572	A	15294	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYL.SACRHPMEDSMDMD MSPLRPQNYLFGSLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS

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15205	45573	A	15295	3	1024	CGGIHSLVLRGCSLEPAFFYLRSASFPTISACRHPMEDSMDMDMSPLRPQNYLFGCELEKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIKVTLVATLKMSVQPTVFPWGAFEITPTQWSRLRLKCGSGPVHISGQIIFSKLLEEDAESEDEEEEDVKLALSISGKRSAPGGGSKVPQKSKTLLLMKDDDDDEEDDDEDGD*WMDFGWMEEAEEKAPSERNPIRDTPAKNAQKSNQNGKDSKPSSTPRSKQGESFKKQEKTPKTPKGSSVEDIKAKMQASIEKGGSLLPKVEAKFINYVKNCFRMTDQEAIQDLWQWRKSL
15206	45574	B	15296	1	1107	MLASMGVVAEKMKYLSSPYQGHAFHTRJLSMTVNFQAQLWL PNEAGPTGDDWGGDTHGCPSFSPHLPRFIQKQPWGTGRLLQEHFSCSKSLVPVPSRDIEAFHLHADLILNTLPSLVIIQIEHSEELRARVSTYESGEDTIQCITVTWKPKYGATRWKDPGSPDGPLEER RLEDLSTRNNSIRLFRGCGYRVKQNSSQRPNKVCGLPDTGVLLQTKCGLVRNSQRSAPNTNKQH EELFSTAGIPENLSRRQEVLPGHGFTGWVGWTWKLTSGEGVTFHHLSATHKLSHASCRQGNFKPKGAMSVTRSTVHPHLAFLSAEINGKCGRPCVFLGIWAINCGMAILYERLSALVCVSVSERHLDYTMRFDFDIPSTLEARIGSPLWALSLHPLRSSVTSSVELILPECTVAVLEIQYVFLGDTILFTTVGKARSCTRDRDGGRAQIMQVLQGGKGRELDAAPQPEGQLLREVRVLGVFPFIPRARVDAWLVTVAVGSADEAHGLLGAAASSTGGAGASVDGGSQAVQGGGGDPRAARSGPLDAGEEEKAPAEPTAQVADAGGCASEENEVLREKHEAVDHSOREENEERVSALKENSLQQNNDDENKIAEKPDWEAEKTSERNERHLNGADTSFVSEDLFQLL
15207	45575	A	15297	1	1968	

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15208	45576	A	15298	1	2104	MKHLKR VWSAGGGLLHLTL LSLAGLRVDLDLYLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRLGVFPVPTSV DAWLVSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGG/CASEE NGVLREKHEA\VDHSSQHEENE ERVSAQKENSLLQNNDDENKI AEKPDWEAEKTTESGNE\RLH NGTDTSFSLAEDLFQLLSSQPAEN SL\EGISIWGD\PLPGISIDGHEF FKHIYHVNFQPRLS\QD\VNHL EAILLCNNTRFRDPTARTSQSQ EPFLQLNSHTTNPEQTLPGTNLT GFLSPVDNHRNLTSQLLYD LDINIFDEINMLSLATEDNFDP DVSQLFDEPDSDSGLSLDSSH NTSVIKSNSSHSVCDGAGYCT DHSSSSHHLEGA VGGYYPEPS KLCHLDQSDSDFHGDLTQHV HNHTYHLQPTAPESTSEPPWP GKSQKIRSRYLETDRNLSRDE QRAKALHIPFSVDEIVGMPVDS FNSMLSRYYLTDLQVSLRIDRR RGKNKVAQAQNCRRKLDIILNL EDDVCNLQAKKETLKREQAQC NKAINIMKQKLHDLYHDFSR RDDQGRPVNPNHYALQCTHDG SILIVPKELVASGHKKETQKGK
15209	45577	A	15299	2	342	RRFRVAAAAGVTA*AVVLSA RPSETWETRGR*RICPSSWP* GI*VNNG*K*RRHSVCQCSLWF PARCIKPYHSMARITQPGTRNKE NGPAGPTALDNVASSDDTGRH RPQT

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15210	45578	A	15300	710	1831	IRMKSKEIHARCIPYHSMARTQ PGTRNKENGPAIPTALDNNVASS DDTGRHRPQTITQLAPGFHPLQ LASFRMRVLFSLSGEGRSRGGPE LQFPASCRRRGEGSPGVRESGSG GIAATSTPNYPNPQDSKEHDIR GAEHQKQEQPAKPPHTARSAY PPQKSSYPANAKATRHSPETAA AKEARAPAAAQQRHQPNPSP APHTRPATAATRQPERRVPSPT HRHPAATRLSPRRQSPSPRPHH DRRGFPRLAETLQHPMCPLPLV ASAGHHRHHRLLLLAPQAPER EASDEIVFSGRSRSGCTEFQE SAMCFPNPGLPDSGESQAVTI LILRKFKQVIWVIEVPLDYKKG SWEYFSRMETHIMPFENIQSE
15211	45579	A	15301	77	1041	IPSCVVSIGIAAAF/HPGLASDAP ARASSWWTHVEMGPPDPILGV TEGFKRDTNSKKMNLGVSAJR DHNGKPYSIHKAEEAIAAKNLD EDYLSIGRLAEFCKASAEVALG ENSEVSKSGREVTVTQISGTSAL RIRASFLQRFLKFSQDVFLPKPT WGSRTPIFRDTGMQLQGYRY DRKTCGDFDITDVEDISKTPAQ SLLLLHACSHNPTGVDPGPKQQ KEIATVVKKT/RNFLALFDMA YQGFASGNGNKDAWAVRHSAN IRHCRCSQSYTKNMVVLHSEGV A GFTMVCKDADEAKRVESHKI LMCPMYSNPPLNGTRLLLPF
15212	45580	A	15302	1	1263	
15213	45581	A	15303	1	1146	MTGRQSLSPVLSSSLDSMSFT TRSFSTNYLFLGSVQVSNYGA RPASCMASVYAGAGSGSRISV SRSTSFRGGMGSGDLAAGMAG GLAGMGGIQNKETMQSLNDR LASYLDRVRSLETNKRKLESKI REHLEKKGLQVRDWSHYLKT IEDLRVQIFANTVDNAGIVLQID NACLAADDPRVKSLMTNVTWL PLETEMEALKEELLFMKKNHEE EVKGLQAQIASSELTVEIEKSTT VVTQTQTKVGDAEMTLTELRR TVQSLKMDLDSMRNLKASLEN SLREVEARYTLQMEQLNRILLH LESEMAQSRAEGHQIGEYEAAL LNIKVKLEASATYHRLDDDD FNLGDLDNSNSMTI/QKTTT RRKVVSETNDTKVL

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15214	45582	A	15304	184	370	
15215	45583	A	15305	40	1411	RGDPRVRRRTQSLSPVLSLSPDS MSFTIRSFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL ESKNPEHLEKKGPQVRDWSHY FKIIEDLRAQIFANTVEQCPTTV L/LRIDS\RLA\ADDFRVKYET EAGPCAQS\VENNIHGLCKVIDD TNVTRLQLEIEALKEELLFM KKNHEEEVKGL*AQIASSELTV EVDAPKSQLAEIMADIRAQYD ELARKNREELDKYWSQQIEEST TVVTTQSAEVGAAETTLTELRR TVQSLIEDLDSMRNLKASLENS LREVEARYALQMEQLNGILLHL ESELAQTRAEGQRQAQVEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
15216	45584	A	15306	392	1449	GPWEMLMTIKSHPD\AERQQR VKKLTVQVFWSSASLRER/GKTY LFWPKLKKA\A\IPAA\YREALDE ALGISGGGRDVG\ERVYKGPSM MANPQKPVLEALSSNKYLHLIC AKHCDRHEGYKDEIKVKEASS RVNGC\VEAMLSAPLPLDRRNE HVESKGKPFMTGLSPRVLSASR RDGLRERKGSFFRTVVLHDTKT DSNSDTE\TNSSTPPRTLLEMQIL SPTWTY\EISSRTLGC\GPSVFQG RASYS\PSVSGPRLGCPLMDGGR MRCPPGNPESC\VEANLIPISVP VAPHAHQHLVLSV\FK\ITVIG GKTCVAQNH\SN\EA\KMKQRPEI NHASPPGAF\AWSQS\GEPIASAM TVPA

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15217	45585	A	15307	1	785	MWDVVGQDSSLLRGAGGPGQLQWFGRLQLHLGGLREHRDAWVHSRGLGSCSGMQGAATPTQNGRGCLSPAPASSMEHAAPAVPPCCSWCDSSSRSRWPATATTETGPRTPVPSAQESAVGLLTASLLKGDSGSTGFCPLLMSLAAPGTQQC SLGFCCTFERKRSVSPAAPGTAPELAAALMLMPRKNQIAVYELLFKQGMVVAKEGVHLPRHPELADKNVPNLHIMKAMQSLKSQGHREEQFAWRHFYWHLTREGIQSIQ
15218	45586	A	15308	1	392	
15219	45587	A	15309	1	716	
15220	45588	A	15310	150	372	RRSNEWGVVPVVPARTGGG/HGQKTPPSPLPPSPSPSPSPPPPAVAPAKIPPLPLPLPPREAPPAPGPALP
15221	45589	A	15311	218	740	KSCPETVSRRKNVGSIKKHQGD KFNVPVCLKMTTKEFVLCGWVPCRCL/REGEEETVTTLDYSHCS\LEQVPKKEIFTFEKLTLEELYLDAQIEELPKQLFNCQSLHKLSPDNDLTTLPASIANLNLREL DVSKNGIQEFPENIKNCKVLTIVEASVNPISKLPDGFSQLLNLQ
15222	45590	A	15312	96	297	
15223	45591	A	15313	469	5174	KMTSLAQQLQRLALPQSDASLLSRDEVASLLFDPKEAATIDRDTAFAIGCTGLEELLGIDPSFEQFEAPLFSQLAKTLERSVQTKAVNKQLDENISFLIHLSPYFLKPAQKCLEWLIHRFHIHLYNQDSLACVLPYHETRIJFVRVIQLLKINNSKHRWFVLLPVKQSGVPLAKGT LITHCYKDLGFMDFICSLVTKSVKVFAYEPGSSAQLRVLLAFYASTIVSALVAEDVSDNIIAKLFPYIQKGLKSSL
15224	45592	A	15314	267	495	GCLL**CLCIRL/SKNRAERALRPYSDEALRLSSDPFRQRPKGSGWSLLSVEINQYGYGRVMIGRSNSEVVVL

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15225	45593	A	15315	3	3027	AMEQAGTRPAATEHPRLRRPM PWLLLLPLLLLLLLLLPGPAASQ LRYSVPEEQAPGALVGNVARA LGLELRLRGPGCLRNHLGAPSP RYLELDLTSGALFVNERIDREA LCEQRPRCLLSLEVLAHNPVAV SAVEVEILDINDNSPRFPRPNYQ LQVSVSAPGARFHIESAQDPD VGANSVQTYELSPSEHFELDLK PLQENSKVLELVLRKGLDREQA ALHHLVLTAVDGGIPARSGTAQ ISVRVLDTNDNS
15226	45594	A	15316	1	775	MPCVNGKYNSTIQAGLQMAQI LQDEGPYEVGIDEETGSQKGDG IIRSSRKLFTMALFLETNLLKD PLSRERRWRLELDGSGGREKG VAVFLRSAGIRQVQVAMEQAG TRP/AATEHPRLRRMPWLLL/L PLLLLLLLLLPGPAA/SQLRYSV PEEQAPGAL/VGNVARALGLEL RRLGPG/CLRNHLGAPSPRYLE/ LDLTSGALFVNERIDREACLSG AGANPVA/SAVEVEILDIN/DNS PRFPRPNYQLQVTARCWWTSW
15227	45595	A	15317	2	165	
15228	45596	A	15318	1239	2251	TCSSRRARRPRGRTVSQVRGPA PWAPRRARLQQRGSLRGAARS PASPTSA/PSYSRASASAGPAAL QPQGA VTPGPSANLAAPGGTL VPAEGPRMPVTAQSASSHPAP SASQPSPPAAASRGSLSVPEVT ATLLASASSPTLDATRDAPATP RIAAPPGSATSSRGLGSAQGS LGTKEISIDSFGLGSPAVTQRTT APPDSAAALSQDTRPEAAGSWPG PQTGACSVGSGTDRRDTAAAT EAQHLSSESKEKTSAQKSGNCF GILKADFTISTLMDPEEMKDQF LRQVRLPSTDALKKQSI SNYRP PGKGPQYYLGDSA WNMVSA GTIEGFYKE
15229	45597	A	15319	46	2859	

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15230	45598	A	15320	240	924	NGEQKCILCHIVYSSKKRHSHE CRRCGPTEVSLSAYAKHISGQL HKDNVDAQEREDDGKGEESSE DYFDKELIQLIKQRKEQSRQEPS SSSQEVNSDDSSATFSVSFVYV WLKTILLTWPKEVKRLDTPGL ELWL.VPNMAELSEPEGVDWK ERCVALESQMKFRVQASKIRE LLAEKLLHNERLEYRDQRKDS ASFQKKQFTYKASGIEMASDL SKAPLEIRG
15231	45599	A	15321	3	755	LRLPRSTRTRRGIVWRTGAAM GKVNVAKLRYMSRDDFRVLTA VEMGMKNHEIVPGSLIASIASL KHGGCNKVLREL VKHKLIAWE RTKTVOGYRLTNAGDYDLALK TLSSRQVVECVGINQMGVKGIE SYIYIVANEEGQQFALKLHLRL RTSFRNLKNKRDYHIHRHNVS WLYLSRLSGMKFCYMKQPCD EQGSQRLRIHMMGGQMWAAPIC QPRDLFVWFVLRAEACACCGA TSQORGALGVTSTCYRD
15232	45600	A	15322	1	1028	MNKTITTQEEVLPLQADV VQRE EELNSLKQKLA AALLAEQEPQP ERLVSELQLPRKAAVFDQDEILR SSRQLVLPVLGVHRHVLVCC GGLRCLAGGLAAA SVGRGLG VDCDVVEMS NLAYQVLHGEAL AAQAKAASAAASLRGLNLAPP PAETVTNCADGGMLRVLTGVL GCLQPLKVLKIAASLGPSYSGS LLLFDALRGHFCCIRLSRCLDC AACGKWPTVTTHLLDYEAFCGS SATDKCRSLQLLGPEDRVSVTD YKRLLDSGAPHL LDIRPKMEL PRKAAVFHDEILRSSQLVLP GVLRLHLLVGGCGGLRCLPAQY LAAAI VGRGLVA YDVV
15233	45601	A	15323	92	778	QGTTRRWSLGTCSLMTRTQFEV CTKVCVQESLQRPGEELKTRCP SVGAGYVNYGTPAHERJ/GAAV KTGREADKPEVTQTQFSTRK DE/TSLFGVPLQ*LLARHRAPP* RRT/RRLLEVARTPMLPAQASR SELAARQDSA WASPAAPASN/ RSVLRRCLLSARPPLCGPL/LRV LPSWRRQIIRENSAED* LHSEY RANRIRRRRGHPEN/WTKS*LE NPENLTRSSSAPAPC
15234	45602	A	15324	142	500	

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15235	45603	A	15325	3	343	
15236	45604	A	15326	1164	1648	PLMTAPWPSCCWRSLSSGRP AGRQRQLPTSTTANQPA ^P SR ^R KKSTSRKKQRNLPAVSPAMVAI VRRSCDLYRWSVLHIYASQERR VRDAAKPESD ^R KKRTT ^T KTR ^R /H WRYIKELESRQPGVADMRQQP TQLVEVPWNEQTPEQRQQT ^L Q RQHGRETRCSV
15237	45605	A	15327	28	417	
15238	45606	A	15328	2	440	
15239	45607	B	15329	1	441	
15240	45608	A	15330	22	584	IRGRVDP ^P PSAVEPPPKMQIFVKT LTGKTIT ^L LEVEPLGYG [*] KNVK AQASRD ^K EG ^I PPDQQL ^I IFAG KQLEDGRTLS ^I DYNIQK [\] ESTL/ HIFVLR ^L RGGAKRKK ^S YT ^T PKK ^I KHKR ^K KG [*] SLAVLKY ^Y K VDE ^I NGKIS ^R LRLREC ^P S ^I DECGC WG ^V YGQVTFDRHYCG ^I KCLLT LLFQQTRMTSNCMS
15241	45609	A	15331	3	954	LDARRHWEGTPG ^T FHTSPDAW ADAWGKMAGEKVEKPD ^T KEK KPEAKK ^V DAGGKVK ^K GNLKA KKPKKGK ^P HCSRNPVLLRGIG RYSRSAMYSRKAMYK ^R KYSA AKSKVEKKKK ^E VLATVTKPV GGDKNGGTRVVKLRKMP ^R YY PTEDVPRKLLSHGK ^K PFSQHV RKLRASITPGTIL ^I L ^I L ^I TGRHRGKR VVFLKQLASGLLLVTG ^L PLVLNR VPLRRTHQKFV ^I ATFTKIDIS ^N VKIPKHLTDAYFKK ^K KLK ^R PRH QEGEIFDTEKE ^E YEITEQRKIDQ KA ^V DSQILPKIAIPQLQGNLRS VFALNGIYPHQLVF
15242	45610	A	15332	670	1008	WCILGVTPSLMSRTALFLSRHT FFA/RSHSAASKL/EKKKKEKVL ATVTKPVGDKNGGTRVVK ^I R KMP ^R YYPTEDVPRKLLSHGK ^K PFSQHVRKLRPSITPG/TIL ^I L ^I L ^I TG/ RHRG
15243	45611	A	15333	1	708	

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15244	45612	A	15334	1	1754	MRNEISDLTEELHQKEITIAITVT KKAALLEKQLKMELEIKEKML AKQKPWACLNVNAMP AIQVVFN LGRFRKCQDPHKAQEWVYPGY SGSDCEVFPEIMTSKNREEAMP EWKLWKKVVLSGATDAPSWD GPTFTDLNVFAGNMGLSDCTL LGKIWKIPGHFLHTSGPVSFHT KGLLNTPTKERWVGFGSEGR GVPEPGGCGVLAVPRRTPPSA AAMTGERLGRAWAGDRAAA SRSAVPVGTFGMMGWRPVAFG KNAKAYRGFGGIVTSLTPSCDK VTLLFVRILPGSGQSRDQSSPEK LTDTKSTSNKAYGFPECLRRPE STHIFFYDHLQLGSEQPRGTGKT PLKWVSQKTLERETRQCQALVI WTD CDREGENIGFEIIVCKAV KPNLQVLRARFSEITPHAVRTA CENLTEPDQRVSDA VDV RQEL DLRIGAAFTRFQTLRLQRIFPEV LAEQLISYGSCQFPTLGFVVERF KAIAQAFVPEIFHRIKVTDHKD GIVEFNWKR/LSTL*PHGLPSSL SVVCGVRSLSRCSVGF CWRSTP DPVCLCITSGGCRTASIAEQQL LPDPYSRFSIPEGQPP
15245	45613	A	15335	3	125	
15246	45614	A	15336	764	1005	
15247	45615	A	15337	1	3533	MELVNCVLMSTLGN TCCPMAL AMFRSSSLPRPGHSLTGSPLRV NLIHIFPLNDFHQNVVKINK DPPLGAAIGKESCPADNELHSL ERRPLSPKL VQALGVAGLSRPG PPHTGCAIWL LITDHKLLSEIL YDLLHQGLDILADPPDEGGIPR GKNLVELLQLPGLEEDKAFQKE IGLKILVFKAYSTLSSDGPPLFS ALRSLQGVSQSKVGESREEKSQ TEEEDPGNPWPQSLGASVSS GKWGCLRTKP

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15248	45616	A	15338	1	2800	SISGPGQEA VPLRPKAEPEPGSG MVWDRQTKMEYEWKPDQGL QQILQLLKESQSPD TT I QRTVQQ KLEQLNQY P D F N N Y L I F V L T K L KSEDEPTRSLSG L I L K N N V K A H FQNF P N G V T D F I K S E C L N N I G D S SPLIRATV G I L I T T I A S K G E L Q N WPDLLPKLCSLLDSE D Y N T C E G A F G A L Q K I C E D S A E I L D S D V L D R P L N I M I P K F L Q F F K H S S P K I R S H A V A C V N Q F I I S R T Q A L M L H I D S F T E N L F A L A
15249	45617	A	15339	8	450	TWSWSPQAPS W A R P S S Q A R A V S L L V A R G Q L C Q G S R R R S G V G S R V D A G A A R T A L R T L G T R P R L R R P C G L G S H E T K A A A S G Q D G Q R G S R G R G S L G G R E L G A N E P L Y Q / W R A H T L T V L F I L T C T L G Y V T L L E E T P Q D T A Y N T K S E I A V V H L S
15250	45618	A	15340	246	559	MPVA VMAES / A F S F K L L D Q C E N Q E L A P G G I A T P P V Y G Q L L A L Y L L H N / G Q R J W Q R D F P G I Y T T I N A H Q W S E T V Q P I M E A L R D A T R R R A F A L V S Q A Y T S I I A D D F A
15251	45619	A	15341	129	915	R S G T Q G R S A A T A A L N V I A G A T P E Q S W G L A V R T V Q R R G R P A K M P V A V M A E S A V S F K L L D Q C E N Q E L A P G G I A T P K V Y G Q L L A L Y L F H N D M N N A R Y L * K R I P P A I K S A N S E L G G I W S V G Q R I W Q R D F P W G / Y T T I N G H Q W S E T V Q P I M E A L R D A T R E T A P L P V W S Q A Y T S I I A R * F C Q P L L G L P V E E A V K G I L E Q G W Q A D S T T R N G S C P G K P V C R G P W D V F P F N K F I S L Y S E P A P V P P I N E Q Q L A R L T D Y V A F L E N
15252	45620	A	15342	1	529	M A T L T I S R A Q T E D E A D Y Y C H R I K L V K E G L D E R T H K A Y L S S S G K G C E F H M V K P G S P L G P D I L G S W A Q S A L I Q P P S V S G S P G Q S V T I S C T G T S S D V G S Y D Y V S W Y Q Q H P G T V P K P M I Y N V N T Q P S R V P D R F S G S K S G N T A S M T I S G L Q A E D E A D Y Y C C S Y A G S Y P V V F G G G T K L T
15253	45621	A	15343	399	737	W I S G G N S C A T T / L S D A G L S T T S N S I G S A T V G A R Q A E S A S S Q S G G G A L G R H C G A S G K C A E S L R R E P V G S A T N Q W A P G W V V G R P A S D S S H V V I G L G R S A W S P A E V T P S L I P G R G R T K

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15254	45622	A	15344	1	4320	
15255	45623	A	15345	1	966	MNVNLAEESEKGETVGEIKG GGIQMVMLASQPLTSYCAARFI TGHGQKLKSELKKTLLQVIMLNI QKVRIPTRDGYNEKDILSTGKN VEKLELSNIAGYPSNIEKKEYQE QSVLSCCSEKIDANPKSVVCSF FMQEQCTKGKRFILPGLTSLVD RHLRYFGILPTVSNAAVVKEVP TVSNAAVVTEAPTGSNAAVVT EAPTGSNAARVMEVPTGSNA VVTEVPTGSNAAVVTEAPTGSN AAVVKEAPTGSNAARVMEVPT GSNAAVVKEAPTGSNAARVME VPTGSNAAVVKEVPTGSNA VKEVPT/GSNAAVVKEAPTGSN AARVMEVPTGSNAAVVKEAPT GSNAARVMEVPTGSNAAVVKE VPTGSNAAVVKEVPTGVTLRW SRKRPRE
15256	45624	A	15346	1	702	
15257	45625	B	15347	238	546	
15258	45626	A	15348	632	2361	FQSRFTLKNWNPGEQSQKII/CF QLGERAYQTDVLVKVPRQSSV FSENQRMNNPERWFESTGCGK TYNQNRFAFNQHQRFHSGEKTY EHNECGKAFSWPSILSKHQRIH TGKLLYTCEDCGKSFVSHSYFI QHCKIHTREKPYCEIKCGKAFS THSSYVQHLKIHTGEKHHECNQ CGKAFSHSSNLIHHQRIHSGEKP YKCKECGKAFNRQSNLIHQRI HSGEKPYDCKECGKAFSTQLFL IQHQRIHTGEKPYECNECAKFS LNRTLTVHQRIHTGEKPYRCNE CGKSFQSCSQVQHQRIHTGEK PYICNECGKSFGARLSLIHQRI HTGEKPYGCREKPYECSECGK AFSQSFNLIHHQRTNNGEKSYE CNECDKAFSLSSLVQHQRHIN GDKPYECHKCGKAFSQGSHLIQ HQRSHIGEKPYECNECGKTFGQ ISTLIKHERTHNGEKPYECSDCG KAFSQSAHLIHHQRIHTGENPY ECSECGKAFNVCSLIQHHRHT GEKPYECSDCGKAFSQHSQFIQ HQRHTGEKPYMCNECEKSFSA CLSLIQHKRIHTGEKPYVCAKC

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15259	45627	A	15349	3	354	EAFGGERVSSMSGLSGPPARR GPPFLALLLLFLLGPRVLAI HLPINSRKCLREEIQGPASDW RVRDLRPVWGRWRPAQ/RTSR S QILLAI ⁺ STPKRMQPRGNLPLTT EDYDMF
15260	45628	A	15350	283	393	YVYRRYGRFE*NDPSSALMST* GKRCQDCLDQRENKK
15261	45629	A	15351	1	351	
15262	45630	A	15352	1	867	
15263	45631	B	15353	1	1323	
15264	45632	A	15354	1	3669	
15265	45633	A	15355	362	1039	LESYLQPSAEGKTVSVFGETC ATPVGP/AAGPHTQ/LAQNIVTS WL.TGGRFIELKTVQILDRIELE KPCIDAEDCFNTEWSTFTLL KAWDEYLKAWFALHLEAMF QPSDSGKSFIFNMSVGYNLEGQ PLNPKNYPSQGVPRVLKSHRQD YLVGNKLSWADIHLVELFYVY EELDSSLISSFPLKPHTHVDNT KKGSHPHMCA ⁺ YTDYVNNPND RMPQREITFVS
15266	45634	A	15356	74	208	QRLTKLRETSRRLSSWQRSPSS TTSMHGAEWSPRWLLAAGV EFEEKFIKSAEDLDKVRNDGYL MFQQVPRLRLMG*SWSRV
15267	45635	A	15357	308	735	NQRCTWAYYSMTMEIFLISCVKI LSVRYAVQQLKTGVFCSLETQP SKMAPAKKGGKKKGHS/AIIE VVTQENTINIQQHIHEVGFKKC APRALKEIQKFAMKEMGTPVY LIDTRLNKA ⁺ VWAKIRNVNTRI HLCIS ⁺ RKCNEDE
15268	45636	A	15358	3	323	LSSLASMSFTTCSAFTNYWSPG SVQVPSYGTQPVSHAASVYAG LGGSGSRISVSHSPMAGGLAG MGGIQNEKETMQSLDRDLASY LDRVRGLETENWKLESKIQEH
15269	45637	B	15359	1	991	

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15270	45638	A	15360	40	1030	RGDPRVRRRTQSLSPVL.SLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL VESKIREHLEKKGPQVRDWSHY FKIHEDLRAQIFANTVDNARIVL QIDNARLAADDFRVKYETELA MRQSVENDIHGLRNVDDTN YHTDLQLETEIEALKKEELFMK KNHEEEVKGLQAQIASSGLTV EVDAPKISQDLAKIMAIDIRAQ YDELARKNREELDKYWSQOI EESTTVVTQSAEVGAAETTLT
15271	45639	A	15361	1	438	LHSDDL.SLQML.RCSPVATAASY TSGPGAPISSSFSRVGSSSFQGG LGGGFGGASGIGGITA VMVNQS LLRPLNLEVDPNIQARF/VHTQE KEQIKTF/NNKFASFDKVRFL EQNRMLEAKWSLLQQQKMAQ SNMDNMFQSYNNL
15272	45640	A	15362	176	1455	EIFPLVIQKSYKVSTSGPRAFSS RISYTS GPGAPISSSFSRVGSSS FQGG LGGGFGGASGIGGITA VM /VQVLHTQEKEQIKTF/NNKFAS FDKVRFL EQNRMLEAKWSL LQQQKMAQSNMDNMFQSYIN NLRWQLET LGQEKLLKLEAELG NMQELVEDFKKKYHDEINKHT EMENEFVLEKDVDEAYKNKV ELES HLEGLTDEINFLRQLHEEE IWELQSLSDTSVVLSSSHSLD MDNIITEVKAQYKEIANCSWAK ADSMYQIKYEDLQMLARKHGD NLRCTKT DISEMNQNVSWLQA EIKGLKGQRASLEATITDAEKR RELAIKDANTKLLLEAALQW AKQDMAQQLRVYQELMNVKL ALDIKTATYKKLLEGEESWQES RMQNMSIYSKTTSGYAGGLSS AYGGLTSPPLSYGLSS
15273	45641	B	15363	70	915	
15274	45642	C	15364	62	217	
15275	45643	B	15365	1	612	

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15276	45644	A	15366	3	841	STPKMPKGGKAKGKKVAPAPA VVKKQEAKKVNVNLFKRPKN FGIGQDIQPKRDLTRFVKWPRY IRLQQRQAILYKRLKVPPAINQF TQALDRQQTATQLLKLAIKYRP ETKQEKQRL/LARA/EKKA PKGTFTKRPV/LRAGVNTVT LVENKKAQLVVIADVDPIELV VFLPAL/CRKMGVPYCIKKGAS LGRIVHRKCTTVAFTQVNSD KGVALAK/LVEAIRTNYNDRYD EIRRHVGGNVLG/PKSV/ARIAK LEKAKAKELATKLGLNVHC
15277	45645	A	15367	2	1006	WINLKGNI LLRKRSLTSNFWPCK LRSRKRHTTRNLRLMNLWLSSH PPQQSNTKPPWCCQLSCSTSLT LLGTSLPLLSYL IHLIPGPRQYP VIHRTSTLLQHISVGKEKFHKS QHWGFCNNVMMQLQLSPLK GLSLVDKVNRPALSGTRVLAS KTAWRJFQEP/SEPKTKAAAPG VEDEPLL RGNPCRFVIFPIEYHD IWQMYEKA EASFWTTEEVDLS KDIRHWESLKP EERYFISHVLVF FAASDGIINENLVERFSQIVQ/TE ARCFYGFQIAMIENIHEMYSLLI DTYIKDPKEREFLFNAI/ETMPC VKKKADWALRWIGDKEATYG
15278	45646	A	15368	3	1368	QAQPMGRVGGMAQPMGRAGA PKPMGRAGSARRGRFGKCWSE GSPVHPVPAVL SWLLALLRCAS TMLSLRVPLAPITDPQQLQLSPL KGLSLVDKENTPPALSGTRVL ASKTARRIFQEPTPKTKAAAP GVEDEPLLRENPRRFVIFPIEYH DIWQMYKKA EASFWTAEVVD LSKDIQHWESLKP EERYFISHVL AFFAASDGIVNENLVERFSQEV QITEA/RCFYGFQIAMIENIHEM YSLLDITYIKDPKEREFLFNAI/E TMPCVKKKADWALRWIGDKE ATYGERVVFAA AVEGIFFGSGF ASIFWLKKGRLMPLGTFSNELIS RDEGLHCDFACLMFKHLVHKP SEERVREIINAVRIEQEFLTEAL PVKLIGMNCTLMKQYIEFVADR LMLELGFSKVFVRVENPFDFMEN ISLEGKTNFFEKRVGEYQRMGV MSSPTENSFTLDADF

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15279	45647	A	15369	2	621	RFIKMLSRHHQHVVHVLPLRLA PLPVAMEEEIPALFIDNGSGM/C KSSFA/GDNALRAIFPSIIGHPRH QGVVMVGMGQKDSYVGDQAQS KCGILTLKYPIKHGIVTNWDDM EKIWHHVFYNELCVALEEQVV LLTEAPLNPRANREKMTQIMFK TFNTQAMYVAIQAVLTLHSSGC TTGIVMDSGDGVTHTVPIYERH TLPHTILHLDL
15280	45648	B	15370	1	966	
15281	45649	A	15371	2	228	
15282	45650	B	15372	1	816	
15283	45651	A	15373	256	384	RKLLNEAPC*PMR*HSLLNRLA TSCNSWTVPVVPKFSKLRRGL
15284	45652	A	15374	145	375	KIAGKNRLNRNQCKERKVVQL WISEKKQREAVEDPSLDCCH KFFPGS*ERLHG*KRQWF*PP HTVEKQMRSCLL
15285	45653	A	15375	319	482	
15286	45654	A	15376	4776	5910	VCSTAGDVNGVCLLYDLHLHIA VASGSAGKECFARKPLLAEQV IYDCLQEFKEKKLVPA TPHAQV LSYEALLSAHD TIAQKDFEPLLP PLPDNIPESSEAMRIVCLVKNQ QPLGATIKRHEMTGDILVARIH GGLAERSGLLYAGDKLVEVNG VSVEGLDPEQVIHILAPRCLSP MSLADLPPLPREVLVLGAKLPV PSSSFLLPREDCCGQPQSSLIT WFAPLETEPGVDRA MRSRGTIME KVVPVSDPPVNSQMVVYVRA MTEYWPQEDPDIPCMDAGLPF QKGDILQIVDQNDALWWQARK ISDPATCAGLVPSNHLK/RIWT EPGICIFTKRLRCSGKQREFW SQPYQPHTCLKSTLCEYCNCPT
15287	45655	A	15377	2	405	WSLVTRRALARVGLPG/SPPPRL LLLPLLLGWGLRVAAAASASS GAAAEDSSAMEELATEKEAEE HRQDSVSLTLTILLTLTILTIWL FKHRRVRLHETGLAMIVGLEK ITIGVLDITGWPYCTIQPYNGFL
15288	45656	A	15378	1	3804	
15289	45657	A	15379	349	622	RPDVANLAFLARKEGTGRGFLS KKTAEASRWHEKWFALYQNV LFYFEGEQSCRPGMYLLEGCS GGTSPRSFRSSSRDSPISPLHPT AK
15290	45658	A	15380	314	483	

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15291	45659	A	15381	352	822	DPRRVQAFPAKMKFNPVTSDR SKNRKRHFNA ¹ SHIRRKIMSSP LSKELRQKYNVSRMP ¹ IRKDDDEV QVVRGHYKGQ ¹ QIGKV ¹ VQVYR KKYVY ¹ YIERVQREKANGTTVHV GI ¹ HP ¹ SRVVITRLKLDK ¹ DRKRIS DRKAKSRQVGKEKGKYKEETI EKMQE
15292	45660	B	15382	80	432	
15293	45661	A	15383	11	888	VKCRKAEGRR ¹ ESRLQTFEESQA VEAAMANVPWA ¹ EVCEK ¹ FQAA LALSRVELHKNPEKEPYKSKYS ARANM ¹ EEVKALLGPAP ¹ EDED ERPEAEDGPGAG ¹ DHLAGLPAE VVEPEG ¹ PVAQANRLRLAVNEF HLGVNHIDTEELSAGEEHLVKC LRLRRYRLSHDCISLCIAQQT WRCIGVRDPTTSSCAFLSTSTPT VH ¹ SVKKIQTPGLRPSNSTLVD DMESSFQTCFASPLSQDYVNGS NQEEIGTGVDRCIHKFLDIARQ NISFLQKRLQLSVQKPEQVINED VDVSELN ¹ EE
15294	45662	A	15384	1864	2705	WPGKVL ¹ AHRGLHPWHRDPHGS GGGAGQELRRQGGCLEQLLYD AAHAQRLPPLDSVLPRAALPQD CQRASACEGDP ¹ TLRPSHSPGH PRGAER/VPSTACI ¹ QRSWEGR/ WNRALQQVGG ¹ LKSPWRGEYK EPRHPPPNQANYHQTL/ACPAE R/CFRQGPQGGPQLRRQQAEP SSLLSHQSPQSTSLP* ¹ L*AR RSLGCGNPYLCPPWSQPLPETP AHQSGKQPSRSRNCSSWK* ¹ NYS STACPSHFLWRSR ¹ KFSRASAST ASPCRM ¹ TVRRTHQRFKARGTP
15295	45663	A	15385	1113	1378	RPHAESFVSGGIDPPGPGPGST GPGPL/ERQPCSLTSWPREPPSSS SMKMLTQGP ¹ SLTAPYKGTILGE VNPAHAISSARNTSSRTSV
15296	45664	A	15386	285	722	TPAHGVPVPGQSGRHRHW/QSA ARSLQ ¹ QPSAW*PKTGS ¹ LFA ¹ TTW RCQTRASTCSAHWPLMAASPG AGGSSMASWR/DRP* ¹ PCPPPPAP HLPEAAFLR/CHDACP* ¹ NTGSA VPRGSCQPPAQQWDQGLAATR WGQAERLPRIYNWALAPP

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15297	45665	A	15387	207	605	FQASAEERFGTEDD/GSLRTRPPV MQSHQWPWRRPRPLVSRGRPQ TTPERHDSGGSPLTPRMESH EDEDLA/EGCRWP/EAGTVGV GPRAQGAQR/QAVLARKKHR RRPSKRRHWRPYLELSWA EKKQQRDERQS
15298	45666	A	15388	193	407	ACPKTSKNLRQRRLWNLA KHEF/SVDMTCGGCAEAVSR VLISLEVRVKYDIDL PNK/KVCIESEHSMDTLLATL
15299	45667	B	15389	321	625	
15300	45668	A	15390	275	690	SLWPPVIRG/SPKGNRPAIL TYHDVGLNMANKKSGDHP EREGTPRSFREVVS AFPGSSKLQIPKGS APRCGVPGRGARRELQ SFRAGPRTQGS PVGPRCQSRRLSAQEE SAKARHGGLRAHRS FSWDIRMSKERKFS
15301	45669	A	15391	2	137	PGRYRPN*LLSDASPGAG NEFQSTFLTPTILPSLRFP VLYTPNS
15302	45670	A	15392	1	648	MSLRKLTIMVEGKGGPN IPHACGCRQRSSIKVSL LPAVTSKSESPKEPE QLRKLFIGLSFETD ESLRSHFEQRRTLT DCAVMRDPNTKCSK GFGFVYATMEEKYHT VNGHSCEARKALS KQEVASASSQR/GR SGSGNFGGGHGGG FGGNDNFGHGENFR GHSSFGGSHGGS GYGGSGDDYSGFG NDGSGNFGGGGS YNDFGNYSNQSSN FGP
15303	45671	A	15393	1	3629	MTGICYTTEDETSYKKN AOPTASKKQKETQK FCLRVDDGQKQV KLSVLQEKSAQLTV QLKSQKFLGHPTA GRGRSELCLDLP PPEDPVALET RSVGTWVRERDL GMPPDGEAALAAK VAVLETQLKKAL QELQAAQARQAD PQPQAWPPPDS PVRVDTVRVVEG PREVEVVASTAAG APAQRAQSLEPY GTGLRALAMPGR PESPPVRSQEVV ETMCPVPAATSN VHMVKKISITERS CDGAEMKWEDQ NIGD

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15304	45672	A	15394	1	1515	MGQVFRVVTGVGEQPGHPDQF PYIDSWLSIIQNHKWLQACFET YCKTLMAQIKPGTIERDCKASV KEKDSQEKQKKPVLQAPPEELE SPALYAPIYPSLARLRQEAAPA APRGSDSEESTPQATPCREEPEP LPEKETSSSYRSNAVHFLHNPT WADCKQLQLSFLNTEEHHRVI QAAFWLENNAPAGTGYIRQY AQQALPIEADTGWDPNQAQGL QSLQWYREALLNGIKAGGKKA TNIGKSVSEVCQKPDSEPFYER LCEAYQLYT*FDPEAAGNQCM VNVAFVSQAQGDIKRKLQKLE AKAVLRGKFIALNTYIKKAERA QTDILRSHLKKELKQEQTKSKA SRRKDVTKIRAELEIETTTTKI QKINETKSWFFEKINTINRPLAR LTKKSRKELQITSLRKEMGDDTT TDTTEIQKIIQGYEHLVYAHKLE NLEEMNKFLEKYNAPSLNQEEL HTLNRPIRNSIEVVVIKKLPTKK/ SPGQDGFRAESYQIFKEALV
15305	45673	B	15395	1	1077	
15306	45674	A	15396	69	290	YYFDSPIHPLHLSGTLRPGGSRQ FPCDPQFLCRLHLTLASL*SLPG DLLRGLLHKLVCVRERLDLASL YAVGR
15307	45675	A	15397	62	201	
15308	45676	A	15398	3	429	LPSSVPRQPKMQARCLSRISIRA VEIYESDLEEGQGLLHEFSQFVL DRPPPTQSYAQELVHTCYLHT LASL*SLPGDLQRGLLHKLVCVR AERLLDASHHAAVGRSEFFW TPYTHSPPGAGVGHPPWHTRL PWGVPAEGHQ
15309	45677	A	15399	303	612	PSSSIPVYHCSLRGICIPVLGLKR AANVGVSLEASPLLSTPGGLGI CLSCGGTRTVGSRVGSIFPW*G EGTTGITGSISCKGSSDVGSNRT SGVDFPRRVE
15310	45678	A	15400	1	273	

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15311	45679	A	15401	1	406	MEEGWIRLPDGRVAAPQLLGA AVVLAVQETTHRQESLEKLL GRYFYISPLSAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWVVLGLTDFKN EATDPPGVKLQTFVSVTTHKG SVDPNSEKQDQLLQRAKEQSFH SVEGDPSRDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVVKRKTLPANTQTA SPRALADSLMQLARQVSR*RAI SCCPSH*LPSAKCISVSGIGGL VSLTSRMKPRTLLE
15312	45680	B	15402	1	930	
15313	45681	A	15403	391	617	LQLQPTG/CNFLFYFYGYMKIL GFCFHIVEERGGLWYPCFYC NLSSLGG*RSCSHTRIVPSLLMP KLGPGGQVC
15314	45682	A	15404	1	1860	
15315	45683	A	15405	1	531	
15316	45684	A	15406	2302	2691	
15317	45685	A	15407	520	2883	
15318	45686	A	15408	3690	4727	ENCHWGCHEPCDIGSSIISPLA YWEQYHRVTYISRDTGESSIVFP ALVTMLRNLFILAGSSDPHFHT PMYFFLSNLSWADIGFTSATVP KMIVDMQSHSRVISYAGCLTQ MSFFVLFIACIEDMLLTLMAYDR FVAICRPLHYVPVIVNPHLCVFFV LVSFLLSLLDSQLHSWIVLQFTF FKNVEISNFVCDPSQLNLACS DSVINSIFIYLDSIMFGFLPSIGIL LSYANNVPSILRISSDRKSKAF STCGSHLAVVCLFYGTGIGVYL TSAIVSPPPRNGVMASVMYAV VTPMLNLFYISLRNRDIQSALRR LLSRTVESHDLLSQDLLHPFSC VGEKGQPH
15319	45687	B	15409	1	3195	
15320	45688	B	15410	1	1819	

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15321	45689	A	15411	399	1089	LLTPRTDLQEMPLDNAIEIWEYWT DGSYLGRGEVFQWYDHLALIFVP QTGIEDVIWHIEALPNYIQKVCE RRNPYNQILSLQCAQHEIFLVS WKLVCQKQLEGDDMLVGTTA SNLLLESEQSTSNLNEKINHLEY EDQYKDNNFGEGNDGGILEDK LISN/NMGGPDSPDSVNPVE/P/M PTMTDQTTLPVNEEEAFALPEI DITVKETNAKRKRKLIVDSVKN LDSKTIRAQLNDY
15322	45690	A	15412	3	809	FKDDDDMLVSTTTSNLLLESEQS TSNLEKINHLEYEDQYKVDNF GEGNDGGILDDKLISNNDGGIF DDPPALSEAGVMLPEQPAHDD MDEDDNVSMGGPDSPDSVDPV EPMPTMTDQTTLPVNEEEAFAL EPIDITVKETNAKRKRKLIVDSV KELDSKTIRAHLSDYSDIGTTLD LAPPTKKLMMWKETGGVQKLF SLPAQPLWNNRLLKLFTRCLTP LVPQDLIKRRKGGEADNLDEFL KEFEHPVFPREDQQQ*HQQRD VIDEPII
15323	45691	A	15413	1	595	MVNRSHFRGVGPECHQQNSHG HLNSITETSNSTLRAAPLQPTR DPSDMAVFEIDELPEGA VKPPA NKYPIFFFGTHETAFLGPKDLFP YKEYKDKFGKSNKRKGFNEGL WEIENNPGVKFTGYQAIQQQS SSETE GEGGNTADASSEE EGD VEEDGKGKRKNEKAGSKRKKS YTSKVTKKLLIVINVICISIKHF
15324	45692	A	15414	41	785	GKGWAGGASGPANHGPAAGG RSPGMLRGDQGLPGRGAAGM ARPRSREYKAGDLVFAKMKG YPHWPARIDELPEASVKPPTNK YPIFFFWHPMKPAFLGPQDLFP Y*EYRGKFGKSNNRKGFNEGL WEIENNPGS/IRFTGYQAIIQQQ SSFRTEGEGGNTADASSEE EGD RVERDGKGKVRKNEKAGSKRK KSYTSKSSKQSIRKSPGDEDAID KDCKEEENKSSSEGGDAGNDT RNTTSDLOKTSEGT

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15325	45693	A	15415	1	1272	MWSGAGPGLAVWPQLVTVLSL SLSRNLCKWGLSFLACLLGSD MADAAMQHYGVNGYSLHAM NSLSAMYNLHQQAQQQAQHA PDYRPSVIALTLAERLADIILEA RYGSQHRKQRRSRTAFTAQQL EALEKTFQKTHYPDVVMRERL AMCTNLPEARVQVWFKNRRA KFRKKQSLQKEQLQKQKEAE GSHGEGKAEAPTDQLDTEQP PRLPGSDPPAELHLSLSEQSASE SAPEDQPDREEDPRAGAEDPKA EKSPGADSKGLGCKRGSPKADS PGSLTITPVAPGGGLLGPSSHSYS SSPL/SPLPSAGAIPPAHGGHQQ PGALLVLRSGSGPCCSGGCC CALPGRQHGPAGLTA/SASPTTS PCQQPLLP/SQGVWGSPLLPA AGLAPASATLNSKTTSIENLRRL AKQHAASLGLDTLPN
15326	45694	A	15416	1	1152	
15327	45695	A	15417	8	82	
15328	45696	A	15418	1	1350	MGSEKDSSEPRSTSLHAAAPDP KCRSGGRRRLTLHSVFSASAR GRRARAKPQAEPPPPAAQPPPA PAPAAAQGPPEALPAEPAAEA EAEAAAAAEPGFDEEAAEG GGPGAEEVECPCLVRLPPERA PRLLSCPHRSCDCLRHLYLRLEI SESVPISCPECSERLNPHDIRLL LADPPLMHKYEEMLRRLYLAS DPDCRWCPAPDCGYAVIAYGC ASCPKLTCEREGCQTEFCYHCK QIWHPNQTCDMARQORAQTLR VRTKHTSGLSYGQESGPADDIK PCPRCAYIHKMNDGSCNHMTC AVCGCEFCWLCMKEISDLHYL SPSGCTFWGKKPWSRKKKILW QLGLTGIAPVIGISLIAGIAPAM VIGIPVYVGRNIHSRYDGKEN/S KHKRNLAITGGVTLVSIASPVIA AVSVIGVPIMLAYVYGVVPI SLCRGGGCGS
15329	45697	A	15419	2	540	

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15330	45698	A	15420	1	530	SRTTPGKAPKETWGDQAGSGK GGQGPTRKIPRRTSSHLPPSPA AGDCPLATPESPPLAPETPDE AASVAADSDVQVPAGPAASPKP LGRLRPPRESKVTRRLPGARPD AGDGDHLSAVAERP KVS LHF D TETDGVYFSDGEMSDSDVEAED GGVQGRPREAGAKEVVRMGV LAS
15331	45699	A	15421	1	2989	MLLVMYWAPAPPPVHMSQFLT TGPKCLELSLDHGRDSQETAS GLLWLQHAACGLAQWNQKPH PPFLTLLQAEPPFERARSCDIYIR IKMLQTAQQHQVGLAPTERKE ALRGSPQKSASGQRPGSLDR ELLMLIKISKCLRVPSGPSSVLG TESTGPVPGELVLCQQDAGATQ EGVCYGRELMICRCDSPRLME PWGVKGTPFVRTDLITAMKIP DSYQLSPDDYYILADPWRQEW EKG VQVPAGAEAIPE
15332	45700	A	15422	218	404	
15333	45701	A	15423	1	422	
15334	45702	A	15424	160	470	LTMLFAACVFSGDEIMASEERQ PMEEEWSRSSTISGEDGERWTP DTAGKAAQGIAGDVVWVSLP PSKVSAASKPPKS/HHPFFKWH NFSNLMKMFYKMYFSKN
15335	45703	A	15425	21	375	TFENTRFWDVQIPVPTGERRNE WALPPPGAGSV PAGGWSRPLTP GRCD SQGRGRSRRAAPLSRSP PPLRRSPTLPGEPHPAHRPLRVH PRHGPRPSHLACLNSQAPDASR LRASANQ
15336	45704	A	15426	155	340	

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15337	45705	A	15427	1	2658	MIINTIITTTTITITITIMSSPIT ITNITIIQHHHHHNDQRPSLGK CRGLYIRVRKVPGERATANSRC PINAQGIESCWNGVMALWLG NSTCSRLELTDSQCQPADSP GDEDPKPWWDPHEAPLTGYF HPYGAAAFVPRHAGNFKDRREV PHQDTSFCSAQGFWILPSACKT GRVALTLTLIGAYQTLTEADV KGLTAARAASPGAKWRTQFPC PAGTCSSQAGNGQLEDCLPYPP GPSAPVGSLSRSSANGEFIIGRVI KAMNNSWHPECFRCDLCQEV ADIGFVKNAGRHLRCRPNRE KARGLGKYICQKCHAIIDEQPLI FKNDPYHPDHFNACANGIKLG VFLTDRKDLTADAQELKGELY CLPCHDKMGVPICGACRRPIEG RVVNAMGKQWHVEHFVCAKC EKPFLGHRHYERKGLAYCETH YNQLFGDVCFHCNRVIEGDDE GDGFAHRYSPYDSCEVDQSPLE GQQLKSIRKGLAQSQPLPTPV MLHPGCKTQIREAPGSAALLESV RRRPRPGLVPEEESAAVEAV RHHHLQNFSLLETLNGQKLG GHFCDVTVCHEASLRAHRCGL AIGSPSFQDKLLGPSEIRVPSV VPVQTVRQLVELLYSGSLVVA QSEAPQVLMAASVLRIDSYRR MHADYRTRSSAPASTSAPALP TPVPPPLAPEQLRHRLRHLLAA
15338	45706	A	15428	708	892	
15339	45707	A	15429	2	713	
15340	45708	A	15430	212	1246	DLPLAVHGVQSDSGAQAVASR SGDESSIVCLKEESTVNMTRFCS LPLAVISVSTAKCQVKSFEII GRVIKAMNNSWHPECSAVTSA RKFWQILHLSRMLVDRKDLTA DAQELKGELYCLPCHDKMGVP ICGACRRPIEGRVVNAMGKQW HVEREQYMDPGILSALIDPKYL LILSHRGLHMKSMKGFYFAKL YYEAKEDLAKKYICTYINVQE RDPKAHRFLGLLYELEENTEKA VECYRRSVELNPTQKDLVLKIA ELLCKNDVTDGRAKYWVERA AKLFPGPSAIYKLN/DGWVRG QMVPKPDDEGVQVRGRSGRPD AGWRLNRRSSVGSASWLRPQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
15341	45709	A	15431	129	444	WGGPGRQPDGGRVPGRCGPRR PATWESPAACRPRQSRHHSFE *GGSRSRSGSHKRPCSPSPAVLRA RDQVVLHTSFATEGDSSEHEDR STPLARRCLCSHRSGEA
15342	45710	A	15432	1	2446	METSLMVQVCGGRDCNALLPG NLCSQPTQVPLEVDGDDGPG GLPLNAAAPPSSVPPVPPEALPP PACPSAPAPWRSIISRLFTGSPA AEAAHPPPGGALDFGALRTSSC LSQSHGHIPGGPGLGLGAVRVP VPSEEDPASLFTEVPAAEAPAT VQSVEDFVANDRLDRSFLEDM TPARDEKKVGAKAAQDSDTG RASRAPEQQIPHGGHWRGHSRS YERFRPPDMVSAGPGPSDGEAL GGNPVAVGFQDDVDLEDQPRGS PPPPAGVPVPSQDITLSSEEAEV ADPPKGPAPAPQCCEPETKWS SIPASKPQRGTAPMTAAASPPWP GGASVHTGLEKCSSTRPPAEIEP GKGEQASSESDEPGIAAQMQL SFVMDDPDFESEASDTQCRAVR RVLPAQRAENAYGSAFQPGAL KPECRPTLKGPGPVPSKAGKK TEATSPRPTGGASPLAHGATVG AAWGLGMASWPIGSSLAPTRA RTREPRQLQRRVGSELPGDPCSG SGASCRQVCARGRATSVRLPAL ESLWPLSSDGSAAAREGLEGPR LRQAAAPGGPGPPLPLSRPPSP ARRMRGGAAYAGRGAAAPLE GRVRLGVGFLAETAVRAGAGA LAAADAPPGSRTPRARPLVAAG SGAAGGRCPVPSRRQREAPSPL GGAGVDLQLECLTSEKAGVGA ATGGVLEALARAIRQKKEIEIQ

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15343	45711	A	15433	26	963	FMIWAGQNRKVQDFVIQLRML TPVVPVPPQAAPNAQQPRAAASA PQTRVRAPRWPLGNVVVLGTE DAAGPSRPASEPPASPALPGPAL ELGLPNHPKQT/IRPRLAPRRSH PKDSCITIFKLSFLKNIFNNSV GDQVNLDYKLISGTEYDILNFW NFRILAKTGCSKDGHRNPRSRP TQEEGSGKPKKSLVKERSGAQE DLVPVPPEEKLELSGTSMGPCCFS KTSYGPHIYILSYKGTATAG HRWPAAYAPLNCVPPPETTM PVSDLGSLPHWASRIATPPSMW LCCLAAALRVLAYSNSSAEYV SQS
15344	45712	A	15434	803	1305	RSKPCRSHNVFSWVAHSRPC CPWSGYSSRLCCLSCCITLGPY QLKNRQQRNGSYKSGNYLCV GNRLLFWVWIFQKGGRS/WLP RSDWVTSYKVMVSNDSHTWV TVKNGSGDMIFEGNSEKEIPVL NELPVPVMVARYIRINPQSWFDN GSICMRMEILGCPLPGWEH
15345	45713	A	15435	2	377	ARELLKAVWRPHKVA VMHCR GHQRATSLVGLGNSRADSEAR KAPSAPFRASVTAPLLPQAPDL VPTYSKKEENDFLQAKGGQVME EG*IRLPDGRVA AVVLAVHETT HRGQELLEKLLGWYFYISH
15346	45714	A	15436	77	679	KMKTNQMGKLSKVVMENATIS EIRLINNRKDV EYQQEILQLEAV WKLHKVAVMHCKGHQRATSL VGLGNSRTDSESPKAASAPLRA SVTAPLLPQAPDLVPTYSKKEE DFLQVEGGQVMEEGCIRLLDG RVAVPQLLGAAILVAVHETTHL RS/ESSLGKLLGQLFSTISHFVSL CQNLTQRCVTCRQHNAHQGPA VPPGMQ

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15347	45715	A	15437	2	881	HARCTGIAARAGLLDPRHTGEA LAARSRIDLARRPHWPRGCGTG GGGGGCAGLGGAWLRGNDVA VPARALVTAAPASSMSPPIPA AARPVSSSIPAASPSPRCGLRAG PAELRCPRRLRQARAEEPPRAG PAPGRRRPTPGICAPLSPLRLA GGTAPSLPGVTRGSRVGRRLRP SLGGAGCRVGRKPRLLPPGRR CSTGLPPPAGTGAPAGVCWED GDPGHLEAAALLRRLGGQIRAL AGHRTAGWAQHGLSPREAVRP APAARGTLLRRSNSRRHLQNP ANFGGTAT
15348	45716	A	15438	3	502	GRRDSCLPVVVAPRACLHPRG QVPRLGSVGKMATPGMSWQQ HYYGSAAKFAPSATAQLAG HSMDSQEMHLKMSKKIAQLT KVYIALNTKNDHEHSAIQALKD AHEEEIQHILAETREKNLQYKS KVTEELDRLRRKIQVLESSLEDHI KMKQQUALTEFEAYKHH
15349	45717	A	15439	29	230	LQIDCKNKPAILRGPTDPLKEA DCYCRTWERPQILLPKWEGTR KPILVI*QNKAHQHAQITLLHQ
15350	45718	A	15440	73	335	FFWGGIEEPCFVILSGSVFWFLL JWVGASASPVVGDVFGRGGSPP PTSTVGAFITVLWGVSVWLKRV CGSSWDC*FVLAINLELKFTM
15351	45719	A	15441	373	513	
15352	45720	A	15442	1585	1649	KNSNIQHSFKITLVHQWFQTK KKFLIYLKKNSSGLVDP*MVHT TRLCADNPQYQPRARKSHS*VK GESTTLREHPMGQKNLNSLQP
15353	45721	B	15443	1	696	
15354	45722	B	15444	49	525	
15355	45723	A	15445	113	474	SIPYKNKEEEEGKGGEYYIKGT CHGTGKSEQQPSALDLPDRAY PNEKEPEN*W*LI*QNKAL*HS PKNHTSSP/RNGSKPRKKSILNL KKNSGG*LLS*LGRHQKVKPN ARKSKNQYKK
15356	45724	A	15446	47	614	TGCPRCQKQNSTCIAAVKMEGPI SVFGDRSTGETIRSQNDVTITN DGATILKLLVEHPAAKVLCEL ADLQDKVEVDGTTSVVIAAEL LKNADELVKQKIHPTSVISGYR LACKEAVFYLTENLIVNTDELG RDCLINAAKTSMSSDIIGINGDF FAN/MVVDVAVLAIHARRGQ/P RYPVTLLY*SHGES

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15357	45725	B	15447	707	1826	
15358	45726	A	15448	108	397	
15359	45727	A	15449	1726	2464	SKAVQLEAGGLQLFCCKMAP DPNITDVFGR TALHYAVYNEDT SMIEKLLSYGANIEECSEDEYPP LFLA VSQRKVKMVEFLKKKA NINAVDYLGRSALIHAVTLGEK DIVILLQHNDVFSRDVYGKL AEDYASEAKNRVIFELIYEYER KKHEELSINSNPVSSQKQPALK ATSGKEDSISNIA TEIKDGQKSG TVSSQKQPALKDOTSDKNDSVSN TATEIKDEQKSGTVSSQKQPAL KDOTSDKNDSVNTATEIKDEQK SGTSVFSETTGLEGYK
15360	45728	A	15450	2	675	
15361	45729	A	15451	1	467	DHSSSPAREQNWMEFDEL EVGFRRWVITNSSELKKHVL TQCKEAKNLEKRLGELLTRITSL KNINDLMELKNTARELHEAYTS INSWINQAEERLSEIEDQLNEIK REDKITEKMKNSTTVRVAAASM QSKLLQGVAAEEGPLRLTRSAF
15362	45730	A	15452	2	632	
15363	45731	B	15453	355	894	
15364	45732	B	15454	99	716	
15365	45733	A	15455	1	1140	
15366	45734	A	15456	1	1476	MEVNREKQLNELEVIGSEEQNL EEEGLMIGGVA VRLVPDDIVIP GGVNATNGTEARDALRVKVA MSVTLLSGIIQYLLSALGWSYY TVDGVSQKNPRALGVTADQLH AIFTTMSDEQASFRGFVAIYLT EPLVRGFTTAAAVHVFTSMKL YLFVGKTKRYSGIFSVVYSTVA VLQNVKNLNVCSLGVGLMVFG LLLGKKEFNRFKEKLPAPIPLE FFADHNSSPAREQKWMENEF EWTVEVSFRRWVITNSSELKEH LTQCKEAKNLEKRLLELLTRITS LEKNINDLMELKNTAQEFHEA YTSINS/RNQTEERVSEIEDQLN EI*CKDKIR/EKKRMKRNEQSLQ EIWDCVKRPNRLTGVPESDGE NGTKLENTLQDIIQENFHNLAR QANSQIQEIQRTPQRYSSRATP RHIIIRFTK VEMKEKMLRAARE KGRVTHKGNPIRLIADLSADTL QARRQWEPFINILKENFQTRISH
15367	45735	A	15457	1	1185	
15368	45736	A	15458	1	2367	

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15369	45737	A	15459	1	744	
15370	45738	B	15460	337	1515	
15371	45739	A	15461	1	1197	
15372	45740	A	15462	1	714	
15373	45741	A	15463	142	601	HQRTKVYKFTKMRKNQPKKPE NSK/TQNPPSPSKDHNSLPAREE NWMENEFDKLTEVGFRRVWIT NSSELKEHVLTCCKEAKNPD RLEKLLTRIISLEKNINDLVELK NTA*ELLEAYTNINSQIDQVEEK I/S/SIEDQLNEIKLEDEIREKKKK
15374	45742	A	15464	153	474	OTKSNVNIKKQDVHTKTPSEG HQHQRPKADHNSLPAREQNWIE NEFDELTEVGFRRVWITNSSEL KEHVLTCCKEAKNLEKRLQEL LTRITSEKNINDLMELKNTA
15375	45743	A	15465	1	2172	
15376	45744	A	15466	1	1640	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRTRLRAEDVFPPI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNPDQGT SMYHGWWPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPLDI IPSCALAHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGITINVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEFDHLPAGNC YVVRNEDCIGFSGFYNVISL GVYLVQQKGWEDTHSKTPSK GHQHRKSKVDKSTKMRKNWS KNAENSKNQNALSPNDRNSSP ARAQNWMMENKFDKLTVEGFR RQVITNTSELKEHILTQSKAKN LDKRLQELLTRITSEKNINDL MELKNTARELREAFVFCVNCE AVSLITSLREDSHWLEDKSGHR M/RRHQE*KCEYFHPPHGLQF YQLPESDSSHDPWPHGGSFSL
15377	45745	B	15467	50	1603	

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15378	45746	A	15468	528	1413	QTERNSTSTSKTPSEGHQHQRPKVDKSTKMGRNQCKKA*NSK SQNACPPKDHSSLPAREQWTW MENEFDLTVGFRRWVITNSS KLKEIIVLTQCKEAKNLEKRLE ELLTRITNLEKNINDLMELKNT ARELREAYTSINSRIDQAKERM SEIVDQLNERNDRENGTKLENT LQDITQDNFPYLARQVNIQIET QRMPQRYYSRRVTPRHIIVRFA KVMEMKEKMLRAAREKDTSVK QKVNKDIQELNSALHQVDLIAI YRTLHPKSTEYTFSSAPHHTYS KTDHIVHSILCDSG
15379	45747	A	15469	368	679	SSQLNKAPSLFNPVSEEFCLWL LLLQKELLTRITNLEKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK
15380	45748	A	15470	865	2055	QTERNSININKKDNIAKTPSKG HQQQRPKVDKSTKMGRNQHK KA*KFPKPGMPSPPK/DHNCSP ARE/QNW/MENEFNEFDLTGA GFRRWVITNSSSELKEHVVTQCK EAKNLEKRL/QELLTRITNLEKN INDLMELKQDITQENFMKHTQ VSIAQADQGRKERVSEIEDPTL MDIKCEDKIREKK/IKKRNEQSL QEIWGYVVKRPNLRLLISVPESDG ENGNK*ENILQDIIQENF/FPNL TRQANIQIETQRTLQRYPLRR ATPRHIIIRFTKVMEMKMLRA AREKGRVTHGKPIRLTENLSA ETL*ARRE**PILNILEKRNFPQR ISYRAKLSFISK/GKREIKSFIDK QILRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKLKRLPT
15381	45749	A	15471	1	315	
15382	45750	A	15472	1	2775	
15383	45751	A	15473	1	1017	
15384	45752	B	15474	1	3105	

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15385	45753	A	15475	1	1115	MKWL LLLGLVASECIMYKVP LIRKKSRLRRLSERGLLKDFLK KHNLNPARKYFPQWEAPTLVD EQPLENYLDMYFGTIGTGA QDFTVVFDTGSSNLWVPSVYCS SLACTNHNRFNPEDSSTYQSTS ETVSITYGTGSMTGILGYDTVQ SGYHHGNHRLNLKGLCSSKRSS TTPPLYDLGQVAPPSGVS SSC DDQSGSVVIFGGYSSYYTGGL NWWPVTVEGYWQITVDSITMN GEA\IACAEGCQA\VEPGTFFVT GP\TSPIA\NIQSDIEA\SEELDGD SVLICSAISS\LPDI\VFIT\NGVQY PVPPSA\YILQSEGCISGFQGM NLPTSEELWILGDVFHPASTLT VF\DRANNQVGLAPVA
15386	45754	A	15476	1	765	
15387	45755	A	15477	470	479	PRNPSSFLQVQVQHRFLQLFVP FHFVFFLASLYVMVTLTTWFR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT
15388	45756	A	15478	1	896	CLPFGGPKPNPWDKDGCGQR PQPRHLPGPGTAAQRRQCPSE KSL\CRWPSLTATSCSLFYIL LHV GAS/CNLLPPAVKDSGKG VGQDTQVLSGSGAVYRVCA GT ATFHLLQAVLLVHLHSPSPRA QLHNSFWLLKLLFLLGLCAIAF CIPDEHLFPAWHYIGICGGAFAI LLQLVLITAFHNSWNKNCNEAS YLAEVFGPLWVVKVYSYEFQKP SLCFCPCPETVEADKGQRGGA RPADQETPPAPPVQVQHLFLQL FCLPLRLLPWLTLCHGYPPYQLV QASAGCGCKPFAPYSL

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15389	45757	A	15479	1	1016	MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARI VFIRIARPRDGSFAYESVPWQQS ATQPAGLSVVTTVWGVGNAT QSQVLGNPMGPAGSPSGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQQGVYSRGGYP GAPGFTTGYAGGPGGLGLPSH AARPTDFTQAAAAA ATATATAT/GHRGCSGAE AEPDAGAMGAGQSFNSQFLQHG GPRGPSVPAGMNPTGIGGVMG PSGLSPLAMNPTAAGMTPLY AGQRLPQHGYPPQAQPLPRQ GVKRTYSEVYPGQQYLQAYP VHSGLSQFPTWQETPRHP
15390	45758	C	15480	1	585	
15391	45759	B	15481	1	885	
15392	45760	A	15482	3	440	GPWPRPVAYLSKQLYRVSKGW PPGLRALAEMALLAQEADKLT LRQNPNI/IGPHAVVTLMTTKG HH*FTNARLTYVKIPT*PLKF/G NTLNPITLLPVSESPVEHNCVD VLDSVYSSRPNLRDHP*TSVDC ERYVDRSSFTNRCKVTR
15393	45761	A	15483	3	368	
15394	45762	C	15484	109	276	
15395	45763	A	15485	1	1710	
15396	45764	A	15486	221	784	QNSLRSMCQKEKKMAAGVLT HTC/GPWPRPVAYLSKQLDRIS KGWPPGLRALAATALLAQEAD KLTLGKT*IRPPHAVVTLMTNT KGHHWLTNARLTKYQSLCEN PHITTEVCNTLNPITLLVSESL VEHNCVEVLDSVYSSRLNLRD HP*TSVDW*LVHDGSSFTNPCK VTLKKMTSAAPVTPRS
15397	45765	B	15487	509	661	

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15398	45766	A	15488	1370	2243	LGKLRLESCGLVAAVRPHSGGL AMPLPNATRPASGRSED/AELK LALHGHRSLSLQGRKHRGVH DNSDIPQAALVGGTTMIIHGVH PDKETSLVDAYEKCRGLADPK VCCDYALHVIGITWWAPKVKA EMETLVREKGVNSFQMFMTYK DLYMLRDSELYQVLHACKDIG AIARVHAENGELVAEGAKEAL DLGITGPEGIEISRPELEAEATH RVITIANRTHCPIYLVNVSSISA GDVIAAAKMQGKVVLAETTTA HATLTGLHYHHQDWSHAAAY VTVPLRLGIPPH
15399	45767	A	15489	307	600	VSRRASSGSPVPLGSLHLQHSA PA/PSAAPKPRSPPARLSRPHLR GESAAPSLSPGPASLAAAAA RVPAQSPAPSTTPAPRTTLAPR VPHRLAPAP
15400	45768	A	15490	3	222	
15401	45769	B	15491	1	1131	
15402	45770	A	15492	136	201	
15403	45771	A	15493	3	556	ELPRRLVCSKLADPGRLTDA CARPGMSRYLLPLSALGTVAG AAVLLKDYVTGGACPSKATIPG KTVIVTGANTGIGKQTALELAR RGGNIILACRDMEKCEAAK/ID IRGETLNHHVNAHLDLDSLKS IREFAAKIIIEEERV DILINNAGV MRCPHWTTEDGFEMQFVGNHL GHFLTTWC
15404	45772	A	15494	11	559	
15405	45773	A	15495	1	312	MAPAADREGYWGPTTSLDW CEENYSVTWYIAEFVWLMMSGF LPTPSSLRDLTASRWVRSLLPSPR SPAGRQPGPAEELPKASPCPWG KLSLRPFASFSSSGPS

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15406	45774	A	15496	2	1605	WQLPHPPAAPSAARQILRACQLS SVTAVAQSCLYGKQLC/GLTTG NIAGAGLLFFGGGIGGTILYAK WASHFRERVEKTIPYSDKLFV VLGSAPYNVPLPKKSTQSGPLK ISSVSEVTKEFKQPASQLQKQK GDTPASATAGDTVLVPGVQHE ESLKTDPAPIDEKGKPTALSEEA SSSSIRERPCEEIAACLAQEEKQ EQVKTESLAKSFEDALRQTANV TLQAIAAQNTVVQAVNAHSNII KAAMDNSEIEGKKKSAKWHTV QGALKEHRKAVDEAANALLKA KEEVQAAQFESKLVSQYHEL GQAQDDFKRQLDSITPEVLPGW KGMSVSDPADKISTDDLNSLIA RAHRHIDQLNRELAQEKATEK QHITLAEKQTLLEEKVQEQELK YEFQNLSEKLSEQLQFHHL SEQVHNFTLDINTAYARL GIEHAVQSHAVAEERKAYQLW LSVEALKYSMTSSAEMPAVPL GSAVEAIKANCSDNEFTKALAT AIPPESLTHGVYSEETLRVRFYA VQKLARRVAMID

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15407	45775	A	15497	89	2490	PKCCFFCLLSGETAAQSCLCG KVVLRLPLRCRRYSTSGSSGLT TGKIAGAGLLFVGGGIGGTILY AKWDSHFRESVEKTIPYSDKLF EMVLGPAAYNVPLPKKSIQSGP L*ISSVSEVMKESNRPAQQLQK QK/GDTPASATAPTEAAQIISAA GDTLSVPAPAVQPEESLKT DHP EIGEKGPTPALSEEASSSIRERP PEEVAAARLAQQEKQEQVKIESL AKSLEDALRQTASVTLQAIQAAQ NAAVQAVNAHSNLIKAAAMDNS EIAGEKKSQAQWRTVEGALKER RKAVDEAADALLKAK*LLMDF NKEELEKMKSVIENAKKKEVA GAKPHITAAEGKLHNMIVDLD NVVKKVQAAQSEAKVVSQYH ELVVQARDDFKRELD SITPEVL PGWKGMVSVDLADKLSDDL N SLIAHAHRRIDQLNRELAEQKA TEKHITLAL/EKQKL/EKRAF/ DSAVAKAFNRHRLKLYRA*TG QKR*KEVRDAME/NEMRTQLR RQAAAHTDHLRDVLRVQEQEL KSEFEQNLSEKLSEQLQFRRLS QEQVDNFTLDINTAYARLRGIE QAVQSHAVAEERARKAHQLW LSVEALKYSMTSSAETTSIPL GSAV/EATKANCSDNFTQALT AATPESLTRGVTVKRPLGAR FYAVQKLARRVAMIDETRNSL YQFVLSYLSQLLLFPQQQLKPPP
15408	45776	A	15498	1	1212	MPKKRQALVEFEDVLGACNAV NYAADNQIYIAGHPAFVNYSTS QKISRPGDSDSRVNSVLLFTI LNPIYSITPTRLNVFKNDQDT WDYTNPNLSGGQDGPSPNKR QRQPPLLDGHPAEYGGPHGGY HSHYHDEGYGPPPHYEGRRM GPPVGEYGPADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVE KVKISLKKQSPGGRPMGEEWL/ DGYAVDRAITHLNNFMFGQK LNV/CVGAQAREGSRGTGERK GGEWGPAEEHSEAEVLTHTM GCGSVSKQPAIMPQSYGLEDE SCSYKDFSESRRNRFTPEQAA KNRIQHPNSVLHFFNAPLEVTE ENFFEICDELGVKRPSSVKVFSG KSERSSSGLLEWESKSDALET LFLNHYQMKNPSINLVT

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15409	45777	A	15499	1	645	
15410	45778	A	15500	3	677	SPPNPRAPYLFPASLQNPANWS PHFYQLPILSQPRSVLTAFRQQA QPRISMPQAQTPFRPQMERLDQ NIRRSNQPHSLKPKLIQSKALT LFNSVKAEEKDEEAEEKFEVTR VVHIRGLIDGVVEADIVEALQE FGLISYVMVMSKKRQALVEFE DVLACNAVNYTADNQIHIAH HPAFVNYSTQKISRPGNSDDIR SVNSVLLFTILNPIYSITTDVLYT
15411	45779	A	15501	2	1712	DEQRRRSGAMVKMAAAGGGG GGGRYYGGGSEGGRAPKRLKT DNAGDQHGSGGGGGGGAGAA GGGGGGENYDDPHKTPASPVV HIRGLIDGVVEADLVEALQEFQ PISYVVVMPKKRQSLV*FEDVL GAGNAVNYAADNQIYIAGHPA FVNYSTQKISRPGSDSDSRVS NSVLLFTILNPIYSITTDVLYT CNPCGPVQRIVIFRKNGVQAMV EFDSVQSAQRAKASLNGADIYS GCCTLKIEYAKPTRLNVFNQNDQ DTWDYTNPNLSSGQDGPSSNP KRQRQPPLLDGHPAEYGGPHG GYHSHYHDEGYGPPPHYEGR RMGPPVGGHRRGPSRYGPQYG HPPPPPPPEYGPHADSPVLMV YGLDQSKMNGDRVFNVFCLYG NVEKVKFMKSKPGAAMVEMA DGYAVDRAITHLNNFMFGQK LNVCSVKQPAIMPQSYGLED GSCSYKDFSESNNRFSPEQA AKNRIQHPSNVLHFFNAPLEV EENFFEICDELGVKRPSSVKVFS GKSERSSSGLLEWESKSDALET LGFLNHYQMKNPNGPPYTLK
15412	45780	A	15502	1	528	NHQIRNDFITSPGVKADSRTSP PQQPASSFDITEAAVSFAKDSL GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP TQALNFTFKDKYKQIFLDGVDK RSQFWRYFAGNLASGGATGAT SLCFYYPPLDFAHTRVAADVKG AGAERELRGFGDCLVKIYKSDG IK
15413	45781	A	15503	1	1452	

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15414	45782	A	15504	2	991	RSAGVKGASRSPVLQQSASSF NMTDAAVSFAKDFLAGGVAA AISKTA VAPIERVKLL/LQVQ/H ASKQIAADKQYKGIIIGCVVRIP KEQGVLSFWRGNLANVIRYFPT QALNFAFKDKYKQIFLGGVDK RTQFWRYFARNLASGGAAGA TSLCFVYPLDFARTRLAADVGK AGAEREFRGLGDCLVKIYKSDG IKGLYQGFNVSVQGIIYRAAYF GIY/DTAG/MLPDPK/NTHIV/S WMIAQTVHCCCPG*LPYPFDT RS/VRNE*MQSGRK/GT/DIMY TGTLDCWRKIARDEGGKAFFK GAWSNVLRGMGGAF/VLVLYE *KSKKYYT
15415	45783	A	15505	1	613	
15416	45784	A	15506	1	1695	
15417	45785	A	15507	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSA MEDEINEMKRE EKFREKRVRKNEQSLQEIWDYL KRPNLRLIGVPESDGENGTKE NTLQDIIQENFPNLARQANI/Q EIQRMPQRYSLRRATPRHII VRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL
15418	45786	A	15508	1	3156	
15419	45787	A	15509	1	879	
15420	45788	A	15510	1	804	
15421	45789	B	15511	1	1230	
15422	45790	A	15512	2	827	
15423	45791	A	15513	1	1011	
15424	45792	A	15514	1	1722	
15425	45793	B	15515	1	780	
15426	45794	A	15516	1	2712	
15427	45795	B	15517	1	855	

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15428	45796	A	15518	3	1263	GRTIQTGKGEVNFENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECSRSLRSCDQLEERVASAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNRLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTQRYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRALFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGL IGVPESDVKEKTKLETTLQDIIQ ENFPILARQANVQIQEIQRTPQR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTTRPALKELL KEALNMERNNRYQLQNHAK
15429	45797	A	15519	1	1137	
15430	45798	A	15520	1	1578	
15431	45799	A	15521	1	1656	
15432	45800	A	15522	1	1120	
15433	45801	B	15523	1	1541	
15434	45802	B	15524	1	1632	
15435	45803	C	15525	53	352	
15436	45804	A	15526	1	973	MGKKQNRKTGNSKMQSASPPP KERSSSPATEQSWMENDFDELRL EEGFRRSNYSELREDIQTGKKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELQRYSAMADE MNEMKREGKFREKRIKRNQES LQEIWDYVKRPNRLRLIGVPESD GENGTKELENTLQDIIQENFPNL ARQANIQEIQLRIPQRYSSRRA TPRHIIVRFTKVEMKEKMLRAA REKGRVTLKGKPIRLTVDSLAE TLQARREWGPIFNILKEKNFQPR RISYPAKLSFISEGEIKYFTDKQ MLRDFVTTTRPALQELLKEALN MERNNRYQLQNHAKM
15437	45805	A	15527	1	2896	
15438	45806	B	15528	50	658	
15439	45807	A	15529	1065	1260	RSHALALDSAGSSSPESH*RAS IPHTALGQNAGSWAGTAHSHH GPFLWSDPRHPQVVPVRTCCP
15440	45808	A	15530	96	219	EFSTKPRLSGP*SSWEMLEIPL APDTTIDLKLLYSRDRF

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15441	45809	A	15531	5459	6324	LLANVSQLLADISQLLANFTQL FSHFSQLLTYLSKLFTHLPQLLT HFPKLLTHQPELFSNQSQLHPNI TRYSPTSPSYSPSPSPNYTPTSPN YSPTSPSYSPSPSPSY/SDLTKLL PFQPTIHTVSNLYPKLTQLQPQ FAQLQPNLTQV/PPTSPSPSPSP EYTPTSPKYSPTSPKYSPTSPKY SPTSPTYSPTTPKYSPTSPYSIQ PLQSTPQPLPSTHLLAPLTRPLP PSTRPPAPPTRPPPKAQPTLPLP LVTRPPAPPTVSQARLSARMTV TRRTEGTWGAAAG
15442	45810	A	15532	13	941	SVVLRPLVVAAATATTPVAA AAANTAKKTATVMVGEMVA GERGVLQMGHDITRFFYSNIQT VINNWLLIEGHTIGIDSIADSK TYQDIQNTIKKAKQDVIETFEN QVPRILNDARDKTGSSAQKSL EYNNFKSMVVSAGAKGSKINISQ GGGSGGGRGPPISMWLLALC LVGLAGAQRGGGGPGGGAPG GPGGLGLSLGEERFPVNTAYG RVRGVRRRELNNEILGPVVQFLG VPYATPPLGARRFQPEAPASW PGVRNATTLPPACQNLHGALP AIMLPVWFTDNLEAAATYGGC FRVPKKA
15443	45811	A	15533	207	696	TNLQEKNKQPHQKVGRYKQT LLKRRHLCSQQAHEKMLIITGH QRNANQHNHEIPSHTS*NGDH* KVRKQQLERMWRNRNRAFTL WVG*TSSTIVEDSMAIPQGR TRNTI*LSHPITGYIPKGL*IMLL *RHMHTYAYCGSIHNSKDLEPT QRSINDRLD
15444	45812	A	15534	1	307	
15445	45813	A	15535	1	381	LPPPHDRLWCVMFPTLCPSVLI VQFPMPSENMRCLVFPCNSLL RMMVSSFIHVPTKDMNSGIL*S RPADIELFSINLVNKKIFLKGF GDPLSLQRQLRNIVSMPCCFPS FLLPWVFSQLSVKPH
15446	45814	A	15536	134	278	DPAFLAPSPV/LMKQAPQATSG LMEPPGPSTPIVQRPRILLVIDD AHTD
15447	45815	B	15537	1	840	
15448	45816	C	15538	1	891	

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15449	45817	A	15539	1	3102	MYSHVITVCRHVKNKDILLNR QPTLHRPSIQAHRARILPEEKVL RLHYANCKAYNADFDDGDEM AHFPQSELGRAEAYVLACTDQ QYLVPKDGQPLAGLIQDHMVS GASMTTRGCFFTREHYMELVY RGLTDKVGRVKLLSPSILKPFPL WTGKQHINRTKDKNHMIISIDA EKAFDKIQQPFMLKTLNKLGD GTYLKIIIRAIYDKPTASIIINGQK LEAFPLKTGTRQGCPLSPLFNI VLEVLARAIROEK
15450	45818	A	15540	1	779	IPMKDHDAIKLFIQIPRNLDK DLKPLFEFGKIYELTVLKDRFT GMHKGCAFLTYCERESALKAQ SALHEQKTLPGMNRPIQVKPAD SESREGDKKLFVGMNKQQSE DDVRR/LFEAFGNIEECTILRGP ERQTAKGCAVVKYSSHAEAAAG RPSTRLHGSQTMPGAFAVPVWV GQVSADTDKERTMR/RMQQMA GQMGMFNPMAIPFGAYGAYA QALMQQAALMASVAQGGYL NPMAAFAAAMQMQMAALNM NGLAA
15451	45819	A	15541	1	1413	MEYYAAIKKDEFISFVGTWMK LETIILSKLSQMOKTKHRIFSLIV LCDITDILKEFTVAEAGGFALNE IMKEICKSRFSKVSLSHWKMW HSTASLGYHRVNVNTPDPLNLC LGHCWLGRLDTGQKQACGGP GVCPGMFRACGNGAPCKEAP SVTEASSPDGSLCLGSHVPIPT APLSSAQMVCHMVEDRRTVEL ILGATHNLFFSTSLTWSLRAIP GNCVLFLLKDYVTEPVRQSILHI AGPTFKQTPNLPFLKFPEATKA HGPNNVYQNDSTCEPTAQVSH WSSVSTLIASPVPGEDRKLFLV GMLNKQSQSDDVRR/LFEAFGN IEECTILRGPDGNSKARPLASSQ GAPSVKYSSHAEAAQAINALH GSQTMPLMQQAALMASVAQ GGYLNMAAFAAAMQMQMAA LNPNGLAAAPMTPTQANGQP AAEENFANGIHPYPAQSPTAAD PLQQAAYAGVQYAGR

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15452	45820	A	15542	254	883	DLRKDSPWEHRQCCKREPGNS APPAPHSWGFAVFNPRAGDVR QLCKRADTRTPSPRAPFGSAGA CRGCGRAGARSLASPKARTCIS SARRRAGGPLQLGAGSGQAKR PDR*TRREGANA*KTLHL/HSSL APSPGGVLAGFQEPGRPVAC CAATAAGGIRAGERR/PAAAAA AAPWAQKLRLRLQRRGPPGC R**MVSFPRLFSGTSR
15453	45821	A	15543	1	768	MCDFGKSTSLPASPTSSANGR DNSTYRLKEQGGFMHSVASRD SCAESARYTDAHYAKSGYGAY TPSSYGANLAASLLEKEKLGFK PVPTSSFLTRPRTYGPFSSLLDYD RGRPLLRPDITGGGKRAESQTR GTERPLGSGLSGGSGFPYGVTN NCLSYLPINAYDQGVTLTQKLD SQSDLARDFSSLRTSDSYRIDPR NLGRSPMLARTRKELCTLQGL YQTASCPYLVLDYLENYGRKG SASQVPSQAPPSRVP

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15454	45822	A	15544	85	2249	SAEAMSGDGA TEQAAEYVPEK VKKA EKKLEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEIKAKNYDK GEKLFQRCLMKVLHIDLWKCY LSYVRETKGKLP SYKGKMAQ AYDFALDKIGMEIMSYQI WVD YINFLKGVEAVG SYAENQRITA VRRVYQRCGVNPMINIEQLWR DYNKYEEGINIH LAKKMIEDRS RDYMNARRVAKEYETVMKGL DRNAPSVPQNTQQAQQVDM WKKYIQWEKSNPLRTEDQTLIT KRVMFAYEQCLLV LGGHPDIW YEAAYLEQSSKLLAEKGMN NAKLFSDEAANIYERAISTLLK KNMLLYFAYADYEESRMKYEK VHSIYNRLLAIEDIDPTLVYIQY MKFARRAEGIKSGRMIFKKARE DTRTRHHVYVTAALMEYYCSK DKSVAFKIFELGLKKYGDIP EY VLAYIDYLSHLNEDNNTRVLF E RVLTSGSLPPEKSGEIWARFLAF ESNIGDLASILKVEKRRFTAFKE EYEGKETALLVD RYKFMDLYP CSASELKALGYKDVSRAKLAAI JPDVPVAPSIVPVLKDEVD RKP E YPKPD TQMIPFQPRHLAPGL HPVPGGVFPVPPAAVVL MKLLP PPICFQGPVQVDELMEIFRRCK JPNTEVEAVRITGGAPELAVEG NGPVESNAVLTKA VCRPNEDS
15455	45823	A	15545	12	427	SAEAMSGDGA TEQAAEYVPEK VKKA EKKLEENPYDLDAWSIL IREAQV**YRITFPSLWVQSHYL VLPVNNIFIITL*MLFIGFQF*N QPIDKARKTYERLVAQFPSSGR FWKLYIEAEVTLFYFFLYQYCS IHL
15456	45824	A	15546	150	469	SAEAMSGDGA TEQAAEYVPEK VKKA EKELEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEVTLFYFIFS YISIAAFTVVIENKLG T
15457	45825	A	15547	1	834	
15458	45826	A	15548	443	732	SFMRWQKGQLPQLCLHRESHC SPYPQPSFLGMEPADIHETTFN SIMKCDVDIHKGLYANAVLSSG TTMYPGIANRMQKEITALAPS MMKKIHIAPA

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15459	45827	A	15549	1	1214	MEEIEIALVIDNGSGMCKAGF AGDDAPRAVFPISVGRPRHQGV MVGMMQKDSYVVGDEAQSKRG ILTLKYPIEHGIVTNWDDMEKI WHHTFYNELRVAPEEHPVLLTE APLNPKANREKMTQIMFETNT PAMYVAIQAVLSLYASGRTTGI VMDSGGDVHTHTPIYEGYALP HAILRLDLAGRDLTDYLMKILT ERGYSFTTTAEREIVRDIKEKLC YVALDFEQEMATAAASSSSLEK SYELPDSRSTSNWQLSGFRLPL RHSFQPSFLGWMESCGMHETTF NSIMKCDVDIRKDLVANTVLS GRTPPCTLGADRMQKEITALA PSTMKIKIIPPERKYSVWIGGF HPWAWLSHLSKMWVQQARS MTESGPLHSSTANGFLGGLLTL VAFTPLWTKP
15460	45828	A	15550	1	2355	MKQITFAPRNLHLLTNTNTWTPD SQWL VDMRTSGASFTGETIER VNIPTGYVEKPNKQCRHSVTRY GHGGHSDHTPSLTATVATQIT PRHSGHSGHCDRNLSLATATA ATLITPHLLWPRWPLGSHSVT WCGHGGHSDHTPSPTTATAVT RITSRHPLRPQQSLGSHPVTHYS HGSHSDCIPVTRYAHGGHSDHT PSLAMATAATQMALCHSLWPR QPLGYLVNKIRRKRCTDGVSPS GKAPVFDTGIPWFESRYP SHLL RVSGSPPGYWGIAKRHQILNVS NMFQKFTNLLGYRQAVRHRI LIPAFRGSNPRTPANLFKTLTIS NMRALENDFFNSPPRKT VQFG GTVTEVLLKYKTAIEKRLEKLA VDPHRDRAQMLKVENVQQA W QQWINKLPARREDEDVKEIR WMIEELRVSYFAQQLGKNSRA ESMLWSFHKAIEAARTNIIQA QTRVEAAQATERRIAADIDDSE LKAPRDGRVQYRVAKPGEVLA AGGRVLNMVDLSDVYMTFFLP TEQAGTLKLGGEARLILDAAPD LRIPATISFVASVAQFTPKTVET SDERLKL MFRVKARIPPELLQ HLEYVKTGLPGVAWSFLYSINQ TICLRDLSIEAKLQALEATCKSL EEKLDLVTNKQHSPIQVPMVA GSPLRTTQMCKNVR/CVNP*AT VVPPVPVQPTTQQYQGLDAGA

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15461	45829	A	15551	1	956	MSSGRRDALARGLNSGDGAP HLGEHRQLEDVGGVTVTVTWT GRLQAAGCWTRSVSTAAAGR REPSTRDGAALSTEPPDPPERLG HRGSRAGLTALGHVTRGSSQ RGGRPPEWEHWLENGTRRTEL VDGVSYESWRRRPCRQQLER LVLENHVATDEDEPALKCQRL EINCQDPSIKSFLYSINQITCLRL DSIEAKLQALEATCKSLEEKLD LVTNKHQSPIQVPMVAGSPLRT TQMCNKVR/CAMHWLCVSCIF TCLPGWRPAAPDQGPAAISLCS LPSSSQGHREPLALGLPSALPPA HRQLRGSATVPIPP
15462	45830	B	15552	161	925	
15463	45831	A	15553	31	856	GGFLHHASFFVGRGRTLLMYFS LLGATPKPEPEPEQVIKNYTEEL KVPPDEDICMEKLSAASGYS DVTDSKAVGPLAVGCLTKCSH AFHLLCLLAMYCNNGKGEHP NPGKPFRTARGFPAASATFTQTP GPQELVPYTPQITAWDLEGKVT ATTFSLQPRCVFDGLASTNDT VWLVAFAFNSASRGFQNPETLA DIPASQQLTDGHYMTLPVSPD QLPCDDPMAGSGGAPVLRVGH DHGCHQPPFCNAPLPGPGPYR WVVP TGALGLGLCLG
15464	45832	A	15554	827	1371	GSSAGEASSLRRLSPSQISRPL LPAGEKVLVVWIEDQTSNINPL SQQSKT/TLFNSMKAERGKEVT EEKLEARRGW/MRFKERSCFPN VKVQGEAANADIEAVACYPEY LAKITDEGGYTEQQIFSVDETA LYWKKMPSTRFLARRKNCHSH PSFSSQHLVQSAAINIKAKSSTS KKIMTP
15465	45833	A	15555	799	906	FLNKLAFALRCGLALNSFLRKI QEPSLGSKSGSL
15466	45834	A	15556	143	560	

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15467	45835	A	15557	1059	1940	QQMQQEMRRKSKWMAMLGK WETYQNS/TKGHLMKRVYKGI PMNVRAEVWSVLLNIEIKAK NPRQYRVMKEKGKRSSEIHQI DLAVSQTLRNHMFRRDRYGTK QQELFYLLAYSXNYPVVGVCYR DLSHIAALFLI.YLPEEDTFWAL VQLLASERHSCRVGEQLPLGLH AARPGDGHGPGPHLPCVASLL GAFRTSLLTPKEGTDPPPKS DAFHHPHQKASHPPRGCPCLPG ATPSGSDSVQLALRLNLRVLLPF SCSGSSCPWYPRKEALHPGGLE EQRLQLPLMGLVTG
15468	45836	A	15558	123	448	ALAAAVYPVSHSERTGEEAKKIC SVR*LLRSAQEEI/FLRGKNSRT GVL*KLLQRK*RYQRALGLAM LSEWTISPKGPVSTGITKPLMTA SRVTVPRMTMSALLDFIHGA
15469	45837	A	15559	1	6387	
15470	45838	A	15560	52	3218	
15471	45839	A	15561	3602	4015	GSVESPLGQKTPRTSSASPCWPS TNLYRMELEYGPHVTSQVVK STRCAPIRWSAAPSILCEVRVPV TMWTCLPLPATGRLSMW*IW RQWPCVLTSAATQS*LTRCGGGT RAVSLAPQSHL*VCPAQSSWTS IILWT
15472	45840	A	15562	932	1316	RVQDIPAKRGIPQFRPKIGIGQ SYKQHYPARPWNVLAQKVVV FEDQDALLPCLLTDPVLEAGVS LVRVVRGRPLMRHTNYSFSPWH GFTIHRAKFIQSQDYQCSALMG GRKVMISIRLKVQKAVNRA
15473	45841	A	15563	1	263	
15474	45842	A	15564	66	185	
15475	45843	A	15565	1	4217	MRLAEERAALAAENADGEPGA DRRLRLLLGTYVAMSLRPAAGA WERCAGSAEAEQLLQAFGRD AAEGPRPLL.VVRGPRGLAIRP GLEVGPEAGLAGAKALFFLRGT PEPPGPDSEFRGAVVCGDLPAAP LEHLAALFSEVVLPLVLANEKNR LNWPHMICEDVRRHAHSLQCD LSVILEQVKGKTLPLPAGSEK MEFADSKSETVLDSIDKSVIYAI ESAVIKWSYQVQVVLKRESSQP LLQGENPTPKVELEF

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15476	45844	A	15566	26	494	RPGCGEVLGNAELWGQECQL HYSPPVSPWENSSGPRFSISKTG SLIPPLNDICQNQKPQIILSHPA RCLGLLDHFPQQWERRQAQNR AETG*GQSAQGGTFRQRPLSV SGNCRVPPRATVSRK/PRPAPAY ALSLSKSPRRRPPRTGPAAPPGLVP
15477	45845	A	15567	1	1242	
15478	45846	A	15568	114	1219	VDLPPGAPVRQSGSHGSVLRDH KTEGEARVPLHQRVVGKAGGR GATPGPHVHEDPVTICCGHSFC RP/C/ICLSWEEAQSPANCRA EPSQKKDFKTNILLKNLVTIAR KASLWQFLSSEKQICGTHRQTK KMFCDMDKSLCLLCSNSQEH GAHKHYPIEEAAEEHREKLLKQ MRILWKKIQENQRDLYEERT AFLWRKRTLRLKGMTSGAQGT SQKVALGLLQPLCHTVRAQS NSARVHKQRGGDAVSSGAGIP DPKAQRFPATLRSQAFTCTAGR RWGSGETVLHPLQRAGVRGAV AELHRQLLLSSAAAGFEECEGL CTSGPHITQGPDHQELYLSHEG VWTLFTCTGDRWKVLGSGVPCP

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15479	45847	A	15569	1	2694	MRMAATAWAGLQGPPPLTLCP AVRTGLYCRDQAHAEATDVV LLAPFCQPKTRSHGTCPPTERDP RGEGSTYVPRVDGIQGWGTR ALTGWTDRLLCQACQTLPPR HWFLPGARGWLGGSPPAHGQE SLPSQSPILLRVESVKSRLRR RAQEEDSTVLIDVSPPEAEKRG SYGSTAHASEPGGQAAAAACRA GSPAKPRIADFLVWEEDLKLD RQQDSAAARDTDMHRTWRETF LDNLRAAGLCVDQDDVDQGN TTVHYALLSASWAVLCYYAED LRLKLPLQDYPTPTPTGRPA/ CAWLGIPIVLLVVDVPPPEYY SCRFRVKNLPRFLGSDNQDTFF TSTKRHQLFEILAKTPYGHEKK NLLGIHQLLAEGVLSAFLHD GPFKTPPEGPOAPRLNQRQVLF QHWARWGKWNKYQPLDHVR RYFGEKVALYFAWLGFYTGWL LPAAVVGTLLVFLVGCFLVFSDI PTQELCGSKDSFEMCPLCLDPC FWLLSSACALAQVREEAGRLF DHGGTVFFSLFMAWVALLLE YWKRSATLAYRWDCSDYED TEERPRQFAASAPMTAPNPITG EDEPYFPERSRARRMLAGSVVI VVMVAVVVMCLVSIILYRAIM AIVVSRSGNTLLAAWASRIASL TGSVNVLFILISKIYVSLAHV LTRWEMHRTQKFEDAFTLKV
15480	45848	A	15570	1	924	MISQIFENYFSGKSSATSGWA RAQRDRFVAGSARPALLSGRL APPALGSERLSTRASSCGGLPR ATPRGRAPPAIRIIPVSTAQR LRSAAARQLLAGSSARGRDAL GKASWAPESVLEVLARAVRQE KEIKGILLGKEVKLSLFAQDMI VYLENPIISAQNLKLMNSFSK VSGYKISVQKSHAFVYTNNRQS ESQIMSELPFTVATKRIKYLGIQ LTRDVKDLFKENYKPLLNEIQE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTVFTE LEKTKFIWNQKRAHIAKTIL
15481	45849	A	15571	1	825	
15482	45850	A	15572	1	1488	

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15483	45851	A	15573	1	1476	MPIKVDWIKSRTHTPRDTMSP KRGINISIQEYRNTPDASILSEL LERDINTQVYTYEQEHTNKN GHQAIDKQNKGHIRRESDRGEY YPLDCRPTGSLTDKGWGMMLC GMMTAGKPTPILTLFDVGLPG GTAINKSSVIRVRNREEGNVEK WGERQVDQDAMVRVRCGIR NNVEAGLKYPGTMKVLSVF YTTQCCRRYLSVLCFAGLARAS VPFNEFDQMSLDEKLFSLHPL GSSSSPPKSLHCLLEHQFTML GFSDLGAQLASPSGSHTRAAGV AACQAPPTLTWLSPPVARGLG TLEQGVVLVGEARAAQEPMEW VGGSCMVGCRSRAALPRGKAAK AWREIQRASAGGAPVSPWSG GAPSRACPPSASSVRFLCAARR LACNTYSPVLYCVRNWWILGL TDFNNEATDPRDFLANVPQGL AAVAIGTCGNNVYSAGDRDYR FALESILKACTLALEEVGP VQDKIGADP/TGLPF
15484	45852	A	15574	140	448	GFLGACAGREFKMAP*SSLG *KLSVSPCPGLLISAEGPEAVFSI V*NARVRGFILEVSETKNPPID TISTKHASLMSDSYREKKLV VYPHSSTPSFQ
15485	45853	A	15575	1	1001	MEAPQGALEQDGPVLSQQRH RKKPFTATPIDPSYHRSHAIL S VIIGYCVPPSHAAEMAAYGWT MGKSKLMAGQWITQSQVFCDS STDGPRQHKQAQTALTQLSQSQ RSTNNSTVSHRQQWVNCRLR VKCQRLRAHKELLVPQRWLWR QGRCPVTTSLVAVSETAGAGA AALALSRCLCLQVSASARPF SRTLSPPQKCVAMAAASHQPIK G ILKNKTSRTSSMVALSEQPCRT VHEELSKKCQKWDEMNILSTY HPADKDYGLMKIDEPSPYHG LTGDDENACSDTETETMVS DI LAKKLAEEGLEPKYVWVQEQE SSGEEDLLAEE
15486	45854	A	15576	1	1851	
15487	45855	A	15577	73	418	GKPDGDKVSHQLLLWKG/YSF/ PPSLMKLSLAGYEILS*KFFSLR TLNIGPPLSSGFRVSAERSTVSL MDFPLCITQCFSAPALNIFSFIST LVNLTIMCLGVALLEQYLCCVL
15488	45856	A	15578	2	460	

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15489	45857	A	15579	1	2031	MATEVFLIPYALLQCSLASYPSP KPGIYVPSQPMWVGSVTCSDQ KNTIEVLVPKAYTLARQQYKSL SEQVYSCHQGTNLNTRAQESAAS LLKPARPRTRQKKETPNTSEHQ KEQTLDTPLRTVTLTRVRGFI LEVSETKNPPISDTMGLDISKQE EVLGRESDEQGEQSQGLSEMQ TALAMLLTREPISAKQAPHEPP RRQEDNTQAREGETRSRKTRA EGQKGHAHAENERNAKERESE RKRQEAEDENGKEKQERNEGT HARHMKRRKRDEKKRQGQNK PGNKRPEGNEEAQRRRKKNRE RQRFSEFYQSGPSAAGLLVFAGG PLQSLFAWVSPLEAAEQQRFLS VPSSGPLRKFCLYFGFVGNATP LRGLNTHGRLLTPAHGTRRRHT RPLNSPVPEKAGSTTESNGSPY GQNPGLPPKGNRAQGEKWM GRRIQGTTRPRAREANHKMT QIMFETNTPAVYMAIQAMLSL YTYGCTTGIVMDSSDGVTHITVP IYEGYALPRAILCLDVAGRDLT NYLMKILTEHSYSFTTMAEREI VCDIKEKLYYVTLDFEQEMAT AASSSSLEKSYELSDGQVITIGN ELSCCPEALFQPSFLSMESCDIH KTTFNSIMKCDMDIRKDLTYNT VLFGGNNMYPGIANRVQKIVTL VVMGSSILALLSTFQQMWVSK
15490	45858	A	15580	485	886	VPYFHFTCSHSSASQLPFLQMM KIAKTCSLGLNRLPEAKLKAFP TPRVTS/LWPRQGRPRR/GCGR NRSGSLVSAARGVGGRSQAAA ARRDAPSPPATSRMPRQGSVS WGCARNAPGRRADPEVRRQPG PSCT
15491	45859	A	15581	1	435	
15492	45860	A	15582	2	339	HRCSTGAFSTAASNSNADRP ARRRGLPR/RGPP/SRRRSRPPR REPWPRTRRPRTRTAKARRRAT LEGRCCRACGHWPRAAAAAA AAAAAAVAAAAA GASATW

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15493	45861	A	15583	1067	2093	RRNTSSKCRSRNCRCPSPHRRH RPSLRPSRQPKCKCRPSRRSS RAPSSRRSRPQGLVPC*RAPPW PTSRWPGSPGFPLLNCSRKGRC RPRHPSQPRCPCSLRWCPSRQ LWSPHRESPPCP*TSRGSAAWRS VSIHRRQQDRPWWTQPVHMQQ LLKLLKQAAVQQQKAIQPAQAQ GPAAVQQKITAQQITTPGAQQK VAYAAQRALKNPVSYHTLPG PETGRGPASADPDGCKTSSSCS TANTRGQHPASCLCFPAGFSTD CGAHAGDGGRAAGADDPSCSDR DCPGGSAETHSAAGGDHGVGP APDSRRSQSPGARQLRQPKPA AQVTDEGPPCCQAKDITY
15494	45862	A	15584	10	607	RALCGESRLPLARKLS*AKKSV QRSTLQSRRIWVCWFHFAN*SL F*KQGR*ESPL*L*LIPAS*RPS TSESPL*KANFQQPHRGL*EKV AEGRRGP**EYVTSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSS SNSSNSRHRRRRRRRLSFLSR RRRHSRCCLSRSPRRRPRRHP ARLWLSRCTDQRKNFQLPRK TV
15495	45863	A	15585	217	1012	AKNDSKRQNFGRGQPTFGAD KAKGERVRTSSITRTSYLDTIT GPYLTGQWPRDPHGHPSCMK DKATQTPSCWAEEGAERSHQ RSAISWGSADQLKEETPTDLQ NAQQKLYKPEEVGCLISDFLKE KENCQPRILYAGKLSSECTPDE EAVNIVEMITKDEYYINLVDK EWQGLRGLTPILKEVLRVKCY QTASHATKSGMKGVQSFGK LHCYFKKLPLQLPSATAILISQ LTSTRQELHHKKDCNLLKTQMI
15496	45864	A	15586	2	387	
15497	45865	A	15587	1	165	LFMFCCLYIR*QLLHPGYNAPP QNTAATRGRGIAQTAEAAFL FLHQRVRFH
15498	45866	A	15588	172	359	PDGDGIESINYLGGYGHFHDIDS SYP*AWNVLFPVCLFYFIEQWF IVLLEEVFHIPCKLDS
15499	45867	B	15589	1	2850	
15500	45868	C	15590	1	2835	
15501	45869	C	15591	78	491	

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15502	45870	A	15592	1	5721	MAVLSLPLAPPTLMPPAHFNLV EMQVKATLKKEYWQRKSPGIPA GANRKKKINGSSPDATSGGYH SPGDSATGIYEGGHASSATLED LELRQPTPSTSPNDCSLVPSQS SSNSSSLHAPHSQYRELAVALH SSSAIISQLSENINSLNENKKSAL QLERQVKELKLGELKETVTS DP SNNGWEAVTSLWEGERLPARG AEEPRGSESTAAARPVPVSPAA VRGRLVAGEPGSYQPAETAAK AQLSLMALPGEY
15503	45871	C	15593	178	1287	
15504	45872	B	15594	52	855	
15505	45873	C	15595	1	1698	
15506	45874	A	15596	302	617	NLAVNPSGPGLFLIGKLLIASIS EHVIGLFRDSTSSWFLSRGVYV SRNLSVSSRFSLVFDDGDVQMG FWCGCPLCLLVFLLTAGPSAA GLLEFAGGHLQTLFA
15507	45875	A	15597	1	2762	MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIGCDFSGTCRQ TLSILTQPLRWGLEGIKKPNS WIIEESVSNNGPPLIPRQTAS GVDLQQTPTDLQRLVTVRRK TNKQKGIASSTKRTSTPKPHL YVTIHKDQSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWYDVYKRPDLRLIGVPD SDGENTRLNTLQDI
15508	45876	B	15598	1	1989	
15509	45877	B	15599	1	762	
15510	45878	A	15600	686	850	GQPERKVGLPTKGSPSD*QRISR QKLYKPKESGGQYSTFLKKRIF NPEFHIQPN
15511	45879	A	15601	2	382	
15512	45880	A	15602	1	993	
15513	45881	A	15603	3	460	SPCWGQLLQATQP/ATAFAQKD LLVGAVLFGHNGSLSSRNTLAF SMDVGPSQWMWGLLNGCGAS AHRQCTRCTLQVITALEGLPLAP LKLAWHKKIYIFLGAAEIRRD QLEAERELFHSRAEQGRFLVGR PGQAAHMLPPGDCVSIWTOH MIT
15514	45882	A	15604	1	130	
15515	45883	B	15605	1	561	

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15516	45884	A	15606	94	420	EKAVGRWIFQSKRYRSPCEKPY SKGLQVQRTVPEGPSKAAARA QAPGPNLLPLCT/PQTPEFIIEP LANMYSCGNQNTLMELEAEQA QQHDEMLHMHALKEALSIIIS
15517	45885	B	15607	46	747	
15518	45886	A	15608	186	364	AFAPAPCTLVPGVLRGPPILLRE TGLAH*CPAVISPPKSLPWLPTA YVESQOVILFGL
15519	45887	A	15609	155	511	GAAVAGTQNLCLGGGAVGG S*RGALNGEGLHPGYNAFPQN TAATRDGRGIAQTAEAAQFLFL HQRVRFHC*FLLWREGRGR*AR REPLSRPQPPAGPLGGALPAPPL PDASTLVGVG
15520	45888	A	15610	1352	1684	MSIRSAWCRAEFNSWISLLTFC LVDLSLVFDDGDIQMGFWCCG PFCLLVFLTTAGPSAAGLLEFA GGPLQTLFAWASAVVAEEQOI LVSSKCCCLIVPLEVLSQRSTWP
15521	45889	A	15611	98	367	
15522	45890	A	15612	426	738	VCCVWGDPGPPAGHGHEAAATL WKEKVDLKERVEKLELQFIHLS GQTDITGRKYISQGVASETQHW ERTTSSGWP*GPGGDEGEPA AGQVLQLVGDHKEGKGK
15523	45891	B	15613	86	1411	
15524	45892	A	15614	950	1493	GTVFLWRRRGTILFRVSGFSAL FFPPSLWFYLPFVDDGDLQME FWYELSFLLMLLLFLCACWFSF *QSGPSAAGLLEFAGGPLQTLF AWVSAVAEEQWILVNRKCCC LIVPLEVLSQRSTRPCEVSVHPY VHCCLGIEELNIYCSLHSLGLFE AILLGKAFELGCCDPSLFATV
15525	45893	A	15615	1	5731	MDSHRPTAWPAAVLAGRSPVA AESERYCSRQPLPRRQALLSV LVLASDTRLPPFWSSQTFCGILS KPLVLSGPLQTQGETNENGLV GGGEVGMQPLVLFERSLFPGR CVLERRIVPWMRQESYSSSSI WVDSDELNLTSVLECLEDDK NNNLLHQQLKWLICGLCRLYN LPKHLDVAMPDQPLPMGQSGP SAAGLLEFTGGPLQTLFAWVSA ALAAEKQILVNCKCCCLIVPLE VLSQRSTWQYELKEYW
15526	45894	A	15616	2	521	

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15527	45895	A	15617	1	1261	MSEHNITEECQQENQSQIEWRSI AHSDSIEVSWLHEVIKTYLKAK STKLDLMKKLKESSQPSRKPK PFIPSQEGTGDNDVIYSTERLSK LLNQKKGSTRLYDKPLSNLLNQ KKVSTRTEGLIVDSRADMRNV TTILLSTESSSTDSSSSMDSSSM DSSSSIGRIVETATCAMIPVQKSK RSGPPQGPSAATGDGAEGRFLP RCSRWPADRLAWSQPRRLAP GPSAATGDGAEGRFPPLCSCCG TDRLAWPQPQGHLLALLPRCGE CGRARELPGDCCLHAEGGCSSV LEVLAIRAIKQKEIEIQIGKQE VKLSLVADDIIFCLENATDSSRN LLELIKEFSKVSRYKINGHKSV LPYINSYQAENHIKNSTPFTIA TNNNNKK\KNLGIYLAKESKDS YNENYKTATERNHRWSQAR
15528	45896	B	15618	60	499	
15529	45897	A	15619	134	1416	RTSICWTMDSSVQNTVLGPTRS SVKGVMEWLQYLMERR/CTL SISMESMPRVAEDAGDVGAEE PLHLEPPAGPLEVEQQLQAEIK HLRKTLESALGQLAQVEANE GSSHLNRQQDERLREWKAELW EEQGETGRSSVQKDRTTISHAL SQNHQLEEQLAKEERLEATSQ NQQLQSQMSLMALPGEGDELG SKEEEEAPQPMPSILEDLKAREA MVAFLNSALVSAEEEQQAQLH GQLKEQRVCCQHLAHPVALAQ KEPEAAAPTPTGTGDSAVWTV DLQVEKTKFIMFTIKPGEVVK DMAQSIYRSGKNLDKDMYGH DLEARRKTNRLPFTTFFYLSYE LDYSRCFIGCLKCLCLPSPATI GSFLKPSQKQKPVCLLYSLQNH EPIKPLFFINYPDSYSRYHTQVIR ILLSGSIHVQVPATKTPPL

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15530	45898	A	15620	1	1665	MGGHVGGRRHMLTPKLIPETL AAGSMKINPEEPNRPPINGAPG GPALPLAAGDSGSEQAGEPALA ASELQGWDSLGLSGPSLGRGTGI VATRSRSGRGLSPASLGRRSR DRKTKELAFAGSGLATRCQRA SSDAAGPPLSRCSPARTPQLPV RGLSLTGPRAPAPPRARVCLLSC SCRQPPPLTGGLNVGRPSGGS WKICPRSLPSASAEIGIRRRRAA AHPPLQPPPLCGESLPSVQCSA NADSSIPVPSRWQDACRNTGA AGPPGYPACVNNRNRDTKNSQ LDETHHMKTKVTDGRGGGAFT MLLRVVDGTHTSCSGSVEWDP RLYGDQADLSRSGHLDRPGA HDYYTAIKKCEEGSLDITTVK VKAGVNGFGRIEHLVTKPAFNS GKVDIVTINDPFVDLNNMVYM FQYDSTHGKFCGTVKAENRKL VASGNPITVFQ/ERDPSKIKWYI AESTCIFTTMEKAGADLQGGGA KRVIIAPSADAPMFVMDVNHE KYDNSLKIVNSASCITNCLAPL ANVIHNFIVGEGPMTTVHAIITA TQKIVDGPSPGKLA
15531	45899	A	15621	2	1105	GRVGCSTVSRIFSCVASRATSLR TPMGKVKVGVNGFGRIGRLVT RAAFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFGHTVK AENGKLVINGNPITTFQERVPS KIKWGDAGAEYFVESTGVFTT MEKAGAH\QGGAKRVIIAPS ADAPMFVMGVNHEKYDNSLKI ISNASCITNCLTPLAKVIHDF GIVEGLMTTVHAIATQKTLD GPSGKLWRDGRGAFQNIIPAS TGAAKAVGKVI* AERGLTGL MAFRVPTANVSVVDLTCRLEK PAKYDDIK\VKQGVGGPPQG AILGYTEH\QVVSDDCNSGPPV FPPFDAGVAGIALNDHFVKLISW YDNEFGYSNRVVDLMAHMAS
15532	45900	A	15622	121	221	
15533	45901	A	15623	189	538	

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15534	45902	A	15624	3	1015	DRAGPPGAPRLGQQLLCATILL GLAKKKKEINITIIKQLKKFLN KKPSYGLERQMETTQNLVDSY MAIVNKTIVWDLVGVMPKTI MHVMINNTKEFISELLSNLYS RGDQKTLMEESAQAQWRDE MLRMYHVLKEALGIIIGDINTTII STVPWGPVDNSWLQVQSVLARR R/SPGLAPTAPSLPTPHRI.SLGA LGTGSVPTLLHHPGSSSVSSLSG LVA/DCFLPKARGGPGQRLPF PSLPGRLECDLAVAPPAPKAAP FICDFVYCCDQASEPVGCGQGT APHRLHGSGLIPQAPPGSIQA WLRAAVFWKGALCPRCGRHIQ EFLHRTLVSL
15535	45903	A	15625	547	1242	PKALIKTSNKSLSYQLTTHSGT MACPWIRHEVLLSRLGFLVLEN TNMDKRPKLLRWLERQMETT QNLVDSYMAIVNKTIVWDLV GVMPKTIHVMINNTKEFISE LLSNLYSRGDQKTLMEESAQA AQRDEMLRMYHVLKEALGII GNINTTTISTVPWGPVDNSCLQV QSVLAGCSFILLVQAVFLLYQA W/LLFWAPQGERWPWTSGL DTV TREEGSPKGLSISL
15536	45904	A	15626	108	308	AQKHHLT*LSFLPRH*ILT*NL KIPTS KIKKT PRSRPRSTSCFL DNLAPSCGCSGKSSWRIC
15537	45905	A	15627	687	1910	KDHQLRKKLRRRGKQGAFTAA LPPGSPRPLRGGRSGGVGLGV RGQRTQAPQAVTPSEGPEPLW GPVLGGGGEHRRGTGASAAAG ASMRRLLGAAGGGAGAGPQRG VGARVVVSEEA NSPGA AITSNR ETQDANEGLSAPRPECLLHPTC RLLYVPLIVRDWVCHTRSVVLL QVVNVGTGIAVGTGLASAYDTL MSQSFQVKNLKRVGIIHQRGVL ILMLCCFFCWADLVNTERILL LKQDPKSPGWTR ECFQEWGSI HLVIPSMFMVCTEQWTFEIGNF LAGLIDVME LGTQGIICELASV AYMNYFRLNPQPPISDFITINLAF LTLTERKILGYIQLRKGPDIVGP YGLLQPFDTAVKFTKEPLWPS TSTITLYIIAPTALSHIVLLALPT RMLAATPRPRGT
15538	45906	A	15628	1	1173	
15539	45907	A	15629	3	1447	

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15540	45908	A	15630	1	215	MDPKQEEIPDSPEKEFRYYRIAE WIRIHQPIICLQETHLTHKDSH KLKV/KGWNKAFHANGHQKSA ARETK
15541	45909	A	15631	1	1524	
15542	45910	A	15632	1	575	MALSERSQPQDHVSHDRIYVK HPEYANLYRQKVVDYTLPRVSI IHVGQAGVQIGNARWELCYCLE LAIQPDGQMPSDKTIGGGDDSF NMFFSEIGAGKHVPRAVFDLE PTVVDRLGHWMAAFLEGEV HTGTYRQLFHPEQLISGKEDAA NNYSRGHYTIGK/EDLVLDRIH KLLTSQCRKPKATMWLSQAT
15543	45911	A	15633	208	465	
15544	45912	A	15634	107	827	EARRPCTLHLRSALHPATMCEL YSKRDTLGLRKKHIGPSCVFF ASDPIKIVRAQRQYMFDENGEQ YLDGINNVAVHVGHCHEVVK ALKQMELLNTNSRFLHDNIVEY AKRLSATLPGETLCLLFYKFRG YWPSSNTNPSRPAAPASPPAAE RAGDFRAGRKPSVPGSRVS PRGPCSRLSLSTFCTRYCPLSAL TSGPGCPYPMCFLLSPRVSRLLY SSHMVAGCRALRRCKNSH
15545	45913	A	15635	3	1218	GGLWEKMAAAA\QSRVVRYLS MSRSAITA\ATSVCCHGPCCRQL HHALMPHGKGRSSVSIVAT VFGATGFLG\RYVVNHLGTAW GSQVIIP\YRV\IKY*QSMHLSFP WG*PGGQLSVFLGNWGTARD* RFLFRYVSYNTGNVGSILFGTR LGETKNF\DFWRDVFVKIPQAIA QLSKGSWEFEKFISCFHIWNGG II*KALS*DI*GNKAVGEKVVRD AFPEAIIIVKPSDIFGREDRFLNS FASMRHFGPIPLGLSLGWKT KQPVVYVDVSKGIVNAVKDPD ANGKSFAFVGPSRYLLFHLVK YIFAVAHRLFLPFPLPFAYRW VARVFEISPFEPWITRDKVERM HITDMKLPPLGLLEDLGQATP LELKAIEVLRHRTYRWLSAEI EDVKPAKTVNI

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15546	45914	A	15636	2	799	GLWEKMAAAQSRVVRVLS/ MSRSAITAIATSVCHGPPCRQL HHALMPHGKGGRSSVSGIVAT GFGA/TGFLRRYV/VNH/LGRMG SQVIIPYRC DKYD/MHL/RPMGD LGQLLFLEW/DARDKDS/IRRVV QHSNVVINL/IGTRP/WKSKNSD YEDVFVKIPQAI/AQLSK/EAG/V EKFIHVSHLNA/NIKSSSRYLRN KNRKREKEEMKKDLLSKKEPE PEDLENSQLIHIAKNEKACFEEN TKSVAEQPFDEEIVDATHQLTS YLGRSQE
15547	45915	A	15637	560	1394	RKSSSVHNAASGLLGSRA PGAH RHLGRRCRCHRLVSPSPAMAE DLSAATSYTEDDFYCPVCQEV KTPVRTTACQHVFCRCKFLTA MRESGAHCLPCRGVTRRERA CPERALDLENIMR/KFSGSCRCC AK/QIKFYMRHHYKSKCKYQ DEYGVSSHPNFQISQDSVGNRIE NNTGIKQIPGAPFGDGRVVGCR QRNAKTELLAAAGESPCTMSL GSGPNLGPSPRSKSSSVTSPOPC FTEHPRERFVSFPVHYVLEGRS MSFLLWSLKTDRIFGH
15548	45916	A	15638	1	1026	MKVVCKEVKFEKQCPAEVLLH WEQTDDDENKRCDLREPRKPE THTKGPGLLVPTTQPGRNEGQS GADGKHARCCKTSCCLSGKEPS FIITEHCPLVPVQNTTIKPDGIR ILQTLDSRETFTMSTALDVLQM KEEDVLKFLAAGTHLGGTDLD FRMEQHICKRKSGGIYIINLKRS WEKLLLVAPAIVA IENPADVSV ISSSSTGQRAMLKCAAATGATP IAGHFTPGFTFNQIQATFPNPRV LVVTD CRTGHQPLAEASYV/NN LPTIALCHTDSPLHHVDIAIPCN R/KAHSVDLMWMLAREILPMIR GTIARKHWEDPEEIEKEEQQA AADKALTKEEFQGE
15549	45917	A	15639	20	441	TAEIAIPCNNKGAHSV*G/MWR MLAREDLRMRGITSGEHPWEV MPDLFYFYRDTEEIEKEEQAAAD KAVTKEEFQGEWTAPAEFTAT QPEAADWSEGVQVPSVPIQQFP TEDWSAQPATEDWSAAPTAAQ TEWVGATTDWS
15550	45918	B	15640	88	531	
15551	45919	A	15641	1	1302	

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15552	45920	A	15642	150	957	KAGASCCGSANPYVSVGKSCV LLAMAQLQTRFYTDNKKYAVD DVPLSIPAASEIADLSNIINKLLK DKNEFHKHVEFDLIKGFRLRM PLDRHMEMENISSEEVVEIEYV EKYTAPQARSNAWFHDDWISSI KRGRGRILTGSYDKTSRIWSLE GKSIMTIVGHTDVVKDVAWVK KDSLSCLLSASMDQTILLWEW NVERNKVKALHCCCKGHAGSV NSIAVDGSGTKYFGLRIEPPKA VSLVEEINSLSYRWTADNYKV GSGGKEED
15553	45921	A	15643	3	393	VFCCPHCSLTFSKSFSSFSRLVR HQQTHWKQSYLCPICDLSFGE KEGLMD/HLEGL*RQGPQSSH HKCRVILQWLGFSDVPTMA GEEWKHGGDQSPRIHTPRRRG LREKACKGDKTKEA VSILKHK
15554	45922	A	15644	335	537	VYFKQVTLDSRCRL*ERQVKST SSWNILSSTWRLPFCPTSVVLR LTWICLRTITSSISWFPADSS
15555	45923	A	15645	153	828	

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15556	45924	A	15646	1	2002	MLESAGNQDIEDVDIVLRQIQV KNRSTTEVGQNGNLQVEVSYT QAHIAPRPLASQGTWPHFVSSA PQPCFQVQNHISKYQNLYYSGFI RETEPISKGDVGEWLSAGKGES SAMFASEQEISKDEQGTPLVGS FYWEVDSPRKESQAWAPGQE WIKLERDITTEKMFELKPIEP VQKTLPWVGEVAATLQEAMK RDCWREARVKKKPVTFEDVAV NFTQEWDCLDASQRVLYQDVS MSETFKNLTSVEGKKKELREQ HPSLRDEGTSDDKVFLACRGA GQCPLSAPAGTMDRTRVLQAS QAGPP/FFATTVGKCFSSRSYL YSHQFVHNPKLTNSCSCQCGKLF RSPKLSYHRRMHLGERPFCCT LCDKTYCDASGLSRHRRVHLG YRPHSCSVCGKSFDRDQSELKRH QKIHQNEPVDGNQECETLRIPG TQAEFQTPARSQRSIQGLLDVN HAPVARSQEPFIREGPMANQ ASVLKNQAPVTRTQAPITGTLC QDARSNSHPVKPSRLNVFCCPH CSLTFSKSKSYLSRHQKAHLTEP PNYCFHCKSFSSFSRLVRHQQ THWKQKSYLCPICDLSFGEKEG LMDHWRGYYKGKDLQSSHHK CRVILGQWLGFSHDVPTMAGE EWHKGDDQSPPRJHTPRRRGLR EKACKGDKTKEAVSILKHK
15557	45925	A	15647	1	1048	MPSLAELFEGSSKAFGAAASQL NFPVASGEMLKFKYGLRNLPLH AVAAEPIASRTSRLNLFQGGKPP FMTQQQMSPLSREGILDALFVL FEESQPALMKIKHVSNFVRKY SDTIAELQELQPSAKDFEVRSLV GCGHFAEVQVVRKATGDIYA MKVMKKKALLAQEQVSFFEEE RNILSRSTSPWIPQLQYAFQDK NHLVLMMEYQPGDLSLLNR YEDQLDENLIQFYLAELILAVH SVHLMGYVHRDIKPENILVDRT GHIKLVDFGSAKMNSNMVN AKLPIGTPDYMAPEVLTVMNG DGKGTGYLDCDWSVGVIAIY EMYGRSPFAEGTSARTFNNIM

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15558	45926	A	15648	101	220	KRQQAFLGLDLHQWFARGSQG FRLQTEGCIIGPPTFEV*RHSGFL SCQSSCTGSFSSVWADVPLMFE GAAQPV*PVPSRGADFRPLSIC *RSSRILLVKRCENSGVR
15559	45927	A	15649	597	808	ITMKSQRQIIKAVTTKEMKSV CRRD/TPAFMFIAALFKIAKIRIQ RLCLSTDEWIKKMWYIHTMEY YSTLK
15560	45928	B	15650	161	3156	
15561	45929	A	15651	14	270	
15562	45930	B	15652	787	1821	
15563	45931	A	15653	1	2412	MAKSKGCSAATLSTHQILVTP WSCDNQKCLQTLPNVPGGTLK LLCEDHWFRNDSCNQAIPTIAT LLSFPSLQASLWTTHTFLPLNH HPVNPDSHLEQPPQSPRLNFE AGDPERAPHALGCKRSRTRATS DRQPMASRDPGWGKASVGGKA CALGSAVLPAGNDCTTDNLGL GSAGFEDLRLRLGQGP RRQGA LQAAPRKASSCAAGQRLAPDSS FSRKR RPSRQLGCEAAVADT AEAKSSEAPAFGWSTMDEAGS SASGGGFRALDEPPNSRIFLVI SKYTPESVLRERFSPFGDIQDIW VVRDKHTKESKGIAFVKFARSS QACRAM EEMHGQCLGPNDTKP IKVVRPGSGCPRGKEWASWTS LHLLCRGEGGV EHPFPAADQT APGLGTGAALRRGSPPTKLRRV AGKGTGCGVFAPRERTROPRPP GDRTA VAGLPSPSPSLIHQLSS LPNSS*PTLSTFLTFLSQMPRFP YIKNGKTL/PFPQVFIAQSRSSGS HRDVEDEELTRIFVMIPKSYTEE DLREKFKVYGDIEYCSIKNKVT GESKGLGVYRLKPSQAQAIE NCDRSFRILAEPKNKASESSE QDYYSNM RQEALGHEPRVNM PFHG VVQYFNVASAIYAKYK LHGFQYPPGNRIGVSFIDGNS ATEKMATQMVAAQLASMVVN NPSQQQFMQFGGSGSQLPQIQ

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15564	45932	A	15654	375	2059	DSSVWQTPQKQRAVRPLHSGG APWTKLAALRATRGFRPGVDS LDEPPNSRIFLVISKYTPESVLRE RFSFPGDIQDIWVVRDKHTKES KGIAFVKFARSSQACRAMEEM HGQCLGPNDTKPIKVRVPGSGC PRGKEWASWTSLLHLLCRGEG GVEHPFAADQTAPGLGTGAA LRRGSPPTKLRRVAGKGTGCG VFAPRERTRQRPDPGDRTA VAG LPLSLALTNPPELFTAKLVLA YFEYFSDLPLSDAQISYIKKRKN STFPQVFIAQSRSSGSHRDVEDE ELTRIFVMIPKSYTEEDLREKFK VYGDIEYCSIIKNKVTGESKGL GYVRYLKPQAAQAIENCDRSF RAILAEPKNKASESSEQDYYSN MRQEALGHEPRVNMFPFGHGV VQYFNVASAIYAKYKLHGFQY PPGNRIGVSFIDGNSATDLLIK MATQMVA AQ/RLHQWCGITQV SNNL/WQFGSGSSQLPQIQTD VVLPSCKKKAPAE TPVKERLFI VFNPPLPLDVLIEDIFCRFQNL EVYLVSGKNVGYAKYADRISA NDAIATLHWKDWSEWGET
15565	45933	A	15655	257	412	
15566	45934	A	15656	3	866	HAASPCCCYEKQSPQLQHLRV CSLRTWSLAARVAEGTAETVD PSAAPKTSVWSSRVCWGRLLA TISPSVNETDTCGMEDRRLVVC RPWRAQCHMKAWGWRHP EEG GTHSGAPSAVLQALAVAIQLGG HLADPLLQVDPLSSCGAVSLDI LIYLVFYRTASVPETYIVKTLF KKLESQSLIQSNVLT RSNSMKA ERGEEAAKEKSEASRGWFMRF KERSCLHNIKMQGEAASADVE AAASYPKDLAKITDEHGYYTKQ QFDVYKTAFCWRVMLKKYVK LLFVLCPLP

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15567	45935	A	15657	333	1034	RLSTTVMRGAFVFMHMKMPRL WLDYCCQFLMDQGRVTHTRRT FDRALRALPITQHSRIWPLYLRF LRSHPLPETAVRGYRRFLKLS ESAEEYIEYLKSSDRLDEAAQR LATVVNDERFVSKAGKSNYQL WHELCDLISQNPDKVQSLNVD AIIRGGLTRFTDQLGKLWCSLA DYYIRSGHFEKIRKAPVNGGPT WMVGQNSVPRFQTRRLTPLKR KGPLVTDFREKQPTPLAQE
15568	45936	A	15658	172	346	ARPCRWCPSG*TSASAPGGLR PCPPAGGDRTPASPLHNQAAA APPGPTWRGAAAS
15569	45937	A	15659	293	482	
15570	45938	A	15660	468	791	LAKCGCLEARGRARQTSGRPRP TDGGP*SPCWETGKGHPVLGR RGS/PGKQGL*SLPQSCQGW CAASRLSSKNSWACMGSGREA VSQETGTSSSSLGLMRPSDKKP
15571	45939	A	15661	366	609	
15572	45940	B	15662	321	739	
15573	45941	A	15663	1	1815	
15574	45942	A	15664	1	1911	
15575	45943	A	15665	437	1125	PVSCSGHSRWAAAIAISIALSMIE TVNMVFTFYSRHHGTISTRVL/I GKRPERQDQDQTVNLGTLEET ASPSPVVTTSPQPMLPSAFPPL SEEINPALPEATVMASPEAVAR QDNVDSAQEPPTPLCASRPTT RQKSWWGARGEVESVTHEEM HYTGKELLEFSNL YKEKSGEQA WEWILRVVDNNGRNIQLDHPE FVDLGPLSRNSAFNAVVRGVK KGSKSLFAWLGEI
15576	45944	C	15666	49	186	
15577	45945	A	15667	80	877	GAERLPEPGPKRMVFRFRVE/V GRVAYVSFGPHAGKI/VSAMVD VFIDQNKGFWSNGPCTQVR/RQ AVMPFKCMQLTDFILKFPHSAH QKYVRQSLGRREDINTKLGQP TRWQGGRFESQEEKEKRLTDF *SVF**RAKEN*RDRIINPRNE V*EAFKRAAFPGKASSQKAPG Y*GVLLAAAAAAAAAAAAA AAAAAAKIVPAKKITVAASKK APAQKVPAAQKATGQKVAAPAP KAQNGSKSKKQKAPAPKASG KESISGNHKK
15578	45946	A	15668	253	1218	
15579	45947	A	15669	1	1819	

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15580	45948	A	15670	1	2422	MCPILREHRGSTEGRKRRQKRLP LELTLKDEEVLAAHRQEIEVAKA SPSKGNIIHFGYKGV EYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKLELTKA EK HVVHFMMDTQLTKRHCPWAA TIQPKLSFLISLP GCDYRGESAR ARPLSHPPQLGLGKDARYLRI CDRSLLCVCAAAGNAGLRPRD SPHTLLHWSRSPYFFSPKPVPP QLLGGQPAAHRRDDLGEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPAPGQGDVMPVLVRPT NRRRLDSTGAGMGPSHHQQQ ESPLPTITHCAGCTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPPP RSSHLHCQQQQSQDKPCPPFA PLPHPHHHPHLAHQQPASGGSS PCLRCNSCASSGAPAAAGADNL SLLLR TSSPGGAFRTTSSPLSG SSCCCCSSRRGSQ LNVSELTP SSHASALRQYYAQSAQQSAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHHHPAHHQH HQPARRESNPFT EIAMSSCRY NGGVMRPLSNLSASRRNLHEM DSEAQPLQPPASVGGGGGASSP SAAAAAAA VSSAPEIVVSKP EHNNSN LALYGTGGGGSTGG GGGGGSGHGSSSGTKSKKKK NQNIGYKLGHRRALFEKRRKRLS
15581	45949	A	15671	1	246	SEPPHRRPTGALPSGAVRRGPL SSRPQIGRSTD SLHCVP GKATD AQRQP VKAAGSGAVPCKATG WSCP KL*EPISCINVTIC
15582	45950	B	15672	43	741	
15583	45951	A	15673	687	1012	FHTSRPFWNISELSRFICQKYKK PWHSVSDFYRYQFFICQGTACC PASLRM*HCPN*ILQGTSSQNCC SCSGKSCSPMQRRHRSTVCSGS GTFCVGSCESEFEGTYFSR

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15584	45952	A	15674	1	1640	MSCDTNGEVEGGRVDSKTRGR QEVERTNTETHLGSGLNCDIPLIF LTYEWRGILEYKIFSVKTEGEVL GKPGQLGHPTGQTTFETGTQV TSMQEMGSYSFGQHPVALQG TAPLPAFTGWRLASVAFPGTQ CKLSVDLPIWGLEDSGPLLTAP LGSAPVGPLCGGSDPTFPFCTA LTGPSAASLLEFARGPLQTLFA WVSAEVSABEQGFFVNHECCCL VPLEVLQSRSTRPCEVSVCPYW GVPPRDRSNQCPSGFTLDSVGP FCADEDECAAGNPCSHSCHNA MGTYCYCPCPKGLTIAADGRTC QDIDECALGRHTCHAGQDCDN TIGSYRCVVRGSGFRRTSDGL SCQDINECQESSPCHQRCFNAIG SFHCGCEPGYQLKGRKCMDVN ECRQNVCRPDQHCNTRGGYK CIDLCPNGMTKAENGTCIGECL AVSVTEIS/CAVNKSNIDECKDG THQCRYNQICENTRGSYRCVCP RGYRSQGVGRPCMDIDECENT DACQHECKNFTGSYQCICPPGY QLTHNGKTCQKGLPFKQIESGG
15585	45953	A	15675	1	669	MGFCHDGRSIAFRGERGNDESA IEMIKVSHLKQYLA VVFRDKPL ELWDVRTCTLLREMSKNFPITIT ALILTGRCASLKWRSKPKKEEF MGYRQWNPTQESSKGDFEIQ EGGPSMATVYRTEMQPVQIGIE LLPSPLSFHSPNSGIPNDPSWL LSTATLHPPTGVERSSSPATEQR WTENDFDELREEGFRRSNYSEL REDTQTQKGEVENFEK/NLEECI
15586	45954	A	15676	1	323	MAHESAEDLFHFNVGWWHFSV PRSKLSQFPDSSLWKEASALT SESQRLFIDRDGSTFRHHVHYL YTSKLSFSSCAELNLLYEALG LQLMPLLQVRCSCFLGVVDQ
15587	45955	B	15677	1	1443	

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15588	45956	A	15678	1	708	* EVTASPPQGVSAVSKGDKQKWT ALGKGLTFIKAVGSIQRNRWRG WQLKALYQCTTIAGATGVFLR VYRALDVLQMEEDVLKFLAA GIHLGGTNLDFQMKQYIYKKK CDGVYIHLKRTWEKLLLAACA IVAIENPADVRVVISSRNTGQRAI LKFAAATGATPIAGRFTPGIFTN QIQATFQEPQHLFFTDSDRH/S PLTEASYVNLHTIAPRNTDPLC YVDIAIPCKKGAHSVGL
15589	45957	A	15679	78	757	REIFINVRSLLMACFVKEEDVL KFLAAGTHLGGTNLDFQMEQY IYKRKSDGIYIHLKRTWEKLLL AARAIVAIENPADVSIVSSRNTG QRAVLKFAAATGATPIAGRFT GTFTNQIAAAREVPRLLVVTDP RADHQPLTEASYVNLPTIALCN TDSPLRYVDIAIPCNKGAHSV GLMWWMLAREVLRMRGTISR EHPWEVMPDLYFYRDPPEIEKE EQAAAE
15590	45958	B	15680	1	1767	
15591	45959	A	15681	98	412	
15592	45960	A	15682	521	600	PSPGES/PPLQDPDPVPPWPPPEE EPRA
15593	45961	A	15683	117	285	
15594	45962	C	15684	12	468	
15595	45963	B	15685	1	840	
15596	45964	A	15686	1	1173	
15597	45965	A	15687	1	2931	MDLFMNVAMLRARYLWSEA VSOFGAQDPKSLALRTHCQTSG WSLTEQDPYNNVIRTIEALAA TLGGTQSLHTNVFDEALGLPTD FSARIARNTQIIQEESEL CRTVD PLAGSYIYIESLTDQIVKQARAI QQIDEAGGMAKAEAGLPKRMI EEASAREQSLIDQGKRVIIVGVN KYKLDHEDETVDLEIDNVMVR NEQIASLERIRATRDDAASDTR EIVDLTNGNIKTFGNSIIHARFD TGRHLFSGGNT
15598	45966	C	15688	1	1779	
15599	45967	B	15689	22	1531	
15600	45968	A	15690	98	412	
15601	45969	A	15691	521	600	PSPGES/PPLQDPDPVPPWPPPEE EPRA
15602	45970	C	15692	175	454	
15603	45971	A	15693	332	494	RKEMASGFSKGFTLGCCRRAL PDGDTQLQLLRGNHDSVLGA KRRDKGEAGPD

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15604	45972	A	15694	2	1276	HTLHSLVTILGTWALHSGPALL LPRPGSGLDFFLLSPVLPSQPQPG LPTPTPFTNAVQLLLTLKLVSLA SEVQDLHLAQRKEMASGFSKG PTLGLL/RRRALPDGDTQLQLLL RGNHDPVLPPLPHLPGLAGAAAL PRGSA\SLRPLRRAWPAPLFGL LFLSSHLFPLEAVREDAFYARP LPARLFYMPVFFAFRMRFYVA WIAAECGCI AAGFGAYPVA AK ARA\GGGPTLQCPPSSPEKAAS LEYDYE TIRNIDCYSTD FCVRV RDGMRYWNMTVQW WLAQYI YKSAPARSYVLR TAWTMLLSA YWHGLHPGYLSFLTIP LCLAA EGRLESALRGRLSPGGQKA WD VWHWFLKMAYDYMCMGFV LLSLADTLRYWASIYFCIHF LAL AALGLGLALGGGSPSRRKAAS QPTSLAPEKLREE
15605	45973	A	15695	134	601	RDGEQPLWAWGSPCPVAPT L CILWAPSSGPGPSFRPSAPATP WLWPGLSPISCDSEPSASWACP LPCPSPKPDRWLLTLKLVSLAS EVQDLHLAQRKEMASGFSKGP TLGLL/RRRALPDGDTQLQLLL RGNHDSVLGAKRRDKGGQTII FVQV
15606	45974	B	15696	76	504	
15607	45975	A	15697	11	706	HITRGRSCTRWISSAMAKGAPR VILLCLFGAALCLTGSRALQCY SFEHTYFGPFDLRAMKLPSISCP HERFEAILSLDTGYRAPVTLAR KGCWGTGPPAGQDAIEPGRAAA RLLGIVRGCTTDKCNHLMTH DALPNLSQAPDPPTLSGAECYA CIGVHQDDCAIGRSRRVQCHQD QTACFQGNGRMTVGKGLEGW KGLGKGYGGRAAMRVVIPDRP NRETWPCSEVGGMTLV

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15608	45976	A	15698	2	1642	DEGRAKGHHTWQQTRENSQA KGETPYKTIRFRETYVHKNSMG ETTPMIQLSPTGSLPQHVGMG ATIQDKIWVRTGLPGFPGTGL PVSSGFPGPSGFPGLQGGPPVSYG PTGIPGPIGPPGPGMLMVSSGPP GLPGPKVILGLNFQGPKEKVS KGLQGGPPGPGQISEQKRPIDVE FQKGDQVSNQDRGPPGPPGIRG PPVSTGGGEKGEKGEQGEPPGKR VSEKDGENGQPGIPVSSGDGP YPGEPGRDG/EKGKNVMGPPGP PGFPGERGQKGDGPPGISIPGP PGLDQPGAPGLPGPPGAPGH IPPSKLGDTFCNIGTGISGPPGQ PGLPGLPGPPKLA/GAPGAPGFP GSKGEPGDILTFPGMKGDKGEL GSPGAPGLPGLPGTPGDGLPG LPGPKGEPVCTFKGERGPPGN PGLPGLPGNIGPMGPPGFGPPGP VGEKGIQGVAGNPPGQPGIPGKF GDPGQTITQPGKPLPGNPGRD GDVGLPGM*GLPGQGLPGIPG SKGEGPIPGILPGPPGPKGMLL
15609	45977	A	15699	246	433	GLFPLEPGANGI*GC/SGIRAQ RWLPGRPKFTGESFIR*PPRVAK ESQQLIWFGCVPTQISS
15610	45978	A	15700	179	5262	RSCGSRMRMLKRGVSLAAGLFL LALSLWGQPAEAAACYGCSPG SKCDCSGIKGEKGERGFPGLG HPGLPGFPGPEGPPGPRGQKGD DGIPGPPGPKGIRGPPGLPGFPG TPGLPGMPGHGAPGPPGIPGC NGTKGERGFPGSPGFPGLQGGP GPPGIPGMKGEPPGSIIMSSLPGP KGNPYPGPPGIGQLPGPTGIPG PIGPPGPPGLMGPPGPPGLPGPK GNMGLNFQGPKEKGEQGLQG PPGPPGQISEQ
15611	45979	A	15701	155	623	FNLYPPGPSHN/DVGMGATIQD KIWGGPGLPGFPGTGLPGERG FPGSPGFPGLQGGPGLPGTGP GPIGPPGPPGLMGPPGPPGLPGP KGNMGLNFQGPKEKGEQGLQ GPPGPPGQISEQKRPIDVEFQKG DQVSNQDRGPPGPPGIRGPPVS
15612	45980	A	15702	581	687	KKGAGQVV/DDVQLAQRLAQ NEIVLSWNCWMLCKQY
15613	45981	A	15703	7	123	

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15614	45982	A	15704	1	374	RFRKAQCTIVERLTNSMMMHG RNNGKKLMTVRIVKHAFEIHL LTGENPLQVLVNAIIN/DVSPLR RVNHAIWLLCTGAREAAFRNIK TIAECLADELINAAKGSSNSYAI KNKDELERVAKSNR
15615	45983	A	15705	2	892	QAFPLPTPDQLSNYKVFACKTA LWQNDDVHSQHKGEYRNAAG EPKYRNSVTTHSEGGKQSEK KDLGVGYWSMACYKLGHIAG NEQQKHICGGIAKKWKQPKCP PTGKWPAAVVKPATESEGGGAK KEEKAHLPRVVEKELHESSRHI RHSIESVLLQAFQKDYTAVKE KYAKYLPISAERYAAKRFKA QCPIVECLTYSMMTHGRNRRK KLMIMRIVKHAFEIQLLTGDNP LQVLVNAIINSGPREDSTLTGRA RIVRRQAVAVSPLSRVNQAIWP QCTGALEAAFRNIKTIA
15616	45984	A	15706	1	536	
15617	45985	A	15707	8	437	
15618	45986	B	15708	255	1058	
15619	45987	A	15709	609	1489	LPLSLPRAARPAVAPHLPPREP PALPLPPPQPPRPSLPGSAQGC NS*RTGTAAAGAGPFAPASMSL RVQTPCWQPGAREPPGSCAS WLFCAVWQMVRAHSGCLAPP PAAAAWVAAQLQP*DGHEGPG G*ET/S*VLRRLPTPTPLPTWCC TVRPRRPVLPFLIMRRRTAGPP CAPIAAAPTTPSSLRRGKVP TGR PPVL*G*AAVMLTMAVTITRTV TTSNAAAVMPKGTGAHRAP LTPGTV*RDCLVKPTAQMPPS APPWTAPPRVAVAPVIVLPAIS NLGAFA
15620	45988	A	15710	173	530	GRERGDKGGAVQTLQDLVNV HLGLTYPPRPGHSGSPSWASQ APLQPPLRGEPGHGWGS/PSGL GQKSEGLGPAHLPRARPAV APHLPPREPGLPLPPPQPPRPP SLPGSAQGCNS
15621	45989	A	15711	1	227	
15622	45990	A	15712	238	498	
15623	45991	B	15713	1	1017	
15624	45992	B	15714	590	649	

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15625	45993	A	15715	3	843	AVFLSTSNEAVYKIFDDSCPPT AKTCNPETFPSSNESRQCPNAR CQFAYFGGESGYHRALLGLQIF NAFMFFWLANFVLALGQVTLA GAFASYWALRKPDDLPAFFLF SAFGRALRYHTGSLAFGALILAI VQIIRVILEYLDQRLKAAENKFS YVCLMTCLKCCFCWLEKFIKFL NRNAYIMIAIYGTNFTCSAR/NA CFLLMRNRIIRDVLDKITDFLFL *GKLLIVGIVGILAFFFFTHIRIRI VQDTSPLNYYWVPILTIVIGS YLIAGHGFQRY
15626	45994	A	15716	1	449	FRGMGDERPHYYGKHGTPQKY DPTFKGPIYNRGCTDIICCVFL LAIVGYVAVGIIAWTHGDPRKV IYPTDSRGFEFCGKGTKNENKP YLFYFNIVKASPLVLAGI/QCP TPQICVEKCPDRYLYLNRSS RDFEYKQFCVPGV/PRTIKKA NGVLEAGNSPCAYLKITPSLGT DY/PWFLLEFQCPITPQICVEKCP DRYLYLNRSSRDFFEYKQFC VPGVQEQ
15627	45995	A	15717	627	1665	EQAGQALSTAPVGDGHELLCE VGSSSFRDVLGTSMGLCGGY/G GAS/GMGGITAVTVNQVLSPL NLEVDPMQGMHTQEKEQVK TLNKSASFVDKVLFLFQQNKM LETNWSLLQQQKPAQSNMDN MFESYINLLGQLEILGQEKLK LEAELGNMQGLCMFFVKEDFK KKYEDEINKPTMENEFVLICK DVDDAYMNKVELEFRLEGLTD EINFLRQLYEEIEPQLSQILDTS VVLSDMNSRSLDMSIIAIEKY EELQTLAGKHWDRLRLTKTKIS EMNRNISRLQAEIEGLPQRPEQ RASLESVIADAEQRGELAIKDA KTKLSELEAAQRAQDMAHG

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15628	45996	A	15718	3	3908	STQOKTARSNMDNMFESYINN LRRHVETLGQEKLLAEELGN MQGLVEDFKNKYEDEINKRTE MENEFVLKKD/VDEAYINKVE LESRLLEGLTDEINFLRQLYEEI RELQSWISDTSVVLMSDNRSL DMNSVIAEVKAQYEEIANRSQA EASMYQIKDEELQSLAGKHG DNLRCTKT*DLLR*TRNIRLQA EIEGLKGQRAFLEAAIADAEQC GELAIKDANAKL/SELEAALQR AKQDMAWQLRLMN
15629	45997	A	15719	1	804	MKPRTLVSSTVTLKDGVSRC SFRCSRVSRISFQWVRLADF RNEATDPHGLDDILTLRQDKG SFMICWLKKGAPPGDPAPPRITP TVRFSTMDLSAASHIRIPLSDGN SIPILGLGTYSPEKSLWATNHVP FMVRPTLERTLRVLQLDYVDL YIIIEVPMFAFKPGDEIYPRDENGK WLYHKSNLCAWAEAMEACK\ DAGLVKSLGVSNNRQRLLELIL NKPGLKHKPVSNQVECHPYFT QPKLLKFCQQHDIVITAYSPLW TSTNP
15630	45998	A	15720	476	906	WKQSHSHQTWYLLTSEACKD AGLVKSLGVSSFNRSR/QLELIQN NPKLKPVPVSNEVECHPYTQP KLLKFRQQHDIVMIAYSPLGTT RNPTWTNMSSLPSLKDALLKR CNKITAQVILRFNIQQGVVPIPK SFNPEKIKENLQA
15631	45999	A	15721	138	217	RHAPQVLGGLSEGT*GGHRCPA RGHW
15632	46000	B	15722	8	578	
15633	46001	A	15723	1	3087	
15634	46002	A	15724	1	2232	
15635	46003	A	15725	1	2085	
15636	46004	A	15726	1	1512	
15637	46005	A	15727	1	1260	
15638	46006	B	15728	1	2145	
15639	46007	A	15729	1	1353	
15640	46008	A	15730	1	1741	
15641	46009	A	15731	1	1995	
15642	46010	B	15732	1	3464	
15643	46011	A	15733	2	109	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL
15644	46012	B	15734	90	1247	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
15645	46013	A	15735	1	1698	MELKAKAQELREECRLSRRC NQLEESVSVMEDMNMKREG KFREKRIRNQEQLQEIWDYVK RPNLRLTGVHESDGENGTKLEN TLQDIIQENFPNLRQANIQIEI QRTPPQRYSSRRATPRHIVRFTK VEMKEKMLRAAREKGWVTHK GKPIRLTVDLSAETLQARREWG PIFNILKEKNFQPRISYPAKLSFI SEGEIKSFTDKQMLTDFVTTRP ALQELLKEALNMERKNRDTHR LKIKGWRKIYQANGKQKAGV AILVSDKTDKFKTKILDKKEGH YHIVGLIQEELTILNTYAPSTG APRFIKQVRSDDLQRLDLSHTLII GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDIYRTLHPK STEYTFPSAPHHTYSKIDHIVGS KALLSKCKRTEIITNYLSDHSAI KLELRICKLTQNHSTTWKLNLL LLNDYWVHNEMKAEIKMFFET NENKDTTYQNLWDTFKVCVTG KFIALNAHKRQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELEIETQKTL/QKINESRS WFFERINKIDRPL
15646	46014	A	15736	1043	1536	TSTELSTPNQONIHFFQHHHTSI PKLTTYLEVKLSS*KKH*TWKG TTGTSCC/INHAKIVTHRLKIKG WRKIYQANGKQKAGVANLV SDKTDFKPTKIKRDKEGHYIMV KGSIQEELTTLNIAYPNTGAPR FIKQVLSDLQRLDLSHTLIMGD FNTPLLTLDSTRQKVNKDTQE LNSALHQADLIDIYRTLHPKSTE YTFFSAPHHTYSKTDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTKNRSTTWKLNLLLN DYVHNEMKAEIKMFFETNE NKDDTTYQNLWDTFKAMCRGK FIAVNAHKRQERSKIDTLTSQ LKELEKQEQTHSKASRRQEITKI
15647	46015	A	15737	1208	1387	KPWQKNYVTHAQASVADLIK WKKGYQ*LKIK*MK*SKRSLE KKE*KETNKASKKYGTI
15648	46016	A	15738	308	487	KPWHKNYIMHAQASVANLINW KKGYQ*LKIK*VK*SEKRSLEK KE*KEMNKASKKYGTM
15649	46017	A	15739	220	1101	
15650	46018	A	15740	1	1534	
15651	46019	B	15741	365	3904	

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15652	46020	A	15742	79	506	EPSQRHSQDLQGWSEHQVCL HRVGVGHGHCATCILPAATASHE GPEAW/TARLLVPQTAVGICSA FSGLPSTSTHEPTGMHFLPSEAHE KPRTPQPDQKGRDDLPCTPSTC LHTSLFLDTGQEFGTCTCRMAGLK EHVAGDNRERRQ
15653	46021	A	15743	2	71	ELKF**FPIPSRKTSPLRQGS
15654	46022	A	15744	1	627	MKAIEIKMFFETNENKDTTYQN LWNTFKAVRRGKFIALNAHKR KQERSKIDTLTSQLEKEKQEQ THSQASRRLNQEEVESLNRPI GSEIEAIINSPLTKRPGPDGFTA EFYQRYKEELPK/YLLKQLQQS LRIPNQCAKITSIPKHQ*QTNRE PNHE*TPHNCFKDNKIPRNPTY KGREGPLQGLRTIAQRNKRGH KQMEEHSMML
15655	46023	A	15746	1	3828	MQLPVQTIAADGYVIKLQKRRT EDGHQSPERHQFPHLSSYSEQE TTRVPFAKAVASGFPGDTTLVF CASPPSPQVHLPTQAVADIFSE FHEHYARJSTAPSVTLKANMM GSEFPTARLSNSKYPETLEVGES AQPVPMYTWKTVAQDRKDGVS SPPLLEKQSITKSISNKPVELSSK VVEVDASKADHMKKMASMGL VHSMAGSGLVLSRSEILKEISSL RNGCAIYRSEFISTDPSSWVVP PRTNEENNGES

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15656	46024	A	15747	1	1639	NCLSDHSAIKLELRJIKLTQNCSTTWKLNLLNDYWVHNEMKAEIKIFFETNENKDTTYQNLWDTFKAVCRGKFTALNAHKRKQERSKIDTLTSQLKELEKQEQTTHSKASRRQEITKIRAEKKEITQKTLQNINESRSLFFEKINKIDRPLARLIKKKREKDQIEAIKNDKGDITDTPTEIQTITREYVYKHLVANKLEYLEEMMDKFLDITYTLPRLTQEEVESLNRPTTGSEIEAIINSLPTKKSPGPDGFTAIFYQRYKEELVPFLKLKLFQSIEKEGILPNSFYEASIIIPKPGRDTTKKNFRPISLMNIDAKILNKILANRIQQHIKKLIHIIDQVGFIPGMQGWFNIRKSNVIQHINRAKDKNHMIIISIDAGKAFDKIQQSFMLKALNKLDIDGTAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLSNFASKVSGYKINVQKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDINKWKINIPCSWVGRJN
15657	46025	B	15748	1	1563	
15658	46026	A	15749	1	4332	

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15659	46027	A	15750	1	2319	MRIDGAQELTLALPFASGVACR DVKPGPRRRPLRYRCFQKPSNR LGSASLGAGFWAGRRDAKSGH DDDPGALFSVTMDRDLEQAL DRAENIIIEIAQQRPPIRRYS PRA GKTLQEKLYDIYVEECGKEPED PQELRSNVNLLLEKLVRRSLPC LLVNLYPGNQGYSVMLQREDG SFAETIRLPYEERALLDYLDAEE LPPALGDVLDKASVNIHSGCV IVEVRDYGQSSNMQPPGYQSRH ILLRPTMTQLAPEVKTMTDRDGE KWSQEDKFPLESQLILATAEPL CLDPSVAVACTANRLLYNKQK MNTDPMEQCLQRYSWPSVKPQ QEQSDCPPPPELRVSTSGQKEE RKVGQPCELNITKAGSCVDTW KGRPCDLAVPSEVDVEKLAKG YQSVTAADPQLPVWPAQEVED PFRHAWAEGCQAWDTKPNIMQ SFNDPLLCGKIRPRKKARQKSQ KSPWQPPDPDHSALWRPGETD AGRAVSQAQESVQSKVKGPGK MSHSSSGPASVSQSSWKTPEQ PDPVWVQSSVSGKEKHPPT QLPSSSGKISSGNSFPQAGSP LKRPFPAAPAAAAAPAPAPA PAAAPALAAAAAAGGAAP SHSQKPSVPLIKASRRRPAAGRP TRFVKIAPAIQVRTGSTGLIGH QRGGPSPGSPGISGSLQSSGGP LPDARFGSSAGCAPLCLGQQP

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15660	46028	A	15751	409	1874	YDSYIVVIDDADITRGDDAVPR DHHSSSTSMVVFRRHRLDVIVVD GDDQHRRMVGRRCRSWFRFR GSLDVDQVIGDTAAGRLNVMG DITRDARRDKVKNERYGVA PSVAFGLGTANRLYLYLHVTQH NTPDGGIPTIGLPGYSAPSAGTA ALNHSGKVDTHNFYGTSDSDYD DSTTDATMRFEHDINDNTTIR NTTRWSR/S/WTWSRTANTKDV SNKILTNQTNLTSTFYTGSGHGD VSTGVEFTRETQNTNYGVNPVTL PAVNIYHPDSSIHPPGLTRNGA NANGQTDTFIAYAFDTLQITRD FELNGGIRLDNYHTEYDSATAC GGSGRGAITCPTGVAKGSPVTT VDTAKSGNLMNWKAGALYHL TENGNVYINYAVSQPPGGNN FALAQSGSGNSANRTDFNPQK ANTSEIGTKWQVRGSSRVNVM HEVNTPHQCVRFRPARSAPGCC QSPCHRSGKHMQYGLSKCQPG QYNSVKSGERVNGVTFQ
15661	46029	A	15752	421	441	P*ARMPSPLGPPCLPVMDPETT LEEPETARLRFRCYQEVAGP REALARLRELCCQWLQPEAHS KEQMLEMLVLEQFLGTLPTIEH AWVRGQRPGSPPEAAALIEGLQ HDPGQLLG
15662	46030	A	15753	1	346	PAFGGSAPSERLELHVDGPPPRP QAPGD/CGVGRSWRAEM/HR ALRGNTNPRHILRSCCARARRRP *RRSAPPGRAN:PS*SSWGPSTP GNYRCRYRSWVPHTFKSELND PVELLVA

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15663	46031	A	15754	1	2091	MKPGRLRRRRGRGLGCGLPQL RATWSGAVLAGRDAVLRCGEP IPDVTFELLREGETKAVKTVRT PGAGAKLELIFVGPQHAGNYRC RYRSLVAHTFESELSDPVELLV A VAATLNHILRLVHMLHIPAAG EGSFREGTHFLKSPVKMPLVF RVGRRRLVNLQGPQGVPIPIRSC EHLNWQKGLCGVTKCAAPLLR GPCCPAVLRKEIPFVSLKPLGMS SKASEAEPGLPRLGSHQSTAAA LGPRYNGSADAIRPHTA WAVIQ TTISRFTWSLTQVNVPSRTVSLA VRRDRYMTSRTTTNPEEGRG TFWARRNGCPSACAVAEAL EACLADVRYPPVALSCGRLQK RRDFRETNAAMSNEKSLASA RFFVEVQVTLGALCTVQATGQ SMLVFSTTQMSSYSEKFLTSH ASLSPLQLADRWRDQGMKW QSPQWGLRPAASHTAEQEPGL AASKAFRDLQNLNSAFLSLTS LSAGHQCSAIVVMMSKKEITP QGQLAAASFGELQPVALKCPW LK.SQHVESWL/RPEAHSKEQML EMLVLEQFLGTLPEIQAWVRG QRPGPSPEEAALVEGLQHDGP QLLGWITAHVLKQEVLPAAQK TEEPLGSPHPSGTVESPGEGPD TRIEGSVQLSCSVKEPNVDGQ EVAPSSPLAAQSPGNGHGHQ PASTSFHPPRIQVSSPKWEV
15664	46032	A	15755	1	208	EVAQMPRVSTPATLPSLPQPAL
15665	46033	A	15756	3	373	MAPWTPVPYDQLMEEKARAR YAGTIQKWTAAALQLPRTSLK DSGEGTSKWGRSVDTTQPLSPA IPVIFQ* AHEQSGHSGMDGGYA WALQHGLALNTDLA
15666	46034	A	15757	3	266	
15667	46035	A	15758	3	587	YPASAGLMLQNFVIGLRYHF AIHSPAAGGLDGLHAAVAIQG ITKIETTPNHQAPAHWTLLTQ QAHLQSPPLHFNPLTLCLMHC PTAIPHCADARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVGAYGAQQL
15668	46036	A	15759	1	1566	

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15669	46037	A	15760	1	981	MVAIAKVLIAVKEDSDSHNQPN TRMTVSKGVPVSAVEGGRRGQD SDDCVVEENDAVRTWPPSRILRT ESHSPHTCSWRRHLLSSCPYT GMSEFIPSSGNISSTHAVISFPPL SEEMNPMLPKATVMTSLEAAA RQNLKSRQAPRCEVESVTHEEV YYTRKELFEFSNLYRKKSGEQI REWILRKTDGSWRITVDYRKL NQMVTPIAAAVPDV/VVSLLEQ INTSPGTWLNCHNLIWRDLDCFL LPQNITLVHYTDDIMQIGSSEQE VANTLDLLPALMASW/ENSP*SI DRGRED*SLVHKWFCTICRHHP KVDSCTTAPF*DIEGQQQL
15670	46038	A	15761	349	718	AGPEGTTTACPI/COOQRPILS LRYGTISWG/DQSATWQVVDY IRTLISWKWQSAKATTIHGLT KCLIHHDIPHSIAD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHHPCSFNP
15671	46039	A	15762	143	469	ARIQ/GSRNQGVVEVAVPLTVT PSDPLANVLLPVATLPSAGLEI LVPEEGRLLPGDITMMPLNWN LRLPHGHFGLLLPLNQAKKKG VAVLGGVIALDCQDEISLLLYK
15672	46040	A	15763	1	2712	
15673	46041	A	15764	3	578	LKSRQAPRCEVESVTHEEYVYT RKELFEFSNLYRKKSGEQIREWI LRKTDGSWRITVDYRKLNQMV TPIAAAVPDV/VVSLLEQINTSP GTWLNCHNLIWRDLDCFLLPQN ITLVHYTDDIMQIGSSEQEVAN TLDLLPALMASW/ENSP*SIDRG RED*SLVHKWFCTICRHHPKVD SCSTTAPF*DIEGQQQL
15674	46042	A	15765	1	461	MTVDYRKFNQVVTPTMAA/AVP DAVSLLEQINTFGTWYAAIDL ANAFSPVPVHEAHQKQFALPQ GYINFPALCHNLIIRRELDFFLLL QDITLVHYIDILLIGSSEQEVV NTDLLIHKRSKEAETHAASRIR VSCLPEQKSHEQTLPEWQVVP
15675	46043	A	15766	1	1371	
15676	46044	B	15767	54	864	

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15677	46045	A	15768	2	1148	PRGRNRRRKTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PIEFHCLSKLIHLLIPGMQPLT WQ/HALFSIPVHKGYINSLALC/ Q*CYLERT*LLFTSTRYHTGPLH **HYADWJQCARSRKQTLGTG KGQRFLVTERDTYVGYFTYPAH NASAKTTIHGCTECLTHPHVIPH SIASEQDTHFTAKEVWQWAHG NGHHWSYHVPHPHPEIARLIEWW NGLLSQVQCHLGDNTLQGW GKVLQKAVYALNQYPIYGTVS PIARIHGSRNQGVVEVAPLTIT PSDPLAKCLFPVPKTLCAACLE VLLPGGGMPLPGDTTTTPLNRK LRFPLEHFGLL
15678	46046	A	15769	917	2352	DTISHQLEWRSLSKQETTGAIEI SATIKDLKGAGVVIPTTSLFNSS VWPVQKTDKSWRMVTDYCKL NQVLTPNAAAAPDVVPLLEQIN TSPGTWYAAIDLANAIFSPVHK AQKQKQFAFSWQGGQYFTFVLP QGYISSLALCHNLIRRDLDGFL LQNTITLVHYVDDIMLIGSSEQE VANALDLLVRHLICVRGWEISPT KIQGPSTLVKFLGVQWCGACR DILSKVKDKLLHLAPPTTKEA QRLVGLFGFWRQHIFHLGGLLQ PLYLVIOKAAIFEWNPEKVL QKVQAAVQAAALPLGPDPTDPI MLEVLVADRDAVWSLWQALI GESQQRPGFWSMALPSSADN YSPFERQLFACSWALVETECLT MGHQVTMQPELPIMNWMLSDP SSHKVVAQQH/QEVAQMPRV STPATLPSLPQALMAPWTVPY DQLMEEKARARYAGTIQKWT AAALQPLSRSTLSKDSGEGTSKW
15679	46047	A	15770	1	861	
15680	46048	A	15771	5	90	
15681	46049	A	15772	1	324	MVQEASEVIGQLQSSAAK*AM HWAGFSYLTCKSLNAN
15682	46050	C	15773	1	726	
15683	46051	A	15774	364	543	ARGAARSMKHTSGDETQRQKL D*VRLTGIRASREEVTKAGPR KRIMCSGMDLNGGLQL
15684	46052	B	15775	1	1056	
15685	46053	A	15776	1	282	

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15686	46054	A	15777	167	954	KRVTSKLSKSPRRGSPHCSRNPV LLRGIGRYSRSAMYSRKAMYK\ RKYSAAKSKVEKKKKKVLAT VTKPVGGDKNGGTRVVKLRK MPRYYPTEDEVPRKLLSHGKK\p FSQHVRKLRASITPGTILILTGR HRGKR VVFLKQLASGLLVGTG PLVLNRVPLRRTHQKFVIAFTT KIDISNVKIPKHLTDAYFKKKK LRKPRHQEGEIFDTEKEKYEITE QRKIDQKAVDSQILPKIAIPQL QGYLRSVFALTNGIYPHKLVF
15687	46055	A	15778	1054	1403	MVEGGILRVNTSVECKTGPFF SPHILWREPFCSVQVGGKKKKK VLATVTKPVGGDKNGGTRVVK LRKMPRYYPTEDEVPRKLLSHG KKPFSQHVRKLRPSITPGVTILIL TGRHRG
15688	46056	A	15779	1	388	
15689	46057	A	15780	1	456	MKLPEEGSLSDICCSAIFAVLQP LLVIPRETGSGVDLQQTPTDLQ LRQTESQIMSELPFTVASKRIKY LGIQLTKDVKDLFKEIYKPLLSE IKEDTNKWKSIKPSWLGRINIVK MAILPKVTYIFNAIHKLPMTTEL EKT/KFIWNRKRACI
15690	46058	A	15781	1	504	
15691	46059	A	15782	1	1836	

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15692	46060	A	15783	285	1949	RGEMNSRGRNLSIINKTDFPFI ALNAHKRKHRSKIDTLTSQK ELEKQEQTNSKASRSHEITKIRA ELKEIETHNKPFFKISESR/SWFF IFYF/ERJNKIDRPLARLIKKKRE KNQIDTIKNDKGDITDPTIEIQT TIREYYKHLAYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGSEIEAIINSLPTKRSPGPDGFT AEFYQRI.KQCRKAHLDPVSLT HRSGPGAREDR LSDSGDASRGC WNLSQHAAVTSPSEERRIRTL SCRSVGVCCRSTPDPVCLGISSG GCRTVNIGEQQMLLPDRSSGSF VSEGYRCPCEVSAPTGGCPPVRC LMINTVSLIGVKFTEVFD SINISE HLELACLDHNSLLAREQNW EDEFDELTEVGFRRWVITNSSE LKEEVQTHCKEVKNLETRLDE WLTRITNAEKSLKDLMEKTM AGELRDACTRFSSRFNQL EERV TEIEDQMNMEMKQEEKFREKRIK RNEQSLQEIWDYVKRPNLHWL GVPESDRENGTKLENTLQDI IQE NFPNLARQTNIQEMQRM P
15693	46061	B	15784	596	1414	

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15694	46062	A	15785	610	2986	QTERNSININRNGHQHQNPICRS PSSKTKGSIKPQRSGRNQSRKA ENSKDQRTSSPTKDCSSSPATE QRWMENDFDELTEV/VLQKPG RDTTKQKEKFRPISLMNIDVKI LNKILANRIQQHIKKLIHHDQV GFISGMQGWFNICKSINVIIHIN RTNDKNHMIISIDAEKAFDKIQ QPFMLKTLKKLIGDGTYLKIIIRA IYDKSTASIIILNGQKLEAFPLKD RTRQGCPSPPLFNIALEVLARA IRQEKDIKICQLGKEKVRSLFA EDMIVYLENPVSAFNLFKLISN FSKVSGYKINVQKQSVFLYINN RQRESQIMNEFPPTIARRRIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNNMPCSWIGRINIM KMAILAKVIYRFNAIPIKLPMTF FTELEKVTTLKCI*NQKRAHIAK PILSQKNKAGGITLPDFKLHYK AAVTKTAWYWYQNRDIDQRN RTEPTEIMLIHYNHLIFDKPDKN KKWGNDSLFNKWCWENWLAI CRKLKRDPLTPYTKINSRWIE DLNIRPETIKTEENLGNITQDIA MGKDFMSKTPKAMATKAKIDK WDLIKLKNFCTAKETTIRVNRQ PTEWEKIFAIISSDKGIISRIYNE LKQIYKKKNPNPIKKWAKDINR HFSKEDIQAASKHYKKHSTSRI MQIKTTLGYHLTPVRMATIKKS KNNRCWCGCGEKGTLIHCW/M
15695	46063	A	15786	1	906	MVNQKRYHIPGGTAEISGTIKK LKNAGVVIPTTSPNSPIWVPQ KTDGSRWRTMDYHKLNQVVT PIAVAPPVVVALLEQINTFSC WYAAIDLANTFFFSVHKA/HK K*FAPSROQQYTFTVHPAYDN YSPFERQLLACYWASVETEHLT MGYQVTIQLLEPIMNWVLS DPS SHKLGHAQHSIIKWKWYIRD RARAGPEGTARIHRSRNQGV EVAPLTITPSDPLARFLLPVPTIL HSAGLEVLVPEGGTLPLGDTT IPFNWKLRLPPGHFRLLLPLNQ QAKKGVTVFAGVIEAIKMK

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15696	46064	A	15787	1	909	MVLEVSVDSDRAVWRI.WRAPI GESQQRSLGFWSKVL.PYSADN YFPPERQLLACY.WALLETDRLT VGHQVTLQPELPIMNWLSDPS SHKVGHVHQHSIIKWKWYIRD QTRAGPEGTTTTPTVITQ.WDAHE QSGLSGRDG/KGQRFVLTGVDT YSGYWFAYPAHNASAKTSIYG FTECLIHCHGIPHSIASDQGT.LFT AKEVWQWAHAHGIHWSYHIP HHPIAAGLIEWWNGLLKSQLQ CQLGDNTLQG.WGKDLQKAMY SLNQRLIYSTVSPISRIHGSRNQ RVEVEVAPLTITLSDPLAKFFFL
15697	46065	A	15788	1	754	MQNNVDSFQEPPTPLFSSRPIA RLKSKQAPRGEAESVTHEELES RLAKTSDKISSLTFRRGWGKV LQKAMYALNQHPYGTVPPIPRI DGSRNQGVVEKVAPLTITLSDP LAKFLPLVLSALHSAGLEVLVP EGGILPPGAGDMRMIQLNWK SLPPGYFGLLLPSQQTKKGVT DLGGVIDLDYQDEISLLFHINKV NGKLQQPNPDRTTSGPDPSGM KVWVTPPGK/EPQPAEGLAEGK GNTIEWVVEE
15698	46066	A	15789	686	1506	VETVHMLMQIGEFKKTDSV/WK TVDYHKLNVQVVTPTAAAVPDV VSLLEQINTYPGTWYAVIDLEN AFFSVPVHNAHQKGEAFWSQG QQYTFTVLPQGYINSPTLCHNLI RRDPGHFSYPQDITLVHYIDDI MLIGSSEKEVANTLDLLPIYQV TLKAANYEWGPQEKA VQVQV QAAVQAALPLGQHNPADPTVL EVSVAADRDAIWNWQAPIARIH GSRNQGVVEVAPLTITPSDPL AKFLPPVPATFCSAGLEVLVPE GGMLPPGEIETIPLK
15699	46067	A	15790	422	537	VNQGVVFCAIIN*YECLKQSF KTQTDYFPSPLNTSQ
15700	46068	B	15791	1	519	

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15701	46069	A	15792	53	753	SLGTGTLRVLLGTAAEQMLQFS HLIYADYGGKPALEDINLTLESG ELLVVLG/PSGCGKTTLLNLIAG FVPPYQHGSIQLAGKRIECPGAE RGVVFQNEGLLPWRNVQDITVA FGLQLAGIKKMQRKFAHQML KKVGLEGADKRYIWQLSGGQR QRVGIARALANPQLLLDDEPF GALDAFTRDQMOTLLNLWQE TGKQVLLITHDIEEAVFMATEL VLLSSAPGRVLERLPHI
15702	46070	A	15793	2348	2760	LWLVCINCFIPAFLLMLRWLPR LKPLSQLSVPTYRLPSVPFLKPT GMESPEAISRVSGKGL*RDSDA YSVLSYHYPIIRHPSIIVDIIRS SIDP*PIVDHSSIAKRSCTFPLG YWEVVFVQLTFGQQRQASGILQ
15703	46071	A	15794	2	415	HPGLETTDLLSPLPAALEPQQQ GRPSIQGAPRGSFTRIEAGTPHV PAPCPAAQRNQGWGLVGAWL GFMAP*EQSVASSWK*PLMKS QYSREVISHLPLVPMQQRVPM TQSMWGWLVWFPALFLVQIGH LVMSSGHS
15704	46072	A	15795	428	885	GISMKLSRISAI/NWNKISDDKD LEVWNR/LTSNFWLPEKVPLSN DIGAWQTLTVVEQQLTMRVFT GLTLVDTLQNVIGAPSLMPDAL TPHEEAGLSNISFMEAGHARSY SSIFSTLCQTKDVDAAYAWSEE NAPLQRKAQIIQQHYRGDDPLK K
15705	46073	A	15796	1	1125	
15706	46074	A	15797	57	303	SHKHADALLYPADPVCTAC* LLRGNRRDQSKSITAKRHLTAA HFRFVRMVRHGNH/SRLRPDSF R*PVSPDR*PPLRAAHFR
15707	46075	A	15798	3	430	
15708	46076	B	15799	1	1338	
15709	46077	A	15800	380	1043	WTRWRASADNLAHGRWGEO KLVTVTGASGAPDQAAARCGC IWRKISWYRSKGSKHPLTPKEV EKTGWGLKIRGMGKQQA/ERV KEAARILELDGLKRRPRELSG GQRQRVAMARAIVRDPVFLF DEPLSNLDKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVEVDGDDTLEIL GADNLAHDAGRAEAGGDWRI RSARRSSTCAH

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15710	46078	A	15801	1	900	MAAIAFLITWFLSHDKKRIRILK RLSGGNGMADEFPGGAVVFTV LNLTHWLEDWGLPVHWRSSC MPSGLEYLIVLIFKGVIVAVHLL IVDALNLIRRIHAV/QGSPCVET CQHALDQLIMHSQPTHAVAVF DDENRSSGWRHQGLPDYKAGR PPMPEELHDEMPALRAAFE/QR GVPCWSTSGNEADDLAATLAV KVTQAGHQATIVSTDKGVCQL LSPTLRIRDYFQKRWLDAPFID KEFGVQPQQLPDYWGLAGISS KVPGVAGIGPKSATQLLVEFQS LDGIYENLADVAEKRWHKL
15711	46079	A	15802	1	1350	
15712	46080	A	15803	1618	2082	
15713	46081	A	15804	1	803	MINLIGSDVNYDWLKLPLVHL HWYDKEVRPGRKVGHLNLTDS DTSRLTATLEALIPLLPPEYASG VIWAQSLIRCCKHRIRHCPIAG CGTGCRPDKTRQASHQAQMSN AYDYSEIQGIGKQKAANRVAEP RTYHSFASITDRRADLLKPGNH AQDGRLTAAARRADKHDELFIG NFQKADNRGQVSDSVEGNSNC APVKPAPIPTERIPALMASMPA CASSMPIHACGGTPSPAQAARK ISGSGFEFLSWEASAQKVKNRS SSSAKIVGAFRETEASPTICC ARRSASKEKMPG*ARADPHRA HTAGVNGVNARLRIFNADTCL RRHAQPCTGGEKDFRVRFRVF KLGSIRAEQEKLALQRR

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15714	46082	A	15805	1	1655	MRGHNWIDMDQARQSTPHPT DRKICHKNDPRKTTPLRKIDAH PHTLILPAESTLSTTKYKLRLAL LVENTNKDKSAVS VFRGSVL HQAANFPNMLCFQLKNGVN ACNDFIMLFVDDNAAGSIERAA SPCINEKQHAFSESVPAlAAVRG LGSMAVFEFNDPQTGEPSAAIA QKIQQRALAQGLLLLTGAYG NACKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKLT PVIQPRASGEYNEEFSLP VVN YLKDKLSNPVRLVKDYLDGVD VAEGELVVLLENVRFNKGEEKD DETLKKYAAALCDVFVMDAFG TAHLRAGFLLTGIGKLRCSLRC AGPLLAELDALGKALKEPARP MVAIVGSKVSTKLTVLDSLK IADQLVGGGIANTFIAAQGH VGKSLYeadLVDEAKRLTTC NIPVPSDVRVATEFSETAPANL KSVNDVKADEQILDIVRDLDA NVVINAVFSYVTNVWG WAF WYMVVMLFGWFWL VFGPYAK KRLGNPEPFSTASWIFMMFAL
15715	46083	A	15806	1	1359	
15716	46084	A	15807	670	1008	
15717	46085	A	15808	455	1137	GTKPRDIDHILGTFITPGMPKGG KLDVYAAPLPLKLLGRPTGE YNEEF/SLLPVVNYLKDLSNP V/RLDGVDAEGEL/VVLENVR FNKGEEKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLK /IADQLVGGGIANTFIAAQGH VGKSLYeadLV/DEAKRLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPVAVMLEERG
15718	46086	A	15809	465	888	RGLVALSSERRCRLRRNHPS GTRSPDPAGAASLSRRFFYAPP GTPETGCGYSSRSQRKR/LST WRCNS*ETPKSPKACCRPARIP APRSSSVKKASACGPAAMKK RCRKASITPISKITCAIHRMRRW TCTKRAAF
15719	46087	A	15810	417	707	IQIHERSWRYLHWWSSVRRRA A*YGAPL*RDGIQRGTRRISQV YQ*SSVRQLRRDASAGSAPRV CREYAAACYLRHEHWSCDAVS PTPRMLKSFV
15720	46088	B	15811	1	4350	

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15721	46089	B	15812	1	2862	
15722	46090	A	15813	1	1471	MLHSRGFLAEVFGILARHNISV DLITTSVSVALTLDITGSTSTG DTLLTQSLLMELSALCRVEVEE GLALVALIGNDLSKACGVGKE VFGVLEPFNIRMICYGASSHNL CFLVPGEDAEQDGTGTSIGAGQ KKKMYANNGAIDRKLLFEATF VTIEKCCDTNQKGGDDTHALGQ PIRGHDKSLAGSFCYACRSEEG LSQYRAYDSRQGLIAVKDTQG HETRYEYNIAGDLTAVIAPDGS RNGTQYDAWGKAVRTTQGGGL TRSMEYDAAAGRVIRLTSENGS HTTFRYDVLDRLIQETGFDGRT QRYHHDLTGKLIRSEDEGLVTH WHYDEADRLTHRTVKGETAER WQYDERGWLTDISHISEGHRV AVHYRYDEKGRLTGERQTVHH PQTEALLWQHETRHAUNAQGL ANRCIPDSLPAVEWLTYSGYL AGMKLGDTPLVEYTRDRLHRE TLRSFGRYELTTAYTPAGQLQS QHLNSLLTYRHFANFAL
15723	46091	A	15814	1	1367	MSKLLERFRYFKQKGETFADG HGQVMHSNRDWEDSYRQRWQ FDKIVRSTHGVNCTGSCSWKIY VKNGLVTWEIQQTDYPRTRPD LPNHEPRGCPRGASYSWLYSA NRLKYPLIRKRLIELWREALKQ HSDPAADNDLIARFQSFTNQPI ANRLTGNDRARFNLTIFVNNQH ATAITTTGTFLPEWSTTFIITLIL QSKVQAIDLTKAIVTVGCNTIS TTVHEVVSASIGIATKFWQHIGP CFYVIYDVTVTIVESRTTEYSP DVTGLITRITTPDGRASAFYN NHHSQLTSAATPDGLEIRREYD EWGRLIETAPDGDITRYRYDN PHSDLPCATEDATGSRKMTW SRYGQLLSFTDCSGYVTRYDH DRFGQVTAHVHREGLSQYRAY DSRGQLIAVKDTQGHETRYEY NAA/GDIRQCESDLQSPSCSQYR AIDGESLSETARYSVHQ

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15724	46092	A	15815	357	1733	TADSPETLRCQTSGENARGAGT VERAGKSLWRSR*SHRP*STR TGDHHCQQTNFSLFN*QHPGQH RVYSGSTAIINQSLITHDPEYPEN LPAAPLVRYGWTGPRGELAVVY DRSGKQVRSFTYDDKYRGRMV AHRHTGRPEIRYRYSDDGRVTE QLNPAGLSYTYQYEKDRITITD SLDRREVLHTQGEAGLKRVRV KEHADGVSVTQSQFDAVGRRLRA QTDAAGRTTEYSPDVVTGLITR ITTPDGRASAFYYNHHNQLTSA TGPDGLRLREYDELGRLIQET APDGDITRYRYDNPHSDLPCAT EDATGSRKTMTWRSRYGQLLSF TDCSGYVTRYDHRFGQMTAV HREERLSQYRAFDRRGTVIAVK ETQGLETFEYHFVPDGVIAV KG/SRNGNSQSVGKRRSTEDIR G*TRWRGYTADRRAAKTHARV E*HLRARPRVCALFFPKQGERH
15725	46093	A	15816	1595	3228	DNNAKLFRAGQMKVLKPYVDS GKIKVVGQWVDGWLPENAL KIMENALTANNKIDAVVASN DATAGGAIQALSAQGLSGKVAI SGQDADLAGIKRIAAGTQTMT VYKPITLLANTAAEIAVELGNG QEPKADTTLNNGLKDVPSRLLT PIDVNKNNIKDTNLPAAPLVRY GWTGPRGELAVVYDRSGKQVRT FTYDDKYRGRMV AHRHTGRPE IRYRYDSDGRVTEQLNPAGLSY TYQYEKDRITITDSDLRREVLH TQGEAGLKRVRVKEHADGVS VSQFDAVGRRLRAQTDAAGRTT EYSPDVVTGLITRITTPDGRASA FYNNHHNQLTSA TGPDGLRLR REYDELGRLIQETAPDGDITRY RYDNPHSDLPCATEDATGSRKT MTWSRYGQLLSFTDCSGYVTR YDHRFGQMTAVHR/EEG/USQ YRAYDSRGQLIAVKDTQGHET RYEYNIAGDLTA VIAPDGSRRNG TQYDAWGKAVRTTQGGLTRS MEYDAAGRVIRLTSENGSHTTF RYDVLEQYCGQVIKAHAVSRF
15726	46094	A	15817	1	627	
15727	46095	A	15818	701	895	

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15728	46096	A	15819	1412	1705	LASISTSCAPPKVNCGVMAIFLASD SRLWSGLRAQATSRSTLSLM TRSGWLAIQ*NALRSWLASHE TKRPPSTLGGNTVPS*ALRLGIL ASSRILL
15729	46097	A	15820	344	547	
15730	46098	A	15821	1	1518	
15731	46099	A	15822	1693	2455	VLAAFTRSKQRYGAPRLTDELRA AQGYPFNVKTVAAASMRQGLR AKASRKFPVSYRAHGLPVSEN LLEQDFYASSPNQKWAGDITYL RTDEGWLYLAVVIDLWSRAMA LLRRKSPGNVIVHTDRGGQYCS ADYQAQLKRHNLRGSMASAKG CCYDNACVESFFHSLKVECHIG EHFISREIMRATVFIISNVITIGG GGTVAARGGVP*AVKSNVNDV RRNCLARSSNNGWIFPPVVVNG WRQQALTIVAGICC
15732	46100	B	15823	1	1407	
15733	46101	A	15824	1	3252	
15734	46102	A	15825	1	2409	
15735	46103	B	15826	1	2802	
15736	46104	A	15827	1715	1824	
15737	46105	A	15828	410	720	PGSRAVIGWSMSPRMTAHWPA MPCRWRCGGVRTYAPEPTG*R RWLQNCACSS**LRKTSRKNR TT*RTPARSSAPPLMLKQPFTR QWPLNTPWKPPRLSPS
15738	46106	A	15829	905	1008	SCDSYRLSSRAAAVTPMRSASF RASGFLLVILFVCRVSVVGCVRV LAWSGGSVFRRGVPLAWTVLR WVRRRCGCGVGRCRGLSAVV YPSGIITVDSARSWRIMGRSGSP LAITVGLAGCWSQRL*TDAFS KLQGRVFTGDTICM
15739	46107	B	15830	1	3148	
15740	46108	A	15831	1896	2062	SVCYPRN*IPSG*N*PRIWSDP VQRRERAGKKWLHENPGWRK **PDYHYRSEAD

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15741	46109	A	15832	1	1456	MSTEIARLKRQLADGMKSWLS SKRPRHSTRAPEMKYVFIEKHQ AEFASKQCAACSGWPATAGNV VSAADKDKHASAVPPHCDSVV LAAFTRSKQRLPLNVKTVAASL RRQGLRARPPGSSARSATAHTA CLVRKSVGAGFLRQWPPEPKWA GDITYLRTDEGWLYLAVVIDL WSRAVIGWSMSPRMTAQLACD ALQMALWRRKKPRNVIVHTDR GGQFGDRWK/ALANALNIPLDQ LSARISANPKGGFIYLAREVNP DMADYIKKLLPGIHVREESRR YYPSGEVTAHLIGFTNVDSQGI EGVEKSFDKWLTTGQPGERIVRK DRYGRVIEDISSDTSQAHLNLA LSIDERLQALVYRELNNVAFN KAESGSAVLVDVNTGEVLAMA NSPSYNPNNLSGTPKEAMRNRT ITDVFEPGSTVKPMVVM TALQR GVVRENSVLTIPYRINGHEIKD VARITTEEDFNHASAARFVCAA AERALQNH
15742	46110	A	15833	2	929	
15743	46111	A	15834	1	472	
15744	46112	A	15835	1	513	
15745	46113	A	15836	1	254	CDNLKTCHTSHGVSMAETAVI NHKKRKNSPRIVQSNDLTGAA YLSLRDQKRV/LRYEPVSQFRLS ETQKHQSVCFAFIRIPVSVS

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15746	46114	A	15837	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECNLTCTHT SHGVSMAETAVINHKRRKNSP RIVQNSNDLTEAAYSLSRDQKRM LYLFPVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIR/PSRGLYSV HINPYLIPFFIG/LQNRFTQRLS ETKEITNPNYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPPDFRRRLQGFCFRFNH IHQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCALHRIETEL MGKFDEGKLPTDPLMLRLAIE TVAHDYDVIVIDSAAPNLGIGTIN VVCAADVLIVPTPAELFDYTS LQFFDMLRDLKNVDLKGNSN GSQSPWMEEQIRDAWGSVMVLK NVVRETDEVGKGQIRMRVTVE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLK
15747	46115	B	15838	1	1734	
15748	46116	A	15839	1	971	
15749	46117	A	15840	1	1143	
15750	46118	A	15841	1	556	
15751	46119	B	15842	8	1000	
15752	46120	A	15843	1	1169	MLTLILLDLQFMAQLAGYQMS FNSTKSQTKNNFAVGYRTGD FQLHTNVNDGAIEFGGSVYQKV CEELDALINLAWTSSTSCTRFG LAAKFQLKPIAFISTKVNHWLT GVSYPPLLEAGVKLNLSALCDN LKTCHTSHGVSMAETAVINHK KRKNSPRIVQNSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIRAH SPSRGLYSVINPYLIPFFIGLQN RFTQRLSETKEITNPNYAMRLY ESLCQYRKPDGSGIVSLKIDWII ERYQLPQ/TYQRMPPDFRRRLQ EEFESLNRQITGSEIVAMINSLST KKSPGPDGFTAIFYQ
15753	46121	A	15844	1	1509	

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15754	46122	A	15845	1	558	
15755	46123	A	15846	1	1773	
15756	46124	A	15847	1	2256	
15757	46125	A	15848	1	812	MEVLASWATFTLGQTEQHVD WISAGAAPQGPVVKQLPSPVPPT EQLEQEKPTVIGSAPSTPNKLLL SHSNCQLPRPLRSITNISACFSLE LAIDHRGFPHSPGARSLYSNSVF GTYQLCDLCDNLKCTHTSHGS VMAETAVINHKKRKN SPLIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVYRPEEDAGDEK GYESFPWFIKRSPE*RRGKFPFT QMGQD
15758	46126	A	15849	1	1773	
15759	46127	B	15850	1	1755	
15760	46128	A	15851	1	726	MPASGNENDLNMPSGTIEIFVR CYVEVERIMSAWTEQPNHRT MMWSVLLQPCDNLKTCHTSHG SVMAETAVINHKKRKN SPRIVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVYRPEEDAGDEK GYESFPWFIKRAHSPSRG/LYSV HINPYLIPFFIGLQNRFTQRLSE TKEITNPYAMRLYESLCQYRKS
15761	46129	B	15852	356	671	
15762	46130	A	15853	1	2121	
15763	46131	B	15854	721	2739	
15764	46132	A	15855	1	5828	MQEQQQASSLIRSGNGRLPGSG AQRTPCHIRRDGQRRVCD DCK QQWWKAKYNIPSGLHACTATL EETHILDSGAHVQVYFKGQLH VMRVPC TDYFDTKNPNLSHL HGSVMAETAVINHKKRKN SPRI VQSNLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQN
15765	46133	B	15856	537	1318	
15766	46134	B	15857	1	411	
15767	46135	A	15858	1	1356	

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15768	46136	A	15859	1	1215	MPYDRPFTVMAAFPLCPACDK EYRDPLDRRFHAQPVACPECGP HLEWLKMGKIVAIGGIGFHLA CDARNSNAVATLRARKHRPAK PLAVMLPVADGLPDAARQLLT TPAAPVLVDKKYVPELCCDDIA PDLNEVGVMPLPANPLQHLLQ ELQCPLVMTSGNLGKPPAISN EQALADLQGIADGFLIHRDIV QRMDDSVVREIRRNAAPF/AGA VLSQHLGDLSDDGIMQWWRER YSLMQNIYDFTQYVVDHAHP GYVSSQWAREMNLPTQTVLHH HAHAACLAEHQWPLDGGDVI ALTLDGIAQPDERSSEDVDRA HQRGHERDRRRRSGTSHLTR VDLKEDGKGLKIVRQSLPYGTA SGTHGLYFCAYCARLHNIEQQL LSMFGDTGKRDAMLRSPNR
15769	46137	B	15860	74	2050	
15770	46138	A	15861	2	703	LQARFPLSWRNPITFACYAGL FCLSAIY/PDHLCPVSVPRFAA GPRHRRHLLVLRGCGLRH/TK RPGPGPGPARALAIWPPDGC* RCRRPSPASSLRSSATPTCTST QPALEWCVAVYAIICFILAAIAIL LNLGECTNVLPIPFPSFLSALAL LSVLLYATLVLPYQFDEK YGGQPRSRDVSRRHAYYV GAWDRRLAEAILTAIINLLTYVA DLMHSAHLDFSKV
15771	46139	A	15862	1	849	MAQPLAKQWTPVSPRALLVSIS SMPPRPAADVT/CRHRNCTLRE LLYGFAAAAQQLNLHGDVCN DGDG/VEVRLREDPETFLVQLY/ QHCPPLA/RTGGTMNTQIVPDA ATCPASLSEMNTPGERRYYPF INCTHYGPSFPIIRAMPYDRPFT VMAAFPLCPAC/DKEYRDPLDR RFHAQPVACPECGPHLE/WGIG GFHLAC/DARNSNAVATLRARK H/RPAKPLAVMLPVADGLPD/A ARQLLTTPAGAGLWLGNGYP RAPDNANSTAMSCASHAHSFG GGHPRGR
15772	46140	B	15863	1	2688	
15773	46141	A	15864	1	1578	

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15774	46142	A	15865	1	877	MQAAHRLRPAYRIKTKGKPPAL ADYHPAYQEMLSRKQDRVIDQ IDFGIKDTVEILHMGQIQSMGREG FALSRLFSIHGHNVHGNESPEM GPERRSGFYDEWSPERIQQYYRP AREQLMNELVQILKNTRQHLM TGVSHMIPFVSSGGILLAVSVM LYGKGAVPDADPNLKKLFD IGVAGLTLMVPFLAAYIGYSIA ERSALAPCAIGAVVWNSFGAGF FGALIDAFPLSEEINPALPEAK VMACLEAVARQDNVDSPPQLP PTPLFASRPITRLKSWWAPGGE VESGTHKK
15775	46143	A	15866	3	423	
15776	46144	A	15867	633	771	NNRSHPALCTNRPPTRLVFYP LLAPNA*LAALQKGWAYGAGH NA
15777	46145	A	15868	1	4014	
15778	46146	A	15869	1	180	SGHPFIPLKDLTQIAIGDVFNNN LILWANREIHSVP*RY*HDANI QCFVVISSFVRSQQ
15779	46147	A	15870	815	1905	IFQEHIMDHLPMKFGPLAGLR VVFSEM/WRAEVIWIENVAWA DTIRVQPNYPQLSRRNLHALSL NIFKDEGREAFKLMMETTDIFIE ASKGPAFARRGITDEVLWEDKP KLVIHLSGFAHQVSQISTHQG SSNWVSPDQLQCNQTQNSPKQ LFSTHCMQCRPNSTTNSRFQFS NPVNHALNHQSKPHHPLVYVYQ HKAKRAHRAKSITASRKQATTF QQVGAPAGGHTTSSSHPQTT KALEQVKHLTTQAILSKAKPQ ATSPIPRDTGPIRGRQFHALNPS TTVIGQAPANRQIQGHHPQFKP KTPFWPQPEKVPNRQCTSKTY SNGEQNIPQTYAIRTKNRSTYPR NLKQQPLNPGKAKT
15780	46148	A	15871	1	361	QTTGISFGGRGAGPGVPTRTQ/ CLRCHGGRHG/HPSHLCKPNKG DPRKIRLKMSWR*PWFAIGPRD WSSSRPKPTSPRGSCRSFIEASK MSAPVVVSTKTHSSRSMLSFSL MEDFVTALSIL
15781	46149	A	15872	1	447	

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15782	46150	A	15873	1	1424	MILLEQLSQHKLDMIISDCPIDST QQEGLFSVRIGECGVSWFCTNP PPEKFPFACLEERRLLIPGRSSM LGRKLLNWFNSQGLNVEILGEF DDAALMKAFAGMHNNAIFVAPT LYAYDFYADKTVVEIGRVENV MEEYHAIFAERMIQHPAVQRIC NTDYSALFSPAKLRALYHPAS TELHPACGKDFRQLYRRIQNQI QRHALWHKIFDVEIPHPILIIAR VSANMPHTGCRJAEIWPVKVVE AILRLTNDAPLEYLPIGNHKS MRSEGMNPHYQRQFMELALS VLKCGEFTLNRGRKSPYFFNAG LFNTGRDLALLARFYAALVDS GIEFDLLAPAYKGIPIATTAV ALAEHHDLDLPYCFNRKEAKD HGEENLVGSALQGRVMLVD DVITAGTAIRESMEIIQANGATL AGVLISLDRQERGR*CDHRRNG DSRVDG DYSGQWRD ACWRVD FARSSGTRARRDFGDSGS*A*L QLQSDLYHHPERPDCLPGREAG NGGTSGGG
15783	46151	B	15874	1	1086	
15784	46152	A	15875	484	729	CTQFRKTCFTCKASNGFCFATS CNLIYTSEIIICRGPTG*HNLIASL LQRIDNLRKFIVPTLKYLRTRCR LDDNIMIFYAQGI
15785	46153	A	15876	1717	1971	PANAWAEMWEYSAWQRRMYS MG*TSKVVVHPGATDRW*NTN GCYRIFWIAAPFVPAAVIHGNIL PTHGACVHKFGGRAPAGAAVE
15786	46154	B	15877	1	765	
15787	46155	A	15878	103	823	VPACAGLKKEARSLASPPRLL NTKLQASCRA LFSPPIQSRQTTG ISFQGRGGAGPGVPTRTQ/CLRC HGGRRHG/HPSHLCKPNKGDPRK IRLKM SWR*PWFAIGPRDWSSS RPRPTSPRGSCRSFIEASKMSAP VWVSTKTHSSRSMLSFSLMEM PARMPITSSMPSTPLRQGSVKFE DFVTALSILLRGTVHEKLRWTF NLYDINKDGYINQEEMMDIVK AIYDMMGKYTYPVLKEDTPRQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
15788	46156	A	15879	1	2926	MVKDASQSASLGLDAFLPAS GVQYTHERSPDSPKSEQECP VVNEDTFKQIYAQFFPHGGLMS ENGTGKASVFGSTGSGALLLE EGERRRQPLIEMRKPPHVLIN YQAKVGGNSIPSPSLCKPAFPPL PSWAVDLASARQKEDASRS LQNK EEDFYTSQPGFPALALGCCL RVNLLGHRGISAGSSYRPITST PCHLCKLGQEVFAKPLNLQDQ CQQNLVMQVLKVLNCLNDFD IGSSADESADDLCTV
15789	46157	A	15880	1	1521	MDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKSPGPD GFTAEFYQRYKEELVPFLKLF QSIEKEGILPNSFYEASILIPKPG RDTTKKENFRPISLMNIDAKILY KILAKRIQQHIKLLIHDQVGF PGMQGWFNIRKSNVVIQHINRA KDKNHMIIISIDA EKAFDKIQPF MLKTLNKLQANLLKLSNFNKV SGYKINVQKSQAFLYTSNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKINIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRAHIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYCYQNRHIDQWNR/PSEI TPHIYNYLIF
15790	46158	A	15881	1	1182	
15791	46159	A	15882	1	690	
15792	46160	B	15883	1	458	
15793	46161	A	15884	1	719	
15794	46162	B	15885	1	3552	
15795	46163	A	15886	1	321	
15796	46164	A	15887	1	362	
15797	46165	B	15888	1	489	
15798	46166	B	15889	1	1660	

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15799	46167	A	15890	1	1593	MGKKQNRKRTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSLEQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRLSR SRCDQLEERVVSAMEDEMNMK REGKFREKRJRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIHQENFPNARINKI DRPLARLIKKEKNQIDTIKN DKGDITNPTIEJTIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPTGAIEIVAINS LPTKKSPGPDGSAIEFYQRYKE E/PADKQLQQLSLSIQNQCTKITSI LIHQQQTNREPNE*TPHNCFK ENKIPRNPTYKGCEGLLPGLQ TTAQGNKRGYKQTEHSMLM GRKNQYRENGHTAQGNF*IQ HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKEQSWR HHTT*LQTLQGYSNQNSMVLV PKQGYRSMQNRALRNNAAYL QLSDL*QT*EKHAMGK/EPPI**
15800	46168	A	15891	1	1177	
15801	46169	A	15892	1	3663	
15802	46170	A	15893	1	1995	
15803	46171	A	15894	1	4191	MVKGSIQEEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHIK STEYFFSAPHHIYSKIDHILGSK ALLSKCKRTEITNYLSDHSAIK LELWIKNLTONHSTTWELNNLL LNDYVWHNEMKAEIKMFFETN ENKDDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQETKIR AELKEIETQ

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15804	46172	A	15895	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRSLH AKSTEYTFSSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKLNLTQNRSTTWKLN NLLNDYWIHDEMKAIEKMFF ETNENKDDTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGGDI TTDPTEIQTIREYYKHLYANK LENLEEMDKFLDITYLPRLNQE EVESLNRPIITGAEIVAIINSLPTK KSPGPDGFTA NRAKDKNHMIIISIDA EKAFDKI QQPFMLKTLNKLIGIDGTYFKIIR AIYDKPTANILNGQKLEAFPLK TGTRQGCPLSPLFNIVLEVLR AIRQEKEIKGIQLGKEEVKLSLF ADDMTYYLENPIVSAQNLLKLI SNFSKVSQYKINVQKSAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWNIPCSVWGRIN IMKMAILPKVIYRFNAIPKLP TFFTELEKTTLKFIVNQKIRARI AKAILSQKNEAGGITLP
15805	46173	A	15896	1	1740	
15806	46174	A	15897	1	880	
15807	46175	A	15898	1	2777	MGKKQNRKTGNSKKQSTPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKG EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAEMEDEMNEK REGKFREKRJKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIHQENFPNLASTLSD HSGIKLEINSKRNPQNHAHTWK LSNLLNAHWVNNEIKMKVKKN FFELNDNSDTIYQNFSD
15808	46176	A	15899	326	3096	QTERSTPKTHLYVTIHKDQK*I KPQRRGKNRGEKLETLSRAP VLLQRNAVQQQQRNKAAGRRM TLTS*EKKSSDNQITPSYRRKF KPMACKLKT/LRKKLDECITRIT NAEKCLMELMELKAKARELRE ECKSLRSQCNOLEER/INKIDRP LARLIKRRKREKNQIDAIDKGD ITTDPTIQTIREYYKHLYANK LENLEEMDKFLDITYLPRLNQE EVESLNRPIITGAEIVAIINSLPTK KSPGPDGFTA

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15809	46177	A	15900	1	2047	MENDFEELREEGFRSSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTQKCLKELMELKTKARELR EECRSLRSRCDQLEERVVSAMED EMNEMKREGKFRKRIQRNEQ SLQEIWDYVVKRPNLRLIGVPET LHPRDEAHLKLNLDIAIKNDKGD ITTDPTETQTTIREYYKHLVANK LENLEETDKFLDTYTLPRNLQE EVESLNRPTGSEIVAIHNSLPTK KSPGPDGFTAIFYQRYKEEL/PD KQLQQSLRIQNQCTKITSILHQ QQTNREPNE*TPIHNCFKENKI PRNPTYKGCEGLQGLQTTAQ GNKRGYKQMEHSMMLMGRKN QYHENGHTAQGNLQIQCHP* ATNAFLHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT *LQTLQGSYNQNSMVLVPKQR YRSMQNRALRNAAVYQLQSD L*QT*EKQEMGKGFP**MVLG KLASHIM*KAETGSLPYTYLYKN QFKMD*RLKR*T*NHKNPRRK RHYHSGHRHGQGLHV*NTKSN GNKSN*QMGSN*TKELLHSK KKKNY*QTEQATCKMGENFHN LLI*QRANIQNLQ*TQTNLQEK KQPHQKVGKGHEQTLLKRRHL CSQKINHEKMTITGHQRNAN QNHNEIPSHAS*NGNH*KVRKQ VLERMCRNRNTFTLLVGL*TSS
15810	46178	A	15901	1	3285	
15811	46179	A	15902	1	3681	

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15812	46180	A	15903	1	1854	MKAIEKTFETNENKDDTYQNL WDAFKAVCRGKFTALNAHKR KQERSKIDTLTSQLEKEKQEQ THSKASRRQEIHKIRAELEKIET QKALQKINESRWCFEKIHKID RPLARLIKKKREKNQIDAINKD KGDITDDPTEIQTITREYYKHL ANKLENLEEMDKFLDTYTLPR NQEEVESLNRPIGTSEIVAINSL PTKNSPGPDGFTAIFYQRYKEE/ RENKIPRNPTYKGCCEG/PLQGE QTTAQGNKRGYKQMEHSMML MGRKNQYRENGHTAQGNLQIQ CHIPQATNDFLHRIKGNFYKV HMEPKKSPHRQVNPKEQSW RHHTT*LQTLQGYSNQNSMVL VPKQRYRSTEQNRALRNATY LQLSDL*QT*EKQAMEKGFP** MVLGKLASHM*KAETGSLPYT LYKNQFKMD*RLKR*T*NHKN PRRKPRHYHSGHRHGGQLHV* NTKSNNGKSN*QMGSN*TKE LLHSKRNYHQSEQATYKMGEN FRNLLI*QRANIQNLQ*QTNLQ EKNKPPHQKVDEGHEQTLKKR RHLCSQKTHEKMLIITGHQRNA NQNHNEIPSHTS*NGNH*KVRK QQVLERMWRNRNTFTLLVGL* TSSTIVEVSVV
15813	46181	B	15904	1	2718	
15814	46182	A	15905	1896	5031	TWKGTTSTSRCKIMPKYRSTRQ KVNKDQELNSALHQADLIDIY RTLHTKSTEYTFSSAPHHTYSK TDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKNPTQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDDTYQNLWDT FKAVCRGKFIALYAHKRKQERS KIDTLTSQLEKEKQAQTHSKA SRQEIHKIRAELEKIETQKTLQ KINESRSWFFERJNKIDRPLAR LIKKKREKNQ
15815	46183	A	15906	4	133	

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15816	46184	A	15907	95	1875	PFFGRKNYRLPSKNMPRRCRSS PLPCSMKMTI*CVLTSTATITRL PAASAQW*LDGRTLVTKNSTR YLHTLHTMGPAPEPNLTILWSE ELPIAFKKYAAQVSIVTSSLQYE NDDLMRITDFNSDDYAIACCVS PMVIGKMQOFFGARANLAKTL LYAINGGVDEKLKIQVGPKTAP LMDDVLDYDKVMDSLDHFMD WLAQYISALNIIHYMHDKYSY EASLMALHDDRVDYRTMACGIA GLSVATDSLSAIKYARVKPIRD ENGLAKDIQGTTEPQFRNSHSR TSGTVTLVLPVSTFVGTGFFIRV DPPKKPLKIRKIEFVEIYEPFSEG QAKAQADRCLSCGNPYCEWKC PVHNYIPNWLKLANEGRIFEAA ELSHQNTLPEVCGRVCPQDRL CEGSCTLNDEFGAVTIGNIERYI NDKAFEMGWRPDMSGVKQTG KKVAIIGAGPAGLACADVLRN GVKAVVFDRHPEIGLLTFGIP AFKLEKEVMTRRREIFTGMGIE FKLNTEVGRDPRESSFYEEKQL IARKALPFIDNKTMAADSSST VMELKLLQDRSGLTLLTNSAE AIHVLAQSEIKVVSTGGELNKN TLSLQGRITKEIIRRYHVDMWL PDELRVKEGFSPTDLKLEAKG QKVALKEAMGSTQSIMVGPDE RRTGFSYLRQNLIRVKF
15817	46185	B	15908	271	2118	
15818	46186	A	15909	597	743	
15819	46187	A	15910	573	1066	IRAQNGSPWLSFLVDSVCVLKA CVDVAVMRAGICSVSYWQYQS GVGANSSALSGFSQGAIMMLES IKAEPGLASRVIAFNTRYSSLE TASTATTIHLHGGEDPVIDLAH AVAAQEALISAGGDVTLDIVED LGHAIDNRSMQFALDHLRYTIP KHYFDEALSG
15820	46188	A	15911	1	2652	
15821	46189	B	15912	1	1494	

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15822	46190	A	15913	1	1733	MGVGSKGITFGSTTTQHGSFIPY LTGYLTYYTHGHSANPKPAVG GQILTAVLPAHMDGYVSRIMTM NTQLTTLPLTTATHTARQTASLIS VIGRQLRCFRHSSQPSVLTHVR DDSTQYAQLDMANGQPTSHGY EHWAQLMYATDRRYGRHMSD AARQGCSDTGIVKFSHPPEMS VRKFTSARSGCVRSQAWNVTV SAQTRVSQALTLLRRVHKSPM NALTVPVMAEAPSQAHRGRQ TRRLSLHQLRLLLTTPDVWGV IRRCVPVVWGCLEHLDTAGFPL PNSHTMPLPIGWNDTRKRLHHS AHNGQHDVAQGRRLVGRKVG LTHPKVQQQLGVDGLSLFCVY LVWYIGLHLRRFPRLAYTICPSL VYGADLRVIVRLFSDSHHMAF GNPQPKHLDCQEYALFLLNSM PDNTAEHYRNKIAIYLHCLPED DRIKAIINEIRMAIHQVSPFREEP VDCVLVWKYSQMLPNDYNPN NVAPPEKKLLQKSIEDGTQPI VVTHTDKNAMEIVDGFHRHEI GKG/SHASLKLRLGYLPVTCL EGTRNQRIATISHNRARGRH ITAMSEVTPELRLLGW
15823	46191	B	15914	1	273	
15824	46192	B	15915	169	292	
15825	46193	A	15916	2	844	KGGVYKTSVSVHLAQDLALKG LRCLLWKGTPPQGTSPMVSRE GDPALHN*CKTQLLCLSYLGEK DDVTYAIKPTCWPLDIIPFLA LDRIETELMGKFDEGKLPTDPH LMRLAIAETVAHDYDVIVIDS HNRGNIGTINVCAADVLIPTP VEMFDYTSALQFFDMLRDLLK NADLKGFEPPVRIIVTKYSNSN GSQFPWMEPIPECLPKHGSKK NNVRNANEVKGQIRMRTVFE QAIDQRSSTGAWRNALSWEV CNEIFDRLIKPRWEIR

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15826	46194	A	15917	1	681	MSIGGSGNSLCTRPKQQGGGTG LKQYEVSVPGTLRCLACPQACT LRKEHWIHFAPKSNYDSCR YIE EYFAYEASFMSVQLTELVIKSL EDLASLFMIHKKNPVSIPHTVW YADDIRRGEEAADVLGLTLYE LMLRAGEAAFQVCRSAYPDTR HWLVLCGHGNGGDDGYVVAR LAKAVGIDDTLLAQESDKPLPE EAPLAHEAWWNAAGGEIHALNI GWPESEHLIV
15827	46195	A	15918	3	774	VKCEKCLFLPLGQFSQFTQKLR WIFLDFLIRKGGQVTPATAFAM HLHEYISQGLSILGALDIEGSS DKQRTITITATPSVGALVLPVIY RAIKTHYPQLLRNPPISDAENQ LSQFQTDLIIDNMFCTNRTVQH HGLFAANMVLICREGNPLLSLE DDREAIANAHHVLLPPEQNFSS GLRQRVQEMFPGRQINFSTSYNI LTIAALVANSMDLAIIPSRLYNL FSRCWPLEKLPHPSLNEEQIDFS IHYNKFSLR
15828	46196	A	15919	1	741	MITVLLIATQFAPYFTEMALKG GFSGFAGESAQISALSVGNMFGW SISELMSLGIGVVVAVGIVASV VLFLRVLSMSWLKEVIGTEKAV IAMCHLRALPGDPSFDAQLGM NWVIDKAWDDLMLQNGGVD AVMFSNEFSLPYLTGKLVPAFLV AREILVRGMYVRGRKMVAFLV CCVALAISAMYELIEWWAALA MGQGADDFLGTQGDQWDTQS/ GYVLRAAWRINDGDIPRSLSLP PATALWLDNRI
15829	46197	A	15920	1	678	MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMLQNGGVD VMFSNEFSLPYLTQVRPETTAA MARIIGQLMSDIRPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHQ HRIGAGEVKTFLNIVPEAAVYL GNRDICSIKSTVFNNHPDALC VSGLTAGIRTDALLKRVKETV PDTVVLANTGVCLENVEEQLSI ADGCVTATTFF
15830	46198	A	15921	624	734	TRTLRQIVDSRAIPFT*ERLHSP NQPKNPYPPEV

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15831	46199	A	15922	1	1923	MPFALGGGDLEETPRSDPGVTF ACSLAQPMRKPTGVLGNRFHD TQEPVPVGGPGLRGFHLWHAPP LDRPAQFAAIRTDSELMSSANP KSFTASPLMTFTPARSRINRYR YPAGTRAKGENEAAFAARIHSF LPYRRPVFWATTMGAKSAIK PMSTAVTRDASVFQTEYERSRF GARPWPLRKAPEAMGRGFHEI GVQCEAPTANTLEPSRRGAVM AAGLSFQRTPWREVLGRGEGSF LGAGSDPVLRLASLASTPFPGE KHVGSWGMGRIVLRSFALASSS LRHSGERIPGTVLPDDIFACHQ RNYAEVFGIWRITSSVLQPIEPV EPKCISQFLYIVLERRSSSLISLS FNSASLCSRHDARYVLQHALF CFTTNDFGQIFTTFFVSGSGTR MSLPAEFGVIAQSDQKVLFIDA DLAVVIRITCLPSTMSWLKEVI GTEKAVI/AMCHLRALPGDPFS DAQ/LGMNWVIDKA WDDLMA LKMVRPETTAAMARI/IGQLMS DIRIPFGVNV/LWDPVASFDLA MATGAK/FIREIFTGAYASDFGV /WDTNVARSRRIRASTVFRLAQ RCQPDASEYGFMRMIARVFDVR GDQNSEASLRVSGSIGPRTCAP VAWQSRFRPRLDRSDDVKRF QADTDSLVLH
15832	46200	A	15923	480	900	KTRYSCRGETWSNPQSSQLSAL IAAVRHPATSNVCRSARSCCIL RALRAIQHTGCSAGNVAPFW CQFAPCWRKPLKIEESDSVFM VIKESLWQELADITDKTQLEWR EVFQDLNHHGVVYHSGEVVGLG NLVCEKCHFH
15833	46201	A	15924	1	431	SKVFAVAGCVLMTTTPDSCN SWQKCRNKTMNKKIHSALLV NLGIYGVAAQAEPTDTPAGVS TITADEIRKNPVARVDVSKIIRT PGVNLTGNTSGQRGNRQIDI RGMGPENTLILIDGKPVSSRNS VRQGYRLECGDG
15834	46202	B	15925	1	1352	

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15835	46203	A	15926	31	546	CYCLFVSFSPNRLCCRSAGVC QRYTPDPFCLGITSRGCRRAKIT ACSFLWKLHPRGALARCQPELS CWRCLSTLLEGVSPSGGTGVR DPYEEAVCLAEKCCAGRSA VLFRAGRQGRSLSLKLPQLPF SPCVLCLSKLVPVSPNSTRTSKL LSIPYSRGPALLEVLS
15836	46204	A	15927	2	479	
15837	46205	A	15928	1082	1386	ADPFQEREAEKYANPIPSREFIL EHLTKREKPARSDELA VELHIE GEEQLEGLRR/RQCYALPERLD LVKGTVIGHRDG YGFLRVEGR KDDL YLS/SEQMKT C
15838	46206	A	15929	3	401	
15839	46207	B	15930	1	3675	
15840	46208	A	15931	1749	1941	SQIPTSEAQVMSNLMGTNGVLR PARAYRNEAVLS*ALVSAMYS QTFRNASFGVPQMFSTTSGV
15841	46209	A	15932	5	1465	KRSTTAQIRWISPLTSLKPRSKR QSKSCATKPKK WYVAAPCCWC SPTGISLKTRLPVPAPMAVGAIQ TRLVDQSLRCDANII VETASAR DPHHFAVLLGFGATAIYPYLY ETLGR LVDTHAIAKDYRTVML NYRNGINKGLYKIMSKMGISTI ASYRCSKLFEAVGLHDDVVG CFQGA VSRIGGASFEDFQDQL NLSKRA WWRCLSATIGCCDC TRGYLGARITGQISSITVWGV IPVVGLCHGWFWFSPTLYVDS WNP HHAPFFSA VGSSIAMTLW AFLGLESA CANTDVVENPERN VPIA VLGGLGAA VIYIVSTNVI AGIVPNMELANSTAPFGLAFAQ MFTPEVGVK VIMALMEMSCAGS ILGGKFTIAQVFKSSSDEGYFLT IFSRVTKVDAPVQGMLTIVIIQS ELALMTISP SLNSQLKEMVNLA VVTNIIPYILSMAALVIIQKVAN VPPSKAKVANFVAVFGARNSF
15842	46210	A	15933	1	3666	

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15843	46211	A	15934	979	1626	FSATITPPFIALQVRVRFHPLDAL LLFVISLWLQLGLPDELSRFTPF CLALPIIALAWHYGWQGALIAI LMNAIALIASQTGLLLGAGIQR LRELNQLSQKELARNQHLEAERL LETEESVRRDVARELHDDIGQT ITAIRTQAGIVQRPAGAGHPLTDA GNGAGRARYCQPSRMANN*IS VKRKVVVEHRCFVDFTFNDDG AVNVDRRAVRGVFIAAS
15844	46212	C	15935	1	666	
15845	46213	A	15936	1	1137	MGKFGHTEIGEVDVRDWSDAL QAKELQKLPGHISRKLEDPPPTSL FMLLNPHSDQFSSNAHHHLHA TAIDDDYTDPTKSTYALGLNWS NSILGGFNISGYKTYSYDGDND SSNLNINWNKAFFKATVSVNVW QHQLSASENNEDDGLFYVNIS IPFGRSNTATLYTRHDDHKTHY GTGVMGVVSDEMSYYVNAER DHDEPTLPAQNKAQEVLLDVV LDEAKIGVASMLGSRVRVKTW SWFADDKQEIQRGGFAGWLTD GTPLWVTGSGTSKTVLTRYAT VLNRVLVPVPTQVASGQCVEVE LFARYPLKKITAEEKSTTAVNPG VLNGRYRVFTFTNGNHITFVSHG ETTLSEKGLKLQSHLDREEY VARVLDREAKISTPP
15846	46214	A	15937	323	695	FTGPRRSLEIEVAELKQRDLSDL AIGAGGSVCWTLQGAWSPTRA KAGELKTQLATAASLR/MDKH RSNSVGPDLFTLLDDYLHV VDTALWLSGGKASLDGGTLLT NDAGEMLFAEHFHSAGPL
15847	46215	A	15938	1	235	
15848	46216	A	15939	98	593	MSKVRLMRNLSAPPNAYAKG ESKPGIMSGWVF*AEWAYLITG *AKKKVYGSS/ARIHLRALRY SNWRQYFAGYTFGRQYWQSPE DDHLPLLREFLARHEYMQKYL LGTESGIQGEELGASDGKPEEV EWQTAIEGKLDLLVTLDFRM SSTCLFSDIVLPTAT
15849	46217	A	15940	367	677	LSSCLRATQSAAPVRNWKARFL RCTVWVWQKRSSTGRNMYLPV RPTILKLRPVHTVW*LSGASL RNWVHCCTRKKKVKCSSAVA* RKRNICPMKLHVSSTRK

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15850	46218	A	15941	1	921	MEMSSLEFLHSCSHLKCHLLY YIASAYNYDWYTPAKLSFISE GEIKYFTDKQMLRDFVTTRPAL KEL.LKEAVNMERRNRWVDIGP GTELDCISQAYAQFVASTAECC GEGGIKAWDYVRMGFLSRMG VLNNWLTRRRKLLWSARSRIH LRALRYYSNWRQYFAGYTFGR QYWQSPEDDHLPLREFLARYE RPMKKLAGRSSIILAFRGHDQ RDYEFPSKALNIN*LRWALAS VK*TTACATGVFPVSVTGARRF
15851	46219	A	15942	531	637	SIFARLNASRRCT*SYALLVLR LPIIQITAKGIL
15852	46220	B	15943	120	881	
15853	46221	A	15944	1	1583	MADRVDSKCSRSRPGAVAHNY NPSTLGGRGGRITFWLLSANPSI NRGTLEKESRTVAQRLSVLHGI NAPEFFDKAVFSSLVLTLRDEG YISDSGDAEPAETMKVYQLLAE LITSDLMIFNISATVLYITAFIAC SAAVDLTSLRGTRPYNQRAAA SKEIEDLKKKLTEGEEISGCDVS GSDGDDNEEGKIGEDEEKRNT GGNKVFPERTVETPATADAER KALETKLDVEEETRLQLNSRNR KKDLKTRQEHQSLPEKFSGLQK NVLLEAVIDPALIAQLRQAYEE ALRIAQAPAKSVWQPEEYEEA EHEILLAFRALLASDSERFLPSA WQRFIQQLNYCSMEEIDELRWS LCTIAMNTAHLSEFCVVLAEER LRWLQEENTGEIDEEESFLY AIAKGNVNFQITILHLPVAVQN DTIDFYQMFIWLPGAPGAYC DGLHTSKRKTCTTSTHQRQRKD TPPALNPHATCTPPHTWLGAP PPASMRSGPHNAPTPPFTGSTPR HTHDHTNITNANIPHNVNSN

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15854	46222	A	15945	1	1228	MGVLNNWLSEEEELWQSRHIL RALRYYSNWRQYFAGYTFRGQ YWQSPEDDHLPLREFLAYER PMKNCWKILDIETTDVDIIRRA YLALLPSFHPETDPQDFKQLRQ AYEEALRVAQSPAKSVWQPEE YEVAEHEILLAYRALLASDSER FLPSAWQRFIQQNLNYCSMEEID ELRWSLCTIAMNTAHLSEFCVV LLAERLRWLQENTGEIDEEEL GSFLYAIAGKGNVFNFTLHLPV ARRPDICTQHNDQSRCEGYQIL SDKRGHQHGGGITALYQCGNA DPRAKGERLFFDAPAKDSTQTR AEDAHYAGSNMSPDPDQGDG RKQIWESVRVHTPVRCQQRSLP VTSYLNNGGEIFNLIGLICRTRRIA ARWVKSHNRNARSFECLKRHR FVVAFNRRKPLV
15855	46223	A	15946	71	323	AAGAVVSAMPKAKGKTRRQK FGYSVNRKRLNRNARRKAAIR GSNDLEAEASLPEKKGNLTLSRD LIDYVRYMVENHGEDYKVS GS
15856	46224	A	15947	48	627	AAGAVVSAMPKAKGKTRRQK\ FGYSVNRKR\MSRNAKRAAR\ GLECSHIRHAWDHAKSVRQNL AEMGLA\VDPNRA\VP SRKRKV KAMEVDIEEEA*KNLYRKPYY LNDLEAEASLSEKKGNLTLSRD LHLMYRYMV\ENHGE\DYKAI ARD\EKNY\QDTPKQIR\KIN VYKRFPYAEWQDFLDSLQKRC MEVE
15857	46225	A	15948	796	1301	LTKKDYISPNAKAFVQRLPER NLLTRGLKRQRQPCLSWCWCGG QARMPKAKGKTRRQKFGYSV NRKRLNRNARRKAAPRJE/CVR GLGFRVAVGLGRDGRDDGSA MSLFAGSSHIRHAWDHAKSVR QNLAEMGLAVDPNMAVPLRK RKVLTWQGLGPCLLYSSPAILT
15858	46226	A	15949	512	675	SQDFGPPSAAPSPGMP\PGPSG CSSHRQQEDPPDGA AAPGHGL RPGRLQELLV
15859	46227	B	15950	1	717	

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15860	46228	A	15951	587	1387	RARSRLGNPLRLAPAPNSDV GVQRAIFRPICRKAQVPVGSV ANRRRLRQHTRPDPLGTNRSEP GWWDRSWSPDQAKSGQSCVA KIKKNHMHISTDSEKAFDKIQH RFMIKTLKISIQGTHFWKIIKAIC DKLTANIILNGEKLKAFPLRTE MRQGCPRLSLLFNIVLEVLAKA IRQEKEIKDIQIAKEEVRLSLFA DDMIVYLENPKDSFRKLELIK EFSKVSGYKIKNQYCENDHTA VSGVGSFQWICGLADVKNEAA
15861	46229	A	15952	3	3201	SERGFAGDLRYPTHFLSTNSV LASVTASLKEHPRGTLSDGSP ALSRNVGMTVSQKGGPQTSP AGPGTQLGPITGEMDEADSAFL KFKQTADDSLSLTPNTESIFVE DPYTASLRSEIESDGHFEAE WSLAVDAAYAKKQKREVVKR QDVLVELMQTEVHHVRTLKIM LKVYSRALQEVLAQFISTAIGRL FPCADDLLETHSHFLARLKERR QESLEEGSDRNYVIQKIGDLLV QQFSGENGDRLEIK
15862	46230	B	15953	83	1969	
15863	46231	A	15954	1	444	SSESAVEFSEPASGSSPSWELGS EGAIRDKKTSLGAHVGLSALGR ALENTIAFQGGKETDVQKSYDSP QGDCLQDVKGKRPTLE*PSLE NPETRRFLDASYAWRESCLSW HHHTAHDIFAGKPVDPDLPGSTR GQDSAVCSQGQFLIVR
15864	46232	A	15955	2	236	SEGAKRDKKTSALGAHVLSAL GRALEKTIAFGSS/APSKGRKL RSRKVMTRPKGIAWQDVKGKR PTLE*PSLENPEVR
15865	46233	A	15956	1	459	KKVGNYYTTPYRFRMKCHLC VNYIEMQTDPA NC DYVIVSGA QRKEERWDMADNEQVLTTGE RHPLTCLGAL/DPESALGPPKPS RALIVAHEHEKKQKLETDAMFR LEHGEADRSTLKKALAHTVDHI QEAQSAWKDDFALNSMLRRRF REKKKA

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15866	46234	A	15957	564	1189	AAPKMGERRGVNKKYPPDFNP EEAWLSSTDYHNSHPFRERASG SCSQGLIIRFEMPYNIWCEG/C RTNFGMGVRYNAEKKKVGNY YTTPIYRFRMKCHLCVNYIEMQ TDPANFDYVIVSGAQRKEERL GHWRTMNRLLTHRGIEEEAEA WKTDAMFRAGTMRPTAAHF KKALPKLEPHSGRPRAPWKDD FALNSMLRRRRFRVPSKP
15867	46235	A	15958	2	1047	FVDGKLHGRGSTDIGPVAGWI NALEAYQKTGQETPVNVRECL EGMEESGSEGLDELIFARKDTF FKDVDVCISDNYWLGKKKPCI TYGLRGICYFFIEVECSNKLHLS GVYGGVHEAMTDILLMGS VDKRGNILIPGINEAVAAVTEEE HKLYDDIDFIDKEFAKDVGAQI LLHSHKKDILMHRWRYPSLSLH GIEGAFSGSGAKTVIPRVVGK FSIRLVPNMTPEVVGEQVTSYL TKKFAELRSPNEFKVYMGHGG KPWVSDFSHPHYLAGRRAMK TVFGVEPDLTREGGSIPVTLTFQ EATGKNVMLLPVGSADDDGHS QNEKLNRNYIEGTKMLAAYL
15868	46236	A	15959	163	1388	RLVERWRPSGTLFKYIDENQDR YIKKLAKWVAIQSVSAWPEKR GEIRRMMEVAAADVQKLGGSV ELVDIGKQKLPDGSEIPLPILL GRLGSDPQMKTVCIYGHLDVQ PAALEDGWDEPFTLVERDGLT WCSSCRGPYCRGSS/DRLSWKL PSVMWGDREPHLARLD/HPSG LEPQRPGSTWGGDDRRGGRA LSRQLPYAGYAAAQCKGEVPR QVSSSRLVVECSNKLHSGVY GGSVHEAMTDILLMEEHKLY DDIDFIDEEFAKDVGAQILLHSH KSHLHLDLLPVVVRLLGQALFH TAHFDPDNIPSSKDILMHRWRY PSLSLHGIEGAFSGSGAKTVIPR KVVGKFSIRLVPNMTPEVVGEQ ACGAGTRESMSSLYGPSRAED DSGLSALPSQPQPFILYAT

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15869	46237	A	15960	3	433	FETLFSQVQLFISTCNGEHIRYA TDTFAGLCIQLTNALVERKQPL RGIGILKQAIDKMQMNTNQLTS IHADLCQAITPAMAVSHIMLE SYKKYILVSLILGKVVQLPKY TSP/QLVGRFHKPLSNAIYHEL HKLYSTNNPC
15870	46238	A	15961	46	1481	TGSDVAAREDLRWIAAAPPR AAAFSRACCLRRSGRPGENMA SALEQFVNSVRLLLSQGCSCFP GQMTQLCELINMSGELLAKNLS HLADTVLGAADVQEHSLGVL VLFVKFSMPSPVDFEILFSQVQ LFISTCNGEHIRYATDTWQETV LLKSMVLVLVVIYYQLRGIGIL KQAIDKMQMNTNQLTSIHADL CQLCLLAKCFKAALPYLDGDM MDICKENGAYDAKHFCLY GGMIYTLGKNFERALYFYGQ AITTPAMAVRHIIW/ESYKKY ILVSLILGKVVQLPKIFHLKLV G*IPLSLLSNAYHELAQVYSTN NPSELRLNVNKHSETFTRDNN MGLVKQCLSSLYKKNIQRLTKT FLTSLQDMASRVQLSGPQEA KYVLHMIEDGEIFASINQKDG VSFHDNPEKYNPNPMLHNIDQ EMLKCIELDERLKAMDQEITVN PQFVQKSMGSEDDSGNKPSS
15871	46239	B	15962	1	3411	
15872	46240	A	15963	689	925	
15873	46241	A	15964	1	244	GSAPQSCASAPVSRSAAPGTA EAAEPWAIIVGVEQKNYYVCV PLGLIGNCTVTSSGSLDCADW CLKWKSILMESLEVP
15874	46242	A	15965	469	604	
15875	46243	A	15966	286	433	
15876	46244	A	15967	4356	4643	DCPLARNKSKPOTVCLKARQTF QAINFSRALRITGYLTSFPLSRS TLPSAGDFRASAWA*SGPTV* TLTSVPSVGINSSYIEPVFRTLL SGE
15877	46245	B	15968	1	1472	

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15878	46246	A	15969	918	1619	KTHVLSWGSPPKSTWKAGWLQ KQKTTQEKKAESKAPIEEEPAG AGLNKDKETEERSDGERVAEV APEERENVAVAKLQESQPGNA VSCSGGRRKEDEREDWGKRTQ RTHPPAAAQAPGQCPPPGSTEVG AGGGLRWTPSPGRQPAGVAAD MGITVLTVP LQRCLQNSWAKE PVLVVSFVIGSLTVILPPLSPYTK YSIMINEATPYNYPVPVHDDGN M/PDMCSHPQGPQGSLEWL
15879	46247	B	15970	183	459	
15880	46248	A	15971	864	1197	GSFRLGHGRIPPFHLRGMKESL GPDFGDPCVPCLNSGPGPPGV SAGGAGAGCGGMGRDDAWVP TGPVAESPGGHLAPISPRQGA PWGGPCGQLGAGTLGQAVCG MTQDP
15881	46249	A	15972	1	441	
15882	46250	A	15973	3	182	
15883	46251	A	15974	23	475	PLEKGRQFPQYEDQITFTDYL EEYPTDDELVWLWKQHLLKT EKSLLSDISARLWFTYRRKFS /ILGGTGPSSDAGWGCMLRCG QMMLAIQALICRHLGRDWSW EKQIEQPQEQRIQLQCFLNRKD CCYSIHQMAQMGVGEKGSIGE
15884	46252	A	15975	224	418	
15885	46253	A	15976	743	1220	WCWGHVRVRLVLAAGPSSRGVL LLLVLVLPWSASFVVRCAVWG VLGDDGVVGGFLLWLGVVGR LAVLRADLAVCVGVVCACVPF VVLPICAALVRVGCSLVEAALG L GARPLKTFFAVVVPLTKGGV VAGSMLVFVPAVGEFVPELLG GPDIVIGRV
15886	46254	A	15977	3	3492	RKHKVGILYCKPGQSSEEMSN NEEAGPAFEKFLSLIGEVCLK GFTKYAAQLDVKTDSTGTHSL YTMYYQDYIMFHVSTLLPYTPN NRQQLLRKRHIGNDIVTIIQEP GALPFTPKNIRSHFQHVFIIVRV HNPCTDNVCYSMAVTRSKDAP PFGPIPSGTTFRKSDVFR/DFLL AKVI*RLRNAAEQVPTSFTPWA TRTRQEYLKDLAENCVSNTPID STGKFNILISTSKKKEKTKARA GAEQHSAGAIA
15887	46255	B	15978	402	2884	

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15888	46256	A	15979	294	1721	AVRPGRHDPASAGLRSAASQ* VRGHPGGLCA*GSIQGPASAA EGPPAHSRAA*SKGGAELRTR* AGGRRPAGPHAQR*LP*GPRV PLRPPSGTFLLP/PACTPITSRPS *KSCSRASPTPTWSS*IPASGTSP GMVRTPEGA/PGEPEPVVPG PGAARVLPPGVE/PRPCLWARK SPGVFRPSSGGRPPS*KTKWS KPTSTAPRP/P*TLRCTGLAFPL PPREGEPALGRGALEWTCAPLP LPAAAGPRGRRLGCGAAPPPR GRVDQEEK/PGRVPEGPPQANR NHPALPLSPPLSPPT/*PPPAWVP TPALAAAPAPVPTASSHSPSPG NAPVPTGSPRCLFRLPYFPVGS ILLPFRCLISPCRFLRRQFYG WSSAAYALLPHTPLSAACPSGP TTALHGQPQSSCCQEAFTTV KSGVVQSGRPSLRQFYVHDFCK IQPQQLLVSHATTKATTDTRYST ASCVAR
15889	46257	B	15980	35	314	
15890	46258	A	15981	1	197	
15891	46259	A	15982	3	3889	
15892	46260	B	15983	172	287	
15893	46261	A	15984	8	166	
15894	46262	A	15985	250	1095	
15895	46263	A	15986	366	870	NHSLAKKGTAHGLGMEKCCGR SPFFSFFPWSIAKPTLRSSSSWPH SSSSPSMSSPLQRAVGDT/KRAL SASSSSASLPFDDRSNHPSEA CTTPGGGWEVADGNTDSLAD EGSDFEDSFNRNVKKKAAKRP KTPPV/AKQPKGSRVVHRHSR KQSEPPANDLFNAV
15896	46264	A	15987	30	229	ALETNIGSSYNYGSEDQAEFLC VVSSELHSTPNGLSSESSRKT/ CYKPEAPGCEAPDHLQLGLGVI
15897	46265	C	15988	1	930	
15898	46266	A	15989	1	609	

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15899	46267	A	15990	1	875	MRMEAGEAAPPAGAGGRAAG GWGKWVRLNVGGTVFLTTRQ TLCREQKSFLSRLCQGEELQSD RDETGAYLIDRDPYFGPILNFL RHGKLVLDKDMAEEGVLEEAE FYNIGPLIRIIKDRMEEKDYTVT QVPPKHVYRVLQCQEEELTQ MVSTMSDGRFEQLVNISSY NYGSEDQAEFLCVSKELHSTP NGLSSESRKTKSTEEQLEEQQ QQEEVEVEVEVQVQVEADAQ EKGSRPHPLRPEAELAVRASPR PLARPQSCHPCCYKPEEPGCEA PDHLQGLGVPI
15900	46268	A	15991	1	2448	MRRGETRSRRPPQCFWAFAHV SRSSRRGEFFSDFRWKKHSEV RESAQVPTTKREPVLQHKINIK IVIALVDILFALGLNLVCVSPV QLFSVQTDSRATGDQRLPSWT AQRYGTRTLGPDGFTERCYPGP SPESLLCSALPWLRDLGMPVAE APQVAGGQGDGDGEEAEPEG MFKACEDSKRKARGYLRLVPL FVLLALLVLASAGLEMLSDPGS RSYGSGLPAPWAKCPKAPHQR SLIPPDYAPGVNHPPPPQERCSM GLRTQGTGLGRHRVLSAQQVAF SVSLLMAKIAFAKQKSDDIIPDF KLFMVTLVHRPNRLSARVLT VPVLPAPCPMLLPLEGKYAEV MVSQVYSGSLRVLNRHFSQDL TRRESSAFRSETAKAQKMLKEL ITSTRLGTYYNSSSVYSFGEGPL TCFFWFILQIPEHRRLLMSPEVV QALLVEELLSTVNSSAAVPYRA EYEVDPPEGLVILGQYCEWKPPG RRMQTPRPAMRMEAGEAAPP GAGGRAAGGWGKWVRLNVG GTVFLTTRQTLCREQKSFLSRL CQGEELQSDRDETGAYLIDRDP TYFGPILNFLRHGKLVLDKDMA EEGSQVWTVTSGGWGDRNAV LTGMGRALSFLWLIQYLFCL VRAWVLEAEFYNIGPLIRIIKD RMEEKDYTVTQVPPKHVYRVL QCQEEELTQMSTMSDGRFE

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15901	46269	A	15992	1	573	MPGLLSRPRRGLRARPCGGGE ALPEHVAIDVCPGPIRPIQGISG YFPHFPRDLPHDAPARPATASA GRRRPSDGDARDHDKDGDHLFG SLTIQHRPW/PAPSPDFPFTEFAV LYPGULKPMMDHNLADPCVKL HLRPGARKVPEACQLAPDLQD SSCLTAITKAHDVLTVFLPAAL KIQGNKYLTFFECQKLF
15902	46270	A	15993	500	2022	WTREKEPPGVETHGKASRTTL GLSLWCCLHLSEIQSSFISDCAR PRCSGRLPGSGPMLLATPHVLA TVVASSCSKQLWWLPPKVATD QQQMKLLKGLFIAGAPPGSPR/G VQPHLQPIRNMVSVRTMEDSCE LDLVVYTERIIAVSFSTANEEN FRSNI.REVAQMLKSKHGGNYL LFNLSERRPDITKLHAKVLEFG WPDLHTPALEKICSICKAMDTW LNADPHNVVVLHNKGNRGRIG VVIAAYMHYSNISASADQALD RFAMKRFYEDKIVPIGQPSQRR YVHYFSGLLSGSIKMNNKPLFL HHVIMHGIPNFESKGGCRPFLRI YQAMQPVYTSGIYNIPGDSQTS VCITIEPGLLLKGDILNSEILFGV DELSLTGFGLKCYHKKFRSPAR DVIFRVQFHTCAIHDLGVVFGK EDLDDAFKDDRFPEYGVVEFVF SYGPEKIQGMEHLENGPSVSVD YNTSDPLIRWDSYDNFSGHRDD GMEGAQHPIQGDTPPGPSDPP
15903	46271	A	15994	171	720	LSGSAGKVAAPCVPPSNHEL PITTENAPKNVLDKGERPSRGG NTRKSLVTTASTGSPR/GVQPH LQPIINMNVSVRTMEDSCELGPV YRTERNIAVSFPSTANEENFRSN LREVAQMLKSKHGGNYLQRN VSL/RR/LSPLRHPGPWPSPQEP GMCQGEPPGPPATLWPMPCGPT VLESPGGPGP
15904	46272	B	15995	145	972	

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15905	46273	A	15996	2	1096	W P V L T A A G C W L Q D P A G H R G G R A G G A G R A V L F Q L Q A G R A E L R G L R A R G W A R S W A P A P G C Q R T G R D A A A A G R R A G A G A L L G F T C L L L A A L C G H L G P S W R G G L A P G G E W I W L R A S E T R G P S G P R P A L M G S Q K I R N I T R T R H G P L H W L H S G C T T A T P F C L T R S C S D A A C S L K G L P C L C P C G L S V L I R V R L E L R R H Q R A G H T I P R I F Q A V V Q R Q P E R L A L V D A G T G E C W T F A Q L D A Y S N A V A N L F R Q L G F A P G D V V A I F L E G R P E F V G L W L G L A K A G / M E A A L L N V N L R R E P L A F / C L G T S G A K A L I F G G E M V R A P P P N A Q A P P L T P V S P A D R L F Y I Y T S G T T G L P K A A I V V H S S A R P S C P S S R T L R A A H R
15906	46274	A	15997	397	597	S I K S P E I H S P S T R I R M G C S S L P T E E A H A E G V I E L S R I K C V E I V K S D / D R I P C H Y K Y P F Q V S P S G G S S P
15907	46275	A	15998	1922	3886	E G D N K L R P R I R R K L F P L V V L R G D A Q G A P P F K N W I M N N F I L L E E Q L I K K S Q Q K R R T S P S N F K V R F V L T K A S L A Y F E D R H G K K R T R K G S I E L S R I K C V E I V K S D I S I P C H Y K Y P F Q V V H D N Y L L Y V F A P D R E S R Q R W V L A L K E E T R N N S N S L V P K Y H P N F W M D G K W R C C S Q L E K L A T G C A Q Y D P T K N A S K K L P P T P E D N R R R L W E P E E T V V I A L Y D Y Q T N D P Q E L A L R R N E E Y C L L D S S E I H W W R V Q D R N G H E G Y V P S S Y L V E K S P N N L E T Y E W Y N K S I R D K A E K L L D T G K E G A F M V R D S R T A G T Y T V S V F T K A V V S E N N P C I K I Y H I K E T N D N P K R Y Y V A E K Y V F D S I P L L N Y H Q H N G G G L V T R L R Y P V C F G R Q K A P V T A G L R Y G K W W I D P S E L T F V Q E I G S G Q F G L V H L G Y W L N K D K V A I K T I R E G A M S E E D F I E E A E V M M K L S H P K L V Q L Y G V C L E Q A P I C L V F E F M E H G C L S D Y L R T Q R G L F A A E T L L G M C L D V C E G M A Y L E E A C V I H R D L A A R N C L V G E N Q I K V S D F G M T R F V L D D Q Y T S S T G T K F P V K W A S P E V F S F S R Y S S K S D V W S F G V L M W E V F S E G K I P Y E N R S N S E V V E D I S T G F R L Y K P R L A S T H V Y Q I M N H C W K E R P E D R P A F S R L L R Q L A E I A
15908	46276	B	15999	58	1526	

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15909	46277	A	16000	3	378	GASPDGLGGRVLGAGASAEPR GRFPGPSPLGGPPVPGCQCAAP SLRDPWGLWAPVLQMTGSYEF KLNQPPEDGISSVKLSPHTLPS GLSPSWETSRLYDVPGNFM AVKYQHTGARPGNGPF
15910	46278	B	16001	83	2851	
15911	46279	A	16002	296	1186	AENHPGPIVVEGKMTAPERM KHESNYLRGTAEINLNDGLTG GFKGANFLIRFHGMYYQDDR DIRAERAEQKLEPRHAMLLRCR LPGGVITTKWQAIKDFAGENT IYGSIRLTNRQTFQFHGILKKNV KPVHQMHLHSVGLDALATAND MNRNVLCTSNPYESQLHAEAY EWAKKISKQLLPRTRAYAEIWL DQEKVATTDEEPILGQTYLPRK FKTTVVIPPQNDIDLHANDMNF VAIAENGKLVGFNLLVGGGLSI EHGNKKTYARTASEFGYLPLEH TLAVAEAVVTTQDWDG
15912	46280	A	16003	225	386	GLCIPVVRSPCQLWGQKGPCM LRDEGRVFT*ISTKKNCPGNMR RKYETVDCRR
15913	46281	A	16004	386	739	PLLIHWRFTIEEADHRLAAG ARTFQ/PLCGPPQAQAVWR*AQ *FQFADRFPPASRWRRASSGRRF SRSGRRARCQSVAKRRRQIHEC GRSTPDCRCRMRQQYRCRDA RRYQNRAPRR
15914	46282	B	16005	10	1468	
15915	46283	A	16006	3	1267	GRSRR**PPSAVPHDPAVQRER DTQSLSVII*MQIYNFSNTHTLT NHNTLTLFHKTTAETFQHIGP QPTTDTPYHTAEAYCCQLVKLI RRQALRRCWQGAAILKCNKSP TNHCTS

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15916	46284	A	16007	1	1673	MTPICTVFRALSRLPDLWHRSI GTLTEALPQTDKRQEIAVALT SYSGLYGLGYGSKEIQLTYSGT ESGIWPFPPYSPNATHKGCGRHR FACPIAPHFLVIEPQSALGSCPS VEVDPGGCVFGAIRLLVLRDAP SFSRLNLTLASGESLQGGPGFV GVSKVYAFLVVRNPTGTPMFT GTFEIPKWPTFPIPPVFORLGSF VLQLQGPRSPGQCEYDRELVS SRSVSSCLLVGLTHLLSYKDA GVDIDAGNALVGRIKGVVKKT RRPEVMGGLGGFGALCALPQK YREPVLVSGTDGVTGTRRLAL VLKRFVFIGIDLAMCGNDLVV QGAEPFLFDYYATGKLDVDT ASAMISGIAEEKSEILDGSKVSD GDVLIAGSSGLHNGYSLVRQ ILEVHRAAADVLSADAVSW RAPYQTSSGLRKKINQGVSVF DLHLSEVAQMVNYPGFQDIDV AVIEASALAPDGRVWLTSGIRN APTWLLRAKKVIIELNHYHDP VAELADIVIPGAASRRNNGSIFH AMDRLGNPHVQIDPEKIVAVV
15917	46285	A	16008	425	595	
15918	46286	A	16009	315	721	QCFRALGGHRRRIADRGENIQV WIEPGC/INDLLKWLNALDEKY RSRLVWARSSKNSLCASEANW LEMNNRLSKGDLPCIRPILIMLI R*TCSYGFTALR*TQNAAGGGD SLAGGIGIFTLVFFTLPAYAIRW LPR
15919	46287	B	16010	652	858	
15920	46288	A	16011	238	2526	
15921	46289	A	16012	21	522	IPCCRSTRKTSAGLSITSEQRR AAVSRISVTSLLASAG/VRVYRQ HHARDVRERPVDKL/PR**TPC SARLSLYGPSR*WW/MARVLIF VTLPVRSRIVTVSPMRIGFSNRH RPEIKLAKISCKPKPRPTPSAAT SHCNFDHSIPIIEKTPSPISIRY LVMVMA
15922	46290	A	16013	2	527	

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15923	46291	A	16014	1	1734	MVNGCDSTNASSYANVNGCDS TNASSYANGERCDS TNASSYA NGQVRSTNASSYANGERVRL DNASSYAIGERVRLDERTSYAN GERVRLDERILLANGDRVRHHE RILERKATFNNSGTTCCRAVYS RVSAMTAPDKAFTPHRQCRCLP DATLARLIRPQIPAPSVGRIRRL RRIGNSANCLMRRLRVLSGHKF PHHPMPNVSAANGYRSFFPMAS YMTFFFGYLTAWSYCLCGCRW GSLKSPPLALCPVLVPGDGA VD TRIDAVALVALANLAAVRLYA KSSSAAGIINFVLTAAALLAVT AACTVATYALRTGKNRQYRA MQSFRSSIDNRVDTFFKGTGA LGISVTVIAVTCKSRLVYPIPVY TGLSLPQRPVAVVKVNEGSMET KDLIVI/GAGINGAGIAADAAGR G/LSVLMLEAQDLACATSS/ASS KLIHGGRLYLEHYESACEALAE REVLLK/MAPHIAFPMRFRPLPH RP/HLRPAWMIRIAENIS/DFVEP KLCLPRMGTRESVLPGVCRNY ESTITSVISVSPCERDMANYVPR HSAGYRRRFYPMTQPIKDAVEP VDQDWKAGKEMAASRS
15924	46292	A	16015	1	5895	
15925	46293	A	16016	170	371	
15926	46294	A	16017	216	477	
15927	46295	A	16018	2	263	
15928	46296	A	16019	1	2862	

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15929	46297	A	16020	1	1567	MKLNKAGFNVPEYSLLKMPP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLSPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDV AHD SRSIQLAML RD DEILTHPVFNRYHSEMMRY MHSLEKDLALNQAMIPLGST MKLNAAEMIPITWPEFAELHP FCPPEQAEGYQOMIAQLADWL VKLTGYDAVCMQPN SGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLDAEIARIEKMGPV(IKCTTEV GNTLTLEQVKAENRAVLVTVG LSSGSGPLPLFEHSDVEIADVFLQ RARQAQGDIPQSALIIGGGDV AMDVASTLKVLGCAVTCVAR EELDEFPASEKFTSARELGVSII DGFTPVAVEGNKVTFKHGDLR TAPFLGVADKRKNSAGNHP
15930	46298	A	16021	62	329	
15931	46299	B	16022	289	334	
15932	46300	A	16023	1	2991	
15933	46301	A	16024	418	3156	
15934	46302	A	16025	1	2169	

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15935	46303	A	16026	800	2406	SSRRMFPPAIRLLLICLPARRWK SALGEEQLQNLQIHSQEMGISP SLFSTQPLWQIAMVQLATQAQ KLGRLAEYGDYQLLQAAKQQ HKPVIELEGAENQIAMLLQLPD KGLALLDDTLTHWHTNARLLQ QMMSWWLECEGGERERIFPVS KRMGKKLDVFGDNHTASL TE TEEYRKSQVHFICIDKRERSSG NYQSIQGCERSA AFFIPSNSTRK RGESMYRMDKLTGGAAYGAS AGSILNGMLNAYSPEQWNAIG VLTTAAAGAEMNPTRLNKLVG AIVGSGGAITIAAVMLGNADGL EGRYYAYQDVVGVTVC DG HTGTDIRRGHRYTDKECDNLL KADLRKAIITYISGYSGTNGIRDS LLFSSLWLIPVFLFPKRKIIAAVI GVAFSRFIASHLAVAFESDPEAE IRQLNSRRVELERALSNHENDN QQQRJQFEQAKEGVTALNRILP RLNLLADDSLARDVDEIRERLD EAQEAARFVQQFGNQLAKLEPI VSVLQSDPEQFEQLKEDYAYSQ QMQRDARQPGVCP
15936	46304	A	16027	2336	3105	HGNAIALIASQTWRDHPVDLLL SLLVQSLT/GRLELNQSLQKEL ARNQHLAERLLETEESVRRDV ARELHDDIGQTITAIRTQAGIVQ RLAADNASVKQSGQLIEQLSLG VYDAVRRLLGRLPRLDDLT LEQAIRSLMREMELEGRGIVSH LEWRIDESALSENQRVTLFRVC QEGLNINIVKHADASAVTLQGW QQDERLMLVIEDDGSGLPPGSG QQGFGLTGMRERV TALGGAFH ISCLHGTRVSVSLAQRHV
15937	46305	C	16028	1	1374	

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15938	46306	A	16029	1298	2896	GAFTCCATAGGCMNIRKKNRL WIACAVLAGLALTIGLVLYALR SNIDLFTYTPGEILYGKRETQQM PEVGQRLRVGGMVMPGVSQR DPNSLKVTFITYDAEGSVDVSY EGILPDLFREGQGVVVQGELEK GNHILAKEVLAKHDENYTPPEV EKAMEANHRRPARPSIMMPEIG NGLLCLALGIALLLSVYPLWGW ARGDARMMASSRLFAWLLFMS VAGAFVLVNAFVVNDFTVTY VASNSNTQLPVVYRVAATWG AHEGSLLLWVLLMSGWTFAVA IFSQRIPDIVARVLAIMGVSV GFLFILFTSNPFSRTLHLAYPN RCQPINWRGRHLVWYLLFVIS LWLQLGLPDELSRFTPFCLALPI IALAWHYGWQGALIALTMNAI ALIASQWRDHPVDLLSLLVQ SLTGLLGAGIQRLELNQSLQ KELARNQHLAERVLETEQSVR RDVARELHYDIGQTITAIRTHA GIVQRLAADNASVKQSGQLIEQ LSLGVYDAVRPLLGRLRPAQLD DLTLEQAIPLT
15939	46307	A	16030	15	277	KIGQKAPLGEARGGERTSRTA KNFGYEEMLSELEA/HRRG/WL KRV*PRMKLPPEALVETFIQLF DAPSQIMPLTSPILLIAIEMGS
15940	46308	A	16031	1	2916	
15941	46309	A	16032	1	2862	
15942	46310	A	16033	1	3099	

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15943	46311	A	16034	1	1567	MKLNKAGFNVPESYSLKMPVP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLSGPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDV AHD SRSIQLAMLRD DEILTHPVFNRYHSETEMMRV MHSLERKDLALNQAMIPLGSGT MKLNAAAEIMPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVLT.TTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLD AEIARIEKMGPV.IKCTTEV GNTLTLEQVKAENRAVLVTVG LSSGSGPLPEHSDVEIADFLQ RARQAQGDISI PQSALIIGGGDV AMDVASTLKVLGCQAVTCVAR EELDEFFASEKFTSARELGVSII DGFPTPAVEGNKVTFKHGDRL TAPFLGVADKRNKSAGNHP
15944	46312	A	16035	367	849	NNFCSTSHHGQHHTDHRGC EQNVCHRDAICQTLFRITTKDDS NFICLIEAQSACHKDVNYNHDS QKNAADHHDKQQ*SPANFMPD TINDGFAERCINHQNGRLVSF RNPFPIARHPVTNPRPGKMPQH KRQQQLQHNFTDLLKAAPCTV NIHHQTNNQW
15945	46313	A	16036	1	1066	MHQRPRTRNAVEQHFRSRLQY YALHAFETIPIPLMRGRSIPAL VNNKLRSLERFSTRKIDDDA LARLVSCAWPGNDFELYSVIE LALSSDNGRIRVSDLPEHLFTEQ ATDDVSATRLSTLSFAEVEKE AIINAAQVTGAPFWWLGDKVL TIPLTLGMVAAALTDLDDRLAG RLRNLIITLFCFFIASASVELLFP WPWLFIAIGLTLTSGFILLGGLG QRYATHAFGAILLNAIYTM LGT SLYEHWYQQPMYLLAGAVWY NVLT.LIGHLLFPVRPLQDNLAR CYEQLARYLELKS RMFDPIED QSQAPLYDLA L ANGLLMATLN QTKLSLLTLRGDRGQRGTRRT GIL
15946	46314	A	16037	1	951	
15947	46315	A	16038	576	669	

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15948	46316	A	16039	1	1047	
15949	46317	A	16040	2	425	
15950	46318	A	16041	148	1052	RARRGVSVKAKKQETAATMK DVALKAKVSTATVSRALMNP KVSQATRRNRVEKAAREVGYP QPMGRNVKRNESRTILVIVP DIDPFFSEIIRGIEVTAANHGYL VLIGDCALIQQEKPFIDLITKQ IDGMILLGSRLPFDASIEEQRN LPPMVMANEFAPELELPTVH IDNLTAAFDVAVNYLYEQGHK RIGCIA GPEEMTLCHYRLQGY VQALRR CGIMFCRFTAEGVQ EIDYKDIA TLKNYITESGGVTE LIHFFIAEY SDNQRANAGGGV EDEIEVLES LRLNENHAIKER CRS
15951	46319	A	16042	3	741	
15952	46320	A	16043	237	1542	FHRLWTRGFLSPSPSRRTG DNAAGRTKMPPSPVIF/WFALA QFVGVKHSRSHIPFAAVRSHK ARIRISRSRSDVATSILPQLS *RMPF*SQKALVARFPARQNC AFRLPGV*/LDPGMDHAAV VARLVTVGRGGIVWFG RDFYRSVDDIHFGAWGDL AKECFDIVIPQNTARTY PHANAIEIGVRTMKQINAAIG RQTNRMMAHWVIRSSRHYR RQLNSLCFITGADVCRWFPQ HIVPGRDSVAHVVVQHVITY RLLRGLLHFAGDGGVNAITV FIGTFAITVIHLLAHHFAQV RRRESNLRVIVSVNRLSAC LIELLLGDIPFIQHPRQHD VTPRDGTIHRVERVEGRRFR QPGYHRHFVQRQLVDRFSEI DLCRSTDITIGAVTKVNLVQ IKLEDLVFRQQLFNANREED FLNLTHIQRAFWTEEEVSRQ LLNGTCLP
15953	46321	A	16044	1	1059	
15954	46322	A	16045	104	349	RSAAAPWKTARKALVCCSA VVISPALKISMIVTISVQA HG*LRKGS GVKAAALSWW KFPQTMKPTITS LTGRRIS CRSRVKR

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15955	46323	A	16046	1056	2373	GPRLVQRSDHRPHDANYRQYL AGLSVHDDPLHGLAEVIPDDL YEASMDGAGPFQNFVKITLPL LKPLTPLMIAFAFNFNFLI QL.TNNGGPDRLGTTTPAGYTDL LVNYTYRIAFEGGGQDFGLA AAIATLIFLLRIPRRTTALQGM SNLNMESSRWARANRRLKAIN TLSLTLITQSCETYLIQNTPELI TDTFREFFDTPVETAQDVHKQL KRLRRVIAWTGERETPVITYSW VAAATRYQLLRGVISNTKINA TEEELQGEPEVKVESAERHHA MVNFWRTLSCLGLTFLFWLT GWTSGSGAMVMIADVTSLAM RLPNPRMVAIDFIYGTALALPY GGGRPVAVGVFYGGCYCTRDG LTRAPPPNAAPTAARYGPRTTP RTLKRGITDVRCEKRHHQQA RNAGYQTVFSDLRLRHPALR

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15956	46324	A	16047	1	2581	MVLMGLAQNIWQFLILRALLG LLGGFVFPNANALIAATQVPRNKS GWLALGTSLTGGVSGALLGPMA GGLLADSYGLRPVFITASVLIL CFFVTLCIREKFPQVSKKEML HMRVVTSLKNPKLVLSLFVTT LIIQVATGSLAPILTLVRELAG NVSNVAFISGMASVPGVAALL SAPRLGKLGDRIGPRKILITALIF SVLAVIPRHFEMRSKESRPSAW VTPKGEWGKGSVELVEIPTNDE TNDNIVAYWTPDQLPEPGKEM NFKYTITFSRDEDKLHAPDNAW VQQTRRSTGDKVQSNLIRQPDG TIAFVVDFGTGAEMKKLPEDTPV TAQTSIGDNGEIVESTVRYNPV TKGWRLVMRVKVKDAKKTTE MRAALRVWNKPGQNHQHLGN GFYGGVYGGYLETMFGGAGAE VLYRPLDSNWAFLDANYVKQ RDWRSAKMMKFTDYSVKTG HLTAYWTPSFAQDVLVKASVG QYLAGDKGGTLEIAKRFDSGV VVGGYATITNVSKEEYGEDFT KGVYVSPLDLFSSGPTRSRAA IGWTLPLTRDGGQQLGPGYTDLL VNYTYRIAFEGGGGQDFGLAA AIALIFLLVAIMFPLLMVVAIS LRQGNFATGSLIPEQISWDHWK LALGFSVEQADGRITPPFPVLL WLWNSVKVAGISAIGIVALSTT CAYAFARMRFPKGATLLKGML
15957	46325	A	16048	1	765	
15958	46326	A	16049	869	1012	MAISFMMSCFVT*VAANSAILL SMSWRA*SNSNGP*LANILLS AAC

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15959	46327	A	16050	1	1854	MTLSGNSDTDFEKTVTSVPALPD VVSDSDMSLNALS SVTLADNVQ LSFRRDSYSGQPSVIYTTQPRRT AGSEDAPVWPEAFTEDVRHNR PPYPVPIPRATRPACLARERMAM YMRPQIKTIGKAPAEALSNPR MQGPQLSSASTIPVTPFHWLFG SHAAGHFSQHAHRTALTGHFS HLATTLKGLALEGNAIFTITRFT RPYGHKNTTPHSP LCSAPHSPIF NSRRK VYGGHQGPQWWAFIHS RPGSSSHSILHCFAL VCPGLV QRDTPHPIRPALCPPIAIAFSLSL WLGNSPSPSGTQHLQGP KTFQ QASPSK VCPKRLICTVIPQQRV ASHHHFHGHNRYYQLGLPVQH CTLQGVIRATHFIPRTARNQISH VSWGAGPAHSDSQGKDLE/H EPIKPLDNSEKASKV/SQALET TTTAEKVQRQ/PVIAHLIRATER FNDR/LGNQFGFVLAS/HPMLL QDIFDKILQNS/DPTLAATLKNT INTAVHSHLVAPAGDGIFLLLRP FDAVCAA WIAIAEYKDYPGMP GKTHLKIRLMRRERLIGIRFYSG LLPGTKAPYSRTLAFKRVLHTA LSLHGLGKTCTTGELCSLTL EYASNAFTYWPDWHINRIKKN N
15960	46328	A	16051	249	724	EKVKKTQRKEIENVTNITGVVRQ IELWRRDDLQHPRLDEVAEEVP VALVYNGISHVVMASPKDLE YFALGFSLSEGDIIESPRDIFGM DVGVPACACNGLEERRALDGR TVAGCGVCGVEQ/LNDIGKPV QPLAFTQT/FDLNKLD DALRHL NDFQPVGN
15961	46329	A	16052	71	408	RYLSTASQTSIQIAGLSRSRA FTTFSKGILLSHTSVFIPDRCT SFSMMPTCSASLTSCHPFQMTS LLSSHHP/FK KKKFGTKTGHCL CPSLNCLPCCFSQIMVIKQVIL
15962	46330	A	16053	668	905	CLHVLHHLTSHCPQMTPKPYST IHFLPRMTSLSSHHP/FK KKKF GTVKTGHCLCPSLNCLPCCFSQI MVIKQVILEKKK
15963	46331	A	16054	834	1057	ARLLFMDLLDERTLVAVERPL VTSLSSHHP/FK KKKFGTKTGH HCLCPSLNCLPCCFSQIMVIKQV ILEKKKTK
15964	46332	A	16055	1	1011	

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15965	46333	A	16056	191	631	NLLRGNKMATQSSPVITDMKVI PVAGHDSMLLNIGGAHNAYFT RNIVVLTDNAGHTGIGETPGGD VITYQLVDAIIPMLVGQEVARL NKMVPQVHKGNQAADFDTFG KGAWTFELRVEAGAGLEARLL DLGKALNVSGCELLGHGS
15966	46334	A	16057	2	335	GARQQQKFVLIAGGFP*QLL*T NAVIGREFRNVQECIGLHTAGF ANAVTKHFGKCAIALHNMAFR IEDNHRSEVMVNGNQLSGLFF LRHFYAGIPYQQRQVINFLGAH
15967	46335	A	16058	736	910	RVSTPRATGTVPQRDYLPSVVA TG*PDSFHTYLFVRTY*K*V*VL AYLNTRQNDGDFP
15968	46336	B	16059	17	1699	
15969	46337	A	16060	3	440	
15970	46338	A	16061	1	564	
15971	46339	A	16062	1	1062	
15972	46340	A	16063	203	425	LNNWISWLLHMMCLMKVAN CFRS*DRRELAVSAFFVLL*AM RLRRSSSGFLANLAHLQKMKL NSSTYVPPTKH
15973	46341	A	16064	402	713	RGVAISLGQSKSHGYIHFQVAQ REPEILG/DSIKA VRWC SLHGRL M***M*RD LKQWFS APEA*VSL GTL CVIGQKAVGSLALMSWEP TPRPMGLLSTSR TLYS
15974	46342	A	16065	944	1305	LPLWFISALRLAGIAVWCVLST GFEQIRMIFAGLED RQSAL/FA ADAEDTGKKNMRVAR/IDARF DPTIGWPSSLGLLFSNRTPWVPF PFFFQVPQLHTFIRGILIWKTFP FWIFFFPASSW
15975	46343	A	16066	1	756	

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15976	46344	A	16067	50	1191	CLTIAVFFPAPQCPMFSPICHT ARDGERAASMIQDYIFCFFSASF MKLKPERMHSHIERAQTSDMLK DCRRHLPIGILMAGGMFAVLRK KHQQTIERPRISLTCMLPSW ATFLWLFTRIGQVLVTCLLMSR ECFVNE/VQVIATVVSVPQVN PDIVAMIGASAAALSLGIPFNGPI GAARVGYINDQYVNLPTQDEL KESKLDLVVAGTEAAVLMVES EAQLLEDQMLGAVVFGHEQQ QVDSRGSPKGNRTCDNYIVIEG LIDYVNDMIENVSEEAFCVENR IMRHSDDHSCIVVRLSLFALD LVLVVIASVVNPCLLEVTRLR AASIVSQPNLNSDTWGIGAILY GAYTCSCIADPHKMMSSGPMY SHSCVEK
15977	46345	A	16068	401	1518	LILFMST/ALLDAVVKKNRVRLI PYMLALYVLAFLDRSNIGLAKQ TYQIDTGLSNEAYALGAGIFFV VYAFLGVPAANLLMRKLGARTW IGTTTLWGFLSAAAWADTE AKFLIVRTLRLRAAEAGFFPGMI YLTSQWFPQRNRASIMGLFYM GAPLALTLGSPLSGALLEMHGF MGHPGWFWFMFVIEGLLAVGA GVFTFFWLDTPQEARFLSKQE KTLINQLASEEQKVTSRLSD ALRNGRVWQLAIHYLTQVAVY GLIFFLPTQVAALLGTVKGFTA SVVTAPWVAALFGTWLIPRY DKSAAKRYTRPHRECGYFSAPY HPPKVRNNAPHSGPGICLIRL RVRVRPNLGIEVYKHDSPPNNA
15978	46346	A	16069	283	822	

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15979	46347	A	16070	1	1400	MTDLIQRPRLRKSPALRAMFE ETTLNLNDLVLPIFVEEIDDYK AVEAMPQVMRIPEKHLAREIER IANAGIRSVMTFGISHHDETGS DAWREDGLVARMSRICKQTVP EMIVMSDTCFCEYTSHGHCYV LCEHGVNDATLENLGKQAVV AAAAGADFIAPSGAMDGQYDV FVRNENYWGKPAIKKITFNVI PDPTRAVAFETGIDLLYGNE GLLPDITFARFSQNPAYHTQLS QPIETVMLALNTAKAPTNELAV REALNYAVNKKSLIDNALYGT QQVADTLFAPSVPYANLGKPS QYDPQKAKALLEKAGWTLFAG KDIREKNGQPLRIELSFITDAL SKSMAEIJQADMRIQADVSLI GEEESSIYARQDRGRFGMIFHR TWGAPYDQRPQSQRVQR*F QAQQD*MKKPTQSKWNRATR VRGGEILTKFVLTAPLKWLKR SNSRRVSFAG
15980	46348	A	16071	592	1427	IPIGVTPCFSTLRLTLFALLACAS FIVHAAAPDEITTAWPVNVGFL NPHLYTLNQMFQAQSMVYEP/LV KYQADGSVIPWLAKSWTHSED GKTWTFTLRDDVKFSNGEPV/D AEA AAENFRAVLNDRQRHAW LELANQIVDVKALSKTELQITL KSAYYPFLQELALPRPFRFIAPS QFKNHETMNGIKAPIGTQPPWN LQESKLNQYHGFGRNENYWGE KPAIKKITFNVIPDPITRAVAF TGIDLLYGNQRLPLDTFARF SQNPVYHTQLSQIWNQ
15981	46349	A	16072	1	1071	
15982	46350	A	16073	585	1072	RPARDVPLPIRGLQPSLRGPQQL PEKPAVEVRLDKWLWAARFYK TRALAIREMIEGGKVHYNGQRS KPSKIVELNATLTLRQGNDETR VIVKAITEQRRPASEAALLYEET AESVEKREKMSRPGPPFVGAP KNPRGFLKLNALTMHPDRRP DKKERRDLLR
15983	46351	A	16074	36	356	ASHTLARKSC*/PSLLYQENQA HNQMPASELKASEIPFHPSTKTQ DPKAEESPRSKR*L*QRQVLP DPAADLSVKPPGLMLPLCYLS GPADITVLKASQDGLIIA

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15984	46352	A	16075	1	2111	MNTPLQSAHTHLTLVEFIAYLV SDSPFPAASTLSLPTCNFDCPT KLGAGTMPAAAGGQRRPHAA PPAAYPHRNKVRAAEARTSRA VRREYEAGDEASGRRGRGGRM KSVQNARADRGMWVRRERAV VRGQENTVVVFAAASPESDFL QIVLRDIAREMVPEYKSDLQPR TQMDAKKPRKCDLTPFLVLKA RKQKQFTSAKHLWVQRKGKG VEDHADWQGGQWVGVEGKSA EQQGLNLTGAFNRSPENKVSFQ GPALNALEIDSSYLDPQALALP QGWQGLLPPLLTGTELVGSKLS VQIQKPPSPNIKNSRMTQVFHKN TSVTSLPFVDTKGKKNTVSFPHI SKKVLLKSSLLYQVSDGLDPE KAGERPGFSPKPVLERPRIVGKS TVAAEEENQAHNQMPASELKA SEIPFHPSIKTQDPKAEKSPKK QKVTLTAAEALKLFKNQLSPYE QSEILGYPELWFLGLEAKKLDL APEKFSKTSFDDEHGFYLVH DHIAIYRYEVLETIGKGSFGQVA KCLDHKNNELVALKIIRNKKRF HQQALMELKILEALRKKDKDN TYNVVHMKDFFYFRNHCITFE LLGINLYELMKNNNFQGFSLSI VRRFTLSVLKCLQMLSVKIIH CDLKPENIVLYQKGQASVKVID FGSSCYEHQKGHLPSRLRSAVT TTSMLNKVLRFSPEKLPHLQFE

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15985	46353	A	16076	28	1327	GYKMPVITLPDGSQRHYDHAV SPMDVALDIGPLAKPLVIRQ GAAGLMAKLVDA CDLIENDAQ LSIITAKDEEGLEIIRHSCAHLG HAIKQLWPHTKMAIGPVIDNGF YYDVLDRLTQEDVEALEKR MHELAEKNYDVIIKKVSWHEA RETfANRGESYTVSIVEENSAD DDKPGLYFHEEYVDMCRGPHV PNMRFCHEFKLMKTAGAYWR GDSNNKMLQRIYGTAWPDKKA LNAYLQRL EEA AKDRHKIGK QLDLYHMQEEAPGMVFWHND GWTIFRELVFVRSKLKEYQYQ EVKGPFMMDRVL WEKTGHWD NYKDAMFTTSSENREYCIKPM NCPGHVQIFNQGLKSYRDLPLR MAEFGSCHRNEPSGSLHGLMR VRGFTQDDAHIFCTEEQIRDEV NGCIRLVYDMYSTfGFEKIVV
15986	46354	A	16077	1692	1776	
15987	46355	C	16078	1	1341	
15988	46356	B	16079	83	373	
15989	46357	A	16080	2	64	
15990	46358	A	16081	1695	2293	EMISNPFIPSSILPLAKIRNIGIMA HIDAGKTTTTTERILYSGYTRSL GDVDDGDTVTDFMAQERERGI TIQSAAATFEWKGYRVNLIDTP GHVDFTLEVERCLRVLDGAVA VFDASAGVEAQTITVWRQADK HNIPRIVFLNKMDKTGASFKEYE VITISLQKSGITKLCFFCVLKL V SQERCQASKCNKIEGQRFNQ
15991	46359	A	16082	1	2901	
15992	46360	A	16083	1196	1740	FWLKAMPTIVTASPRWFSC/LR EIRSAASAIATAIQQAIRPSTV IATLLSNSHGNSSDSTSVMK AIINKLRILRGRSRPQRTRGPTPS SSANGTISQVNMVLKNGSPIEL PSPSCLCTNGSSVPSNTTSIAAT SKTLFANSKSDSRDHSAFTRER TLCPRAANSSSEPANHQHKKGE D
15993	46361	B	16084	49	398	
15994	46362	A	16085	378	566	
15995	46363	A	16086	1	2184	
15996	46364	B	16087	311	4963	
15997	46365	A	16088	12	335	
15998	46366	A	16089	1034	1400	

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15999	46367	A	16090	1767	2973	SGARRLAG*KPGNAVSAAPFY YARPV/SMISPMILIPC*CWKC/D PAAKRQFRERTAVRCVAQFVD VGKLIPFWGLCVGIYATNSAET FLHRVVQLLNDSEVHTLQDAIT IRDEDTATPSPADEVAYIQLSG GTTGTPKLIPR1HNDYYYSVRR SVEICQFTQQTRYLCAIPAAHN YAMSSPGSLGVFLAGGTVVLA ADPSATLCFPLIEKHQVNVTL VPPAVSLWLQALIEGESRAQLA SLKLLQVGGARLSATLAARIPA EIGCQLQQVFGMAEGLVNYTR LDDSAEKIIHTQGYPMCPDDEV WVADAEGNPLPQGEVGRMLMTR GPYTFRGYYKRSSVLGKGSDCS FGVFLPGLLPASSVRRDSNVSI RNVVSLINSSRWKSGFTWHDN VLQLDGSFPLT
16000	46368	A	16091	845	1920	YPMMRK/RLMKLWREAKALHS DPFEPWASHIEDADKAKSSKQA RGRGGFVRSWQEVNELIAASN VYTIKNYGPDRVAGFSPIPAMS MVSYASGARYLSLIGGTCLSFY DWYCDLPPASPQTWGEQTDVP ESADWYNSSYIIAWGSNVQPTR TPDAHFFTEVRYKGTKTVAVTP DYAEIAKLCDLWLAPKQGTDA AMALAMGHPPERESGRYRLIPV PASGYPPDPAPEWDQFPVHVEL CDTANGCPLPELASPAGYTSSIN RVSTCVSTLAKSYRSRVRVKR LRRRFNGGVHFRVVAVVIDQ HICRTAFTIIIWLQREFTEIEKTAT SPLEAFKRPQNSLVVNALFRSN RNAAAAFSAL
16001	46369	A	16092	1	209	VSFMIIAALMMMGIDTGWLLV AAGFVGAI/IAS/ARPGNRSKRL IALISAIGMSIFLQNYVSLTEGSR DVA
16002	46370	A	16093	194	657	CLDHILRAVQSLRLPLSVPAAM RPGAAGYTMVYGIIGMIN/FAH GEVYMIGSYVSFMIIAALMMM GIDTGWLLVAAGFVGAI/IAS/ AYGWSIER/VAYRPVRNSKRLI ALISAIGMSIFLQNYVSLTEGSR GLATEMFLEKGDNGTEDGRAR
16003	46371	A	16094	1	3303	
16004	46372	A	16095	3	5071	
16005	46373	B	16096	144	326	

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16006	46374	A	16097	282	599	IPVSI SGCHLAGAGTQTASGV P VHPHGH LAHQRSFIGNTKTEC WPISVPPHHW*A**TDIGAGSG DDQRVLDVW\WNWRTKE*P*W W*PTNGLCRKVANRQAAR
16007	46375	B	16098	1	276	
16008	46376	A	16099	812	1084	
16009	46377	C	16100	1	1608	
16010	46378	A	16101	173	504	SADSKPVLPRTSASLVSASCSTR CGLRQASMESNNLTMTVFGFSIG K VWMRS*NSATSLAKSRISFGT RRRWHSCTSN/SNTRRAMTMM TRPEFWRRQPCGLSIAAIESVIK V
16011	46379	A	16102	1	816	
16012	46380	A	16103	742	1182	PAFIECSKAQENNHKGNCYQSG SLVSR*AFLIRHTRPVITNARR*F *RKVFHQRHGIAGTGSWRGFPL NLH*RQTVVAFQSRRAIHPM*S GKGREWHHFVGAADIKFIDIF WQHTEFGIRLNTRRAMTMMTR PEFWRRQPTEIVA
16013	46381	A	16104	550	884	KRYGMAASFHSGEITTHRTAP WRMVVMSPARSMADLAQTA WRG/APRPLPDLATMTMPQAY/ NSIQYDAEKLWHNVE/NRQOLD AQFFHMGMGFRRLTLWAGITN AQCGWTA

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16014	46382	A	16105	2363	2856	MLTLWSSPTTTRRWRWAASSV ANTLA*MTLSMAAMLSPQVDV RFATLCHDLGKGLTPPELWPRH HGHGPAGVKLVEQLCQRLRVP NEIRDLARLVAEFHDLIHTFPM LNPKTIVKLFDSIDAWRKPQRV EQLALTSEADVRGRTGFESADY PQGRWLREAWAQAQSVPTKAV VEAGFKGVEIREELTRRRIAA SDTIPQLNEHDHRRRHNAKIN GERDQRNALNQLQEGFNRYQR HHKSGDQPNKGHRDIAACQEA PALVEIERRCAHHHRHQQERK SEQHAARFGIANGDLVRVWNK RGQILTGA VVTDGIKKGVVCV HEGAWPDLENGLCKNGSANVL TADIPSSQLANACAGNSALVYI EKYTGNA PKLTA FDQPAVQAN TRPLRLARNQHRAFRCRITFHR FTRJMWVEIQRFNGNHPFGRV RIQDSLVCVCGALRYISATFNVV RKRAVTCVRSFGSDFTGSPPLR APKGESIRLLALREAGIIHILAL GEDYKMEINESRTVLKTEDNSY SFDVFIDARGORPLKVKDIPFP LREQLQKTGDEIPDVGEDYTLQ QPEDIRGRVAFGALPWLMDHQ PFVQGLTACAEIAAACGPFDDK RIEGGIVVRMAKEGETLVLLDG TEAKLNADTLVIADHNKALAM GGIFGGEHSGVNDETQNVLLEC AFFSPLSITGRARRHGLHTDAS
16015	46383	A	16106	390	636	KFLSFRPDRVCVACAEERAGL CLRQCITGHPEACLAIPVLVCVE CWGGTDADQPVA VFPSRSQV SPDRGT*QWLCWKFL
16016	46384	B	16107	1	520	
16017	46385	A	16108	142	243	
16018	46386	B	16109	275	919	
16019	46387	A	16110	1	693	
16020	46388	A	16111	522	714	

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16021	46389	A	16112	1	900	STCSSRSHLHLIQASPILPNYVA TAAVAARIADVQGISDTCVIAQP SPPHPGALRTLVTFTDEPETPQP PGAAGFQLVQKKQVQLHNVLY VMTPHAFAGQTVITIYLPGEQQT LSVAPLKNVVQLVTQGHRLDR LWWPGAFLLDFAAKVKALKD/ YPNHVMAQRASGEAEADDDV AATIKSVRQQLNLNITGRPLV KLDPDFVRVDENSNPPLVGDT LYTVQRPGTEQGSFKVKRARA RVQRTRAPLFGPKSPAPEHMES ELEFELIGPSKSTSGNPRGLRSE RPVLFCLYPEMPTAAAAR
16022	46390	A	16113	150	649	NALLGTCPGTARFFGTGSAPTL HPDASRSGRGRACPRSAQWS PRPWQSVAGLAWLGAHWGSR STSRTAETTASRKGHPRSPAQA LPPGPRPPRAPQLQRALQSVHP LSRPRAPLA/EPKLTAACWAEA VKITTVRYSDSCSRLLTDLGKP VQSMMLLKDIRKVYNWQ
16023	46391	A	16114	153	740	THQLFLPHHQEISQTTWLSAA WPRHTCAHSLSPLOPPVPSRP HVPLPGPSKTSWSDGPRQLSLPG/ RPSERTPRR/CRSASGQPPHLGG EERLCLAAPSGRICHCEGDDES PLITPCHCTGSLFVHVHQAQLQQ WIKSSDTRCCELCKYEFIMETK LKPLRKWEKLQMTSSERRKIM CFSDIPRHCPRMCGLLVCAH
16024	46392	A	16115	1	1194	
16025	46393	A	16116	323	642	TGYARQKPVPAALGWWTNVSAS TAPPILPSITGSRSLAVIKWLTVS AGKLSALLCASCQKGG/VGEM ANGNGERNHKQIGDVTLPPO HYRKIYQPIAARSCIRCVCGS

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16026	46394	A	16117	1	1782	MAGIRSTLIKEKNMITYEATV VTIDDIHVHEVNLGKRGIVYIK TENKETPFTVVDIDGSPGNVKT LDEGLSLLSLVSVVMKLFYQ YEQRFGMRSTSLNVIGSNTIAI YTTTHRII.VEIFSLTLAQMNAA RWSPQVELTLLVYPFVSLFICT VAGLLNLTVMPEQYRYTLPV KAGEQRLGELTGAPCATLVA EIAERHAGPVVLIAPDMQNALR LHDEISKFTDQMVMNLADWET LPYDSFSLHQDNYLLVAFQPFY QLTDDAAVGVLIIVPNTLMQR VCPHSFLHGHALVMKKGQRLS RDALRTQLDSAGYRHVDQVME HGEYATRGALLDLFPMGSELPY RLAIGVNVAAQAEVLNLESGAK QVLQETFGYQQFRPGQEEIIDT VLSGRDCLVVMPTGGGKSLCY QIPALLNGLTVVVSPLISLMKD QVDQLQANGVAAAACLNSTQTR EQQLEVMTRPRIGDGTGALRK RVAQLAFKNQPMVMGNWAQS ILHGGVIASALDVAAGLVCVGS TLTRHETISEDELQRQYRGWGP LIFALICAQAGASVLLLLVACC VQAIKSPSPALNYTMKNSFILPV
16027	46395	A	16118	380	1431	TALLIRDMPPYVEAYPNENLTT VMPEQYRYTLPVKAGEQRLLG ELTGAACATLVAEIAERHAGPV VLIAPDMQNALRLHDEISQFTD QMVMNLADWETLPYDSFSPH QDISSRLSTLYQLPTIQGGVLI VPVNTLMQRVCPHSFLHGHAL VMKKGQRLSRDALRTQLDRAR YRHVDQPAHAGGKVLLEMIVVG IATWLGFLLFGLNYSLLAVLV GFSVLPIYGAFVVTIPVVGVAL FQFGAGTEFWSCFAVYLIQAL DGNLLVPVLFSEAVNLHPLHHR EQIGGNKMADRQCRKIVCATV RQLPEGGRGEMANGNGERNHK QIGDTVLKATGSKQGDGQNHG
16028	46396	A	16119	1	940	

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16029	46397	A	16120	114	1380	NRVHCRRCSSGGDTGVSHLKG NVKYRYELTDSVGVMA SLGFA ASKKSSTVMTGEDTFHYESLRG RYVSVMAGPVLQISKQVSAYA MAGVAHSRWSGSTMDYRKTEI TPGYMKETTARDESAMRHST VAWSAGIQINPAASVVVDIAVE GSGSGDWRTDGFIVGISGVLKD GTGKPVQNCITQLKARRNSTTV VVNTVGSENPDAGRYSM DVE YGQYSVILQVDGFPPSHAGTIT VYEDSQPGTLNDFLCAMTEDD ARPEVLRLLELMVVEEVARNAS VVAQSTADAKKSAGDASASAA QVAALVTDATDSARAASTSAG QAASSAQEASSGAEEASAKAT EAEKSAAAESSKNAAATSAG AAKTSETNAAASQQAATSAST AATKASEAATSARDAVASKEA AKSSETNASSSADYAAAS
16030	46398	A	16121	165	299	GILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW
16031	46399	A	16122	1	388	MGSKSWVTQKGPAPAKSSQV GRVKQATATDTGRTRDSHMER PKCSKGYLCLPYMALQQHHLL SDVTVRGFGVAGATNILFRQQKH LSDAIVEVRLCGSDLVLYGTST PKNLIWVMHVVGHRPDRR*C CCNA/SVRQTQISLRAFGSFHM AVSGSSSVSGCSLFHSAHLTAL CFSWPLLCYPTLGP
16032	46400	A	16123	130	414	
16033	46401	A	16124	1	387	
16034	46402	C	16125	1	1611	
16035	46403	A	16126	318	401	
16036	46404	A	16127	519	658	YPGSLLASKGTKLDGE*V*RS RLQKVGNNKLLQAKGACSNPT QES

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16037	46405	A	16128	1	1837	FRPRLVAAKPSVFADVQSMES VGTGGGAAEAGGVRSRGLCPT RMLPGLAAAAHRCSSWSSLCR LRLRCRAAACNPSPDRQEWQNL VTFGSPSNVVPCTHPYIGTSLQ EKLYSTNVHKEGQGSHTLREE KVPSFVTAEGVGAKLISPLKQE PLQVRVKAVLKKREYGSKYTQ NNFITGVRAINEFCLKSSDLEQL RKIRRRSPHQDTESFTVYLRSD VDAKSLEVWGSPEALAREKKL RKDAIEYRERLFRNQKILREY RDFLGNTKPSRTASVFFKGGP KVVMVAJICINGLNCFFKFLAWI YTGASMFSEAIHLSDDTCNQG LLALGISKSVQTPDPSPHYGFSN MRYISLISGVGIFMMGAGLSW YHGVMLLHPQIESLLWAYCI LAGSLVSEGATLLVAVNELRRN ARAKGMSFYKYVMESRDPSTN VILLEDTA AVLGVIIAATCMGL TSITGNPLYDSLGLGVGTLLG MVSFLIYTNTAALLGRSIQPEQ VQRLTELENDPSVRAIHVDVKA TDLGLGKVRFKAEVDFDGRVV TRSYLEKQDFDOMLQEIQEVKT PEELETFMLKHGENIIDLGAEV DRLEKELKKRNPEVRHVHVDLEIL
16038	46406	B	16129	1	1065	
16039	46407	A	16130	1248	1658	PLALPEFISKSWKERLTDTTTLF LKARRQSLCLQIGDPLES/ILQ AFCVLSVAKESQLYTYLHAIMR TLKSSIARGARTFQSTSDGTVKS RPSKIIFLPRLHDFRFSALRHL DPKKLDLGDGSRSAIRPDRRF
16040	46408	B	16131	969	1026	
16041	46409	A	16132	339	432	RYMVLSEFRSMQTGITKWKERI L*NCRKRE
16042	46410	A	16133	3	443	HTWNSDRMTMYLQRRHIFKNC FWLQAGYSLGAPSWRSLVTWV QIIFSDFYRKTLCSNSPLF*SLC QRQSTLLGTLIFCSYASSPEAI NSAAPRVRSRPTDPKARSPRG VGGAEGNGSRDTEPKGGRPLA TPSQGERLMAGVTVK
16043	46411	B	16134	34	1426	
16044	46412	C	16135	62	217	

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16045	46413	A	16136	1	609	MIPVSEKSKIGQLNMLKGKKT KGKKVALVPAAVKKQEAKKV VNLLEKFRPNVIG/QDIQPKR DLHFRVFWPRYIRLQQQTAIL D/QFIQALDQQTATQLLKLAK YRPETKQKNKQRLA/RAEKKA ASKGDI PNKRPPVLQAGVKT VTVNLVENKKAQLVVIADHDVDP VELVVFLPVLHCKMGVPYCIH GKARLGHVLRKT
16046	46414	A	16137	1	824	GTRPKMPKGGKAKGKKVAPAP AVVKKQEAKKVNPVFEKRIPK NFGIGQDIQPKRDLTRFVKWPR YIRLQQRQRAILYKRLKVPAINQ FTQALDRQTATQLLKLAKHYR PETKQEKQR/LARAEKKA WPKGTFTPKRPPVLRAGVNTV TTLVENKKAQLVVIADHDVDP IELVVFLPALCRKMGVPYCIH GKASLGRVLRKTCTTVAFTQVNS EDKGALAKLVEAIRSNYNARY DEIRRHWWGNGVLGPKSVARIA KLEKAKAKDLATKLG
16047	46415	A	16138	1	799	
16048	46416	A	16139	1	344	MHQTTAKTPHTSYPNNYEEHN RRANRSKNYDRIRHTTILKRTN PAQTITNLLKSRFNRYNYVQPR SCRSIFIHIPGERDLNLCIAPNP AIFPTSIGYLGPDNLNLPYAPFI TTNLTGPAPTTHPVGNLGTG NPEPGGCILIVWCCVNWACL WDSVVAAPREPYMPAGLLRHR RHYRHRREDLIAVPAARQTDE NRRPALCHEYAVGHRKIKNV EHTEPYILPLITHSQPLNRGAFF CPGVRFVVSVDLDFEKRLAFAS *SCGVQLRIRGKVQGVGFRPFV WQLAQQLNLHGDVCNDGDGV EVRLAYRYLVGQPQHYPRGRP
16049	46417	B	16140	1	1323	
16050	46418	A	16141	1	1356	
16051	46419	A	16142	1	1524	

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16052	46420	A	16143	173	2310	QQWASRTRRWRSLLTLCVDA RSQHDYIALSRLFHTVMLFDVP VMTRLMESEARRFIALVDEFYE RHVKLVVSAEVLVEIYQGDRL KFEFQRCLSRQLQEMQSEYLKR EHLAAKPTVKRDWYVVDAT GKTLGRLATELARRLRGKHKA EYTPHVDTDGYHVLNADKVAV TGNKRTDKVYYHHTGHIGGIK QATFEEMIARRPERVIDNRRGS LRQAGYAIHDGGNSMAKNST CGVQLRIRGKVQGVGRPFVW QLAQQLNLHGDVCNDGDGVE VRLREDPETFLVQLYQHCPPLA RIDSVEREPFIWSQLPTEFTIRQS TGGTMNTQIVPDAATCPACLA MNTPGERRYRYPFINCTHCGPR FTIIRAMPYDRPFTVMAAFPLCP ACDKEYRDLDRRFHAQPVAC PEGPHLEWVSHGEHAEQEA LQAAIAQLKMGKIVAIKIGGG HLACDARNNAVATLRARKHR PAKPLAVMLPVADGLPDAARQ LLTTPA/APVIVLVDKKYVPELC DDIAPDLNEVGVMPLPANPLQH LLQLQLQCPLVMTSGNLGSKPP AISNEQALADLQGIADGLIHN RDIVQRMDSDSVRESGEMLR SRGYVPDALALPPGFKNVPPVL CLGADLKNFTCLVRGEQAVLS QHLGELSDDGVMQMQWGQRLC RMGTQVLPPFTFNIKKVQSARY
16053	46421	C	16144	1	184	
16054	46422	A	16145	85	416	
16055	46423	A	16146	96	570	

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16056	46424	A	16147	2	1690	CCCCPCCPCWGRVSGSVAGG PRQGLGLPLSLCISPGSLNKDPS YSLQVQRQVPVP/EGLCVIVSC NLSYPRDGWDESTAAYGYWFK GWTSPKTGAPVATNNQSREVE MSTRDRFQLTGDPGKGSCLVI RDAQREDEAWYFFRVERGSPL TQKPDVYIPETLEPGQPVTVICV FNWAFKKCAPSFSWTGAALSP RRTRPSTSHFVLSFTSPQDHD TDLTCHVDFSRKGVSAQRTVR LRVASLELQGNVIYLEVQKGQF LRLCAADSQPPATLSWVLQD RVLSSHPWGPRTLGLRLRGVR AGDSGRYTCRAENRLGSQQQA LDLSVQYPPENLRVMVSQLNR TVLENLNGTSLPVLEGQSLRL VCVTHSSPPARLSWTRWGQTV GPSQSDPGVLELPPIQMEHEGE FTCHAQHPLGSGQHVLSLSVH/S PSTAAGPLLLGG*GSAQLLL/ SRPARPPLCAGGLGRSCWRGTA VRAPSRPPAQPGPPTAP*AS MEGSA PASGSAVRPGTSTGPRV ALSSSCYQGSWSMGEDLA WGL PWELASLPCSLSPALSSSG
16057	46425	A	16148	3	1578	VTQLLCTSNRRALFALFPGR RFRPVATNHQSREVEVMSTRGRF QLTGDPKAGNCSLVIRDAQMQ DESQYFFRVERGSYVRYNFMN DGFFLKVTGMWGGNPNCLSH WGGTLGTAYGLSREGSQGPLQ HKNN/HPTTVSVPALTQKPDVYIP ETLEPGQPVTVICVFNWAFEEC PPPSFSWTGAALSSQGTKPTTS HFSVLSFTPRPDHNTDLTCHV DFSRRKGVSVQRTVRLRVAYAP RDLVISISRDNTPALEPQPQGNV PYLASPK/GQFLRLCAADSQPP ATLSWVLQNRVLSSSHWPGRPP LGLELPGVKAGDSGRYTCRAE NRLGSQLRALDLSVQNPPENLR VMVSQLNRVLENLNGTSLP VLEGQSLCLVCVTHRPQPSQAE LDPEGTGSEPLALRPRGSSWSW LVGSSGARRRVHLRPSAFTGAP RRTLLSPCTTPRSCWAPPAPGR LRVCTAAAPPRPARPPLCAGGL GRSCWRGTAAQGLLRGSPPAQ PGPWAQTASPEPSMEGLNSGPQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
16058	46426	A	16149	90	1029	MLLPILLSLLGGSQAMDGRF WIRVQESVMVPEGLCISVPCSF YPRQDWTGSTPAYGYWFKAVT ETTKGASIVAPNPPSREVEMST RGRFQLTGDPKAGNCSLVIRDV QMQDESQYFFRVERGSYVRYN FMNDRVLKVTALTQKPDVYI PETLEPGQPVTVICVFNWAFEE CPTPSFSWTGAALSSQGTKPTTS HFSVLSFTPRQDHTDLTCHV DFSRKGVSARTRVLRVAYPP ETFGISIFTVTNTPDPDENLRVM VSQANRTVLENLNGTSLPVLE GQSLCLVCVTHSSPPARLSWTQ RGQVLS
16059	46427	A	16150	270	1001	CCCTVYRAFIRKRLKRSSDSVY RRKNPSASYDRDAESLAAYK SGEVDLHQLASTWAKAYAETT LEHARPEEPSWDEDFADVYHD LIHSPASETLLNLEHNYFVSISEL IGERDVELKKLRERQGIEMEKV MQELGKSLTDQDVNSLAAQHF ESQQDLENKWSNELKQSTAIQK QEYQEWVVKLHQDLKNPNSS LSEIHKVQPSQFRESVEAIGRIYE EQRKLEESFTIHL*AQLKTMHN
16060	46428	A	16151	60	648	LAMSLSHLYRDGEGRIDDDDD ERENFEITDWDLQNEFNPNRQR HWQTKEEKGSLQRKEFFTDLV GLCFCAIRARDYSAPVNFISAG LKKGAEEEELESDGFLRFFFI LFFH*LSFDFSLQGGNFKPSQK GFAGGTGKSFMDFGSWERHTKG I*FTYMNCCKRKTLLFFC*NSSG IINPIEAKQRKGKGAVGAYG
16061	46429	A	16152	237	450	LAMSLSHLYRDGEGRIDDDDD E/REENFEITDWDLQNEFNPNR QRHWWQTKKEESTYGVWAERDS DDERPSFGG
16062	46430	A	16153	12	85	VSFLSMGSGHCIRSTRGSKMVS WSVIAKIQEIWCEEDERKMARE FLAEFMSTYVMMNIHMIVEKN T*SPFCPPWARATVSGPPVAPKW SPGP
16063	46431	A	16154	49	481	
16064	46432	A	16155	20	248	
16065	46433	A	16156	493	728	VSFLSMSSGHCIRSTRGSKMVS WSVIAKIQEI*CEEDERKMAREF LAEFMSTYVMMVSGRAARSG WALPGSMTSPSPF

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16066	46434	A	16157	136	306	ASSSREGLTAKFAKFTKFKIHQI *ITLTSYSIKSLEKVCADLIRGTK EKNLKVKGVP
16067	46435	A	16158	563	1216	MMFWPELQPRVCWMGLSWVN HQNGRRRRRNQKHH*QKVPLL IMASK*KLLEFLNRETKASANL SETVTKPPLPQKNTAQVGASSQ TRKPNKLAPHPAPVAFVKNTCP SRPRERTHFLRPRPEDRMVAL KPIKIVLPPVFMPPSSPQGRSR MPTQHLRYCRWVAPKALVPTCL PTHLSRKEEKKRMDTPFLPY SRPPSGEWLLIVLWFFNRSQRS
16068	46436	A	16159	1	143	
16069	46437	A	16160	40	230	KQAAQPAVATLSGPLPHCGSFV LSLFAINLVAHSLGPHCLYEL* HSPRRSTASLREGPRLHS
16070	46438	C	16161	233	319	
16071	46439	A	16162	290	472	EFLDTFCYIPKVVDDQ*DTKQ QHNVAIIPHVSSAQMTFC*RT MPTISDDPWHMAMSMRAV
16072	46440	A	16163	3	553	
16073	46441	C	16164	270	608	
16074	46442	A	16165	2598	2943	HSPRGSAAFLKSVRPRTHQFR TQEDRLSPGIQDQPGQPSNTPSL QKL*N*LGVMGRCSPSYLS*P WREDHLSPPGG*GCSEP*LHHCT PAGVTKSDRVSKNK*INKNKIN NDNQ
16075	46443	A	16166	2	58	
16076	46444	A	16167	218	342	
16077	46445	A	16168	734	872	
16078	46446	A	16169	1233	1706	CLVFWLLYYPGQLPFHLLPHS LGSQQSSSEESAATPSLAEGRR EAAFRCPAGLARQAWRPHAR LPGAAPLAAPSLAPLTGRSG RWLPMCAASC*SPSPAMSVYP QRRLGQGGAEDEGGPVSRGC RAPGPQRPLAAPGEQTAAATQ AICLIW
16079	46447	A	16170	598	1159	CRQTGKVIYDVWFFWLLYYPG LQLPFHLLPHSLGSGQQSSSEESA ATPSLAEGRRREAAFRCPAGLA RQAWRPHARLPGAAPLAAPSL APLPTGRSGRWLPMCAASC*S PSPAMSVYPQRRLGQGGAEDE EGGSVSRGCRAPGPQRPLAAPG EQTAARTQASVYLLPHSPPLL SALHIHLLPPS

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16080	46448	A	16171	834	1185	RSLFRHHRPSAAFPRTPCSDCPR CSAGTMEDCWLVLGSPELR*KS LHERPFHWLPSPSRARCCLPRSE TPAGVPVPPRPGPRRARRPRGTS RPPPASSRGRGALGSLPASEPLP ARAT
16081	46449	A	16172	78	478	VVKNSLIFLVNQVLNSRDFHVF FKTT*NCPAQAHAAALYQGLGP ACSQRAASHWSSSSKRSSKSLK KSA*TAFLAAKSIKSPGAASRL GNGKARLCQVRFPKEQVISALQ GHYPHKRRWVRGNRLKLEST F
16082	46450	C	16173	1323	1656	
16083	46451	A	16174	77	231	RSCMTLMWPRSTP*FGLMERR RHMFDWLLITMLWMLPTKLGS SKLSPAA*F*SSCLIL
16084	46452	A	16175	1	255	STSKGEKPAIRAMAHFLEPHPIN FLGARARKADLSPT*YHFFKHL DNFLQKGCFHNQQDAENAFQQ FFKSQSTNFYAGSSFVTEV
16085	46453	A	16176	690	1020	SPVLQRAFKNGPGTANERTVQ WWFKKLCKGDESELEEHS*G PSEIYNNQLRAIFKADPLTITRE EVFPHPLYSPDLSPSYHFFQHL DNFLQKGCFHYQQDAEHAFQE
16086	46454	A	16177	1	383	MHRSCGSDAYALLGERSVSLR RCAVRHAGGIRSANADISNDKA GEKPARRKTKGSCPTLIGAGLV QSLSPIQSAADAGELGSGILPD VESLRIPVQYLANLLTAGDTKP VLRALKRMLAMRHYKRAETV DGKVDTRALEEVGLTEAQAQE MYRYLAIANYEDRFVVPSSHRE LAREAFPEKNGCGFTFGDGCH GSDTKFNLFNRSRIDAID*PCPD *RWTGTLGLPASGLFTRFIVTY VSIRTSDTSSMPHSTPSQA/TERS PNNA*ASLQTC

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16087	46455	A	16178	740	1977	SASASRSLHEHITVTPSTGILTCFP STTPFGLAL/GGTGLGPASGLFT RFIVTKSSIFSVTPLVQPKPSCN GYSPPPPVPHRRERQRRVIAEK IFCQHHRAKLNRLEERQYLTVN FRAIAQRVNIGITGLQITIDANA AINRQPGASCQGRFPGAVRCGG NYRIHFIDIALAVQRWPECQNPF FPAPVTEISTADERPSPLTGCLQ RLVTFGSVIFGHINMIMRLAPIGR FGAMAFITGKYGVGTLLVQLGQ LIICFYITCILFVVVLVLSIAKAT GFSIFKFIRYIRELLIVLGTSSSE SALRRMLDKMEKLGCRKSVVG LVIPITGYSFNLGTSIYLTMAA VFIAQATNSQMDIVHPITLLIVL LLSSKGAAGVTGSGFSVLAATL SAGGPIAGSGSGADPRYSTALC
16088	46456	A	16179	757	1037	FLDPSPPEPNVTVTPSTGILTCFPS TTPFGLALGVDSPCPD*RTWTGT LGLPASGLFTRFIVTVGVTPALD TGLM*LRSCGPPRSML*HRTQQ KC
16089	46457	C	16180	1	313	
16090	46458	A	16181	178	290	LLGLASEN*HCPASEAP*TIT DTELWVTLTVEGKS
16091	46459	A	16182	1	251	
16092	46460	C	16183	129	1136	
16093	46461	C	16184	117	364	
16094	46462	A	16185	636	748	LLGLAAED*RCPIASEAPQTIT DTELWVTLTVEGKS
16095	46463	A	16186	37	444	DPQVGKLLQHCAPARIKMTVTF NNHRKPOLSKFHLQYSEDQQ QHIRETFHLVFKRDENVCKFLGT IWSLTGKLNRGQAPLFGIFHT VELHLEIRSSCQGVHF*LTCSFS CPCSGPFVNSPFYLPESGHSK
16096	46464	A	16187	179	422	LQLGPKEKQSRVLGSFFQVPSC GKMGCGSSGSRHGFPP*PQLSG GPLDPRQSGSGISEMK*TE*GGY PKGSPQHYSRKHQGS
16097	46465	A	16188	1064	1374	KEQCLQALSSVKNREKRPSSFH PICWSAVSVSGREGDMWPLAP FPDSEN VAGAGALLRLAALPG LSWALRPPPPAPVRSWATSGW* GGQGREPGRIIPRW

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16098	46466	A	16189	44	515	VGGGGVQPSMTMGDKKSPTRP KRQAKPAADGFWDCSVCTFR NSAEAFKCSICDVRKGTSTRKP RINSQLVAQQVAQQYATPPPK KEKKEKVEKAGQKRKPEKRPR KFSP/SVVTKKNTNKKTKPKSDI LKDPPSEANSIQSANATTKTSE TNHTSR
16099	46467	A	16190	382	795	DSGRSWKRLSPPRPMCDTWA LGSYPRLCFVSPFSCSLPLPSL FPHSPLGRPKRQAKPAADGFW WDCSVCTFRNSAEAFKCSICDV RKGSTSTRYLKICVTWVVVI*Q VFIEHTAICALGVQWYKDRPGP CSYGA
16100	46468	A	16191	2	343	
16101	46469	A	16192	472	625	KTSLFQHWLWKVTIVIVMF**L RVNVGKLLNNHRYNSENASL GSQWKFP
16102	46470	A	16193	343	693	KTSLFQHWLWKVTIVIVMF**L RVNVGKLLNNHRYNSENASL GSTQIPLKAFNPCHTSFTLCKH MVIQAHEKQLIQILYLGDL ET*HFQAFWQALDENMTLLESI TGFEFG
16103	46471	A	16194	340	534	TAIMNDMVTI*TRKFMNTQRLQ RKQMVIDVLHPGKATVPYLILI EQLRFARHCAWYGGDSDETSH
16104	46472	A	16195	80	552	PIPHLEKFHAPTRTRFRGNQMIV IDVLSPPGKADQCP*AQEIPGKT *PKMYQDPHPDVIVFVWIPELH FGSRGKTKLAFGNDFMSTLGF AKEKWNPKHRTLQGHGPGME/ ERKKTSGKPTERERQGTGLEG KFQGGGLAKGPPFGAWAKRRNE VSSS
16105	46473	A	16196	248	474	YPETPESPTQLSSGQPHREQPPE MPESPTQSSGQSCQEPPETPE LPM*PCLAQPSQKHMIG*QNN KHHENKM
16106	46474	A	16197	223	669	PRPSLPACSPWRIVDDCGSLKS WKRVCQWLQCPNALPCLGSL PLRCEFSGFPRN*LGLGSTTGSF AVWGGFLFSTIDCGLVRRPGPSP FHPVLPALTSVSLPPTPPGGPLA MVGSAAMGGWSGEWEILHLA SSTHPYPSLSPAPPFLE

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16107	46475	A	16202	188	484	HFGRVEVGRSQGEFQTRLAN KAKHHLYSFMNESQISPIGC*P M/PPKLIRKVHREKNCAGRNL T/RQSRGFKTGPPPPARSSPTLP PPPLPRLPRRP
16108	46476	A	16203	36	409	
16109	46477	A	16204	651	893	NTSVKNNFSFMNESQISPIGC*P MAPKLIRKVHREKNCAGRNL T/RAEKRLQTPGLPVPPARPSSPSS PPTPLPAATPGGR
16110	46478	B	16205	13	441	
16111	46479	A	16206	3	205	NSSNSFSIQFCSFAGEELCSFPGG EEAFWFLEFSAFLRCFFLIFRDL STFGL*CAPLEEKRHSGWFNFQ PFCAAFSSSSGIYLPVFDAGDL QMGLCGCPFC
16112	46480	A	16207	23	841	EKAKEFRRAEEKKEVPVAPET LKKRRNF AELKIKRLRKKFAQ KMLRKARRKLIYEKAKH\YHK EYRQMYRTEIRMA\RMARKA\ GNFYVPA\EPKLA\FVIRIQRV S/MGVSPKGSERCCLLRPFVKIF NGNLL*KLNGFRLTML\RV\IE PYIGMGGTPIKSVNELIYKR\G YGKIH\RKRIA\LTDYAL\IARSLG KYGIVCMEELNHEIYTVGKRFK EANNFLWPFKLSSP\QGG\MKK KTHFVEGGDAGNREDQINRL HRRNELTRLTWIFF
16113	46481	A	16208	1137	1200	PPSAPAPG*LRPPALSSGSP*PPS APAPG*HAPPPSAGTPPP

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16114	46482	A	16209	1	1480	MNECRGVEITVCSSEDWIQRHL PGAVVPLKGEENVGVATEDHY QEDSFGLRGTGKPLKLEKSR PGAVTHTSPSDGLTQYVPDSL.T AMPAAA VVIWVIRPGCGVQQQ IGFLRHSNIDDIRPTIIRAVAPV KLHGIRIKMASFTSATRLTDEQ VITAPADSGIVIPFSDNWWAG GKTHLTHKDSHKLKVKGWKK AFHANGHQKQAGVAILTSDKT NFKATAVKKDKEGHYIMVKGL DQENITILNIYAPNTGAPKFM KQLLIDVRNEIDSNTHIAGDFNT PLTALDRSSIQVKNKETMDLNY TLEQMDLKD IYRTLHPTTAEYT IYSTVHGTFSKIDYMTGHKTSL NKFKKSEIHSSSLSDHSGIKLEID SKRNHQNHANTWKLNNLFLNN RWVNNIEIKMEIIQLFELNNND TTYQNLWDTAKVVLRGKFIAL NAYIKKTERAKKTIYHTSGI*K QEQT KPKPSRRKEIIRAELEI TTKKTIQKK
16115	46483	A	16210	32	398	ASERLGGPGSPG*/PVNPRTDGS GAAWLSQRAQCTQSDPRV*EV PEHLSPSTPSQEYRGLPAL\PHTS RPSHCLPACPLPSRTQPVWVPK PGPTACRGFLQHSPTPGSP*S FQGSWWDIDL
16116	46484	A	16211	2	681	AEPWDEGGDVPCRVPSGSGV* V*TLYLDSSVQLCGTEAPQHPV DGPPGGKLCHEGSLHLRQGGIP GPRLVLQFVQQA GVC GPGGNA VYSTPRDSASLVSGRTSMLFLR KFGKTWRKGLHQRGPPASPV LGRECNWG*VIGRIHPAQSS/SGP ACAKDAAEALGAAMPGLVSGPL GAALQPRGAGVQLGAATGPGS CSK/RGSPKADAR/PRHSQEPGQ VPPHAPQGPGLS

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16117	46485	A	16212	102	1005	VQWSARPDATPLSTEPSLADYP EAQSHIPRRGPRRPEKQGRGGK PPRALGRERAGGSRGPPASPD PLSRPCSQAPPPGASAGA*DAP ACRREAGSDGVPCRVPSGVS* V*TLVLDSVQLCGTEAPQHVP DGPPGGKLCHEGSLHLRQGGIP GPRLVLQFVQQAGVCGPGGTD GSGAAWLSQRAQCTQSDPRV* EVPEHLQPVDTHKELYQ*PGG RDGPGWEEPPQCGMGVSEAHG GAGGPGEGAGKRLQRKFGKT WRKGLHQRGPPASPVLRGRPR PE*VLLRCD*EG*PPSAGQLL
16118	46486	A	16213	378	494	GTACLIQIPOTQGV*QRGFLAEY IQWQLRMRSISIPVRTG
16119	46487	A	16214	18	894	SVGSLCCLQETPGLRAFGVPWR SAQRRWPRRASAALLSLVLPGR AHSRPTLAPGLEAQPPPPGG SALAQHSRTAPAGTSAACLWP VSEQGAAPMCQVTRPPGSQAP CSQPSAAHAKHLTTGSSSPA SALPRA*TGSRWETKSSERVS SA*GTACLIQIPQTLRRRTG* VGRRLPGSGGDFGCSIFS* PV TYSLSVSATSSNEATQLGTT* NSIIFECASQASTAVRCRLFT* T DAPWSRSSSTTKTCSITASC S VLPLLEALMEAPCPCLACSSA S
16120	46488	A	16215	340	582	
16121	46489	B	16216	93	711	
16122	46490	A	16217	1378	2081	LSRKKPNWPSMPWYQFSLIWL MSVKTSPSWKPSWFWGWSK YSTLQLGWSRGGMLLGVQM DLLEDWKGDAAIIGTVVQKG PPLDCSGSPRSKAPRTWAYTPA WGVRKLPASCA*ASLPA RPGSA WPASGRSAAPP/AARS*LICS M SVSRRLCMLVSA TSLESSNFSSA WRSSSGILPCRFSMSRESFTSA RCFMDSPASSASLKLDSLPS SF WWIRIRHSRSPSDCG
16123	46491	A	16218	191	288	
16124	46492	A	16219	67	209	
16125	46493	A	16220	96	341	
16126	46494	B	16221	1	1185	

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16127	46495	A	16222	192	703	AMPSCSTRAGLAFVCHVRRRCGLSCRGVIPASSQCLFPAPMGTTATLRMENV DVKEEWQD*DLPRPLPEETGVVELLGSPVEDTSSTSN TLNFNGAHRKRKTLVAPEINISLDHSEGLLFDDFLDTLDDLDIN VDDIETPDETDSLEFLGNGNEL EWEDDTPVATAKNMP
16128	46496	A	16223	8084	8251	TAGDERHGPSVRMFRIKGRRLGWMGPLGRGKR*VTRGMWPG KGPAYPGSSASSF
16129	46497	A	16224	645	1317	WGASRLREPPSPRTLHSPRPGP ASAPPLRPLPQNRTPSPSA STT APPQPSEASRLPA*KAKPKPHPP SAPRRGGSPPRHSAQPA CGRRR PRSVGGAAPYAAERRNSAPQGP PQLRLRTAEGGKRSPNPRQRSH PRQRGDSL*LGWVSRDRRAGR DGRDGSAGGTRSPSPRYASPE PLGPAAPASPA GASWTGGPGRR ADDSWRASVFQAQSSACFPRA RVL
16130	46498	B	16225	72	378	
16131	46499	A	16226	151	372	GGQHWAKAWRQTLGPMPER TGACGCGSL*PFTTPPPAICVD GTFHKYVFTPDGNCNREADFV YLDICDDDDF
16132	46500	A	16227	182	1083	HPGPCPDHEQVSGMGLVEDPV SPGLPLTLNLGPDNPPTCPA VLI WDDAREGKD*EG*SSLGIPPP HGHPVLCDTHRIVIVLKNRQLC PF*DAASSAAHPTPHLHTLGL CELPCGLLAPSLHTTPTSDSLL PQDLASTKPGTSSAPFTINAHQS DIACVSLNPGQTVVASASQKGT LIRRVCMVGW*PHTT*HVGITA DLSSINFSDSSFLFPTLPCPCP PAHLPLYGLASACRLARVGK VGPIMIGYYVDSQWLSAFTTEM PERTGACGCGSL*PFTTPPPAI CVDGTFHKYVF
16133	46501	A	16228	202	517	GVHCHGFSAGQAAGQEPTSVH ETLLPHQLQDQSALRGGVQNR QRHQA AEGPGERAGAAVS VGL GEPQCH*VGAGRAARGPPILEV PAGGADAAAECPAGPHGCGG

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16134	46502	A	16229	141	633	WENARPEPSQGDRLRAASVVSPPR LPPrKGQGGGLGYFGRGAGHAH GTAGQGASESETLLPHQLQDQC ALRGGVQNRQRHQA AEGPGER AGAAVSVGLGEPQCH*VGAGR AARGPPIL.EVPAGGGDAAAECP AGPHGQNRGQQSGISQLRHE REFLLRPFPQAPQL
16135	46503	A	16230	65	466	VVFAEAAEASLMTSGVGGGAA QSPRRRGWWPLGEMPYANQ PTVRITELTDENVKFIIENTDLA* GYRGKRLAALGRGRPKPGPRG RGRGCSGWWGGDVLPELPPCT RALALGACGAGPACRGCSAFTP LGF
16136	46504	A	16231	42	491	SGGKEAQGGSGTDQTVVVLNS PTYYSNDIPYTFHQDNNFLYL CGFQEPDSILVLQSLPGKQLPSH KAILFVPRRDPSELWDGPRSG TDGAIALTGVEAYTLEEFQHL LPKMKGNKWEQKSHYKPDWD *NLSCLFRQVLNFVIVAPP
16137	46505	A	16232	531	976	NQSVIRVNVNDSLIPVIAAELG VRKPSEKGMQKKTKDLGFR AGKESKTEWRK*GLQDMASQ MFASPLK*PVTAAFHDSMPSS LLQIFMEQLFLEARLQLDSKSE ARRNQCDMLLRNQLCSTCQ EMKMVQPRTMKIPDDPKAS
16138	46506	A	16233	2	419	SFLLSSSYTRTKSILRWPSLKKR ESGFPLNSSNSGVRKSC*LSSDP KSGTIVCPRFSTISPSSSSSSI CSKTFLPSFSLPQKAAPNLAR SWGLPGSRTARLSQGPDRGPRG VCLRGSGAAEPSQRRGKPSRDE IV
16139	46507	A	16234	27	792	INSIRILSTCKMGHPRFAPQAPG PLRTSEKGPVLPWAGNSSSDH SSEPSVGFYFNEDSDGSHPLVQ MRACSPDPAQGARPSAEAPGP *HSASRGSDPKVASEWRLPHAE ASPLPGLPGSGAASPAPKHSCTSF SCLPQKAAPNLARSWGLPGSRT ARLSQGPDRGPRGVCLRGSGA AEPSQRRGKPSRGTHRPEPRAG GRLSPAERSPETEHAQCGRRG LRND*TSPLVRGAQKEVGRRD CRGSSAILRAGEL

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16140	46508	A	16235	343	969	YDKTRLFNVTPLPPPHKKIKKII QDIKGEILRAFPLRTGTGKHCRCPL SPLLFNILLEVLARAIQKEIKS IQIGKEEVKLSL.FADDIIILYESP KYSSRKLQELIKEFSKVSRYEIN VHKSVALLYTNSQAENQIKKS TPFTIAAKNKIKYLGILYLT.KDAK DGYKENYKTLMEIIDDKNKQ KYIP*SWKGRINIVKTTILSTAIY
16141	46509	A	16236	15	403	ICESRRGRVCSALVRRYVGEFG GKAGSICMPQAPDKSSRWTLI RPPRFPPSPCSPGKEAPGGSEL /SPLPHAWPSDPVSPGLGDRVTA NPAEIR*EPGPQSAAPGFREQRR RGQMG*IWYLTPTPPGGQ
16142	46510	A	16237	19	454	KGKSLCTSPKVCRCRGLRKS PETKVTHICMPQAPDKTSRWTL LIRPPRFPPSPCSPGKEAPGG EL/SPLPHAWPSDPVSPGLGDRVT ANPAEIR*EPGPQSAAPGFREQRR RGQMG*IWYLTPTPPGGQRRPS SAASPRGFPLV
16143	46511	A	16238	276	898	MKGTA PWRCGSRGRVCSALV PKVCRGLRLKSRKPETKVTHIC MPQAPDKTSRWTLIRPPRFPPS SILQSWEGGTGWLRTPLPHA WPSDPVSPGLGDRVTANPAEIRIL GEDPESPEETLNILIRTPIPPKPR GNAKSHP/GGHRSHR*EPGPQS AAPGFREQRRRGQMG*IWYLT PTPPGGQRPSSAASPRGFPTTN SSRLPAEPE
16144	46512	B	16239	177	284	
16145	46513	A	16240	253	416	CCPVLPGPWAAGHPGD*PDGP G**AQPHKECRGGFAPLQVTLG PK.QPSGKRVNK
16146	46514	A	16241	1401	2246	NIYLLQVDFDCWGLQGLGVSN PSYSIRRCYTAGQSPRGLPDGPR F*G*EESTGEQADCP*GSHRRSR SAAGAADGGLDPGAHTITCGC LSHRGRLVPAQKSSAAL*APSG AKPAPTVAPVHDPARQG*GGQ ARGQGARGPHSHREGLCEC*A VTTL*EPHLRNSSAPA*ERGPGQ IRVPEGQSGDQESSAEHHGGD PGGGKPRCGHQEPLGAGWPS PAGVEPLLGLQKSGDAP**E PQRGCVDEAQSSPGAVPEAK AIAVQPPADPVFAAVARCD

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16147	46515	A	16242	30	461	IPAETTC/EPAKIHFCFTDGSN GKASYSGSKGKVFQTPYISAQK VELVAVIEVLTAFDMPINVISDS SYMVHSTQLIENALQRFHTDEQ LIHTKKGGNRDYGTAQTQLNL ALLTFHFSSLPKGQMLPAAEQH LQKPAAKTQAE
16148	46516	A	16243	1	573	
16149	46517	A	16244	1	1689	
16150	46518	A	16245	1	1416	
16151	46519	A	16246	27	779	KNHFNWKDKFPPLRISFLMVA TVKPPEPTPLKRLTEKPIWIEKW PLSK*KLEALEKLVTEQLENGHI APTFSPWNSPVFIKKKSGKWR MLTDLIAINSVIQPMGALQPPGL PSPAIIPKNWPLIVTDLKDCFFTI TLAQKQDCEWFTFIIPAVNNLQPAKHFCFTDGSNGKASYSGSK VKVFQTPYTSALTAELVAVIEV LTAFNMSINMISDSSYVVHSTQ LVENALQFQTDNDFIYPVA NSS
16152	46520	A	16247	2	394	
16153	46521	A	16248	63	1123	ELDVMGLPEERVSRSGSRGQE EAGAGGRARSWSPPPEVRLVSL LRLNMSQKINDIWASISVAEFW GDIAKEFYWKTPCPGPFRLRYNF DVTGKGIFIEWMKGATL*LCLF LVWGRSYTPNHWFLLVCLREG NEPGGQLDGREQVAARRVHGS YSVLLPAGIQKGDRAVAILSNPFL HSLNPWGFLLSRLSSL*GPM DIVPTRQHGAY*GLECLLLPKD MDMGGSCQVPFEPTRLPL*AFL FSRGFPVRCCIVVKHLALTLSH SLYTWTLQGGGTGVSCPHLELF TVLPCLSLQISWNQIDLWWHE LMQEAGDECEPLPSHLVVSRG GHKLTLCSPFPQGVVHTVGGY
16154	46522	A	16249	35	219	ALGVHFVLGPVGDGSRVDCG QQUPTSSACTTSGLSISRCSGI WRMNQKKQVRGSPSKE

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16155	46523	A	16250	1934	3213	WPAPPSQVPSLDYGLALWFDA YVSVHGTQETSQCSPESSLTPPR LCGLRILQPYAERIPV VATAGIT INFTLRGYAWPNGALPASTVPC GFAACPGFELCSVNGRQAPAGS SGFLPPVPSLCPHTVCRATFQCK EDSTCISLGRFPWGSETHLLCPA PIPSVPGVPCGTFTFQCEDRSCV KSLSASPLLLLCPPHLPPSPD CGLQGPSSRIVGGA VSSEGEWP WQASLQVRGRHILGRGSFLPPH LTPPHPTPPHPSMASTVLWTVF LGKVVQNSRWPGEVSFKVSRL LLHPYHEEDSHDYDVALQLD HPVVRSAAVRPVCLPARGRIEN RGSRLLRSHFCP*PRTGPI SNAL QKV DVQLIPQDLCEVYRSSPG KGGALTLLQSFLSPFGDSSG PLVCKALSGRWFLAGLVSWGL
16156	46524	A	16251	511	853	CCWNMALIQTFQMSMEIPLCTT LS*TAHLASANGNSGVVKLLL DRRCQLNVLNDNKKRTALT KAV QCQEDECALMLLEHGTDPNIPD EYGNTTLHYAIYNEDKLMAKA LLLYGADIESKNKVEEEMKKH ESNNVGLLENLSNGVTAGNGD DGLIPQRKSRTPENQQFPDNESE EYHSHTFELPSRIYP
16157	46525	A	16252	1050	1350	CDPQMCCCCRPEAATPG*REAA SAGPWD SAPPSPARTSLPSAHSS DYPLPRSRSSSAASRSPPRPL STIARRLNPRRSGRSLPSGQPAG PSDPRGFCL

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16158	46526	A	16253	2	3486	SSQSGAAAGAFCLGLCVDELTA SCDLEADSEDRTEHLATLQLRP DFSGSRCPAPQKHLQTHRPHSK PWPIY*PT*RSYLAIHPHSW*AP PPSRRRAPPAFHPTQACPSTCY CHTLASRRGPSNGRYHRPGYPH PTAVQRDPPAGPRGCQSPC*HQ PPACRRPCGRHYR*HGQHDPPP WQ*HC*SRSPCHPPSQORDAVTW PFIHIPAED/SHTQPKQSP/PAFRP HTKTCPTCYCHTFAGRRGPSD GRHHHLGYHHPASVQWDPAC *RGCWRCQREPQTCPCGGR/P PPGTSLA*PPHPRVPLKEKLCQY DEFSEGLRHSALNRHQVRPTG EKSVKSLERGRGVQRNTHIRNH PRAPVGDMPIYRCDVCGKGFRY KSVLLIHQGVHTGRRPYKCEEC GKAfGRSSNLLVHQVRVHTGEK PYKCECGKGFSSYSSVLQVHQ LHTGEKPYTCSECGKGCAKSA LHKHQHIIHPGEKPYSCGECGKG FSCSSHLSSHQKTHTERPYQC DKCGKGFHSNSYLQAHQVRVH MGQHLKYCNVCGKSFSSYSSGL LMHQRLHTGEKPYKCECGKSF GRSSDLHIIHQVRVHTGEKPYKCS ECGKGFRNSDLHSHQVRVHTG ERPYYCDVCGKGFIYSSDLLIH QRVHTGEKPYKCAECGKGFSY SSGLLIHQVRVHTGEKPYRCQEC GKGFRCTSSLHKHQVRVHTGKK
16159	46527	A	16254	333	695	ISVFRSPGQSTSQHDAATWPF HISGEGPTPSRRKAPPAFHPTQ ACPSTCYCHTLASRRGPCNGRY HRPVYPHTAMQORDPPAGPRG CQSPCWHYTPACRHPCGRHYR *HGQHDPPPWQ*HC*FGSPGQS TSQHDAVTWPFLLHIGERPTAS RRKAPPAFHPTQACPSACYCH TLASRRGPSNGRYHRPGYPHPT AVQRDPPAGPRGCQSPC*HEPP ACRHPCGRHYR*HGQHDPPPWW Q
16160	46528	A	16255	9	437	SCNMSLCRCNCVIRAAFKEGTP ALLVYSAILSFPTVSLAKSCSISI AIVSNILSWLDPFKRGVVSLSLR LPSRVLL*L*LVHSLLKETSFRS SSFSSCRACFLRSSQ/STAGPCR HLCRPTSAGIGEQRRCRPESH EIVDRGI

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16161	46529	A	16256	619	1138	SCNMSLCRCNCVIRAAFKEGTTP ALLVYSAILSFTPVSV*DPEAFSP HLPNSNCWSLPPSLSSNVSRDRG AEAMQAGKSPWCVFPP*EPGPT GCEPPRTLPPAPFKLCSL
16162	46530	A	16257	408	801	SQRRGSVCRLVHGRHGQPGKG TSPHSSLWDWQPGPQPSGPPWP EGGASPGTIPSLIPRS*SASCCFP WHPGCSC*GAPASQC*VALSPQ PWFPLPCLSVPSVGAQTGPK HVRTPPGSDSAPPQLQPQSRI
16163	46531	A	16258	1	199	
16164	46532	A	16259	665	1006	IGSPDGRNVIRERTVTNETQTEG EREKEEERESHTGDVLKVGDL GPQGSSEFQLLSNLTVPNFIDI QFPK*VSAAC*DGPSHTSSYIS SSLFIIRASQSSPGDFSISVRY
16165	46533	A	16260	247	404	
16166	46534	B	16261	258	934	
16167	46535	A	16262	519	924	NRTIQADLLYPDDAGNPLPARN TRQASASADPPGARAGERRRG AAGPSPGR*QAPGPPPPGEGA GARPG*EGDAAGGATRFVGED ARLLRAGCHRRGRGEAEPELQ ALRHPGLQGLL*EGAPHGELAL VAFHL
16168	46536	A	16263	121	214	
16169	46537	A	16264	139	272	
16170	46538	B	16265	1	1962	
16171	46539	A	16266	2373	2554	SATPWLPPTGLAAPTGLAAPGT RSPPGQT*PERSPAASPKRPERP ALDFQPFRQPPPPPP
16172	46540	A	16267	919	1653	WNCFVCSADTMAQIMAEQVEVE NLSGLSTNPEKDIFVVRENGTT RRPLQPPPRGRAS*GGAGRLCS QLITEQADIALTRGAEVKGRCG WRPLGLRTQTLRGLKRTSPAQ QESHNSMKGPEATCQLSGTLG* EQ*GF*LLLWALAVAGKHTAN SHHLSALVTPAGKSYECQAQQ TISLASSDPQKTVCRTYDSGCF DQSSLLFFFPAAEHKCPVDEREQ LEETLPLILGLLGLVIMVTLAIY
16173	46541	A	16268	2	321	PAWPPWPPTGFCPCQQDPSNT FVVPAAHTV*CSHPCSYYKGIR QMVGLPQLFHPDCPVPTPQAHT DSLNTLGLVGGPPVCSDATLPQ IINALEEDPAAQKMQALAF
16174	46542	A	16269	120	327	
16175	46543	A	16270	540	791	

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16176	46544	A	16271	1688	1945	DRVSLLPRLRQENRLNPGGRGC SELRSHHCTPAWATE*GSVSKK KKKKKNQKKNQDFISLALPPS PHCPPLSQSLLLQPSSSAN
16177	46545	A	16272	3	343	DIHHVRKSMEVNFLSYVVLTV AALPMLKQSGSIVVVSLSAET AMKAVSGIVHMQAAPKEECAL EIIKGGALRQEEVYYDSSLWTT LILIRNPCRKILEFLYSTSYNMD RFINK
16178	46546	B	16273	48	407	
16179	46547	A	16274	35	646	DLTGFIKFSLLGLFMAYYYYS ANEFRPGKYPCVSFWRNRFK KHRGA*VAYHLAKMGAVVV TARSKETLQKVRVLCQICVPS HAQMCSYI*DMTFAEQFVAQA GKLMGEAVSLTSSSELCPWGH QELLDIHHVRKSMEVNFLSYVV LTVAALPMLKQSGSIVVVSLL AGKWRDICGR*KKKKNARD AVQTPGSKSAI
16180	46548	A	16275	221	393	LLYPANCVYMRCQMLHFQGI QRPIIL/HVSSGGAHLQGTGVET EEMRSAIAPDPIPLT

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16181	46549	A	16276	2025	4146	SDEWIIAGSVSGDYNSAAVS KNDILLGIEHISVFSETNHSSEEA FIKTAKSQLVEIEPATQNPKTSF SYERLQALQETCKENKGVPKQ GDTFLSFSAACTDVSSVTPEK EFEETSATGSSMQSGSELLKE REILTAGKQPSSDEFSASLAGS GKSVAKTGPESNQCLPHHEEQ AYAQTQSSLFYSPSSPMSSDDE SEIEDEDLKVELQRLRFRHIQEV VNLQTQONKELQELYERLRSIK DSKTQSTEIPLPASPRRPRSEKS KLRSRPQSLTHVDNGIVVIDPLC VESNAASCQSPASKKGMFTD DLHKLVDWTKAEAVGNSLIK SLNQLKQSQHKLETENWNKVL QLESVYHREDEATWLPQLRAQI VAYPACAAAIASAHRRSMGVQ GFQEFLEKRCPGA VVPVDLLKL ARTVSRQQQQHLHRQLPPTA ALAPGAPRAARGSVPLQPLPP AALGAYSGGAGPIRHHHPAHH FHIIHGQAQPLHPLPPPPPPQ LPGARVLVDAGSALPRLYGGY QTDWVCGGWNAMLGYSAL CQACAYPGGDGLEVVMFPGG LGKDRLAEWGRRCQAERQTAQ LIVGHVGNKGTTPPRAWFLPPA CLSHCVRLALIRFRF*VFQSLD HHLEVVAFFRENGFHGLLAHD SEYALYNIPSYSSHALKLSWN GKNLTNTQFLMQEVAKQLGLK
16182	46550	A	16277	1	542	MRAPPKSGQLQHCPRSRGALRS GDLPWEINPLSSCSLLHEKDPP MTSGPQTNPKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAPIPYFRTPSY LCAPIPVYRTPSYLCALTPFPL FWRHIRTSKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPQGMPAAQ
16183	46551	A	16278	3	351	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLIS LRPNLCPHPDL/GISVP*PLSRF SGGT*ELPNA*TAAA/AAF/LPEP PPPG/CLLQVPEI*PPQGMPAA QDSS
16184	46552	A	16279	1	513	
16185	46553	A	16280	774	1007	ARSVTSSELCSGSWCLQASRHT HVPWCQL*KLPVVHLVQPQPC RGPAPGAALPAGSLEMPGTTEP ERGCHSPGLGIS

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16186	46554	A	16281	507	520	LLGLAAED*CLIASEAP*TS LFGGLFTRTHMKFGAVTQIRGP PLGDKSPVLLFALERQRRHVL SMDPKLRCSWRTGKAAPWCL IIAEMPDISPTFQRCQTQGRPL WSFTLSSKSRSFSGEGARACYKC QKSDHQAKECPQGPPIPKPCPIC AGPHWKSDCSTHLAATPRAPG TLAQGLTDSFLA
16187	46555	A	16282	269	607	RARSEGAGLWSVVAPSAVSVF VSDPRCAPFHRSPCCSPVDRV CRCLRRVALAPALVLCVSGSH SQSPWNGLKLSDRLLGLAAE D*RCPIASEAP*TTTDAELTIPGL
16188	46556	C	16283	1	1752	
16189	46557	B	16284	146	372	
16190	46558	A	16285	336	753	ARTPLAAASRSGSGTRGGA VAGDDLRGPAEPGPAEPGARRR RGKGTSPSSRPRTQRRPSAAMH GHRCQPARRSREHPNTYFAGR RPPELRRGRSGVPPRP*RRPGE APRAPRPRAEL*ARLPRPSVRP APARRV
16191	46559	A	16286	1	768	FDELREEGFRQSVITNFSELKDD V*THRKEAKNLEKKLDEWLTR INSVEETLNDPMELKTMAQELR DACTT*FREKRVKRNEQSLQEI WDYVKRPNLRLIGVPESDGEN GTKLENTLLDMIENFPKLARQ ANIQIEIQIPQRYSSRRATPR HIIVRFTKVEMKEKMLRAAREK GWVTHKGKPIRLTADLSAETLQ ARREWGPFIINLKEKNFQPRISY PAKLSFISEGEIKYLTDKQMLR DFVTRPALKE
16192	46560	A	16287	345	894	EQRHINIPESLGH*STSAGDTA DRVWSGPPANSRPAEAGPDC* KEN*QARTSNQNPICTPSSSK TKEAKNLEKRLDEWLTRINSIE NTLKDLMEKLTARELRDADR SFSSQFDQVEERVSVIEDQMNE MKKEEFREKRVKRNEQSLQEI WDSVKRPNLHLIGVPESDGENG IKLENTL
16193	46561	A	16288	1	1206	

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16194	46562	A	16289	1	882	MAPVSASEDFWQCPETSLISQL ESAPGIQLMEARDADKSLIMHE IAPTSNRELPHVKISIAKPCSMML MISWFFVNTGQSFKQDQAAIF AVLQPLLVIHRQTGSGVDLQQT PTDLQLRDLTVRRKNNKQKGI ASTSRKRTSTPKPHLQDHSSSPA MEQSWMQKDFDKLAEVGFRR SVITNFSELKEDVQTHHEAKN LEKRLDEWLTRINSVENTLNDL MELKTMALQELHDACTSFQRQF DQVEERVSIEDKISEIKQEEKF REKRVKRNESLQTIWDYVVR PNLHLIGVS
16195	46563	A	16290	1	1008	MVRFGEDELGGRYGGPGGGERA RGGGAGGAGGPGGGLQPGQR VLYKQSIARARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITWPPFEYMILATIANC IVLALEQHLPDGDKTPMSERLD DTEPYFIGIFCFEAGIKIALLGFV FHKGSYLRNGWNVMDFVVVL TGRKAGLGGCGSGVESGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSELKEDVTRHRK EAKNLEKRLDEWLTRMNSVEK TLNDLMELKTMARELRDACT FSSQFDVQEMVSVIQDQISEM KREEKFREKRVKRNE/QSLQ*I WDYVERPNLRL
16196	46564	B	16291	1	1257	
16197	46565	A	16292	3	467	KTPFVGQYHQRPVKDKTTKMG RNQSRKAENSKNQSTSSPPKDP GSLPATEQSWTENDFDELTEVG FRRSAITNFSELKEHVLTRRKEA KNLEKRLDEWLTRINSVEKTLN DLMEKTMALQELRDARTSFNS *FNQVEKRISVIEDQIDEIK*EDK
16198	46566	C	16293	115	498	

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16199	46567	A	16294	2	1455	TERDSININKKDIYTKTQSVGRQ HQRPKVDKTTKMGRNQNRKA ENSKNQASASSPPKDCSSPAME QSWMENNFDLTIQFRRSVIT NFSLEKEDVQTHCKEAKNLEK K\DEWLTRINSIEKNLNDLMEL KTM\AQLRDACTSFSSQFDQVE ERVSVIEDQMNEMKQEEKFRE K\RVKRNEQSLQEIWDCVKRPN LHLIGIPESDGENGTKLDNTLQ DII*ENFPHLAR*ANIQIQEIQEIQ RTPQRYSPRRATPRHIIVRFTKY DMKEKMLRAVREKGFKPTKIR RDKEGHYIMVKGSIQEEELTIL NIYAPNTGGPRFIQVLSDLQR DLDSHTIIMGDFNTPLSTLDRS MRQKINKDIQELNSALHQVDLI DIYRTLQPKSTEYTFSSAPHRTY SKIDHVVGSKTLLSKCKRPEIT TNCLSNRSAIKLEIRIKKLTQNR SAAWKLNNLLNDYVWHNEM KAEIKMFFETRTKIQHARISGIL
16200	46568	A	16295	395	656	FQLQRPASCSSPIQHRKHIPRKP A\SSSLPHTGKSARQPEQPNR ENCLLRILIRVASEATRRWTRPS EFSSRSNPRAHHPRRALR
16201	46569	A	16296	671	1126	RRKVSELEHRRPVWKCPRRPPE VRKPESARVVSFPRGGARRSRP GATRSPQPRVPAAASASFGFGG LGRGGRGERARRGRGPKLEGP ESSAVLA*RNFPSPRRRRPGRG GVEIARLGGTGSSPRPCPKPDPT ASLSELFIPSDIPRRRN
16202	46570	A	16297	2571	2716	THGMLEKRCCLQENMPIPGKD FMTKTLKAIATKVKIGK*DLIKS FCT
16203	46571	B	16298	54	576	
16204	46572	A	16299	475	719	VTWIRNNNACFTLNWFYHERS HIWILKSTLQCGQIIGNDVESR HKICPKPS*LVGSVELEADNVL PQKFPAAKTIFALYF
16205	46573	A	16300	395	830	LSPCHNSFFFFQAFDDIAKYFS KKEWEKMK*ATVPGPSLPLKK *TFCSFLGFKVTLPPFMRSVSLE FGNLYQQRKILM*L*STVEMSLI LFICDLHIVKIMPKPAEEENGL KEVPEASGPQNDGKQLCPPGPNP STLEKINKTS
16206	46574	B	16301	54	576	

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16207	46575	A	16302	475	719	VTWIRNNACFTLWIFYHERS HIWILKSTLQCGQIIIGNDVSR HK/CPKPS*LVGSVELEIADNVL PQKFPAAKTIFALYF
16208	46576	A	16303	393	822	LSPCHNSFFFFQAFDDIAKYFS KKEWEKMKSATVPGPSLPLKK *TFCSLGFKVTLPPFMRNSLSLE FGNLYQQRKILMYF*STVEMSL ILFICDLHIVKIMPKPAEEENG LKEVPEASGPQNDGKQLCPPGN PSTLEKINK
16209	46577	A	16304	1	447	
16210	46578	A	16305	75	565	LLFSGFSLHGYLPHWYLCHLP RSRSLGLRDKRWVKGDTDFL SPSHPEYLLKEENDGHLCSLSFR MGNQFSSPLPAYTPLECILNH W DGFYP*NLEEKHLIALRTKGWP NYDLQEGLSWPQEGTHFNNT WQLELFCRHEDRWSEATYMQ AFYILQGNRDLG
16211	46579	A	16306	1	1620	
16212	46580	A	16307	128	223	
16213	46581	A	16308	1	1578	
16214	46582	B	16309	592	883	
16215	46583	A	16310	1	344	MHQTTAKTPHTSYPNNYEEHN RRANRSKNYDRIHRTIILKRTN PAQTITNLKSRFNRYNYVQPR SCRSIFIHIPGERDLNLCIAPNPP AIFPTSIGYLGPDNLNLPYAPFI TTNLTGPAPTTHPVGNLGTG NPEPGGCGILIVCCYNWACL WDSVVAAPREPYMPAGLLRHR RHYRHRREDLIAVPAARQTDE NRRPALCHEYAVGHRKIKNV EHTPEYILPLITHSQPLNRGAFF CPGVRFVVSVDLFEKRLAFAS *SCGVQLRIRGKVQGVGFVFV WQLAQQLNLHGDVCDNDGDV EVRLAYRVLVGQPPHYPRGRP
16216	46584	A	16311	84	237	DGIVLSTYHYFYWHHF*ILEGP LPANTGDCLPLQVQPDREQVR WALFKK

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16217	46585	A	16312	2887	3537	HLDRSGLFNQIVIPVCRKLKGKE GNDEKQCVTTSRSNAAFFLLHF FLLATFTWMGLEAIHMYIALVK VFNTYIRRYILKFCLIGWGKPLK IFLVLFPHENCQVYGKESYGK EKDEL*VIKTCDE*ISFVS*SG VMFFLNIAFMFIVVMVQICGRNG KRSNRTLREEVLRNLRNVVSLT FLLGMTWGFFAFWGPLNIPF MYLFSIFNSLQGGKINCT
16218	46586	A	16313	302	547	QIGLWTPNFRTFCVWTGGL VLCF*GFCFQEAAGARDTSSFA MGVSPWFEFRHG*LWPEMRSM E QILELLVLEEFLTITGQ
16219	46587	A	16314	1	1174	WEEKENKEYLKSFEILMLMGK QNIPLDGHEADEIPEGLFTPDNF QALLECRINSGEVLRKRKFETT AVNTLFCSTQQRQMLEICESC IREETLREVRDSEFFSIITDDVV DIAGEEHLPLVLRVFDSEHNLR EEFIGFLPYEADAEILAVKFHTM ITEKWGLNMEYCRGQAYIVSS GFSSKMKVVASRLLEKYPQAIY TLCSSCALNMWLAKSVPMGV SVALGTIEEVCSFFHRSPQLLE LDNVISVLFQNSKERGKELKEIC HSQWTRGRDAFEILVELLQALV LCLDGINSNTNIRWNNYIAGRA FVLCSAVSDFDHFVITIVLKNV LSFTRAFGKNLQGGTSDVFFAA GSLTAVLHSLNEVMENIEVYHE FWFEATNLAHQT
16220	46588	A	16315	717	902	GALQSWPCYLPRQCAGATVQNF CGVPTCMRKSTWSNLVVRFP QDPSRCAN**LDCCCTACTQ
16221	46589	A	16316	1	374	EHSEPPIGVQIVDYLLRQEKVT DRMDHSHKVEITVLSFVDDIIS GAKSPCAMPSPQDPK/QAQEIA DKIYNLFNGYTSKEQQTAYN TL.LDLGSPTLHRVLYHYNQHY ESFGEFTWRCEDELGPR
16222	46590	A	16317	2	1293	

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16223	46591	A	16318	219	1912	PHPTRTSAQSVQYIEKDWGPG EGLEEGGVLGQLVAFDSFTVSF HFVSAGNSPSESEERERDPKV LTFPEYITSLSDSGTKHMAAGV RMECHSKGRCPSSCPLCHVTSS PDTPAEPVLLLEVTKAALLNTQS FPCSLMQLLQEATMSSLWCSTG GDVIEDWCRCDSAFGGCVPV CSFLSAHRLRLSTVHEPSSLV LEWEHSEPPIGVQVDYLLRQE KVTDRMDHKSIVETGEHLLHG LVLIQGDKTTKKNALPHGFAP GPQYPRAMQEEQEEEEAVLLL QEAAVLLPLRVDRISCCFRHR ELLFLMLFPFLLWAETVLSFV DDIISGAKSPCAMPSPQVPDKQL TTIYFQPLIARFSFSSRGLLRIM SSHCHGDCDVSTLDSYTVSAN HALPLPARFTLWGV DNTGRRS RPSDVIVYM*ITYFFPPSSEIAD KIYNLFNGYTSGEQQTAYNTL LDLGSPTLHRLVLYHYNQHYESF ASF*LKYPLCLIHRRKAGLILSQL GDLSSWCNGLLQEPKISLRRSS LKYLGCRYSEIKPYGLDWAELS
16224	46592	A	16319	1	2031	
16225	46593	A	16320	1	739	MKRAGSSGGRGECDISGAGRL GLEEAARLSCAVHTSPGGGRRP GQAAGMSAKERPKGKVIKDSV TLLPCFYFVELPILASSVVSLEYF LELTDVFKPVHSGFSCYDRSL MPYIEPTQEAIPFLMLSLAFAG PATTIMVGEGILYCCLSKRRNG VGLEPNINAGGCNFSFLRAV RFVGVHVFGLCSTALITDIHQLY TGHQAPYFLTVRTPNYSLNVS CT*NSYLAEDIRSRSDLTLTHSG

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16226	46594	A	16321	48	1359	GDKNQNPNNWPLGEGKGNSLG RKETGRSNSRSHSSRSKSR*QSS SRSSRSRSHSRKKRHSRSRSTY SRSSWRDRMYSRDDRH*YEVIV DCSRHGREYKGREPRHSGSLE RPTEQETSQPKIRKEIVETKGT RGNCGTTGLLRPKTMMVERSY GPQDRVAVGTWPHPGTERWAS SWDVSSSVRHQSEG VVQGW RCTHKSQQEVGACVNFRTPKVI LIYNLYLPVSHQFSKTFMSIVIV QKNLYLHNDFRALNVTHIYRLT IPNTTTCFATQDEDKQIFHTAA QHRSHSTSSYQYLSLTRSHRYEI VFYTRGLGAPFPAGDGHGKFQ RLGKPYSHSVHFIPODKTQHIS INTPHKNSETTKQHTCSFAYGL YYYQQKEDNPYAWPQVPA EMVSRLAQSRHSQQSILHFSHQ SYHTDHISTV
16227	46595	A	16322	227	3020	SCIKPRRKEMGRSNSRSHSSRSK SRSSQSSSRSSRSRSHSRKKRYSS RSR\SRYSRSDRMYSDY RRDYRNNRGMRRPYGYRGRG RGV/YQQGGGRYHRGGYRPV WNRHRSRSPRR\GRSRSPKR RSVSSQSRSSRSRYSRSPR SSSSRSSSPYSKSPVSKRRGSQE KQTKAEGEPQEEPLKSKSQE EPKDTFEHDPSESIDFNKSSAT SGDIWPGLSAYDNSRSPHSPSP IATPPSQSS
16228	46596	B	16323	258	3728	
16229	46597	B	16324	1	435	
16230	46598	A	16325	1120	1209	ASSDNPP*SEPRVSLTIEGQEIF FLDTGTAFSVLSSCPGWLSSRS VTIRGILGPVTRYFSHLL
16231	46599	A	16326	1291	1582	IHQSAICI*LVCKKHTNQPVSS SGFVNAPIDTLYLATLVGPWRT LCVHTLYLVNLVGMWRTFVSS SGIVNAPISALSKQTTWLYQSA GCGWGQIRE

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16232	46600	A	16327	2	840	APAVATEVLPGAGLTAGVLLWSDPKEPSNPGSSHRVGASDLDPAHPTLLSYTMQKLEELDVVLFDRSGHRTKFTNVGRMLLERGRVLLQAADKLTDAEALARGWETHLTIVTEALVPTPAFFPLIDKLAAKANTQLAIIT*VLGAWERLEQGRADIVIAPDMHFRSSSEINSRKLYTLMNVYVAAPDHPHQEPEPLSEVTRVKYRGIAVADTARERPVLTVQLLDKQRLTVSTIEDKRQALLAGLVATMPYPMVEKDIAEGRLRVVSPESTS
16233	46601	A	16328	3	923	RFLSDGTIISVDSAGKVQFWDSATGTLVKSHLIANADVQSIAVA DFFPGHESRATEALCWAEGQR LFSAGLNGEIMEYDLQALNIKY AMDAFGGPIWSMAASPSGSQL LVGCEDGSVKLFQITPDKIQFER NFDRQKSRILSLSWHPSTHIA AGSIDYISVFDVKSGSAVHKMI VDRQYMGVSKRKCIVWGVAF L SDGTIISVDSAGKVQFWD SATG TLVKSHLIANADVQSIAVADQR RQFRGGHSRGNLSPSAGPCAS NSS*EAVGADKTVPSHS*RAH CGPTAQQR*YLGDTHTLVFRP
16234	46602	A	16329	2	1059	
16235	46603	A	16330	582	1540	
16236	46604	A	16331	1	720	
16237	46605	A	16332	1	477	
16238	46606	A	16333	1	540	
16239	46607	A	16334	1	261	
16240	46608	A	16335	964	1574	LRWCCGSQLFRGYWGGVTGR YLTVLPPHLAVGCMAPWGPFS VRIAAVVFIQIFAGEVFWCPVM CVRGLCTPVLTVGPVGHGNSHIP AIVFTCSLQTLVGGTRRWRC CAAGDVTKFPALVGVGGETPR PQLPIGVTTVILLQVLVVKFGR NVMSVWALRVPLAFQSRH/ ASWKFCRHSFLHCNAYIPLHTQ ECRSSHISFLDQ
16241	46609	A	16336	3	87	
16242	46610	A	16337	1	1398	

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16243	46611	A	16338	1596	2205	LRWCCGSQLFRGYWGGVTGR YLTVLPPHLAVGCMAPWGPFS VRIAAVVFIQIFAGEVFWCPVM CVRGLCTPVLTVGPGNGNSHIP AIVFTCSLQTLVGGTRRWRC CAAGDVAKFPALVGVGGETPR PQLPIGVTTVILLQVLVWKFGR NVSMVVALRVPGLAFAQSRH/ ASWKFCRHSFLHCNAYIPLHTQ ECRSSHSIFLDQ
16244	46612	B	16339	276	442	
16245	46613	A	16340	1	300	
16246	46614	B	16341	1	903	
16247	46615	A	16342	119	889	RQHILESHSRPILCTTWPLLIQ DPRTLQSAAMLLTQSLFGIFT RTRMKFGAVTWGGPPLGDQS PSSCSLLREKDPPTTSGPQTHQ PKEHLTNFKSGVPRRDACLGP SPLAASPAFLGKGQVPQPLISLC PDPFLPHNPLISLRPNPLCPHPD LVSLCPDPFPAFLAHLNFQTP PQQPGIPPEPPPGACYKCKQSD HQAKECLQPRIPPKPCPCAGPH WKSDCS THLAATPRAPGTAE GSLTDSFSA
16248	46616	B	16343	1	498	
16249	46617	A	16344	3	903	
16250	46618	A	16345	1	684	
16251	46619	A	16346	2	1028	
16252	46620	A	16347	1	338	
16253	46621	A	16348	2	392	
16254	46622	A	16349	790	2184	
16255	46623	A	16350	773	890	
16256	46624	A	16351	467	606	
16257	46625	A	16352	1569	1841	
16258	46626	A	16353	430	980	LLTEDALDDLPSFLLTGQQTPA FGRRVSGVIEIADGSRRRKAAA LTESNYRVLVGELDDEQMAAL SRLGNDYRPTSA YERGQRYASR LQNEFAGNISALADAENISRKII TRCINTAKLPKSVVALFSPHGE LSARSGDALQKAFDTKEELLKQ QASNLHEQKKAGVIFEAEVIT LLTSVLKTSASRTSLSSRHQFA PGATVLYKGDKMVLNLDNRSR* RGIT*AAGI*PS*AEKSWGDI*S* RSYHSFNFECA

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16259	46627	A	16354	1	343	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVGMARG NAITLPPVCGRDVKFTLEVSGVI VLRRLPGYGQVMNVTRSCLLR THWMISSLLFY*L VNRHRRSVE EYLV
16260	46628	A	16355	1	584	MLRDLLKNVDLKGFEFDPVRI TKYSNSNGSQSPWMEEQIRDA WGSMLVKNVVRETDEVGKGQI RMRTVFEQAIDQRSSDTNEGAP VIPKHTLNTQPVEDTSLSTPAAP MVDSLIARVGVGMARGNAITL VCGRDVKFTLEVSGVIVLRRL PYGQVMNVTRSCLLRTHWMI SLLFY*L VNRHRRSVEEYLV
16261	46629	A	16356	62	350	SLPNLDNAACSSSSSPTRTR*SL SVSAAALRRRLPSAIDHTREVF STLSRSTSRVNFSTRPHTGKV MALPRAITPTRAINESTIGAAGV DNEV
16262	46630	A	16357	291	502	RLFVHHVHKHLLGDNRYPI WIMQPSAHH/RSPTTR*SLSV SAAALRRRLPSAISMTPDTRLR NAGVC
16263	46631	A	16358	1	378	
16264	46632	A	16359	159	433	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHH/RSPTTR*SLSVS AAALRRRLPSAISMTPDTRLRN AGVC
16265	46633	B	16360	1	624	
16266	46634	A	16361	3	299	
16267	46635	A	16362	163	699	
16268	46636	A	16363	795	980	
16269	46637	A	16364	663	734	
16270	46638	A	16365	391	1248	
16271	46639	A	16366	1	1143	
16272	46640	A	16367	1	271	
16273	46641	A	16368	1	493	MSKRRWLTGNGSDRENIRLDL GFLVSDDEEKRYKCEDCGKAFN RSSNLTHKKIHTGEKPYKCEE CGKAFKRSSLTTHKRIHTGEK YKCEECGKVKYLLSSLTHKIIH TGEKPYKCEECGKAFNWSSHL TTHKRIHMERNPTNVKNVAKA LSTPLPLLNK
16274	46642	A	16369	728	1428	
16275	46643	A	16370	3689	3864	NYKSFFKWS/SQMOSMTKIYRG PLDHPDSPCSNVNDIEGTPPEEI STAQPLHPRPAGSS

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16276	46644	A	16371	2	126	WPLLLGLCLSLTKEWGFQA*LE KHVVRVKFSPSHNLVPGRSI
16277	46645	A	16372	728	2207	
16278	46646	C	16373	1	873	
16279	46647	A	16374	1220	2097	
16280	46648	A	16375	73	1438	QDLRLFYLKDTMFASKLAHLQR FAVLSRGVHSSVASATSVATKK TVQGPPTSDDIFEREYKYGAHN YHPLPVALERKGKIYLDWVEG RKYDFLSSYSVNVQGHCHPKI VNALKSQVQGN*PLTSRAFYN NVLGEYEEYITKLFNYHKVLP MNTGVEAGETA'CKLA'RKWG L'YTVKGIQKYKAKIVFAAGNF WGRTL'SAISSSTDPTS'YDGFPGF MPGFDIIPYNDLPALERALQDP NVAAFMVVEPIQGEAGVVVPDP GYLMGVRELCTRHQVLFIADEI QTGLARTGRWLAVDYENVRPD IVLLGKALSGGLYPVSAVLCDD DIMLTIKPGEHGSTYGGNPLGC RVAIAAL'EVLEENLAENADK LGIILRNELMKLPDSVVTVAVRG KGLLNIAIVIKETKDWDWAKVC LRLRDNGLLAKPTHGDIIRFAPP LVIKEDELRESIEIINKTILSF
16281	46649	A	16376	600	806	

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16282	46650	A	16377	1	2255	EPDVCAKMAGRSMQAARCPD ELSLTNCVVNEKDFQSGQHVI VRTSPNHRVYFTFLKTHPSVVP SIAFSLPQRKWAGLSIGQIEVS LYTFDKAKQICIGMTIIEIDFLQK KSNDSNPYDTDKMAAEFIQQF NNQAYSVGQQLVFSFNEKLFG LLVKDIESMDPSILKGEPATGK RQKIEVGLVVGNQVAFEKAE NSSLNLIGKAKTKENRQSIINPD WNFEKMGIGGLDKGFSDIFRR AFASRVFPPQIVEQMCKHVK GILLYGPPGCGKTLARQIGKM LNAREPKVYVNGPEILNKYVGES EANIRKLFADAEEEQRRLGANS GLHIIIFDEIDAICKQRGSMAGS TGVHDTVVNQLLSKIDGVEQL NNILVIGMTNRPDLIDEALLRPG RLEVKMEIGLPDEKGRQLQILHH TARMRGHQLLSADVDIKELAV ETKNFSGAELEGLVRAAQSTA MNRHIKASTKVEVDMKEAESL QVTRGDFLASLENDIKPAFGTN QEDYASYIMNGIHKWGPVTRV LDDGELLVQQTKNSDRTPLVSV LLEGPPHSGKTLAARIAEESN FPFIKICSPDKMIGFSETAKCQA MKKIFDDAYKSLSCVVDIIE RLLDYVPIGPRFSNLVLAQLV LLKKAPPQGRKLLIGTTSRKDV LQEMEMLNAFSTTIHVPIATG EQLLEALELLGNLKDERTTIA
16283	46651	B	16378	1	2181	
16284	46652	A	16379	1	441	
16285	46653	B	16380	47	482	
16286	46654	A	16381	1	636	MRDPNTRKSRGFGFVTCATVE EVDAAAMNARCKVVGRTVEPK RAVSREDSQRPEDTEELHLRDY FEQYGKIEVIEIMTDQSGGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGSGNFGGGRGGGF GGNDNFGRGGNFGHGGGFGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDNFVNYNNQSSHFPM
16287	46655	A	16382	1	762	
16288	46656	B	16383	59	1042	
16289	46657	B	16384	76	848	
16290	46658	B	16385	179	400	

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16291	46659	A	16386	27	372	VGSLRRPGPPRETRRLRRRRS LEPWAFLLKEAKVG*QPSSLFQ WEGPMGLCSTPLVMNMGDSL TKVHLFQVPPLTITSPGPRTRRPH S*YPSPLATGVWAAVWCKQP HFPAK
16292	46660	B	16387	134	284	
16293	46661	A	16388	1	2013	
16294	46662	A	16389	313	770	IFGFVVMAMHGAPGQAVLELLQ LTGDQSLGLSQRHMAALDALV HLLHGGGLAVLTAGAAPEHET RGIALGREGQRNPRCVKRGW AQEKQA*PGQGGKSSPFWSF TL/DSASAGPRAAHLHLPDVL LQTLHHGLHRLHPPELLQLSHG
16295	46663	A	16390	1	2753	
16296	46664	A	16391	1	1363	
16297	46665	A	16392	26	181	
16298	46666	A	16393	1	867	
16299	46667	A	16394	1	1447	
16300	46668	A	16395	31	659	APALPGCEHMMAIKELKVCLL GDTGVGKSSIVCRFVQDHFH NISPTIGASFMTKTVP CGNELH KFLIWDTAGQERFHSLLPLYL RGSAAAIVVYDFTEAGFHHPK KWWKRLKELGPNIVMAIAG NKCDLSDIREVPPGMLKEYVA ESIGAIVVETSAKNAINNEELFQ GISRQIPPLDPHENGNGTIKVE KPTMQASRRCC
16301	46669	A	16396	1	1182	
16302	46670	A	16397	1	513	
16303	46671	A	16398	146	429	TFYTCFSPSVIPFSFIHTKPYPG HHQSFYMTNVSSNNPTISPLTT RPPFSLISALGSHAAPNPA*SSP EKHRPFSLHTTPQKFRPNTSTL F
16304	46672	A	16399	1	435	
16305	46673	A	16400	56	477	ARAAGESCEGPGVGRCFSS YRQTPCCQRLVNVPKTRRTF CKK/CGKH/PHKVTQYKKGKD SFYA/QGRRRYDRKQSGYGGQT KPIFRKKA/TTK/MGLRECV EPNCRSKR/MLAIKRCKHFELG GDKKRKGQVIQF
16306	46674	A	16402	183	373	IHGSSNPPTPERETLFWHAENG SALASC*KSGGQAPKRVRTTL ILKAEILGLMLVLRSHGM

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16307	46675	A	16403	1	881	MPFKCKKQHTFNKTSPEKGAII FTHGCLCTSPFNSELSEHLGNL KLSSWEHLHHRSQQLSVRLH VPTQPQVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPLWQL KYPKLIIREASSVSEELHKEVQ EAFLLHKHGCFLFRDLVRIQGG DLLTPVSRILIGNPGCTYKYLNT RLFTVPWPVKSGSNIKHTEAIEA AACETFLLKNDYLQIETIQALEE LAAKEKANEDAVPLCMSADFP RVGMGSSYNGQDEVDIKSRAA YNVTLNFMDFPKMPYLKEEP YFGMGKMAVSWHHDENLVDR IQLQLWDPVDGTTASSAVPKQ GRDKRREVPNTLSQPNSEQGLI SAFHSRCVHAVFYKLTSA PKTT SLPDVPSDLLAEGLAASRAGQA LWRCDKKSLTLVRKINLQKG RDGGRSATNQSQPHLDNTGL ERQLEQKVGRCRSPWRGLGHL EGNAQKGHLLHGYNKNGQHL L*MPPSPPLPGGQKGRVLGMLS WVLT*VYKIQH/GT/PAAVEG*D EAFLAVWLGEVGDFSPVPSL LWHS*RGCCSIHGIPLELNPVH QIFIM/SASSLPSPCQNKVPLSG
16308	46676	A	16404	1	459	
16309	46677	A	16405	1	2025	
16310	46678	A	16406	1	816	
16311	46679	A	16407	1	217	
16312	46680	A	16408	3	135	
16313	46681	A	16409	21	218	
16314	46682	A	16410	392	3744	LNYKMLLKNLSPMSMLKAFSF AIPMPQAQTNLPTAKPNGFQP LLLSQYNACPPQ*EAG/QVDL CSTIPLNLLPDSLPLTVPTGPLPQ GSVGLVLGRASSAKGITIHTGL INSDSVDEIKLITSAKVPVSILAG ESIAQLLLLPHILNKGDKTRGP GMGSRGEKAAYWINVISKQRP TCTHIHQGRKFEGLVDTGADV VISSSLWPSSWLKHPTNMGVLV VGKAEVYVGSTFILPCTGLDGG KGTIQPYIM
16315	46683	A	16411	1	783	
16316	46684	A	16412	1	1911	

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16317	46685	A	16413	3	1381	KTPFVG YQHQRPKVDKTTKMG RNQSRKAENSKNQSTSSPPKDR SSLPATEQSWTENDFDELTEVG FRRSAITNFSELKEHVLTRRKEA KNLEKRLDEWLTRINSVEKTLN DLMELKTMAQELRDARTSFNS *FNQVEKRISVIEDQIDEIKQDD KAAETCNWRWVSESRLQLRAS VDAFHARASHYNAGECLHQLA ALNSRLNCAQEMARRDSIGVVP PVPWRVTVGSGIAGEAKLDHL RLVSLIGREVNKENS PAATRWL FSFQAGALAGGQIVLQAAPKN AHGQPVVATRNLLNPAGIVAV LKQRPRLVAAAVQAFYLRDPID LRACRVFKTFLPETRIMTSYYAI EWSLWTLVDVLHAENSEAHM SHNSYDPPSDVARHLTHLPMSP IPDYIARFRYRHR SRVRLTARK LSPAFMRCSEIQRYS TMLERG FNGGYCRSTTVRVVTEATRML
16318	46686	A	16414	1	1191	
16319	46687	A	16415	1	1909	
16320	46688	B	16416	1	1791	
16321	46689	A	16417	1	1818	
16322	46690	A	16418	1	1044	
16323	46691	B	16419	1	1140	
16324	46692	A	16420	1	1062	
16325	46693	B	16421	1	972	

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16326	46694	A	16422	1	1758	MDTFLQAERKDYMEAYELIEQ EEQGVKELNRLPTAPSAHPRD EAHLIMVDKLFVLLDSVCQYF IEDFCIDVHHINSRW/AVCQYFI EDFCIDVHHINSRWIKDLNVRP KTIKLEENLGNTIQDIGMGKD FLSKTPKAMATKAKIDKWDLIK LNNFCTAKETTIRLPVPNPGGPV AETPLSRVFLREARKTLKPHQ STCLSKGRDNSIDSWKTAARVL KTAISSTPTIPILKQDQTQEWVS ATFTSDGKIRLFYTDYSGKHYG KQSLTTAQVNVSKSDDTLKING VEDHKTFIDGGKTYQNVQQFI DEGNYTSGDNHFLRDPHYVED KGHKYLVFEANTGTENG YQGE ESLFNKAYYGGGTNFFRKESQK LQQSAKKRDAELANGALGIEL NNDYTLKVKMKPLITSNTVTDE IERANVFKMNGKWYLGELGW RREWSSGDRKSLARLSKTGTLG LAALT YKCTRDQWTVYCRVIR EKNLCQDMRWYQRCQCTCRD FYANKMSPATAELVTRSPKGRS KLRLRYQLVFISLKGKPKARKGK ASSGSKLSLLSSSKTVALAGMG RGDEFQMELESEDLT SERDGIL TPTSSNQKSKAYGSLIRT
16327	46695	A	16423	1	4449	
16328	46696	A	16424	3	3859	QFLPNLDSTVLGENYFDGTYQ MLYLLVKGTIPVEIHTATVIFVS FQLSVA TEDDFYTSNHLVKNLA LFLKIPSDKIRISKIRGKSLRRKR SMGFHIEIGDPPIQFISNGTTGQ MQLSELQEIAGSLGQAVILGNIS SILGFNISMSITNPLPSPSDSGW IKVTAQPVERSAPVHHVAFVS SLLVITQPVAAPGQPFPPQPSV KATDSDGNCVSVGITALTLRAI LKDSNNNQVNLSGNTTIPFSS CWAN

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16329	46697	A	16425	65	1905	RTSSRKTTNHCSEIKEDTNNWK NIPCSWIGRINIVKMAKLPKPPL VIPRQTGSGVDLQQTPTDLHLR VLTVRRKTNKQKGHPHQNPCT SPSSKTKVLEVLARAFRQEKEI KGIQVGKEEVKLSLFAADMIVY LENPIVSAQNLLKLSNFSKVS YKINVQKSQAFLYTNNRQTESQ IMTELPFTTASRKRIYLGILTR DVKDLFKENYKPLLNEIKEDTN KWKNNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFIELEKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYNYLIFDKPEKNQWGWKDS LFNIWCWENWLAICRKLKDPF LTPYTKINSRWIKDLNVRSKTIK TLEENLGNTIQDIGMGKDFMSK TPKAMATKAKIDKWDLIKLSKF CTAKETTISVNRQPTWEKIFAI YSSDKGLISRIYNELKQIYKKKT NNPIKKWVKDTRNHFSEKEDIYA AKRHMTKCSSSLAVREMCIKT TMRYHLTPVEEVVRAGEMAKTR RCQN VKGASEEGIRA/HCFVSH *PHCP/LWRATTLMETLKFKEPIE VPCKPLEKSVSLLLL
16330	46698	B	16426	1	2348	
16331	46699	A	16427	1	660	MPNFFIDRPIFAWVIAIIMLAGG LAILKLPVAQYPTIAPPAVTISA SYPGADAKTVQDVTVTQVIEQN MNGIDNLMYMSSNSDSTGTVQ ITLTFESGQVQNKILQLAMP/LL PQEVQQQGVSVKSSSSFLMVV GVINTDGMTQEDISDYVAAN MKDAISRTSGVGDVQLFGSQY AMRIWMNPNELNKVERNSRRQ DVGERDISGSRKVNKESREDE EVT
16332	46700	A	16428	1	975	

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16333	46701	A	16429	1171	2007	AVDIVQGLVRGWGRQGWLLS GRGIPEGPLLWGATVGSWRR LLPLTGVCGPLGAVPVLIS*LL GGAQVQLLREEEAGHELVQQL VDGALVLLLDGRLPLHVVADE RCCVLQDLPVLVHKDEVRLAR GGTAALRVLLLVVVDALDLV EQALGAQGLGVVLEHVSLVV KGLEVRLLIILPPDLVEALLGLP PLLFLGLQSFQDNGDSGDRVLL EALDDLRLGLVAIDAINGTALDH LRRASQGVVQPELLLVFRHPR QLLLHTFQHTDCGQVRLQDIV
16334	46702	B	16430	1	768	
16335	46703	A	16431	1	2553	
16336	46704	A	16432	3	573	CEMHSVQKNEHDKTPEHSRKR SRPSLLRPVSAPAKKMKMLRGT KDLISIAAVGKYGTLP/IGIFL*Q GPPGAEPEGGV*KLPPLHRTLQ PGAGVWL*APAAQPISGVSS* LPRAP*GGSVVPNSIYLVFSYCF *AMIVLF*NPVY*LT*LI*LLIPM HL*GAIIHLGLTLQVLPVPTSV VSILTRIQQWVLE
16337	46705	A	16433	110	1347	LTTATGMELSMGTTWTSLCK AENAAQCQKEPHIWLCSISFL RLKRRRTTTKNTGTKKIASTVA VTIPITPLPTAFCAPEAPVLLT SGIPPRLNASENPQLLSGS/SSSD STGTVQITLTFESGTDADIAQVQ VQNKQLQAMPLLPQEVQQQGV SVEKSSSFLMVVGVINDTGTM TQEDISDYVAANMKDAISRTSG VGDVQLFGSQYAMRIWMNPNE LNKFLQTPVDVITAIKAQNAQV AAGQLGGTPPVKGQQLNASIIA QTRLTSTEEFGKILLKVNQDGS RVLLRDVAKIELGGENYDIAEF NGQPASGLGIKATGANALDT AAAIRAELAKMEFFPSGLKIG YYPYDTTPVVNISIEHVGKTLVE ANNLVFLAMNLVLQEFPPADVIS TIAGPPSLRSSRVPLG
16338	46706	B	16434	1	2550	
16339	46707	B	16435	1	630	
16340	46708	A	16436	270	455	
16341	46709	A	16437	174	492	GALQPPPCVTGAPFWAGQGWS PLPQLAGRCGRGTVRGTGAAC GACGPAGVPGGLGLGGPRTRSS RPALLAPNGGLSTRASGCGGC TESPSSGWPTSAAALDFLPGP

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16342	46710	A	16438	3	413	
16343	46711	A	16439	31	507	
16344	46712	A	16440	1	537	
16345	46713	A	16441	152	247	
16346	46714	A	16442	44	208	EEMTSKMYKVIIRKTMKASVC TQVKHPAIASICKAVL*VGPWS GHFKYAGLPIL
16347	46715	A	16443	1	549	
16348	46716	B	16444	376	862	
16349	46717	A	16445	2	1603	TNVSTTIATVVLNALARATKLL PPGHRRSNPATAAASSPPTTLA HCSLRSHHQPLRGEQQQAIR TAGRCCKALSSCPFFECGRSSG APPGACGQIFRVSNAKLEPQAR PSSPVTGGPLDLMACRVVAAST REMAMLIAQALQTINYGRDDE NGHTHSACEVHHGGRVPELSV PSFSWRNRNNSFIMGSIPTDY TLSCVYLPREDVVLIIYCGVSTN EQPDEEVPRTRFPTVAVSIGFAV RQELEFGVIYHCLVYRLYTGR GRGAFCCNGQLRVSGETASGM LPGIQIHQIQEQNLQVGASTEL PCNLHTTRIRVASAPSSAPEDGT ESKTCNFRVTSKGYCLALPRV PFPLTTGYKHLHKPPTGTHSTY HSMCLLNQPGWLRITISILFLNN KICWQKKSGREIKIEDYFPEYA NYTVPEDGHLSAHLIYLSGLCM WLQHSQDSILYTDYRRGGEN SFVMVNSVALNGDGCICSETE AELIEVSHRLNCSREVEHLNA TGELGEERAHGRQQAACGFTIA
16350	46718	A	16446	1	648	

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16351	46719	A	16447	329	2497	GEGQAVLQGKMGEEKPIGA GEEKQKEG/GKKKNKE/GSGDG SRAELNPWPPEYIYTRL KAEHDSILAEKAEKDSKPIKVT LPDGKQVDAESWKTTPYQIAC GISQGLADNTVIAKVNNVVWD LDRPLEEDCTLELLKFEDEEAQ AVYWHSSAHIMGEGMERVYG GCLCYGPIENGFFYDMYLEEG GVSSNDFSSLEALCKKIIKEKQA FERLEVKKETLLAMFKYNKFK CRILNEKVNTPTTIVYRCGPLID LCRGPHVRHTGKIKALKIHKNS STYWEGKADMETLQRIYGISFP DPKMLKEWEKFQEEAKNRDHR KIGRDQELYFFHELSPGSCFFLP KGVYIYNALIEFIRSEYRKRGFQ EVVTPNIFNSRLWMTSGHWQH YSENMFSEFEKELFALKPMNC PGHSLMFDHRPRSWARELPLRLA DFGGLHRNELSGALTGLTRVRR FQDDAHIFCAMEQIEDEIKGC LDLRLTVYSVFGFSFKLNLSTRP EKFLGDIEVWDQAEKQLENSL NEFGEKWELNSGDGAFYGPKI DIQIKDAIGRYHQCATIQLDLDFQL PIRFNLTVVSHDGEDKKRPVIV HRAILGSVERMIAILTENYGGK LAPFWLSRQVMVVPVGPTCD EYAQNVRQQFHDAKFMADIDL DPGCTLNKKIRNAQLAQYNFIL VVGEKEKITGTVNIRTRDNKVH
16352	46720	C	16449	189	456	
16353	46721	A	16450	3	1414	
16354	46722	A	16451	95	293	

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16355	46723	A	16452	1	1136	MKKRPGHSLFQFQFLMFLRFE ARQPLSEEDVASLSWRPLHLP ADWQRAALSLWTHRTFREVLK EEDVHLTYQDWLHLELEIQPEA \MLFQILNGRTSTSGRSMSTFSL SPRLQGAVTETCRLRVFPFLSTH* WISTKAQGYMTTKILIWLSVA AQEMRILFPDCRRW*LTWSCSK TS*CLSATPLPRSTSSLRFSADG SRL*QAGGAWLPFRDRGSC*C TNGSSSACLRLSSAAAASRQNS PSLPDASSSTWSTLR*ETSAPT EVP*HRTSLPTS/QGPPERLSAE QRPLPDGR/RSYWPFSARRNA/RL ILT/FCSGVVAEPGACAALPVEE TLPEAAPGTAEATRRPAVCQR VRVGAIGFPFLLLDGPVVTS DLK
16356	46724	A	16453	3003	3482	HRPRTRPCPWRNRNHLGHRAP L*PQRARR*SPNPEDGSEDEHL *QLC
16357	46725	A	16454	598	759	KVILGLWTEEAQVGQGGLRAP TPRLLHHVLK*DIKR* AHRPDA VAHACNPNTLG
16358	46726	A	16455	1	1767	
16359	46727	A	16456	2	572	
16360	46728	A	16457	1	726	
16361	46729	A	16458	155	1334	HALGRRGGSQELSAAGAASP SGSERRAPGALPCAWAALLV LGAPPASRPGFAAGKTMMLK EYRNCMLPTVDEYKIGQLYM ISKHSH/EQSDRGEGVEVVQKE PFEDPHHGNGQFTEKRVYLSNK LPSWARAVVPKIFYVTEKAWN YYPYTITEYTCFLPKFSIHET KYEDNKGSNDTIFDNEAKDVE REVCFDIACDEIPERYKESD PKHFKSEKTRGQQLREGWRDS HQPMCSYKLVTVKSEVWGLQ TRVEQFVHKVVRDILLIGHRQA FAWVDEWYDMTMDVREFER ATQEATNKKIGIFPAISISSIPLL PSSVRSAPSSAPSTPLSTDAPEFL SVPKDRPRKKSAPETLTLDPPE KKATNLNPGMHSSDKPCRPKSE
16362	46730	A	16459	26	355	
16363	46731	A	16460	86	489	
16364	46732	B	16461	1	201	
16365	46733	A	16462	3	367	

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16366	46734	A	16463	58	553	VARSAPPDGAAGCAGPGSRRT MAEQSDEAVKYITLIEIQKH HSKSTWLILHHKGYDLTKFLE EHPGGEEVLREQAIGDIAENF EDVGHSTDAEMSKTFIIGELH PDDRPKLNKPPPE*RRCFKETLI TTIDSSSSWWTNWVIPAISAVA VALMYRLYMAED
16367	46735	A	16464	185	489	
16368	46736	A	16465	134	345	
16369	46737	A	16466	572	1017	
16370	46738	A	16467	911	1013	
16371	46739	A	16468	1	157	FGGNQKGERGTGQKKGGERGAK RKDFPGAVCSIALGLAKGCG* SWRPSSAN
16372	46740	A	16469	71	369	SCGLSLIKMTTSQKHDFVAEP MGEKPVGSLAGIGEVLGKKLE ERGFDAKYVVLGQFLVLKKDE DLFREWLDKTCG/APNAKQSR DCF*CLREWCDFAFL
16373	46741	A	16470	1	831	
16374	46742	A	16471	368	679	SSQLNKAPSLFNPVSEEFCLWL LLQKELLTRITSLKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK
16375	46743	A	16472	536	717	
16376	46744	A	16473	1	1632	
16377	46745	A	16474	1	651	
16378	46746	A	16475	1	903	GGGGRMKLIDYGLSGYQEESA EIVKAMDFITSTAILPLFGCLG VFGLFRLLQWVRGKAYLRNAV VVITGATSGLGKECAKVFYAA GAKLVLCGRNGGALEELIRELT ASHATKVQTHKPYLVTFDLTDS GAIVAAA AEILQCFGYVDILVN NAGISYRGTIMDTTVDVDDKRV METNYFGPVALTKALLPSMIKR RQGHIVAISSIQGKMISIPFRSGI CQPSKHATQAFVFDCLAVPEM/E QFEIETVISPGYIHTNLNSVNAIT ADGSRGVMDDTTTAQAEALW RWPRMFLLLWGRRRKM
16379	46747	A	16476	359	1094	
16380	46748	A	16477	1	906	
16381	46749	A	16478	1	371	
16382	46750	A	16479	11	257	
16383	46751	A	16480	2	419	
16384	46752	A	16481	1	2514	

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16385	46753	A	16482	262	822	AGCTRKTRIIDVVYNASNNELV RTKTLVKNCIVLIDSTPYRQWY ESHYALALGRKKGAKLV RVTS L*GLWGGQPDSSLVMKTLSSS ATEGREMRAF*AEEGQHWGVQ GSRKLP GP A FL P*AHIFVSPFQT PEEEILNKKRSKKIQKKYDER KKNAKISSLLEEQQFQKGKLLGE KADELEVGSRRD
16386	46754	A	16483	2	799	SQWLKLPSPPLPHAGISRY'NWD QAP*KTGGPRESYPYHKKREVM KLGRPSCPN/NPKIGPPAGIQHSP VCRGG*QVNTRAPEVWTVGNF ISWGLICRCTP*NKDPSIVVLQC HLNNGAWFRTQGPWVEEFCIV ASSDQQQPYRIQWVRSPNLCAC PLGPAKKGEPLDLSLRKEEIFK QKNDLKKLRKEI*LKRKKNCOI PAVLPGREQFPARGKLS CRA/ SR FQGPQQLWAEQDGFCA*EGQK SLEFLSFRKNPRPRKGQIKFLVF VFHPC
16387	46755	A	16484	1	681	
16388	46756	A	16485	287	694	IISSRPAPASAPRRWGLSWSWQ RCWC**TPSPSPRPRPAEG\CLR GRGRGAGGGLPFRPHGSLVHS GAQPPHFPPLPGGARQTCGAPP GSWSCVL/CRPAETGAAAAGSP AAAGSTRKRLGRAQGRGCRVA ALRLSPTH
16389	46757	A	16486	189	381	QGAGSVGR TGQQLKPGPFFLE KLLSLGCT/LSG*ALRARACCSP CCRPGAGCQPAPVAQAGHP

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16390	46758	A	16487	1	2388	QGRLLVAKPPRPARSTAADSSTP RDMLGLRPPLALVGLISLGCV LSQECTKFKVSSCRECIESGPGC TWCQKLNFTGPGDPDSIRCDTR PQLLMRGCAADDIMDPTSLAET QEDHNGGQKQLSPQKVTLYLRL PGQAAAFNVTFRRAGYPIDLY YLMDSLVSMLDDLNRVKKLGG DLLRALNEITESGRIGGFSVDK TVLPFVNTHPDKLRNCPNKEK ECQPPFAFRHVLKLTNNSNQFQ TEVGKQLISGNLDAPEGGLDA MMQVAAACPEEIGWRNVTRLLV FATDDGFHFAGDGKLGAILTPN DGRCHLEDNLYKRSNEFDYPS VGQLA/HKLAENNIQPIFAVTSR MVKTYEKLTEIIPKSAVGELSE DSSNVVHLIKNAYNKLSRVFL DHNALPDTLKVITYDSFCSNGV THRNQPRGDCADGVQINVPITF QVKVTATECIEQSFVIRALGFT DIVTVQVLPQCECRCDQSRDR SLCHGKGFLECGICRCDTGYYG KNCECQTQGRSSQLEGSCKRD NNSIICSLGDCVCGQCLCHTS DVPGLIYGQYCECDTINCERY NGQVCGGPGRGLCFGCKCRCH PGFEGSACQCERTTEGCLNPRR VECSGRGRCRCNVCECHSGYQ LPLCQECPCPCPGCKYISCAEC LKFEKGPFGKNCSAACPLQLS NNPVKGRCTCKERDSEGCWVAY
16391	46759	A	16488	353	1205	
16392	46760	A	16489	11	440	FRALTEGDTQLNWNVISFPVAE ELSHIHENLVFLETVNQPHHQ VSVPSNNVHAPYSSDKEHMCT VVYFDDCMSIHQCKISCESMG SHPNIRWVSLMACCECIGPECID YGSKTVKCMNCMF*RRQMOT KAT**NNRYKKLKK

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16393	46761	A	16490	515	1808	KRKQTGEFGFNSFE WCDSDLCEMNAGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSLENHQQOSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKA NTMANQSKQLASCTLLSEKDS ESSSPRGRIRLTEDDPQIHHPR KRKVS RV P Q P V Q V S P S L L Q A K E K T Q Q S L A A I V D S L K L D E I Q P Y S S F R A N P Y F E Y L H I R K K I E K R K L L C S V I P Q A P Q Y Y D E Y V T F N G S Y L L D G N P L S K I C I P T I T P P S L S D P L K E L F R Q Q E V V R M K L R L Q H S I E R E K L I V S N E Q E V L R V H Y A A R T L A N Q T L P F S A C T V L L D A E V Y N V P L D S Q S D D S K T S V R D R F N A R Q F M S W L Q D V D D K F D K L T C L L M R Q Q H E A A A L N A V Q R L E W Q L K L Q E L D P A T Y K S I S I Y E I Q E F Y V P L V D V N D D F E L T P I
16394	46762	A	16491	1	699	
16395	46763	B	16492	6	5954	
16396	46764	A	16493	22	585	
16397	46765	A	16494	1	837	
16398	46766	A	16495	1	1422	
16399	46767	A	16496	13	189	
16400	46768	A	16497	193	366	GRPGIFKSFRCRW* C * F H M E F I W K S S A * / W S G V W H A G N I C L S I S N P E D L R A S Q F C S S G
16401	46769	A	16498	1	888	
16402	46770	A	16499	3	531	DAWADAWADAWADAWALQS RRRRRRTQTLSSPHDCYRGLQ SLLLILCKMATLKEKLIAPVAEE I E A I T V P N N R I T V L G D G Q V G M A C A I S I L G K S L A D E L A L V D V L E D K L K G G N D G S F Q H G S L F L / Q T P K I V G R I K D Y S G V T A Q F * R I V V G N W Q G V R S A R R G K V R S N L V Q R N V N V F K
16403	46771	A	16500	2	406	
16404	46772	A	16501	2	394	
16405	46773	A	16502	1	399	
16406	46774	A	16503	74	464	FAFNMPPEKASAPAPKKGSKK AVTKAQKKDKGKRRKRSRKESY SVYVYKVLKQVHPDGTISSKA MGIMNSFVNDIFERIAGEASRL AHYNKRSTITSREIQTAVRLLLP GIELAKHAVSEGTKAVTKYHQ
16407	46775	B	16504	84	832	
16408	46776	B	16505	201	829	
16409	46777	A	16506	1	804	

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16410	46778	A	16507	3	615	PECIIGIDILSSGQNP HIGSLTGR VRAIMVGKAKRKP LELPLPRKI LNQKQYRIAGGIEEISATIKDLK DAGVVIPTTSLFDSPIWVPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGP AIFCR* LLSF*ETALGLLLGFGGN*TFDY
16411	46779	C	16508	25	153	
16412	46780	A	16509	1	1317	
16413	46781	A	16510	1	1557	QVPGCIIGIDILSSWQNP HIGSLT GRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIK DLKDTEAVTPTTSPFN SPIWVPV QKTDGSWRMTVDYCKLNQVV TPIAAAVPDV/VSLLEQINTSPG TWFEWSPK/KALQQVQAAVQA ALPFGPYDPADPMVLEVSAD RDAIWSLWNA AIGESQRRPLGF WSKALLSSADNYS PFERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWWLSDPSSHKVSGAQQ HWKCAVHT/IKWKWYIRDWA QAGLEGTS*LYWPRASRYQQG HQDLFILRDLPSQVFIRDKLME RRNRRTGRTEKARIWEVTDRT VRTWIGEAVAAAADGVTFVS PVTPTHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSEVYTKVF ALDVAARHRVQFAMPESDAVA MLKQLS
16414	46782	A	16511	41	428	
16415	46783	A	16512	1	1026	

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16416	46784	A	16513	648	1886	LDPEVAWAKWQHSTVKGPQKQFAFSWQQQYFTFTGLPQGYINSLSLCYNLIPRDLDRFSLPQDITLVHYIDDIMLTGSSEQLAYTLLDLLVRRLLCAKQWEINL TEIQEA STSVKFLRVQWCGACQDIPSK MKDKLLHLFPPTTKKASLFGFRRQCIPHLECGPEQEKALQQAQAAVQAAVPLERYDPADPMVL/V/ELTWLWPLLSAQFASGQDQH*ALHMAPFLGVVSQLPGGKLILDIFHHGKGRVLFSL*TLTPDMGLPILHIMLLPRLPSVNSQNALS TVMPGFTGPGIKGWKWHHSPLVIH*QNFCLFP*HYVLLA*R S*FQRKEPCHQET*Q*FH*TGS*GCQLDTLGS CYF*VNKLRLRELQ CWLG*LTQTIKMKSVYYITEN CWMKRSPVKRRKILELEEA
16417	46785	A	16514	1	402	
16418	46786	A	16515	1	396	PTPRGERSVHVEIPRRVSGSAGHAQWAGPVRVARPOLNAQLE GWLSQVQSTKRPARAIAPHAGYTYCGSCAAHAYKQVDPSTIQ RFRYSYDESQGEIYRSIEHLDKMGMSUEQLDPVSFSNLYKKYH
16419	46787	A	16516	2	358	
16420	46788	A	16517	2	769	
16421	46789	A	16518	1	1017	
16422	46790	C	16519	54	294	
16423	46791	A	16520	159	245	GISVSCSMYL*PDRSAGYYGLF KDRKEK
16424	46792	A	16521	1	1227	
16425	46793	A	16522	1	2697	
16426	46794	A	16523	200	696	YGI VTPGSLCAGDKQPKKQEK NPVLVSPEFVDEALCACEEYLS NLAHMDID/IGPGGPAVPQPPRA GPSSSVTPSGPVSPLQLGLWA VGRCLGIDPFCLVQPLPLPQASR SFTPLFCSTGLEDHCLRD RVW ATFLGSWHSIVTKMSMDCATKW TAHYPKCVLCGC
16427	46795	B	16524	1	960	
16428	46796	B	16525	1	2183	
16429	46797	A	16526	306	1844	
16430	46798	A	16527	59	189	YNSGCLYGSQCSVCRCL*GVRN QVRSQQQAMMAMAILVNKKG G
16431	46799	A	16528	1	2034	
16432	46800	B	16529	1	855	
16433	46801	A	16530	1	834	

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16434	46802	A	16531	65	172	
16435	46803	A	16532	321	429	
16436	46804	A	16533	460	647	
16437	46805	C	16534	529	804	
16438	46806	A	16535	3	433	
16439	46807	A	16536	1	484	
16440	46808	A	16537	511	681	QQGYTPFQSGSGRESFLASSSF WL/PGLPWLAAL*QALTPSSH SLLSYLCSLLFCHP
16441	46809	A	16538	51	634	PVPTFGLPARHTGAEKRRKNSG GEQLSKNNLYIRGLPPGGTDQD LIKLCQPYGKIVS/TRAFLDKTTI RCKGYGFVDFDSPAQAQKAVA SLKANGVQAQMAKLQERDPA\ GLSVSSLL/SMYEQELENMLK PFGHVISTRILRDANGVSRGVG FARMESTEKCEVVIQHFNGKYL KTPPGIPAPSEPLLCCKIADG
16442	46810	A	16539	1	759	
16443	46811	A	16540	74	352	
16444	46812	A	16541	1	747	GSVYLYCYKKSVAKTNTVSYK AGLICRYPQEDYESFSLPESVPL FCLPMGATIECWPSNSKYPLPV FSTFVLTGASAEKVYGAIIQFY EPYSEENLTEKQRLLLGLTSAD GKSDSSKTIHTNKCICLLSHWPF FDAFRKFLTFLYR/YSISGAHV LPIEKHISHFMHKVPFSPQRPRIL VQLSPHDNLILSQPVSSPLPSG GKFSLLQNLGPENAVTLVFA VTEHKLIHSLRPSVLTSVTEAL
16445	46813	A	16542	319	969	
16446	46814	A	16543	131	342	NSDMGLNLGSALTG*PWVAIEF CCFGFFQIIIVFSCLLGWL*VAP HPNLPSSPAEYMDFREAQEGTD VIY
16447	46815	A	16544	1	1086	
16448	46816	A	16545	469	759	
16449	46817	A	16546	3	598	
16450	46818	A	16547	227	604	
16451	46819	A	16548	416	1814	
16452	46820	A	16549	763	867	
16453	46821	A	16550	1	1419	

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16454	46822	A	16551	915	3125	SLAGMRLTGTVSGGVEVR/TAK AGARVGPPELVGRPLEGECWY FSGVSRTOAQQLLLSPNEPGA FLIRPSESSLGGYSLSVRAQAKV CHYRVSMADGSLYLQKGRLF PGLLELLTYKANWKLQNPPL QPCMPQKAPRQDVWERPHSEF ALGRKLGEGYFGEVWEGLWL GSLPVAIKVIKSANMKLTDLAK EIQTLKGLRHERLIRLHACVSG GEPVYIVTELMRKGNLQAFGLT PEGRALRLPPLGFACQVAEGM SYLEEQRVVRDLAARNVLVD DGLACKVADFLARLLKDDIY SPSSSSKIPVKWTAPEAANYRV FSQKSDVWSFGVLLHEVFTYG QCPYEGMTNHTLQIMRGWF FGCISRSEAVRRLQAEGNATGA FLIRVSEKPSADYVLSVRDQA VRHYKIWRRAAGRLHLNEAVS FLSLPELVNYHRAQSLSHGLRL AAPCRKHPEPLPHWDDWERP REEFTLCKRLQSGYFGEVFEG WKDRVQVAIKVISRDNLHQQ MLQSEIQAMKKLRHKHILALY AVVSVGDPVYIITELMAKGSLL ELLRDSDEKVLVPSSELLDIAWQ VAEGMCYLESQNYIHRDLAAR NILVGENTLCKVGDFGLARLIK EDVYLSHDHNIPYKWTAPALAS RGHYSTKSDVWSFGILLHEMFS RGQVPYPGMSNHEAFLRVDA
16455	46823	A	16552	1	990	
16456	46824	A	16553	1	2847	MTAREHSPRHGARARAMQRAS TIDVAADMLGLSLAGEPHRACT GLQTTGYPGLDPSG*TRK*GRG MSALFL*TASAGA*~LH*FSSSLVA GAPPG*CGNVQVF/WLAHAQA MGTNNPIFLSSIAFFQDSLINQM TQVKLSVYDVKDRSQGTVKS ESDRVGNITVIGWQMEEKSDQ RPPVTRSVDTVNGRLHPPAPT MHSLSHRHSKKNSNFRALALM VLPVDESLEALGIRSKYASLR KDTLLKSVFGGAICR
16457	46825	A	16554	1	327	
16458	46826	A	16555	259	3109	
16459	46827	A	16556	262	3159	
16460	46828	A	16557	1	1398	
16461	46829	A	16558	123	393	
16462	46830	A	16559	245	424	

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16463	46831	A	16560	1	531	
16464	46832	A	16561	2348	2775	
16465	46833	A	16562	373	555	LRIQVTFDDVAVEFTPEEWALL DTTQKYL YRDVML ENYMNLA SVGKSNITLLGMVACTCS
16466	46834	A	16563	165	457	
16467	46835	A	16564	310	349	K*TMK*EMGKFK*FY/YLEQED YANANALLSPAPALPKEKRTDS NGRVYFVNHNTRITQWEDPPRS QQQLNEKLPPEGWEMRFTVDG IPYFVDHNRRRTTTYIDPWSTRP
16468	46836	A	16565	1	2217	
16469	46837	A	16566	1402	1860	
16470	46838	A	16567	461	696	KRMCFCTLS SARSSSGSMYMSC RICCSMPFPSSVFRSISRYSR AAFWAWTETRLCWQAAMP RQ QPPGLLHQWTTSP
16471	46839	A	16568	1	601	
16472	46840	A	16569	468	1213	
16473	46841	A	16570	2	365	EGCFQKIKLDHILSPPPMPFWK CSNPDVAFGPGKSLKYKRQLS* DGRQLRRGSLGALTGRVLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPLSTASLPCVSKCW ENIPPMWNCPPIK
16474	46842	C	16571	220	408	
16475	46843	A	16572	840	1091	QSLQHDVTL*VPVLLSYPEPAPS GHGLLRGSQAIAL*TI PADPAGT YLKTR EPTLGQCTVPLPAPHLS VDTVCRCLSSSVWPQ
16476	46844	A	16573	1	1356	
16477	46845	B	16574	1	1084	
16478	46846	A	16575	2	526	QPRGKKFSKKNKPRKQNFPTPKH MRVVLPPF/PPLKFFIFPKGLKFL EGGCPNISPPQKKGSLPKIPR*V LIRPPIRKKLFPCTARVKLGPPQ GSFKTAAPSSSSP*SADPVYLAG K/PRQSSSPGGTGGLNPPRRRLQ PQPHPGPSWHSSSRGPGGHP R RESAERSRCASGNPGGQ
16479	46847	A	16576	36	167	RQLFENTQSDETKQEQNKQNK K*STATESRKVPQIGKSKSYWP
16480	46848	A	16577	171	527	
16481	46849	B	16578	1	471	
16482	46850	A	16579	1	294	
16483	46851	A	16580	185	299	GLQYLKKGKSLKVKRKGKVV*S ACCKKKGAALGTVASPL
16484	46852	A	16581	3	414	

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16485	46853	A	16582	462	928	WGVPGLPGRHLLPLSPQPPPSW LSILYVSWAALTCFLNSGESTA AKFFCPNLSAISYHTEAIPTTWQ GVHLSWAFNGGAPDIFSGPGGL L*PA/PQP/DLALGALFGAGVLV ITTVAGGITTLLFIQHHTTQEI H*QIVQWIKTIL*ILATVSVVIG
16486	46854	A	16583	1	654	
16487	46855	A	16584	66	323	RVSLEIHVIQKRRPHHLSLSFW TRMKTFRRRK/WGEAEESATDT TSETNKVGTGVFVLSLVVPL VRNLAPGVVLGNICKHFPVC
16488	46856	A	16585	1	1530	
16489	46857	A	16586	615	873	FVFLWSLMMVMYRWGFGVAV LSVC*FSF*QSGPSAAGLLEFAG GPFQTPFAWVSVEAAEQRIML NSKRCCVIVPLVVSQRGTRP
16490	46858	A	16587	286	626	PCKLFPCNCTCYSRV*DFFRVA GKRSLNNNTYSWVNTSMLVPR VAFACGFPQLQAAVLCVHLLG SPILGAADSSVTPPFCWMANAH ICGLQLQNTLSFAEPIVLGQEH QLS
16491	46859	A	16588	226	489	PYLSVIFFFDYGINEEQCQRPIQ GDGQNFHRHNGWIKINPSCISF AIFFPFGAEKNMWSTPVEAFN LLST*AF*LFGYKCTLVISS
16492	46860	A	16589	1	1344	
16493	46861	A	16590	1	257	
16494	46862	A	16591	73	374	ESETEHKRPGKHSKPRSCNMCG QWAFHASLTVSYCLLTWCNET CSGDGCEGGMRIDIDPPVSQTR FFITLL*LCFPGAGQPAYFCTQ TQCHVETPRVSQ
16495	46863	A	16592	1	666	
16496	46864	A	16593	95	1840	
16497	46865	A	16594	1740	2026	
16498	46866	A	16595	39	487	SRLDPRVRLFRQFCETRPGLC YIQFLDSVAEYVTPDEKLGEK GKEIMTKYLTPKSPVFIAQVGQ DLVSQTEEKLLQKPKELFSAC AQSVEHYLRGEFFHEYLDMMFF DRFLQWKWLE/RVCACQVRAT GKMYACSRLEKKRIQKRK
16499	46867	A	16596	1	591	

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16500	46868	A	16597	71	1994	EQEQRGRQGGLAPPAPAAAA AARAAAAAAPPQALTAPPAG SVADRRRLSMELINIVANTVLLK AREGGGGKRGKSKKWKELK FPHISQCESLRRITDRDYCRVC DKQPIGARLLFRQFCETRVPGLEC YIQFLDSVAEYEVTPDEKLGEK GKEIMTKYLTTPKSPVFAQVGG DLVSQTEEKLLQKPKCKELFSAC AQSVHEYLRGEPFHEYLDMSFF DRFLQWKWLERQPVTKNTFRQ YRVLGKGGFGEVCACQVRATG KMYACKRLEKKRIKKRKGESM ALNEKQILEKVNSQFVVNLAY AYETKDALCLVLTIMNGGDLK FHIYNMGNGPFEEERALFYAAE ILCGLEDLHRENTVYRDLKPEN ILLDDYGHIRISDLGLAVKIPEG DLIRGRVGTGYGMAPEVLNNQ RYGLSPDYWGLGCLYEMIEGQ SPFRGRKEKVKREEVDRRVLET EEVYSHKFSEAEKICKMLLTK DAKQRLGCGEEGAEEVKRHPF FRNMNFKRLEAGMLDPPFVDP PRAVYCKDVLIDIEQFSTVKGVN LDHTDDDFYSKSTGSVSIPWQ NEMIETECFKELNVFGPNGTLP PDLNRNHPPEPPKGLLQRLFK RQHQNNSKSSPSKTSFNHHNS
16501	46869	A	16598	1	963	
16502	46870	A	16599	192	609	RPGARELRLHPGPRYGRSTSPQ NCPWARPGCLHEAL*GWKICL HCKCPQEEHMTVMPLMEKKT ISKLMFDFQRNSTDDDSGCAL EEYAWVPGLKPEQVHQYYS LPEEKVPYVNSPGEKLRKQLL HQLPPHDNEV
16503	46871	A	16600	1	915	
16504	46872	B	16601	30	820	
16505	46873	A	16602	99	248	RLEKHINCSRVI*SWAASPGLTA AAYRVTLNPPGTFLGVAKVG QYTFT
16506	46874	A	16603	1	717	
16507	46875	A	16604	271	556	TAACLQSHHFSSGQLSFERKW PKVGVTITRSIASLLSGPVGLIHH LAFSAHVPREGPTTPWNYFPRV AAP/RRWTPGEHARTTTGLGAA PCVLLWA
16508	46876	C	16605	135	341	
16509	46877	A	16606	125	226	
16510	46878	A	16607	194	547	

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16511	46879	A	16608	2073	2338	
16512	46880	A	16609	1127	1282	
16513	46881	C	16610	1	2094	
16514	46882	A	16611	523	706	QHPLPNPCCHQPFHLCRLRR*TL HCLRQQ*WPPLRQLPGKIMLIL LRSHPOHPCLLLDLQLD
16515	46883	B	16612	190	805	
16516	46884	B	16613	90	2812	
16517	46885	A	16614	44	216	RCRRRLIPHPRRLSPVVRIRIQVP Q/VQPGAGPSRPGHTRDP/IGAA AAHCPGPGDSGAH
16518	46886	A	16615	1	1107	MTEEPLQALVLSAVLLYQEAY VRRSLTALGLDTFANFAHFSEM QPLSDAPCGLVTGVTRPLVAYS VEVGFTIICGLSLASGNISGWC QLYLLLTQCRGAATLWDSGM GGGRQSSRQTSVPRWTLDSKCI PGPKLTTRPQMDTKALGGQQA HVEHQTHEDIRPQVDTPAGG HKALGEGQDPVGHQASVGYSP QVPQDSLGLAGQATPEIPLG LQLHTVLVQEIQLIEAQTAP GPCAEVRALPAPAAEPEPAWEE APPERALELEGAPAKDQTNEEL PEITA/PYC/EPLALTLELKAWE RKVGGGRGDQHSPPSQLPCCP*S WARWQTCRQRAGHLAWPPVP RCREASLIH*NHSPAAAGPFILL
16519	46887	A	16616	1	792	
16520	46888	A	16617	1	963	
16521	46889	A	16618	1	378	
16522	46890	A	16619	1	494	MKPRTLAVSVTVLKGGSVRVC SFWCSDVFRVSSFVWVRGLAD SGVKLRITFAVSVTPLKAARLEL FVPPGGFVVSLSAGVKLQPFV SVTAHKGSDPKSEKQDQLLQ RGKEQSYHTGEGHPSRLP/PAG SGSLLLSYLAAPTSC*LVQPSG LF*QGADWCINYP
16523	46891	A	16620	137	262	

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16524	46892	A	16621	1	2786	EVSLREATQRKLRRFSELRGKL VARGEFWDIVAITAADEKQELA YNQQLSEKLRKRELPLGVQYH VFVDPAGAKIGNGGSTLCALQC LEKLYGDKWNSFTILLIHSDEW KKKVSESYVITERLEDDLPIKE KELTELNRNIFGDEAFSKVNLN YRTENGLSLLHLCCICGGKKSH IRTLMLKGWRPSRLTRNGFTAL HLAVYKDNAELITSLHSGADI QQVGYGGLTALHIAITAGHLEA ADVLLQHGANGVN
16525	46893	A	16622	174	722	
16526	46894	A	16623	1	1554	
16527	46895	A	16624	1	843	
16528	46896	A	16625	2	745	ECWDGEHDIETPYGLLHVVRIG SPKGNRPAILTYHDVGLNHLKLC FNTFFNFEDMQEITKHFVVCHV DAPGQQVGASQFPQGYQFSPM EQLAAMLPSVVQHFGFKYVIGI GVGAGAYVLAKEFALIFPDLVEG LVLVNDIPNGKGWIDWAATKL SGLTSTLPDTPVLSHLFSQEELVN NTELVSQYRQQIGNVVNQANL QLFWNMYNSRRDLINRPGTV PNAKTLRCPVMLVVGDNAPAE DGVVECNKS
16529	46897	A	16626	3	949	
16530	46898	A	16627	1	633	
16531	46899	A	16628	2	1324	
16532	46900	A	16631	1	591	
16533	46901	A	16632	138	832	
16534	46902	A	16633	55	586	IFVHPTPAASTMPKFDNPEIKV VYLRCCTGGEVGATSAAPKIGP LGLSPKKVGDDIAKATGDWKG LRITVKLTIQNRQAQIEVPSAS ALIIKALK/EPDRDRKKQKNIKH SGNITFDEIVNIARQMRHRSRLAR ELSGTIKELGTASVGCNVVDG RHPHDIIDDINSAGAVECPAS
16535	46903	A	16634	1	735	
16536	46904	A	16636	3	346	
16537	46905	A	16637	57	649	GPRRAYGGRMAGGGDLSTRR LNECISPVANEMNHLPAHSHDL QRMFTEDQGVDDRLLYDIVFK HFQRNKVEISNAIKTFPFLEG LRDRDLITNMFDSDQSCRNL VPVQRVVYNVLSLEKTFNLPV LEALFSDVNMQEYPDLIHYYKG FENVIHDKLPLQSEEEKEREERS GLQLSLEQGTGENSFRSLTWPP

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16538	46906	A	16638	1	1665	
16539	46907	A	16639	348	1534	
16540	46908	A	16640	1	627	
16541	46909	A	16641	1	1343	
16542	46910	A	16642	76	479	IRAVSRSRERPGSRRLYLQAC*G GGAFPPGP*SAEISRLVRSNHLGG YSCT/EGGGGCRKGSCLLQHS LLWHSCLLPASKNTVCSKDLG GCSCQTQESRAPACSWSPRTQGG SASSHDLGSCRNAWETPSRQLG RSW
16543	46911	A	16643	130	675	
16544	46912	C	16644	118	420	
16545	46913	A	16645	1	987	
16546	46914	A	16646	1	494	
16547	46915	A	16647	360	1510	
16548	46916	A	16648	375	2187	VTAAAAATAMAESGESGGPPG SQDSAAGAEAGAGAPAAAASAE PKIMKVTVKTPKEKEEFAPVEN SSVQQFKEEISKRFSHTDQLV LIFAIAGKILKDQDTLSQGHIDG LTVHLVIKTQNRQPDHSAQQTN TAGSNVTTSTPNSNSTSGSATS NPFGLGGLGGLAGLSSGLNTT NFSLEQSQMQRLLSNPMMV QIMENPFVQSMLSNPDLMRQLI MANPQMQLIQRNPEISHMLN NPDIMRQTLELARNPAMMQEM MRNQDRALSNLESIPGGYNALR RMYTDIQEPMLSAAQEFGGN PFASLVNTSSGEGSQPSRTENR DPLPNPWAPQTSQSSASSGTA STVGGTTGSTASGTSGQSTTAP NLVPGVGASMFNTPGMQSLLQ QITENPQLMQNMLSAPYMRSM MQSLSQNPDLAAQMMLNNPLF AGNPQLQEQRQQLPTFLQQM QNPDTLSAMSNPRAMQALLQI QQGLQTLATEAPGLIPGFTPLG GALGSTGGSSGTNGSNATPSEN TSPTAGTTPEGHQQFIQQMLQA LAGVNPQLQNPVRFQQGLEQ LSAMGFLNREANLQALITGG DINAAIERLLGSQHHSISVS
16549	46917	A	16649	269	440	
16550	46918	A	16650	469	746	RLNLPGLPCAGTSILFAVLMFAI GVSCIRQAGGGHVASHIY*GLM /PALAL*DTPEPRNPALPETCLC GSGPQSQMGHQTSHLLSSPGTG LSF
16551	46919	A	16651	1	1026	

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16552	46920	A	16652	719	906	
16553	46921	B	16653	1	1971	
16554	46922	A	16654	200	239	
16555	46923	A	16655	109	177	
16556	46924	A	16656	1	1542	
16557	46925	A	16657	1	453	
16558	46926	A	16658	2	487	
16559	46927	A	16659	1	1260	MEDAEGTVTLAVTLVARDLN CIQPTQTGPSGGIPEESIVIGDVSS MHVIAPEDLVPGQDVEVEDSDI DDPDPVRALPLQIHACGRVGF AHDWSEGGDPAADTLIDPSQ DARYLKCEGMQAPHNSNPVAQ KTEISYHIWIARIPREKSGKVTG TLCDLLKDLTVIHSLIPKQGCSD GLGVLVQGTFPQPGNTDCTC QVSAVEGKGEGMLQLASLRR VTIWAYGDSQERDLKTQLEKIT AIKDMKEMQEKEYRIMEKAHS RQRKQHHKGPKEKQAAIFAV LQPLVITRQTGSGVDPOKTPA DLQKRCRTVRRKTSQKQAVAS TLTKRITTQKLNKADHNSSPTR EQNCTENEFDELTEVGFRRWVI TNSSELKEHVLTCQKEAKNFDK RLEELLIQITSLEKNISDLMEL*S FALSFCVVILFVNVDATAFCWL VFLLTVRHLFCRSAGVFWGSTP DPVCLVITSGGCRTAKIAACSFL SGPLWCCFLCLEWAFSILYSFS CISFMSLIAVIFSNVWLRLSL
16560	46928	A	16660	1	799	
16561	46929	A	16661	1	969	MHVIAPEDLVPGQDVEVEDNDI DDPGQAKMTMEEQWTLVSLLS TSQQQGPVPPGSTASSATDKLS RWELTLLYSTTLFLAREAFRRA CLSGGTQRDWSQTLNLLWLT PLGVFWSLFLGWLWLQLEVPD PNVVPHYATGVVFLGLSAVVE LLGEPFWVLAQAHMFVKLKI AESLSVILKSVLTAFLVLWLP WGLYIFSLAQLFYTTVLGLCYV IYFTKLLGSPSTKLQTLPSRIT DLLPNITRNGAFINWEEAKLAW GFFKQFFLKQILTEGGRYVGG HFLNVLNFGDQGVYDIMNLI SLVARLIFQPIEESFIYS
16562	46930	A	16662	1	1665	

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16563	46931	A	16663	1	1521	MDVSSPPCVDGVSILPLLIPRQ TGSQVLDLQQNPDTDLQLRVLT V KRKTNKKQKQHPHNSICTSPSS KTKEYTFFSVQHHYTSKIDHIV GSKAVLSKRRKTIEIITNCLPDHS AIKLELRKKLTQNHKTWQKN NLLNDYVWHNMKAIEIKMFF ETNKNKDTYKNLWDTVKAV CRGKFIALNAHKRQKERSKIDT LTSQLEKELEKEQTHSKASRRQ EITKIRAELEKIEITQKTQVQIHES RSWFFEKINKIDRPLAGLIKKRR EKSQKDAIKNDKLDITTDPTET QTTIRDYHKHLYAIKENLEEM DKFLDTYTLPLNQESLNRPIGT SEIEAIINSLPTKKKYRTRRIHSR ILSEVQGGAVLEVLAIRQEK EIKCIQLGKEEVKLSLFADDMIV YLENPTVSAQNLLKLSNFSKVS RYKINVQKSAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLEIKED/N KWKISPCPRIGRINIM
16564	46932	A	16664	2	2315	
16565	46933	A	16665	1	912	
16566	46934	A	16666	1	912	
16567	46935	B	16667	199	619	
16568	46936	B	16668	64	1815	
16569	46937	A	16669	1	239	
16570	46938	A	16670	1	242	FREDGKTACGHEPSPVLLGLRL GLQPWG*GWGCSHGAGSAPDL VAGSAHSCGLWLPGLHHHPA QCLPALLCGHLCLSVQDQNG LLGR
16571	46939	A	16671	58	505	ASSRTRPSTLARGRRWFPQPL SGRQRQRRGRRGSRVG/YGTA QNSTLTSPAASASEATVSGHW PSTAPCCV/PAGAGSATMWRSP A*AACGSAAWTSTWSRRSPGP GAAAGYGGVRTFCQPAGLTR/L ANRSTAGLCGWGLTSLCRETEL
16572	46940	A	16672	242	2952	
16573	46941	B	16673	474	2690	
16574	46942	A	16674	97	451	
16575	46943	A	16675	667	893	

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16576	46944	A	16676	3	639	RIRVHPTPAAFMPPKFDPNKIG VGYLRCCTGGEVGATSAAPKIG PLGLSPKKVGGDDIAKATGDWK GLRITVKLTIHNRQAQIEVAPSA SALIHKALKEPPDRKKLKLKL SGNITFDENGNCSTDMR/HRSL SRELSGTTKEILGTAQSVGCNV DGRHPHDHDDINSENDKQPRKS KMRTSFSQIPGHEHFHYLLLL QHVHCQLALTL
16577	46945	A	16677	350	984	VYLEVAPGGESRLPLSALGPQR IGPPGSCLPKKSWNIDICQRP G/DWKG*GLQVKLTHSRGTGQ APDCTRV/VLPSCP*FIQSPSRE PPKRPEKKPEKTFKHQLGIFTL NEICSTLLRQMR/HRSLSPKLS/ GTPLKEIPGGLPQSSWAGNV*W AAIPHDHDDIQQVWLWKCFAV SDIFIVTVGVKGGPPSVFTEISW EVL.EMVTGGVG
16578	46946	A	16678	252	964	
16579	46947	A	16679	1	182	
16580	46948	A	16680	275	639	
16581	46949	A	16681	376	418	
16582	46950	A	16682	1135	1591	
16583	46951	A	16683	3	420	AAKEIEVGGGRKAKFSQKIQV RLVRELEKKFSGKHVVFIAQRR ILPKPTRKSRKTKNQKRRSRRL TAVHDAILEDLVFPSEIVGKRIR VKLDGSRLIKVHLDKAQQNNV EHKVETFSGVYKLTGKDVNF EFPEFQL
16584	46952	A	16684	1	879	
16585	46953	A	16685	2	691	HEEKAMFSSSAKIVKPNGEKP DEFESGHLPLGLELE/MNSD/L KASAQGT*ITAS*RLKLVGGCS ESLFH*SFVPRSLKLKTFPQKNP KVRA*LRRIKKKVPVGKAMS VLYPPSEGEFLPLSPTSEKARTK K*AKSRPPGARTLDKLVHDAH PLRDFGPFPSGNFWAKRIPRSNL DGQPGSIKVPFWTKAQQNQCW NTRVETFFLVSYK/KLTGGGC*F LEFPRVFN

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16586	46954	A	16686	1	452	TLLVIPRKMRSVELQQTSTDL QLRDLTVRKKTNKRKATASTS QKGHLLHQNPICRSPTSKTKEVG FRRSVITNFSLEKEDVRTYHKE AKNLENRLDEWLTRINSVEKTL NDLKLKTMARDLHDACTSFN RRFDQVEERVTVTEDQIN*QTE SNSINFTKRSSTPKPHL/RSPTSK TKEVGFRRSVITNFSLEKEDVR TYHKEAKNLENRLDEWLTRINS VEKTLNDLKLKTMARDLHDA CTSFNRRFDQVEERVTVTEDQI
16587	46955	A	16687	1	618	
16588	46956	A	16688	280	353	SCNSIFARSVRACCS*VASSSFC C
16589	46957	A	16689	1	459	IKYSSPMKSTFVDPVDPVAVAV IYCLAAGLVIRIPFFQLVPLKEE KMLVLLNMDYYEMASLSLVTH RNEAPFSGRVRSSLPATEQSWM ENDFDKLTVEGFRRSVITNFSLE KEHVLTHHKEAKNLEKRLDKW QTRINSVEKTLNDLMELKTM* EEKMVLNMDYYEMASLSLV HRNEAPFSGRVRSSLPATEQSW MENDFDKLTVEGFRRSVITNFS ELKEHVLTHHKEAKNLEKRLD KWQTRINSVEKTLNDLMELKT
16590	46958	A	16690	2	403	LALSGEMTLVLFMLLAGGWVT HDKPEMPRAATSGGTRKGKT KAALKDLIATWKEVCVSSPATE QSWMENDFDELTEVGFRRSVIT NFFKLKEYVLTHHKEAKNLEK MLDEWLTRINSVEKTLNDLME LKNMA*ELTEVGFRRSVITNFF KLKEYVLTHHKEAKNLEKMLD EWLTRINSVEKTLNDLMELKN
16591	46959	A	16691	1	676	
16592	46960	A	16692	1	1965	
16593	46961	C	16693	1	3075	
16594	46962	A	16694	78	152	CAAGFGLPVFY*GFLHRCSLGIL V
16595	46963	B	16695	1	904	

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16596	46964	A	16696	1	2026	EQEASYGRDAFAKAIYERLFC WVTRINDIIEVKNYDITTHGKN TVIGVLDIYGFIEFDNNSFEQFCI NYCNEKLQQLFIQLVLKQEQQE YQREGIPWKHIDYFNNQIIVDL VEQQHKGIIAILDDACMNVGK VTDEMFLEALNSKLGKHAHFSS RKLCSADKILEFDRDFRIRHYA GDVVYSVIGFIDKNKDTLFDQF KRLMYNSSNPVLKNNWPEGKL SITEVTKRPLTAATLFKNSMIAL VDNLASKEPYVVRICPNDDKKS PQIFDDERCRHQVEYLGLLNV RVRRAGFAFRQTYEKLHRYK MISEFTWPNHDLPSDKEAVKKL IERCGFQDDVAYGKTKIFIRTPR TLFTLEELRAQMLIRIVLFLQKV WRGTLARMRYKRTKAALTIIR YYRRYKVKSYIHEVARRFHGV KTMRDYGKHKVWSPPKVLR FEEALQTIFNRWRASQLIKSIPA SDLPQVRAKVA AVEMLKGQRA DLGLQRAWEGNYLASKPDTPQ TSGTFVPVANELKRKDKYMN VLFSCHVVRKVNRFKVEDRAIFV TDRHLYKMDPTKQYKVMKTIP LLQLTCLNWSNGKDQLVVFHT KDNKDLIVCLFSKQPTHESTRIGE LVGVLVNHFSEKRHLQVNV TNPVQCSLHGKKCTVSVETRL NQPPQDFTKNRSGFILSVPGN
16597	46965	A	16697	1	1665	
16598	46966	A	16698	1727	1908	FLFFYIC*RELYFQLCGQFVWNK CNVLLRRMYILLIWGGFECRYQ LGLLGAELNSVPGYHC
16599	46967	A	16699	1	384	
16600	46968	A	16700	1	636	
16601	46969	A	16701	1744	2283	
16602	46970	A	16702	194	368	
16603	46971	C	16703	62	205	
16604	46972	B	16704	1	1257	
16605	46973	A	16705	1	1077	

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16606	46974	A	16706	1213	1228	AQN*QTQRTSTPKPHLSSPSTK TKENDFDELREEGFRRSVITNFS KLKEDVRTHRKEAKNLEKRLD EWLTRINSVEKTLNDLMELKT MAQELRDTYTSFSSRFQVEER VSVIEDQMNDMKREEKFREL/K RVQRNEQSLQEIWDYVVKRTNL RLIGVPEKIQTIREYYKHLNAN KLENLEEMDKFLDTYTCPRLN QEEVESLNRPTVGTSEIEAIINSLP TKKVQDQADSQPNSTRVFKTV CISSLGHTTASADTDVQCQLPV TSLLEQGLSSKSAGFLDYAVQR LWLLGTEPL
16607	46975	A	16707	33	263	
16608	46976	A	16708	204	1756	
16609	46977	A	16709	760	821	TMRTHGHRKGN*QR/**PEST KNSNKFTRKNQTTPSKREWMK LETILSKLSQGGKSKHRMFSLI SGN*TMRTHGHRKGNITHWGL LWG
16610	46978	A	16710	1	879	
16611	46979	A	16711	311	514	KNAHHQWPSKKCKSKLQ*DTIS HQLQWQSLKSSQETTGTMRKME TITLSKLSQGGKSKHCMFSLIGG N
16612	46980	A	16712	24	1268	AGLCAARARMRLFRWLLKQPV PKQIERYSRFSPLSIKQFLDFG RDNACEKTSYMFRLKELPVRL ANTMREVNLLPDNLLNRPSVG LVQSWDMQSFLELL*YENKSP DPQVLDNLFQVLKVRDRHND VVPTMAQGVIEYKEKFGDFPI STNIQYFLDRFYTNRISFRMLN QHTLLFGGDTNPVHPKHGSDIP TCNVADVVKDAYETAKMLCE QYYLVAPLEVEEFNAKAPDKP IQVYVYPSHLFHMFLFELKNSM RATVELYEDRKEGYPAVKTLV TLGKEDLSIKISDLGGGVPLRKI DRLFNYMYSTAPRPSLEPTRA PLAGFGYGLPISRLYARYFQGD LKLYSMEGVGTDAVIYKALSS ESFERLPVFNKSAWRHYKTTPE ADDWSNPSPSEPRDASKYKAKQ
16613	46981	A	16713	175	465	
16614	46982	A	16714	240	381	FFLSFPLQCQS*NQNLLPW/ICA KVCSTPEVSKTTNPLEGRNSG HI
16615	46983	A	16715	268	1524	
16616	46984	A	16716	1	378	

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16617	46985	A	16717	708	987	IQLPGHRSQQQVAGASHTDARQ QDPGNSHSDFVRIISHLPCLER QDRRSAGHNGSATVPGTEACG RAYKAPAGHYHSGAGQSLPAA SHRSFSSP
16618	46986	A	16718	1	2052	
16619	46987	B	16719	1	606	
16620	46988	A	16720	1	541	QHQRKQKRLRAQONLSWEEI AKEYQNEEDSLGGSRVVCDI NKEMLKVGKQKALAQQYRAG LAWVLGDAEELPFDDDKFDIYT IAFGIRNVTHIDQALQEAHRVL KPGGRFLCLEFSQVNNPLISRLY DLYSFVRVPLVGEVIAGDWKSY QYLVE/SIRRFPSQE/KFKD/MIE DAGFHKVTYESLTSGVVAIHSG FKL*FLCLEFSQVNNPLISRLYD LYSFQGHPCGRGHRWRLEVL VPCREVSEGFRLRKEFKDHDRR CRLSTR
16621	46989	A	16721	526	933	
16622	46990	A	16722	191	468	
16623	46991	A	16723	2	677	GKVVHLERRGFHRTMEHLQKI LLLPVLSSSSSDP/STLSVSALV RMFSSADE*SVSEASSSEPSSFS RRSSCSFGSEPSFASFSSFPDL ASLSSVFLFRAFSSSHVM*WL PSSS*VGS/STSARAQLPSYVPSF SVKTKSGLKSALRFFPKAFCL PSTMGPSSSSPESDSALHRLV ILDVWLQIKPRVRKPCRRSHF RKRAQPAVRPLTFRSLLVLR
16624	46992	A	16724	31	187	
16625	46993	A	16725	215	947	
16626	46994	A	16726	1	378	
16627	46995	A	16727	2	7567	GGGGARRQRGDAGGAETAP SEIHLSPAAERSGRSETLRRGT AAGRMATVVVEATE/PEPSGSI ANPAASTSPSLSHRFLDSKFYLL VVVGEIVTEEHLRRAIGSIELGI RSWDTNLIECNLDQELKLFVSR HSARFSPVEVPGIKILHHRSERF *ETVVLIQ/PFLMEGSSGTEVRL MITDAARHKLLVLTGQCFCENT GELLQSGSFSFQNFIEFTDQEI GELLSTTHPANKASLTFCPEE
16628	46996	A	16728	101	365	VITGQPNPTNPNLQATPDIQGT ARLGA/LHPRGIIFIGHQSA/R PHAPAPANPNKRTLFRPPPLSPP SPEPPSGQGAGLGARPALP

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16629	46997	A	16729	1170	2847	VASC*ENACKQNQRQKPCDYLNRCRKGWLQNSTTLHAKNSQ*TVLYKTIKFQLEKTTLKFIWNQKRAHIAKSILSQKNKAVGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNRTEPSEIMPHIYNHLIFDKPDKNKKWGKDSLFNKWCWQNWLAICRKLKLDPFPTPYTKINSRWIKDLHVRPKTIKLTLEENLGNTIQDIGTGKDFMSKTPKAMATKDKIDKWDLJKLKSFACTAKE TTRVNRQPTKWEKIEFTT
16630	46998	A	16730	79	536	
16631	46999	A	16731	232	771	
16632	47000	A	16732	3	339	
16633	47001	A	16733	279	416	
16634	47002	A	16734	1	1760	
16635	47003	A	16735	309	1718	
16636	47004	A	16736	10	417	IAIMNDTVAIRTRKFMNRLLE RKQMVIDVLHPGKATVPKTEILEKLAQMYK TTPDVIFVFGFRTHCGGGKTTGFGMIYDSLDAEK NEPKHRLARHGLYEKKKTS*K QRQERTNRMKKVRGTAKANV VAG*KPNE
16637	47005	A	16737	96	609	EKFMTNRLTSGETKWWI*CPFT PGRRTVP*AQKIRIEKLAQNVQ RPHPDVIFVFGFRTHFGGGKTTGFGMIYDSLADYAEKEMNPKHRLAIRHGPMEEGKRPSKKN GKERKNQN*KRVQGGGLAKGPLLGAGQKEEMKCLGSEIGSQ PKELKVLPMMLAVATVDFSQE
16638	47006	B	16738	1	1041	
16639	47007	A	16739	3	447	VSVPFIFIWLTCKSFLKFDLKSNTNVLQSLGKFQSEVSKRQKLA TVFSSFTSTGLCQGSVAFISRCPLASGSDSVWRGGSVFFSFRP*RLMISLLGSCVSHQFPEKLEF**KKMPYKIPTAHHQQQDDQQRGHEHKQSQPDVAPHLG
16640	47008	A	16740	1	2385	
16641	47009	A	16741	1	639	
16642	47010	A	16742	1	993	
16643	47011	A	16743	127	426	CTDKITLVFGV*MLTPKPKD/CD DSAV*ELLWLTNQLSACVVHPGLYHLHVRISIWIPYRCLFSTMC GVCQTCTVAMQLDCLADSFNA VFKLTEAAGHMAR

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16644	47012	A	16744	3	374	SLRLQFYVYKISFQTQDQANKLS DSDASHLHPLAPCSEPTRTNVH TKLPRERPSQIASPYPLPPCPE RLKKQTNNKKKNW*EPSPHILPP RNAAAHTGQSRASKSLPAPPPT VSPRPRPGAGPT
16645	47013	A	16745	16	253	
16646	47014	A	16746	163	588	TFHAVLHIENAGYFNSIPFFRIL NHNPLTTVEDPYLFKLPAKYLY *VL*YSHESRDDLYSF*IFHQRL SILHLG*NVIMKF*LSY*KKVIGE EKN*EDV*WSRQPAGEREQC*R THIDLE/PCRHMEEYYLTCKAK GKRCSLF
16647	47015	A	16747	2	363	GTSQTLRLSLASACIFQPKVRL SREEIPLNLNY*SVSPNSNPNNHL YSRHTILTAMLTQLQGTVCVLLPI GLLVYPYPCPSPTGLQVTPFLPS PCGSGWPASFTYSSNRFNTNLL FCVFIL
16648	47016	A	16748	1028	1621	
16649	47017	A	16750	1	112	LGNTWG*QPCRLKIWLSLEFT KINVIRHMKKFKRL
16650	47018	A	16751	91	597	LKNRRRSRPSIRQSIGSTSVSRW LTSFLTLYDHTADVQ*V*REFIP LKPRQ*ED*MFQSWLHAWGDT LEEAFEQCAMAMFGYMTDTGT VEPLQTVVEVETQDDQLQSLFH FLDEWLYKFSADFFIP/GWGEE FSLSKHPQGTVEKAITYSAMQV YNEENPEVFVIIDI
16651	47019	A	16752	226	668	IYFFRLHAWGDTLEEAFEQCA MA/MFGYMTDTGTVEPLQTSRS /KTQGDDLQSLFHFLDEWLYK FSADEFFIPREVKVLSIDQRNFK LRFN/GWGEFSLSKHPQGTVE KAITYSAMQVYNEENPGSFC DHWTEKTTQKIKRLPTGKK
16652	47020	A	16753	3	942	
16653	47021	A	16754	3	419	SLYHNSSQKRHWTFSSSEQLAR LRADANKFRCKAVANGKVLP NDPVFLEPHEMTLCKYVEKRL LEFCSVFKAMPERSVVLTCAL ACKVDEFVNSNPQFVGNLRESP LGQEKALEQILEYELLILQQLNF HLIVHN
16654	47022	A	16755	312	537	
16655	47023	B	16756	209	1381	
16656	47024	A	16757	1	927	
16657	47025	A	16758	1	3987	
16658	47026	A	16759	2	175	

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16659	47027	A	16760	2395	2700	
16660	47028	A	16761	2	1118	
16661	47029	A	16762	26	1205	
16662	47030	A	16763	1	1594	
16663	47031	A	16764	1	595	
16664	47032	A	16765	1	1029	
16665	47033	A	16766	1172	1364	
16666	47034	A	16767	253	389	
16667	47035	A	16768	489	855	
16668	47036	A	16769	2	401	
16669	47037	A	16770	415	694	EAKLHLNLCDSMWLCCPTKGK RKQALEVLNILGPFLAPFWIAK SYFFTSPTQVSSL*FLRYKRKIK LQCRPKTCTNPSRTRSCALPGR FIPPF
16670	47038	A	16771	1	765	
16671	47039	B	16772	1	1095	
16672	47040	A	16773	82	311	KANSVDPFGFGVNLLEHLMAC NS/GTNLLNSKRLNNDICILASH TDVSIHARKCCLVVSCLLLRGL SILRSKESHC
16673	47041	A	16774	2	683	
16674	47042	A	16775	1	2703	
16675	47043	A	16776	1	555	DHNSSPAREQ/SSMENKFHELT EVGFRKITSLEKNINDLMELKN TARELREAYTSIKSRIDQAKESI SEIEDQLNEIKCEDKVREKRMK SNKQNFQEIWDYVVRPNLRLT GVPESDRENGTKLENTLQEIHQE NFPNLRQANIQIEIQRATQR QSSSRATPIHIVRFKFEIKEKM LRAAREK
16676	47044	A	16777	1	839	
16677	47045	A	16778	1	504	
16678	47046	A	16779	1	2367	
16679	47047	A	16780	1	1566	
16680	47048	A	16781	146	464	VTGWTNYEGNGRWRESRQLC GCCSRKSSSSWGSLMKGSGAP LRPGRMMWSGFRKCSDTQVM YS*R*LLETMTLASIMR*THTK* NALRKCSALKDCFLGKALTL
16681	47049	A	16782	1	1782	
16682	47050	B	16783	221	1075	
16683	47051	A	16784	1	627	
16684	47052	A	16785	1	1539	

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16685	47053	A	16786	1	1318	LSPVLSLSPDSMSFTTRSTFSTN YRSLGSVQAPSYGARPVSSAAS VYAGAGGLATGIAGGLAGMG GIONKETMQSLNDRLASVLDLR VRSLETENRRLESKIREHLEKK GPQVRDWSHYFKIIEDLRAQIF ANTVDNARIVLQIDNA/RLAAD DFRVKYETELAMRQSVENDIH GLRKVMDDTNITRIQLETEIEAL KEEL/LFMKKNHEE/EVKGLQA QIASSIGLTVV/DAPKF/QDLRQ DSWADIRVAQYDELARKEPRG A*TKYWFSADLRESTTVVTTQ FAEVGAA*DDASQSWRTYS SLGDPWGFWRKS*RASLEN SLREG*RPAYALT/QMEQASTGI LACTFESELGTDPGAEGRQAQ EYVALLNIKVKLEAEI/ATYRRL VLEDGEDFNLDALDSSNSMQT IQKTTTRRIVDGKVVSSETNDTK
16686	47054	A	16787	1	253	RVRTLKSTSTCLYWFEKDS/ DHPERSSP*YMSPSHYGSLVK ASITKPAFLKTSGRFLTCSQFC PLISKISDGFSLPPFST
16687	47055	A	16788	1	276	AAAAGPPGPLVMFTYRERVSG LRSVHLRASHTDARLRQEPT ERLQFHSSGLLIRFSRETEPIGV YIKED*EEWAYKMMVFAKSHD LPFAN
16688	47056	A	16789	1	203	LLHTSTKNELWQ*GKRDPVIF YTQYLF*EKTRK*NQRQAGSL ALGPKPGLRLPGLNPVVENQFI
16689	47057	A	16790	8	361	RGLDGGQGRDGSSSGGGGGR RRRCLLLAPAPAVIRASGRGP R*DCWRAGCA*AWRPC/RLAR RMWTLRSLTRSLYVNMSTSGP GGPAAAGGRKENHQVARKR LNVCVFTRSVSETA
16690	47058	A	16791	674	1076	VQLFRSAGSRDHRFLGRGRN KQTKTLTYPTIPCSLKYQRKQN GSLWLTSRMPSSVFCTLTSPFS LPLRISQTTHPNLRGPSCPKGLG IALISLVRHWLKI*ATSQVQAL WSFSMWMIYFWL/PVQKPHASR
16691	47059	B	16792	296	1470	
16692	47060	A	16793	1	334	
16693	47061	A	16794	718	2541	
16694	47062	A	16795	2	406	
16695	47063	A	16796	74	464	
16696	47064	A	16797	159	610	
16697	47065	A	16798	1	273	

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16698	47066	A	16799	1	543	
16699	47067	B	16800	1	873	
16700	47068	A	16801	1	558	
16701	47069	A	16802	27	136	
16702	47070	A	16803	89	363	
16703	47071	A	16804	579	994	
16704	47072	A	16805	129	362	PKIIQPRRATTRFTSINGWRICPS IPCPEATINRRRCVKVDSVTCH LLTQR*YKSSKVQERC*SCRIQG QKISDCY
16705	47073	A	16806	878	1811	
16706	47074	A	16807	1	843	
16707	47075	C	16808	19	231	
16708	47076	A	16809	1	1650	
16709	47077	A	16810	3	404	
16710	47078	A	16811	279	428	
16711	47079	A	16812	3	507	
16712	47080	A	16813	1	1128	
16713	47081	B	16814	1	567	
16714	47082	A	16815	3	1206	GSEGGAGPGGAAATAAAME DEMPKTLTYVGNLSRDVTEALIL QLFSIQIGCKNCKMIMDTAGN DPYCFVEFHEHRHAAAALAAM NGRKIMGKEVKVNWATTPSSQ KKDTSNHHFHVFGDLSQITTE DIKAAAFAPGRISDARVVKDMA TGKSKGYGFVSFFNKWDAENA IQQMGGQWLGGRQIRTNWATR KPPAPKSTYESNTKQLSYDEVV NQSSPSNCTVYCGGVTSGLTEQ LMRQTFSPFGQIMEIRVFDPKG YISFVRFNS/HMESGRHMAIVSV NGTTIEGHVVVKCYWGKETLID MINPVQQNQIGYPQPYGQWG Q/WYGNAQQIGQYMPNGWQV PIAYGMYGQAWESSQGFSNDT VFLAPWDGDPNFGSCNRLQQQ NGSLLPNRPSGYRVAGYETQ
16715	47083	A	16816	1425	1564	
16716	47084	C	16817	151	339	
16717	47085	A	16818	67	373	FCDCHHIFILMFKSPHIWPVGIFS SWLLCFFWACLHHSLSIALLLSC TKRYSGLILYFLCSSFEITVSSKS SVSF*RRMVFRNQVLGSRACCC C*GVAAPRPPF

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16718	47086	A	16819	1	799	MGPHWLWLHLALVLLPPSALL LPSCEKGVLRVRFYHEKWIYV HKESTKERHGYCTLGEAFNRL DFSSAIQDIRRFNYVVKPLPRY KFQRLNAITKDRQRSSSGVQLP HAGQPQAGADPTQDERRQVAGD TPGDPRALAGGQVVDRTYPGS YEASGRPGLQLALAIEDLLRDS AIGCTFCDCRCPVGAQRLLAHS LALAAPGAEREVVKLLLVAY VRRRPGKNLTQNCQPAAGYI PPGHQ*AASAHARSWKNQPP PRVLIGSA
16719	47087	B	16820	28	438	
16720	47088	A	16821	366	793	AWVEQSKVLKEGGIQLLLTIV DTPGFGDAVDNSNCWQPGINYI DSKFEDYLNESQVNRQCMQPG NRVHCCLYFIAPSGHGPLHN*R LPPSGRIG*YMFVTTWHCLLLR LKPLDIEFTKHLHEKVNIPLIAK ADTLMPPEC
16721	47089	C	16822	228	374	
16722	47090	A	16823	291	604	AWELEKSHLRRLDPSHNINIR VEPKF*SKYGGVQLLLTIVDTP RFGDAVDNSNCWQPVINYIDIK FEDYLNESRVNRQCMQPGNRV Q**LYFIAPSGHGPLHN
16723	47091	A	16824	148	498	
16724	47092	A	16825	1	595	DRPRITGGGKSGTEYPENLPTL KATIENKNSVLNTATKMKDVQ TSTPAEQDLEMA\SEGEQKRLE EYENNQPQVK\QHSRDDLD IIQSSQT\SEGD\SLCCNCKNVI LLIDQHEMKCKDCVHLLKIKNT FCLWKRLLIKLDNHCEQLRVKI RKLKKNASVLQKRISEKEEIKS QLKHEILELEKELCSLFAIQQE
16725	47093	A	16826	1	828	
16726	47094	A	16827	1	540	
16727	47095	A	16828	295	460	
16728	47096	A	16829	2	1355	
16729	47097	A	16830	650	1184	

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16730	47098	A	16831	725	2368	AVDIIKEIKHPQKHKKLPALQRL PFPLREETIPCNVGFPRCEPCL AEVYMCLEMLKDEKKGCMN KSGAGENPQERTAQKRKFPSP HSSNGHSPQDTSTSPIKKKKK GLLNSNNKEQVKQPLECIETQS KAMTMTLIEQLSYLLKFAIQKM KQPGVRRKLKVPVLEQHPDYA EYIFHPMDLCTLEKVGRLQMY GCTEAFADAKWILHNCIYNG GEWLRTQIAKVVIKICEHEVCV SQVCECYLAACQKRDNWFCE PCVSWIYDSACQPV*WKLVIQ MFLPM/WKADIL/RGEEG*YTSE LIGWL*SLSCDCSAGTSISHPSD SD*RWLTEHEGRRVSWPVNNC YLMKSKEIPFVKKTKSIFNSAM QEMEYVYENIRKFGVFNYSPP RTPYTPNSQYQMLLDPTNPSAG TAKIDKQEKVKLNDFMTASPKI LMSKPVLSGGTGRRLSDMPR SPMSTNSSVHTGSDVEQDAEK KATSSHFSASESMDFLDKSTG QLRAGERGGGPLDTGVSHGCT I.GGPKQVSIKQASVLQDTMN
16731	47099	A	16832	2	164	PSTLRAEAWPP*NGSPVPLASS QASSRSRGPTSCIPRYPVASPE RLPLPTAA
16732	47100	A	16833	51	498	
16733	47101	A	16834	1	531	
16734	47102	C	16835	257	358	
16735	47103	A	16836	63	193	SGRLAPHTSRRTSANCSDDAKS SDSCSPSRKT*WSGRNTNRIH
16736	47104	A	16837	1	834	
16737	47105	A	16838	258	545	CQNPQILASPSTKDLMLGRNT NKDTLKACLARVVKRRSECSQ KPAS*MCTERNPTSMREVDLE RKYA VLYQLPFD*AVLKLMLQ FMNLRKEGM
16738	47106	A	16839	66	476	
16739	47107	A	16840	1	1362	
16740	47108	A	16841	1	747	
16741	47109	A	16842	522	687	
16742	47110	A	16843	112	861	
16743	47111	A	16844	87	472	TVTFQCRFGKMLPLEKAFASP QELPSAGSAHAGVSSRSSRK NPRPSLRGPLLTLEFSRLRFREF VYPEAAGPHHTLARLDLCRQ WLMPEARSEQMLELLVLEQF L/SILPDKVRPVPVVAQYPS
16744	47112	A	16845	1	393	

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16745	47113	A	16846	621	1099	
16746	47114	A	16847	1	453	
16747	47115	A	16848	209	1175	
16748	47116	A	16849	1	546	
16749	47117	A	16850	187	421	LGESSQ*GSP/PPPTGGCGPATG Q*PLGQSFRKELAAIFAVSQY SLVVP/PGMGTEATGIWSRPPA NGNSPTVEWHIK
16750	47118	A	16851	3	1654	
16751	47119	A	16852	166	465	
16752	47120	A	16853	1	558	
16753	47121	A	16854	51	380	RNNLLLLTHHFVLIQFLIPRKET KYYLVITP/PSLSINVLNSFFYYS PESLNDNTNCHHEADTPWR*F LAIFEGFLNIAHQMQNMPFLL WKQVPETLVIQQQLPRIN
16754	47122	A	16855	3	550	
16755	47123	A	16856	1	462	
16756	47124	B	16857	1	2811	
16757	47125	A	16858	3	514	ASGTAPEIQARPTRPRKRKRK LLPL/TKAEAKAKALKAKKAVL KGVHSHKKKKIRTSPTRRPKT LRLRRQPKYPRKSAPRRNKLDH YAIKFP/TTESAMKIEDNNTL VFIVDVKANKHQIKQAVKKLY DIDVAKVNTLIRPDGEKKA YVR LAPDYDALDVANKIGII
16758	47126	A	16859	73	396	FFQSP/KNCSCVWWNCAEVL KYKTGETNDFELLKNQLDPDI KRLPWLNRSQTVVEEYLAFLG NLVSAQTVFLRPLCSMIASHFV PPRVIKEGDVDVSDSDDEDD
16759	47127	A	16860	132	357	YVSKFAGRLSSSSSESTSPS LMITRGGTKWGSNHAETRSEE NSLC*YKITKKSQILFYHCFDFY STKAISI
16760	47128	A	16861	380	597	
16761	47129	A	16862	179	280	QRDIKSCVQILQWEGSTRPFTN E**YMANVRNS
16762	47130	A	16863	2	175	
16763	47131	A	16864	178	374	
16764	47132	A	16865	386	2120	
16765	47133	A	16866	887	1104	

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16766	47134	A	16867	1	708	MEVAALEHLDHRLREKVKQQN ALRHQVVLQRRLLEELQLQHS LRLEMAEAQNRHTEVAKTMR NLENRLEKAQMKAEAEHITS VYLQKAYLMDESLNLENRLD SMEAENVRTKHELEALHVVNQ EALNARDIAKNQLQYLEETLVR ERKKRERYISECKKRAEEKKLE NE/LHGAQADPGSDLNPRADPP RAPAATVRRHHPGPACQGGG AAAALEHVPDGGDLWQGGGR HWH
16767	47135	A	16868	1	1327	
16768	47136	A	16869	1	1776	
16769	47137	A	16870	1	397	
16770	47138	A	16871	1	1974	
16771	47139	A	16872	1	336	
16772	47140	A	16873	3	661	GRGGHNFAPNLARSASVTSGL GGPPAAVMVGS.LNCIVASQN MGIGKNGDLPWPPLRNEFRYF QRMTTSSVEGKQNLVIMGKK TWFSIPE/RRNRPFKG*EFNLVL SRELQGNLPQGAHFLSRSLDDA LKLTEQPELANKVGMMVW/IVG GSSNYKESMNHSSSLKLFVTRII QDFESDTFFPEIDLEKYKFLPEY PGVFFDVQEEKGIKYKFVHEK
16773	47141	A	16874	38	755	ALKTCVSNQPDADKDNAGSSGH LRTLSPVVSRSCLKEEERRRRR RMKRRQRSRRRRSRRRRMRRR RRSRSSRRRMKRRRRRRMKR RSSFILMYFFMLLLSGIPLLYME VIMGQWLHVDNIRVWKQLVP WLCMSY/SSQSVCASVSLYNS THISWNFFYSFAHPLPWHCHPLV KNISVTDWAHQYFLYHTTLHA SDHSEAAEALVPNRSLGCLLG RDHRDLDFKPEIRRGAGTGGAR
16774	47142	A	16875	1	1830	
16775	47143	A	16876	2	1142	
16776	47144	A	16877	1	435	
16777	47145	A	16878	1	963	
16778	47146	B	16879	247	1092	
16779	47147	A	16880	1	1653	
16780	47148	A	16881	1	2268	
16781	47149	A	16882	301	555	
16782	47150	A	16883	1	630	
16783	47151	A	16884	731	834	
16784	47152	A	16885	1	2277	
16785	47153	A	16886	45	2446	
16786	47154	B	16887	625	696	

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16787	47155	A	16888	193	315	WPGGGYSLLCFWCPLSFAGAA G/W*PPPGHH*PYSKQEHYRT NSDTLIFLSSRTLVLQGS*GIKV AGSEGPKYNE*PRNPVLPCLCL HLFGC
16788	47156	A	16889	1	588	
16789	47157	A	16890	2	229	
16790	47158	A	16891	1	502	
16791	47159	A	16892	516	576	
16792	47160	A	16893	144	435	
16793	47161	C	16894	1	996	
16794	47162	A	16895	424	632	
16795	47163	B	16896	446	1944	
16796	47164	C	16897	207	470	
16797	47165	A	16898	1	396	
16798	47166	A	16902	1	585	
16799	47167	A	16903	141	906	
16800	47168	B	16904	99	276	
16801	47169	A	16905	1	756	
16802	47170	A	16906	1	383	
16803	47171	A	16907	1	582	
16804	47172	A	16908	3	615	PECIIGIDILSSGQNPHIGSLTGR VRAIMVGKAKRKPLELPRKI LNQKQYRIAGGIEISATIKDLK DAGVVIPTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPALFCR* LLSF*ETALGLLGFGGN*TFDY
16805	47173	A	16909	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVIFPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGAKAKWK*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRG VVIPTTSRFNSPIWPVQKTGDS W*TAADY
16806	47174	A	16910	232	633	
16807	47175	A	16911	1	1677	
16808	47176	A	16912	328	381	LLKLQH*MQSPYLVGPSQ
16809	47177	A	16913	3	811	
16810	47178	A	16914	1	1125	
16811	47179	A	16915	1	1191	
16812	47180	A	16916	113	485	
16813	47181	A	16917	1	357	
16814	47182	A	16918	12	398	
16815	47183	A	16919	498	595	TEMASTTTCT/RFHDEYQLFEEL *KGAFSVNGT
16816	47184	A	16920	5	367	

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16817	47185	A	16921	190	2005	VLYPLHLGTGTGKGAGGASSG EEGSEARRRRIGGLWRRRPHA TLSGHLPSRPAPAHTPSRASYFR TRKVRALGDSAAGVPVGLAA RLASGSPRSQPGHSPGPEMAS TTTCTRFTDEYQLFEEALGRGAF SVVRRCKMKTGQGYAAKIINT KKLSARDHQKLEREARICRLK HPNVIRLHDSISEEGFHYLVFDL VTGGELFEDIVAREYYSEADAS HClQQILES VNCHLNGIVHRD LKPENLLASKSGAAVKLADF GLAIEVQGDQQA WFGFAGTPG YLSPEVLRKDPY GKPVDMWAC GVILYILLVGYPFWDEDQHRL YQQIKAGAYDFSPPEWDTVTPE AKDLINKMLTINPAKRITASEAL KHPWICQRSTVASMHRQETV DCLKKFNARRKLKGAILTTML ATRNFSAAKSLKKPDGVKEST ESSNTTIEDVDKARKQEIIVT EQLEIAINNGDFEAYTKICDPGL TAFEPEALGNLVEGMDHFRFYF ENALSKSNKPIHTILNPHVHLV GDAAACIAYIRLTQYMDGSGM PKTMQSEETRVWHRRDGKWQ NVHFHRS GSPTVPKPPCIPNGK ENFSGGTS LWQNI
16818	47186	A	16922	1	288	
16819	47187	A	16923	318	458	
16820	47188	A	16924	1	578	
16821	47189	A	16925	803	1068	
16822	47190	A	16926	1	660	
16823	47191	A	16927	2	325	TSENNNNGPKR*IHSTESLYLLQ GSVYADHDYIGLPEIPGAYQA NILVEDATIGIVDNELLTSSKDR ELLEVRNTKISPLIDHSSLEKQ TFSLLDSSNQVLEYLS
16824	47192	A	16928	156	573	
16825	47193	A	16929	405	599	GLEPPQKPLVTSILQANPVPLP CGNSQSR* TSTRCWYEHLCQCTQ SHLQMQQYHEAYQSACALA
16826	47194	B	16930	1	1676	
16827	47195	A	16931	1	1125	
16828	47196	A	16932	27	818	
16829	47197	A	16933	1	4986	
16830	47198	A	16934	1	4401	
16831	47199	A	16935	153	370	SVLETCMSTAFVPVCHSSFKTA VLRISLS*ISAQGGPIDLFSQCHP SSSTGVSSNHRGSWDTPGQSL VVICL

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16832	47200	B	16936	47	501	
16833	47201	A	16937	49	1714	
16834	47202	A	16938	1	999	
16835	47203	A	16939	140	2029	FAARAGPGGSRARRGNKWAR MPYEIKKVFASLPQVERGVSKII GGDPKGNFLYTNCKCVILRNI DNPALADIYTEHAHQVVVAKY APSGFYIASGDVSGKLRWDTT QKEHLLKYEQFPAGKIKDIAW TEDSKRIAVVGEGRKFGAVFL WDSGSSVGEITGHNKVINSDI KQSRPYRLATGSDDNCAFFEG PPFKFKFTIGDHSRFFVNCVRFSP DGNRFATASADGQIYIYDGGKTG EKVCALGGSKAIIIDGGIYIISWS PDSHLLSASGDKTSKIWDVSV NSVSTFPFMGSTVLDDQLGCL WQKDHLISVLSGYINYLDRN NPSKPLHVIKGHSKSIQCLTVH KNGGKSIYISGSHGHINYYWD SETGENDSFAGKGHTNQVSRM TVDESGLISCSMDTTRYTSL MLRDYSGQGVVVKLD/VQPKC\
16836	47204	A	16940	31	449	VA VPGGYAVVVCIGQIVLLK DQRKCFSDNPGYEPEVVAH PGG\DTVAIGGVDGNVALYSIL GTTLKDEGKLEAKGPVTDVA YSHDGAFLAVCDASKVTVFS VADGYSENNVYFGHHAKIVCL AWSPDNEHFASGGMDMMVYV WTLSDPETRVKIQAHLRHHS SLAWLDEHTLVTTSHDASVKE
16837	47205	A	16941	1	53	
16838	47206	A	16942	1	389	GMPTSTIASCSQDGRVFIWTC DASNTWSPKLLHKFNDV VWH VSWITANILAVSGGDNKVTEG QQNEQ*QDRWGLAPHPAPGL PLPGPTNQTTGKSPQLQDDYFP RRSYRCSHRLIICLNIGNAL
16839	47207	A	16943	1	438	
16840	47208	B	16944	1	1267	
16841	47209	A	16945	635	808	

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16842	47210	A	16946	37	1319	QGEHGHRGLHGFLGRPEQIP WSRSAPLHRLEIWGALAPSLAD HSEGSPEVSVINTVDTSEHYMI YDAQMDYYGHPPGQPASSDRS VKIF*CAQWEGRSLFADLQGS WRGPVWQVVGWGTPLLRAITS WAFVASLLTGKFIYSWERGKT GTLGRRATSNA GTRLKLNFGC CWAPHGLTVLHWSACWVVS RGPSLLDFTPEGQWEVKKIN NAHTIGCNAVITWAPACCTWK PHRRPHRGQKPNYIKRFASGGC NDNLKLVKEEEDGQWKEEQ LEIGHSDWVRDVAWAPSIGPA HQHHRPAAPRMGRVSIWTCDD ASSNTWSP*IVDKFNDVWHIV SWSITANILAVLCGDNKIVPL WKES*WAKWVVPSSDVKQRG PGLPYQSSDQEGPARNEQVVK DQGGALAPPAQLPGPAPSPGP
16843	47211	A	16947	1	1021	MSGFIDHSHIARIYPGIFGTDA GSCIDQRGITGKLQPPEDRRL GEGKLTNTKDIHTKTPSVRHHH QRPKVDKTTKIGKKQSRKTGNS KNQSAPPPKCESSSPAMEQSW TENDFDELREEGFRRSNYSELK EEFRTHGKEVKNLEKRLDEWL TRITNAEKLKDLMEKLTARG LQRVSVMEDEMNMKEEKFR EKRIKRNKQSLQEIWDYVVRPN LRLIGVPESDGENGTKLENTLQ DIIQESFPNLARQANIQIQEIQ MPQRDSLRRATPRHIVRFTKV EMKEKMLRAAREKAHIALPK LTT*LEVKLSSANVKEQL*QT VFQTTVQSN
16844	47212	A	16948	1	393	
16845	47213	A	16949	1	2631	
16846	47214	A	16950	1	1155	
16847	47215	A	16951	1	1185	
16848	47216	A	16952	1	942	
16849	47217	A	16953	1	615	

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16850	47218	A	16954	474	2678	IKPQRWGGKKQSRKTGNSKNQS ASPPPKERSSSPAMEQSWTEND FDELREDSFRRLVITNYSSELKEE VRTNGKEVKNLEKKLDEWLTR ITNAEKSLKDLMEKMTAQELP DQCTSLSSRCDDLEERVSVMED EMNEMKCEEKFKREKRIKRENEQ SLQEIWHYVVKRPNRLIGVPES DGENGTKLENTLQDIQENFPN LARQANIQIEIQRMPPQYSSR RATPRHIIVRFTKVEMKEKMRLR VAREKGQVTHKGKPIRLTADL LAETLQARREWGPIFNILKEKN FQPRISYPAKLSFIDRSTRQKVN KDTQELNSALHQADLIDYRTL HPKSTEYTFFSAPHHTYSKIDHI VGSKALLSKCKRTEITNCLSDH SAIKLELRILKILTRNHSTTWKL NNLLLLNDYVWHNEMKAEIKM FFETNENKDKTYQNLWDTFKT VCRGKFIALNAHKRKQERSKID TLTSQLKGLEKQEQTTHSKASRR QEITKJRAELKERVGRWRIGEA ADLVGVSSQAIRDAEKAGRLPH PDMEIRGRVEQRVGYTIEQINH MRDVFGRRLRAEDVFPVIGV AAHKGGVYKTSVSVHLAQDLA LKGLRVLLVEGNDPQGTASMY HGWVPLDHIHAEDTLLPFYLG KDDVTYAIKPTCWPGLDIIPSC ALHRIETELMGKFDGKLPDTP HMLRLIAIETVAHDYDVVIDS
16851	47219	A	16955	1	675	
16852	47220	A	16956	1	1032	
16853	47221	A	16957	3	978	HEAKHQMADDAAGSGGGPKA LVGPGMG/NPVAFRRG/GIVIR GPGSRPGGRGRG/GRGARGSK AEDKDWMPVTKLG/RALVKD H*RSKFPWKEIYLFSLPH*RNQR IIDF/LGGLLSKDEGFE*LCVPQ EQDPCPASRTQASRPFAIGGL QMAHVVLGC*VLPRKVA TGHP VGAILAKLSIVPVRG/GYLGNK VLAKPIHTVP/CKVVTGRCGSVL VRLIPAR/RLGGMVSAPVA/KKL LMMAGIDDCYT/SARG/CTATL GQIWPRATL*LPFLRTYKLP*PP DLWKGRLYLPSFPIKEFTDHLV KDPHIPSSVQDSELQLVATT
16854	47222	B	16958	124	274	

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16855	47223	A	16959	202	2264	KWPKMNPQQQRMAAIGTDKE LSDLLDFSAMFSPVNSGKTRP TTLGSSQFSGSIDERG/GTTSW GTSQGQPSPSYDSSRGFTDSPHY SDHLNDSRLGAHEGLSPTPFMN SNLMGKTSEGSFSLYSRDTGL PGCQSSLLRQDLGLGSPAQLSS SGKPGTAYYSFSATSSRRRLPH DSAALDPLQAKKVRKVPVGLPS SVYAPSPNSDDFNRESYPSPK PPTSMFASTFFMQDGTHTSSDL WSSSNGMSQPGFGILGTSTSH MSQSSSYGNLHSHDRLSYPHPS VSPDTINTSLPMSSFHRGTSST SPYVAASHTPPINGSDSILGTRG NAAGSSQTGDALGKALASIYSP DHTSSSFSPNSPTVPVGSPLTG TSQWPRPGGQAPSSPSYENSLH SLQSRMEDRLDRLDDAIHVLRLN HAVGPTSLPAGHSDIHSLGSPS HNAPIGSLNSNYGGSSLVASSR SASMVGTHREDSVSLNGNHVS LSSTVTTSSDNLNKHKTQENYRG GLQSQSGTVVTTEIKTENKEKD ENLHEPPSSDDMKSDDESSQKD IKVSSRGRSTSTNEDEDLNPEQ KIEREKERRMANNARERLVR DINEAFKELGRMCQLHLKSEKP QTKLLILHQA VAVILSLEQQVR ERNLNPKAACLKRREEEKVSA VSAEPTTLPGTHPLSETTNP
16856	47224	A	16960	1190	1327	
16857	47225	A	16961	386	554	ATISFRYSQCK*AEQGCDSLEL LFTKIRKSGYWGV*ATISFRYSQ CKALEIHLTAPVVPSALRIWGF QIPGFNQLSFHPSPEKGSFLPC
16858	47226	B	16962	499	915	
16859	47227	A	16963	1	1785	
16860	47228	A	16964	1	3036	
16861	47229	A	16965	2	710	
16862	47230	A	16966	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGGLHDLKIVVL
16863	47231	A	16967	1	1335	
16864	47232	A	16968	83	426	
16865	47233	A	16969	93	345	APALCLQILLDCXSVNRNTRSF RPREVGIQYKKGGAAGKGG TGNAPGFLLFKDS*KDPTPLPP PLLL*GQRDH*IQHLHQE
16866	47234	A	16970	1	1302	
16867	47235	A	16971	1	1174	
16868	47236	A	16972	274	1428	

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16869	47237	A	16973	411	629	HCLSHFQNTGPRGDVDFQQUELA FPVLMADIRKEERSHLCRSSRR TWTLDKS*IQGSRLLSKEQGW GWGTSRK
16870	47238	A	16974	618	1552	
16871	47239	A	16975	1	558	
16872	47240	A	16976	1	765	
16873	47241	A	16977	2	418	
16874	47242	A	16978	130	1965	
16875	47243	A	16979	1	1062	
16876	47244	A	16980	1	558	
16877	47245	A	16981	37	676	
16878	47246	A	16982	1	1014	
16879	47247	A	16983	1	2964	
16880	47248	B	16984	259	1751	
16881	47249	A	16985	1	987	
16882	47250	A	16986	1	1047	
16883	47251	A	16987	3	1413	GLHAARGPWVYQAWISITM.ER KEVCYQQLGCFSDKWPAGTL QRPVKLLPWSPEIDITRFLLYT NENPNNFQLITGTEPDITIASNF QLDRKTRFIHGFLLDKAEDSWP SDMCKKMFEVEKVNICVDWR HGSRAMYTQAVQNIIRVVGAET AFLIQALSVKPCLPVWVGVGR EGQGDAARGTALEDVHVIAHS LGAHT/AEEAGRSWGPRGRITD DLGTA*YKVDGMG*ERRGVRF SI*P*GGGV*AGFGGERFR*RKN VGKSTAGWRM/GLDPAGPCFO DEPEEVRLDPSDAVFVDVIHTD SSPIVPSLGFMSQKVGHLDFFP NGGKEMPGCKKNVLSTITDIDG IWEIGIGFVSCNHLRSFEYSSS VLNPDGFLGYPCASYDEFQESK CFPCPAEGCCKMGHYADQFKG KTSAVEQTFFLNTGESGNFTSW RYKVSVTLSGKEKVNIGYIRIAL YGSNENSKQYEIFK
16884	47252	B	16988	95	315	
16885	47253	C	16989	1	780	

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16886	47254	A	16990	2	1426	SGTLDRMLIFWTTITLFLGAAK GKEVCYEDLGCFSDTEPWGGT AIRPLKILPWSPEKIGTRFLLYT NENPNNFQILLLLSDPTIEASNF QMDRKTRFIHGFIDKGDSEWV TDMCKKLFEEVEVNCIFV\DWK KGSQATY\TQAANNVRV\GAG VAQMLDILLTEYSYPPSKVHLI GHSIGAHVAGEAGSKTPGLSK/ RLQGLDPVEASFESTPEEVR\AD PSDADFVDVIHTDAAPLIPFLGF GTNQMGHLDFFPNGGESMPG CKKNALSQIVLDLDGIWAGTRDF VACNHLRSYKYYLESLNPDGF AAYPCTSYKSFESDKCFPCPDQ GCPQMGHYADKFAGRTSEEQ KFFLNTGEASNFARWRYGVISIT LSGRATGQIKVALFGNKGNTN QYSIFRGILKPGSTHSYEFDAKL DVGTIKVKFLWNNNVINPTLP KVGATKITVQKGEKTVYNFCS EDTVREDTLTLTTPC
16887	47255	A	16991	1	1407	
16888	47256	A	16992	954	1663	EPSDPAHAPSVALLHTGNQSK VLPWPNRNPCMRRW*K*KMLKI SWVHEWVTSNWISTAVRSLRV FAPKNVFQ**ALGPSGLWLYC
16889	47257	A	16993	3	242	
16890	47258	A	16994	1	1815	
16891	47259	A	16995	1	375	
16892	47260	A	16996	3	2005	
16893	47261	A	16997	1	651	
16894	47262	A	16998	114	275	
16895	47263	A	16999	1	270	
16896	47264	A	17000	140	876	PPALVVGRRQKSWRMFEQMR NVGKLLKGIDR\YNPENLATLE R\YVETQAKENAYDLEPNLAVP ESCTKFNPAAFQTNGSTAQDSC *KALTNLPH\TDFTL\CKC\MIRP GHIQE\ERP\TDFCYLGGPGWE TWPF\SR\AFWESPGMKTVDLLW KV*LG\FEDSV\RK\FICHVVG\IT YQHIDR\WLLAEM\LGDLFGQAS *RCW\MSKYGWSA\DESGQIFIC SPRREHLTPRNIVEKIDFDSVSSI MASSQ

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16897	47265	A	17001	1	777	MSGENVTKVSTFILVGLPTAPG LQYLLFLLTYLFVLVENLAI ILIVWSSTSLHRPMYYFLSSMSF LEIWVYSDITPKMLEGFLQKQ RISFVGCMTQLYFFSSLVCTEC VLLASMGYDRYVAICHPLRYN LACTDFSTAELV/SFILAFILVFP LLATILSYWHITLAVLRIPSATG CWRAFSTCASHLTVVTVFYTA LLFMYVRPQAIDSQSSNKLISA VYTVVTPINPLIYCLRNKEFKD ALKKALGLGQTS
16898	47266	A	17002	2	876	
16899	47267	A	17003	1	894	
16900	47268	A	17004	377	501	
16901	47269	A	17005	3	823	
16902	47270	A	17006	1	874	
16903	47271	C	17007	156	287	
16904	47272	A	17008	1	1140	
16905	47273	A	17009	1299	3135	ISGSVCILLWLQLLPAYNLIHT WEHRHSPPGT/RMSRLAKRNA WEADR/YAEAKLAASRRGQPS LMSSREGGWGEGSQSRNSSHG ALKEAQFIITNAEKS LKDL MEL KTMAQELRDECTSLSSRFQLE EKVSVMEDEINEMKQEEKVRE KRIKRNEQSLQEIWDYVKRPNL HLIGVPESDRENGTKLENTLQDI IQENFPNLARQANIQIEIQRMP QRYSSRRATPRHIVRFTK VEM KEKMLRAAREKEIQTITREYYK HLYTNKLENLEEMDKFLDTYS LPRLNQEEVESLKRPIGSEIGAI INSLPTKKSPGPDGFTAIFYQRY KKELVPFLKLQSTEKERILPN SFYEASIIIPKGRDITTKENFR PISLMNINAKILNKILANQIQHI EKLIHHDQVGFIPGMQGFNIR KSINVIQHINRTEKNHMIISIDA EKAFDKIQPFMLKTLNKL GID GTYLKIVRAIYDKLTANIILNGQ KLEAFPLKTGTRQGCP LSPLLF NIVLEV LARAIQEKEIKGIQLG KEQVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVS GYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIK
16906	47274	C	17010	189	457	
16907	47275	A	17011	2	2600	
16908	47276	A	17012	107	1493	

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16909	47277	A	17013	3	2209	IHTKTPSVCHHHQRPKVDKTTK MGKKQSRNTGNSKNQSTSPPP KECSPAAMEQSWMENDFDEL REEGFRRSNFSELTEVTRHRK EAKNLEKKIRQMVTTRITNVEK SLNDLMELKNMARELRDKCTS FSSRFQLEERVSVIEDQMNM KQEEKFREKRVKRNESLQEI DYVKRPNLRIGIPESDENGT KLENTLDI/QENFPNLAQAN IQIKEIQRMPPQYSSRRATPRQI IVRFTEVEMREKMLRAAREKG RVTHKGKTIRLTVDLSAETIQ RRESTRQKVNKDQELNSAQHQ ADLTDNYRTLHPKSTEYTLFSA PHIITYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELRKIKL TQNLSTTWKLNLLNDYVWH NEMKAEIKMLFETNENKDTTY QNLWDTFKA VCRGKYIALNAH KRKQERSKIDTLTSQKLEKQ EQSHSKASRRQETIKIRAEKKEI ETQKTLQKINESRDWFEKINKI DRQLARLIKKKREKNQIDTIKN VLEFLAKAIRQDKKIGIQLGKE EVKLLFLAEDMIVYLENPIVSA QNLLKLISNFSKVSQYKINVQK SQAFLYTNNRQTESQIMSELPFT IASKRKIKYLGQLTRDMKDLFK ENYKPLLNKIKEDTKKWKNPC SWVGRINIMKMAILPKVIYRFN AIPKLPMTFFTELEKTTLKFTW
16910	47278	A	17014	292	699	
16911	47279	A	17015	269	803	ALGPCSEALPTWVNGEEMA QEIDLSALKELEREAILQVLYRD QAVQNTTEERTRAAGN*KHTC SISGGKGPKNTDWEHKEKCA RCQQVLGFLLRGA VCRGCSH RVCAQCRVFLRGTHAWKCTVC FEDRNVIKGTGEWFYEERAKKF PTGDNSVRTSCTGKHETVGGQ LLQSYQK
16912	47280	A	17016	1	1173	
16913	47281	A	17017	349	718	AGPEGTTTAECP/ICQQQRPILS LRYGTISWG/DQSATWQVVDY IRTLTLLSWKQASAKTTIHGLT KCLIHHDIPHSIAD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHPCSFN

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16914	47282	A	17018	196	577	GSSGQSESAQPQGLWVLPSTRS LAILSTDVNV*QPCFPAGAHQG QPLAWPVFLAWLSWQKRCR* KQQRSSRNLDHRNPGWLHEE GDKTPFFHHFPQLGQSLSQQS LLPAGRR*ARGPQQLPSP
16915	47283	A	17019	1	2523	
16916	47284	A	17020	236	558	
16917	47285	A	17021	1610	2004	VTWSAQMPWAIKNCPTHSPL GGGCLPQPKM*VVQNDFQ*G* WTHCRKGKGGQVGVWPWQ TQNRGKGTFLTPLHSVADAM LYAL*RGSDLDAAQTLPTAAQ DALYAVVPGGEPTGQLQVRHN EFALGQ
16918	47286	A	17022	1	735	
16919	47287	A	17023	88	1871	
16920	47288	A	17024	1	1299	
16921	47289	A	17025	2	260	
16922	47290	A	17026	144	1737	
16923	47291	A	17027	1	1182	
16924	47292	A	17028	262	1132	
16925	47293	A	17029	1	484	
16926	47294	A	17030	3	382	LKGAPDLELDGESRRTWREK GRKRKERALGRVQV*RSRCA* P/STPAALNAPLQGASHSPFLR NCWKGRSVRASSLLRQLAKGG CAARLLSWNLQIVQMYEGHS QQPGLQRLQRWSSQTLRTA
16927	47295	A	17031	1	2022	
16928	47296	A	17032	209	403	
16929	47297	A	17033	213	1993	
16930	47298	A	17034	1	378	
16931	47299	A	17035	64	1180	SASHSGAPATSLYERGVCPPAL RRPPAVLVCRAAASCTLLAMS DLQEEGKNAINSPMSPALVDVH PEDTQLEENEERTMIDPTSKEDP KFKELGKVLLDWINVLAERI IVKQLEEDLYDGQVLQKLF/EK NLAGLQSLNVAEVTQSEIGQKQ KLQKVLQLHDLRPRSWALR IWLGNISHGKLVGNPQLLVSL AMHFRAPIRLPEHVTQVVVV RKREGLLHSHISEELTTITEM MMGRFERDAFDTLFDHAPDKL SVVKKSLITFVNKHLNKLNLV TELETQFADGVYVLLMGLLE DYFVPLHHFYLTPEFDDQKVHN VSFAFELMLGRRPSRNPRVLK TWLTWDLKSLPVLVNLFTKY
16932	47300	A	17036	3	764	

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16933	47301	A	17037	1	1230	
16934	47302	A	17038	1	313	
16935	47303	A	17039	145	263	IFLLYLKKNKVQNK*EIKQHFLG KIMSRDNNNTYLTWGTEN
16936	47304	A	17040	5	982	PTFSRAVATMFSRAGVAGLSA WTLQPQWQVRNMATLKDITR RLKSIKNIQKITKSMKMVA ^{AAK} YARAERELKPARIYGLGSLALY EKADIKGPEDKKHLLIGVSSD RGLCGAIHSSIAQMKSEVATL TAAGKEVMLVGIGDKIRGILYR THSDQFLVAFKEVGRKPPTFGD ASVIALELLNSGYEFDEGSIIFN KFRSVISYRTEEKPIFSLNTVAS ADQHGVSMTDIDADVAAKITQ EY/NIWANIILLTLWKESTTSGG RSARG*QPWDNGQARIAFWRM DLNLDIWTFR/TRQAVITKE LIEIISGAASSVKKENSAS
16937	47305	A	17041	1334	1790	
16938	47306	A	17042	1	930	
16939	47307	A	17043	2	477	SGLGRLPGPWQEAGSSRGPSSG DMAGVKALVALSFSGAIGLTF/ LHMLGCALEDYGVYWPFLVLI FHAISSIPHFIAKRVTYDSDATS SACRELAYFFTTGIVVSCI.WISP VILARVALIKWGACGLVLA/G NAVIFPYNSRGSFLYLRGDDDF SW ^{EQW}
16940	47308	A	17044	130	434	
16941	47309	A	17045	1	1365	
16942	47310	A	17046	656	839	
16943	47311	B	17047	16	149	

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16944	47312	A	17048	1	1317	MTLNEHAAFKHLFNKAHLAPP LIHLTLSGHSTCFREHRRVGVICS HFAQDLWPEQGREDSFQKVLIR RYEKCCHENLQLKIGCTNVDES LTYKRIHTGEKPKCKCEECDKAF SKFSILTKHKVIHTGEKHYKCE ECGKAFTRSSSLIEHKRSHAGE KPYKCEECGKAFAKASTLTAHK TIHAGEKPYKCEECGKAFAFRSS NLMEHKRIHTGEKPKCKCEECG KAFGNFSTLTKHKVIHTGEKPY KCEECGKAFAFWSSSLTEHKRIH AGDKPYKCEECGKTFKWSSTL TKHKIIHTGEKPYKCEECGKAFA TTFSSLTCHKVIHTGEKHYKCE ECGKVFWSSSSLTTHKAIHAGE KLYKCEECGKAFAFWSSSLSEH KRIHTGEKPYKCEECGKAFAFW VSVLKNKKKIHAGKKFYKCEE CGKDFNQSSSLTTHKRIHTGVE KPYKCEECGKAFAKASTLTAHK TIHAGEKPYKCEECGKAFAFRSS NLMEHKRIHTGEKPKCKCEECG KAFGNFSTLTKHKVIHTGEKPY KCEECGKAFAFWSSSLTEHKRIH AGDKPYKCEECGKTFKWSSTL TKHKIIHTGEKPYKCEECGKAFA TTFSSLTCHKVIHTGEKHYKCE ECGKVFWSSSSLTTHKAIHAGE KLYKCEECGKAFAFWSSSLSEH KRIHTGEKPYKCEECGKAFAFW VSVLKNKKKIHAGKKFYKCEE
16945	47313	A	17049	2	2183	

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16946	47314	A	17050	3	1440	IKVLLGENRVNPTMAVWLAQ WLGKGASLTSFPPTASLLRR LGEHIQQFQESSAQGLGLSLGP GAAALPKVGWLEQLDLPFNVS DRRSHLQRYWVNDQHWVVGQ DGPFLHLHLTSPPTHTLFTGH PAALAPAWGALVISLEHRFYGL SIPAGGRLALSRLEFNISSSSPWIC FGGSYAGSLPSHHAPTFPRAQR IS*HFRIPSSAVRPQVVSRLMS TAIGGSLE/CRRWGLVRGGLGG KRGLGCQGRGGPA*VLADIASC FPQCRAAVSVAFAEVERRLRSG GAAQAALRTLSACPLGRAE NQAELLGALQALVGGVVQYD GQTGAPLSVRQLCGLLGGGG NRRGGIYVLCMYIVP*IVLHSLG QKCLSFSAETVAQLRSTEPQL SGVGEAPIYLA PSYPFFPGDTP WHVLSVTQALGSSESTLLIRTG SHCLDMAPERPSDSPSLRLGRQ NIFQQLQTWLKLAKESQIKGEV
16947	47315	B	17051	41	2709	
16948	47316	A	17052	874	1024	
16949	47317	A	17053	1	1602	MDSLWGPAGSHPFVHNSRL SPDLCPGKIVLRALKESGAGMP EQDKDPRVQENPGDQRRVPEV TGDAPSAFRLRDNGGLSPFVP GPGPLQTDLHAQRSEIRYDQSS QTSWTSSCTNRNAISSSYSTGG LPLGKRRRGPASSHCQLTLSSS KTVSEDRPQAVSSGHTQCEKV AEKAPGQTLALRNDSSRSEASR PSTRKFLLPHRRGEPLMLPPPV ELGYRVTAEDLDWEKEAAFQC IKSALQVEDKAISDCRPSRPSHT LSLATGAS/DSAQVTSIPAPFP AASMDAGMRRTRPGTSAPAAA AAAPPSTLNRTLGSLLEWMEA LHISGPQPLQQVPRGQNQRSQ TSRTSSCPK/LKCHLELLQLYGR PPGTKAEEAPASSHCQLTLSSSN TVSEDPQAVSSGHTQCEKTAD TAPGQTLGPRGGSRSQSSRPR RHKFPLPRRRGEPLMLPPLEL GYWVTAEDLDREKEAAFQRIN SALQVEDKAISDCRPSRPSHTLS SLATGASGLPAISKAPMDAQQ ERHKS
16950	47318	A	17054	1	1155	

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16951	47319	A	17055	1	1237	MDSLWGPAGSHPFVGHINTRL SPDLCPGKIVLRALKESGAGMP EQDKDPRVQENPGDQRRVPEV TGDAPSAFRPLRDNRLSPFVP GPGPLQTDLHAQRSEIRYNQTS QISWTSCTNRNAISSYSSMGG LPGLKRRRGPASSHCQLTLSS KTVSEDRPQAVSSGHTQCEKA ADIAPGQTLALRNDSTSEASRP STHKFPLLRRRGEPLMLPPSL EVGVGSLVKELDREKEAAFQ RINSALQVEDKAISDCRPSWPS HTLSSLATGTSLGPAISKAPSM AQQETHKSQDCLGLLAPLASA AGVPSTAPMSGKKHRPPGPLFS SSDPLPATSSHSQDSAQVTSILP APFPAASMDVGMRRTRRGEPL MLPPLELGYRVTAEDLDQEKE AAFRQIKSALQVEDKAI
16952	47320	A	17056	132	835	
16953	47321	A	17057	1	2947	MPEQDKDPRVQENPDQRRVP KVTGDARSAFRPLRDNGVLSF VPRPGPLQTYLHAQRSEIRYNQ TSQNTWTSSCTNQNAISSYSS VGGLGLKWRRGPAQGESGAG MPEQDKDPRVQQNPDDHRTV PEVTGDARSAFWPLRDNGGLSP FVPRPGPLQTDLHAQSSSEIRYN QTSQTSWTSSSTKRNAISSYSS TGGLPGLKQRRGPASSRCQLTL SYSKTVSEDRPQAVSSGHTRCE KAADTAPGQTLAPR
16954	47322	C	17058	229	624	
16955	47323	A	17059	1	1011	MVSTPATLPSLPKPALMASWG VPYDQLTKEEKTRVWFTDGSA RYAGTTQKWTAVLQPLSRTS LKDSSEKSSQWAEQLQAVYL VHFAWKEKWPVGLYTDWSA VANGLAGWSETWEKQDWKIG DKEIWGRGMWMDLSEWSKAV KIFVSHVSAHQRVTSAEFEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYSWAQQTGLPFTKADL AMATAECPCQQRPPLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFLTVIDTYSRYRFAY PAHNASAKTTIHGLIECLHICYG IPHSIASDQSIH/TTKEVQ*WAH AHGHIHWSYHVSHHPEAAGL
16956	47324	B	17060	10	597	
16957	47325	B	17061	6	297	

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16958	47326	B	17062	1	474	
16959	47327	A	17063	1	2712	
16960	47328	B	17064	1	738	
16961	47329	A	17065	3	772	DPADPMVLEVSEADRDAVPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVVEIEHLTM GHQVTMRPELPINCVLSDPCSH KVGHAQQHSIIKWRWYIHYQA QAGPEGTSNLHEEVAQMPTVS TSATLPSLPEPTQMALWEVVPY DQFTEEEKTGAWFTDGSAYHT GTT*KWTVVAALQPLSRTTLKDS CEGKSPHPHPVIAQWAHEQSGH GGRDGGYLWAQQHGFPLTKA DLAMATAECPCQQCKRTLNP
16962	47330	A	17067	1667	2012	LSPHWPPGLPFSALIYAFGLRSS RNKRRLMKTMKVEACEDLSAP KYLRIQLPTGSPRRRSEAEVCI FQGSSVSLVHPPPLSYPSARR* PQTTPRPPRHPSLHPLHPSAQ
16963	47331	A	17068	5	1074	RHSALGTGGSSCRQQRPRDT WVPETILTAWSS/RLQQLGPW LQVTVAGQVNTLAGIQKTIHAE HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCGYQL STAINRNQELCGRKPAVSPSR/G JSPGSPILRPVHGHGYCLQRL SGQKSNRRRTTQKSFQKLHVDK RKPENFSKESDHLIYSREGNPD VASLATPPGIWMMSATDLFYG DPFAFPGGGPFTLSLERGPSVIL GTDASEELLFTKASLAVTSVF QFSTGKIYTEWVWQKNKSFLSP HFPTKPMASPVKGKHSTSLQR LNYRDRWQCLQEGAGLALLSA HMKVPTGSKEPQAGKLPSPK RKQTPTTFKD
16964	47332	A	17069	2	699	CSACPVSHPWLLPWQSGSAFSL P*RALQRPPQHGHRLSKPMQSP RLSVLLRPWPRRLPTDLLY*PS TRGHIHLHDRHHGAPSVSRRW GDKASPPQFPYRSRDSK/RRPPQ HGEVGTVFTNNKGGQS/PATST WEVQSAECQKAPEAGPTTPSTA GDAEGANALRQESEGNWGSEA KSPHVAEAGSWRPQQGSCCHL HPPDKTKDAARKTHSPGDNGC QPRPPRCKTLWSLSRI
16965	47333	A	17070	223	1611	
16966	47334	A	17071	12	310	

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16967	47335	A	17072	31	430	LQAVRLFTLPTSSGL*KLRTVP TWSPSPSCFPHFQSGPRTRTAPT PSTINPGYSGSYSSGPPSLCPRTS RRAPPRHRVPAGRERLHIVVPP YPRPERHLLRVSRRLGILGNRV GRLPESRAIAGRKEEKTDTK
16968	47336	A	17073	1	474	
16969	47337	A	17074	153	1224	RVFSEVSCSPVRNLEFLWRFAP PLAPAGRCPPGVPLQTSPRD AHRSSPLPARASPGQVAAAYR WARCPGCGGRKPRSSGSWQLC RCPTLPPPPRGRSSGRC/RTWP SPSPSCFPHFQSGPRITRAPTPSTIN PGYSGSYSSGPGR*GLSPLHAA/ VSPPLPPGP*GSWARAGLSI ASAHSPCLCRSLIRSR*QTCT RSPT*NCEVPPAS*AA SPLRTM FALVRTAGLKVHLLPLGYCTT MS*SSSMPTVPVVVKVSNIPS VHPP*PCKDCTISRSRIFTRSPI CNPPGFLLPFCSPSTIGQ*SL*KEP PLASWTHFRSDVLLLFVSMNG STLSLGCPSQKAVIALVQVT
16970	47338	A	17075	215	1246	
16971	47339	A	17076	566	675	QPCRQ/CLQPGSPRFHARTLT VTLVHTRTHTAHAH
16972	47340	A	17077	184	584	
16973	47341	A	17078	1	1167	
16974	47342	A	17079	849	2266	
16975	47343	A	17080	1505	1891	DAEKAFDEIQ/PFMIKILRSI QGTLYLVIKTIYDKPTANTILN VEKLKTFPLRTGTQGCPLSAL LFNMVLEVIARIRQEKGIKGIQ ISKKEVKLSLFADDIMVHIENPK DSSRKLLELKEFSKV
16976	47344	A	17081	1	842	
16977	47345	A	17082	155	531	GNLWSVDLRPGTPLRQNFRTI RQQHSRFTKNHCSQTPLLIPRQ TGSVDVLSKLQQTCS*GSCLV TIDLANAFSIPVHKA/HQKQFA FSWQ/YTFTVLPRLTWLQPC*V PNLPAEATNTEPSNGT
16978	47346	A	17083	1	1773	
16979	47347	B	17084	598	1428	
16980	47348	A	17085	3	227	
16981	47349	A	17086	1	207	

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16982	47350	A	17087	1	789	RDLQPFTSVTVHCRKNGNDQTF GGPLDAGSELTIPGDPKHHC PPVKVGAYGGQVINGVLA/HPL IWL VQKTDGS/WRMTVDYCKL NQVVIPIAAAVSDVVSLLEQINT SPGTWYAAIDLANAFFSIPVHK AQQKQFAFSWQGGQYTFVLP QWYINSPALCHNLIRRDLD CFS LPLDITLVHYIDDIMLIGSSEQ VANTLDL FVRHLRARGWEINPT KIQGPSTSVKFLGFQWCGACQA IPSKMRDKLLHLVPPTTKKEAQ
16983	47351	A	17088	1	435	
16984	47352	A	17089	2	808	PLIWL VQKTDGS/WRMTVDY CLNQVVIPIAAAVSDVVSLLEQ NTSPGTWYAAIDLANAFFSIPV HKAQQKQFAFSWQGGQYTFV LPQWYINSPALCHNLIRRDLD C FSLPLDITLVHYIDDIMLIGSSEQ EVANTLDL FVRHLRARGWEINPT KIQGPSTSVKFLGFQWCGACQ AIPSKMRDKLLHLVPPTTKKEA QCLQLLACY/WALVETEHLTIS HQVTMRPELPIMNWVLPDSSH KVGCAQQHSIIKWKVYVHDW ARAGPEGT
16985	47353	A	17090	2	544	
16986	47354	A	17091	1	633	MTVDYRKFNQVVPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFALPQ GYINFPALCHNLIRRELDFFLL QDITLVHYIDDILLIGSSEQE NTLDL LHKRSKEAEHTAASRIR VSCLPEQKSEHTLPWEQVPSS GDIKEYFPNFAVLLTTASLQGG DNTSQLQLTWKAPEDIKMSKT DADAEEIEALRG
16987	47355	A	17092	1	3228	MVTSSLTVAITSLVVVITSLV TSFVVVITSLVVVITSLVVVIT AIAIATLVVVLTFVTVVLTSLV VVITSLVMVITPPFAVITSLGV VITSLVVIITCLVLVITLGVVIT LGVVITSLVMVITPLVAVITPL GVVITSLVVVITSLVMVITSLTV VITSSIVVITPLVMVITSLTVIT LFVVITPLVMVITPLVIVNTSLV VVLITLIVSPPSLCSL VVVITFL VVAITSLVVVITSLVVVITSL
16988	47356	A	17093	1	471	
16989	47357	A	17094	1	1590	

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16990	47358	A	17095	332	1704	RGYVFCSWKKTGDS/WRMTVD YCKLNQVVIPIAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQQQYTF TVLPQWYINSPALCHNLIRDL DCFSLPLDITLVHYIDDIMLIGP RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVLFDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTTPVISQWPHEQCCHG GRDGGYAWAQCRI.PLTKAD LNTATAKRPIQQQRPTLSPQY GTIPQGDQPATWWVDYMG LPSWKGQRFVLGTGIDTYSYGF AYPACNASAKTAICGLTECLIH HHIDIPHSIASDQGTFFMAKEVR QWAHDHGHWSYHVSHPHEA AGLIEWWNGLLKSQLCQLGD NTWQGWGKVLQKVYYALNQH PIYGTVSPIAKIHRRVADSLKGG SGSWVWGFSTLAALDNDLGT RKVRAPSTN
16991	47359	B	17096	1	2061	
16992	47360	A	17097	1	1623	
16993	47361	A	17098	1	741	
16994	47362	A	17099	213	679	
16995	47363	A	17100	33	853	
16996	47364	A	17101	3	1249	
16997	47365	A	17102	17	770	
16998	47366	A	17103	130	469	
16999	47367	A	17104	1	1425	
17000	47368	A	17105	1	882	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
17001	47369	A	17106	227	1519	VTLLKMNAMLETPLFLSAVSDG VKLSAVAALVYVIVRCMNLKS ATAAPDLYLQDSGLSRFLKSC PLLTKYIPPLIWGKSGHIQTAL YGKMGRVRSPPHYGHRKFITM SDGATSTFDLFEPLAEHCVGDD ITMVICPGIANHSEKQYIRTFVD YAQKNGYRCAVLNHLGALPNI ELTSPRMFTYGTWEFGAMVN YIKKTYPLTQLVVVGFSLGGNI VCKYLGGETQANQEKVLCVSV CQGYALSRAQETFMQWDQCR FYNFLMADNMKKIILSHRQALF GDHVKKPQSLEDTL SRLYTAT SLMQIDDNVMRKFHGYNLSKE YEEESC MRYLHRIYVPLMLV NAADDP LVHESLLTIPKSLSEKR ENVMFVLP LHGGHLGFFEGSVL FPEPLTWMDKLVVEYANAICQ WERNKLQCSDETEQVEADLE
17002	47370	A	17107	21	385	SRSSSVVRQEPGRADGQRRRR GGPGLRSPGERQQPRPARPCR AHPGDPAGA/QPPPKTGKTCG APKATTRSTRCSISR*PPFPRSSC PTSPRAPSSASSSTAAMRRWL VTCRMPNWA
17003	47371	A	17108	158	423	
17004	47372	A	17109	1	1851	
17005	47373	A	17110	1	1104	
17006	47374	A	17111	66	432	
17007	47375	A	17112	103	3531	
17008	47376	A	17113	1	1311	
17009	47377	A	17114	1	750	
17010	47378	A	17115	183	373	QPQATTLVHPVHVA*LF*VHW QNRYPADNQGYRHWRCLLPA LPDAGR/VRLSASC*KPPNSRG
17011	47379	A	17116	344	480	SPKDDQEPSISKV***TSLPTSSR SLCLPPARMHFVWLAALLSFA
17012	47380	A	17117	3	3565	HEARRGLKMAACGRVRRMFRL SAAHLHLLLFAGA/RNSPARA SHSQGGQPGANFVSFVGQAGG GGPAGGQLPQLQSSQLQQQQ QQQQQQQQPQPQPPFAGGPP ARRGGAGAGGGWKLAEESCR EDVTRVCPKHTWSNLA VLEC LQDVREPENEISSDCNHLWNY KLNLTTDPKFESVAREVCKSTIT EIKECADEPVGKGYMVSCLVD HRGNITEYQCHQYITKMTAIF DYRLICGFMDDCKNDIN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
17013	47381	A	17118	1	495	PDRRRGCPALSGS*SGPAPRL/C LCNPTLTTFHPSGVIGVCL*RHWC LCRANTRHPSYRGRLSSR
17014	47382	A	17119	1	1479	
17015	47383	B	17120	67	8652	
17016	47384	B	17121	67	9183	
17017	47385	A	17122	1	1440	
17018	47386	A	17123	1	422	FRWKELDRPLEPSPETAQPPPP WLQK/NPTAVERANLLNMAKL SIKGLIESALSFGRTLDSYPPPL QQFFVVMHECLKHGLKVRKSF LSYNKTIWGPLELVEKLYPEAE EIGASVRDLPLGNEFYEYHALM MEEEGAVIVG
17019	47387	A	17124	2	587	WMGSCGLHRAWLQMRWWPE SAWKELDRPREPPETAQPPPP WLQK/NPTAVERANLLNMAKL SIKGLIESALSFGRTLDSYPPPL QQFFVVMHECLKHGLKVRKSF LSYNKTIWGPLELVEKLYPEAE EIGASVRDLPLGLKTPGRARAW LRLALMQKKMADYLRCLIIQR DLLSEFYEYHALMMEEGAVI
17020	47388	A	17125	312	493	
17021	47389	C	17126	102	278	
17022	47390	A	17127	2	140	KAHNCSGLRPPDLNPSVSNRL FASFLSPRDLKGR/ICSD*SQVL
17023	47391	A	17128	1	2051	
17024	47392	A	17129	1	498	
17025	47393	A	17130	2	340	
17026	47394	A	17131	140	396	
17027	47395	A	17132	703	912	
17028	47396	B	17133	201	912	
17029	47397	A	17134	1	1382	
17030	47398	A	17135	2	431	
17031	47399	B	17136	99	1151	
17032	47400	A	17137	1	891	
17033	47401	A	17138	15	2722	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
17034	47402	A	17139	476	2934	TEPKTKTT*LSQ*MQKKPLTKF NNPSC*KLSIN/IVLEVLAIRQ EKEIKGQLGKEEVKLSLFADD MIVYLENPVSAQNLLKLSNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVGRIINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLRFIWNQKRARIAKAI LSQKNKAVGITLPDFKLYKAT VTKTAWYWYQNRDIDQWNRT EPSEITPLIYNYQIFDKPEKNKQ WGKDSL FNKWCWDNWLAI CR KLKLD PFLTPTKINSRWIKAL NLRPKTIKLEENLGITQDIGTG KDFMTKTPKAMATKDKIDKW DLIKLSFCTAKETTIRVNR LPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWEKDMNR HFSKDDILA AKKHKCSSLAI REM QIKTTMR YHLTPVRMAI IK KPGNNSQKDIPDWRNGPKRKD RQITTFRGPTKLQVVVPTLGAA PGRGCPWRRRPRCPGREGEELH PALGGERGQRQAAGSGGARRL APSAGDGLCVGPVEDTGETQT WKTGQPG LREPWWGWRPTEPP PAPSSHSEEWPRRPPVRRAPRP AGEHAGEGGA VADTTAFSPW LPRVGGWHLQVHRGGRSCAGA RRFGGSRGWDLDLSSAPVASL
17035	47403	A	17140	1	2298	
17036	47404	A	17141	3	482	
17037	47405	A	17142	1	1026	
17038	47406	A	17143	1	623	
17039	47407	A	17144	25	392	ESLKGADPKFLRNMR FANKHN KKGLKKMQANSARATSARAD AIKALVKPEKGPDIPKGVSRK LDPLAYIAHPRLGKCAHSCIAK GLKLCRLQAKDKDQTKAQAA APA*APKGARTPTKASE
17040	47408	A	17145	1	507	

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17041	47409	A	17146	2	811	YRFSGPTIRSIQNHTHTNQGRK WHKKGIKKPRAQRYESLKGPE V*PSGQGVTCLLRADWLSPLL SGTYVGPFLRNTRFKKHKNK KGLKKMQANNAKAMSAIAE AVKALVKPEVKPKIPKGG/SR KLRLTLPDIVHP/KLGSARAPY LPRGFRLCLPNANAKSISSQGO GQGGQGSNQGGPFKPLQVVP ASGVNVPRLTKGFQSRYSLA QHEGQERTWVRPPTPRPWGYH FAWGWGSPVAICTNKPEAGKR RNEKEKLCQGDGY
17042	47410	A	17147	1	636	
17043	47411	A	17148	169	410	
17044	47412	A	17149	385	1359	QTNSPNCVRGRVSPVLPGSSS MDVLASYSIQELQLVHDGTGYF SALPSLEETWQTCLELERYLQ TEPRRISETFGEDLD/CFL/HAFP SPCIEESFRRLDPLLPVEAAICE KSSAVDILLSRDKLLSETCLSLQ PASSSLDSYTAVNQAQLNAVTS LTPSPSPELSRHLVKTSTQLSAV DGTVTLLKLVAKKAALSSVKVG GVATAAAAVTAAGAVKSGQS DSDQGGGLGAEACPENKKRVHR CQFNGCRKVYTKSSHKAHQQR THTGKPKYKCSWEGCEWRFRAR SDELTRHYRKHTGAKPFKCNH CDRCFSRSDHLALHMKRHI
17045	47413	A	17150	1	948	
17046	47414	A	17151	400	446	PSFLR*PSFWSREFH
17047	47415	A	17152	7212	10914	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLQDLASRGRAI PFCGQGRGFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLGDGDRAFHRNSLDFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSFFLVN DWLSVETEANGGLVEKEVLAA SDAALLRFRLLV AELQGFDD KHIWLSIWDPRPSRFTRIQRAT CCVLLICFLGANAVWYGAVG DSAYSTGHVSRSLPLSV
17048	47416	B	17153	1	14934	

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17049	47417	A	17154	999	3009	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQGRFKYIELVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHL DGDRAFHNSLDIFRIATP HSLGSVWKIRVWHDNKLSPA WFLQHVIVRDLQTARSAFFLVN DWLSVETEANGGLVEKEVLAA SDAALLRFRRLLVAELQRGFFD KHIWLSIWDRPPRSRFTRIQRAT CCVLLICLFLGANAVWYGAVG DSAYSTGHVSRLSPLSVDTVAV GLVSSVVVYPVYLAILFLFRMS RSKVAGSPSPTPAGQQVLDDSD CLDSSVLDSSTLFTSGLHAEVRT LLGVLGWAGGPAALAQGLKT LCTSQAFVGGMKSDLFLDSD KSLVCWPSGEGTSLWPDLLSDP SIVGSNLRQLARGQAGHGLGPE EDGFSLASPYSPAKSFSASDEDL IQQVLAEGVSSPAPTQDTHMET DLLSSLC AEVHTALPLHCSCLQ DSVQWHA VQGLPAFCRGPDPVT QEAQETARPAQNVLVLIPLHAA PHQAVAEIDALYDVYLDVIDK WGTDMDLFLGDFNADCSYVR AQDWAAILRSSEVFKWLIPDS ADTTVGNSDCAYDRIVACGAR LRRSLKPQSATVHDFQEEFGLD QTQASGPWGGAGLGSPPPGRT QAAGRALAISDHPFVEVTLKFH
17050	47418	A	17155	242	363	TKRQENGRRKKQDRTPTEQQLR VK*KSRSTKKRRKQSRSES
17051	47419	B	17156	1	12879	
17052	47420	A	17157	3	596	NLLFPVRSERGPHRPTPLSLWL LRPCELNKLAAAGGLAAGSSRA GALYLLIYIPRRPARAAPLCPAA ATGAPGASAGSASPASARPPGL ARAAPGLRGRPRSPRTFCV WLGVSLLSYQH YFAEPFESFQ VCCRHCGLCLTIRVHFPCLSAN PFHFSQLHLGPRPGKACHSVGL QIYNSQAHSHPSQERQLFC
17053	47421	A	17158	1	235	FFFVLYNLFLFVITSIPLOKVSIL TQRQLVAEENVKCCTVIPEPQ** *LSNYPFIVEMGFCHVGPQWSR TPTPKSVSR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17054	47422	A	17159	256	4064	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQGRGFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSFFLVN DWLSVETEANGGLVEKEVLAA SDAALLRFRRLLVAELQRGFFD KHIWLSIWDRPPRSRFRTRIQRAT CCVLLICLFLGANAVWYGAVG DSAYSTGHVSRLSPLSV
17055	47423	A	17160	2	347	LTSRGP/LCCVLLICLFLGANAV WYGAVGDSAYSTG/LCVQAEP AERRHSRCWPGVQRGCLSRLP GHPLSLPDVPEQGWEPHPHTC RAAGAGRRQLPGLNPCWTAPS SRSEASTLR
17056	47424	A	17161	9415	9994	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQGRGFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSFFLVN DWLSVETEANGGLVEKEVLAA SKASFRVPTPSRSPVALPAPAGG
17057	47425	A	17162	1030	1222	
17058	47426	A	17163	2	2762	
17059	47427	A	17164	25	115	
17060	47428	A	17165	1	383	
17061	47429	A	17166	120	596	IKAPCASFPTSGFPQRRSFVGR SSSTPEECGHSELGRNEDKASR GRIRQQ/PFAVLKYLLFCSLRW* YPGKQGLEWTSSKLQQTCKRY RERHKDTPQEEQLQDT*LSG/V TK/G*NEGKNVKGSRERSGYS QREAHQTNSRSLGRNSTSQKRV GASIQRS

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17062	47430	A	17167	1	2236	RPSGQPQLPGSVRHPRPVLRRLPL PRAQGSSSFRPRPFAPDPTMD KFWWHAAWGLCLVPLSLAQID LNITCRFAGVFHVEKNGRYSIS RTEAA\NLCKAFNSTLPTMAQM EKALSIGFETCRYGFIEGHVVIP RIHPNSICAANNTGVYILTNTS QYDTYCFNASAPPEEDCTSVTD LPNAFDGPITITIVNRDGRTRYVQ KGEYRTNPEDIYPSNPPTDDVS SGSSSSRSSTSGGYIFYTFSTVH PIPDEDSPWITDSTDRIPATSTSS NTISAGWEPNEENEDERDRHLS FSGSGIDDEDFFISSTITTPRAF DHTKQNQ\DW\TQW\NPSH\SNP EVL\LIQTTTRMTDVDRNGTTA YEGWNWPEAHPLIHHEHHEEE ETPHSTSTIQATPSSTTEETATQ KEQWFGNRWHEGYRQTPREDS HSTTGTAASAHSTHPMQGRT TPSPEDSSWTDFFNPISHPMGRG HQAGRRMDMDSHSTTLQPTA NPNTGLVEDLORTGPLSMTTQ QSNSQSFSSTHEGLEEDKDHP TSTLTSSNRNDVTGGRDPNHS EGSTTLLEGYTSHPHTKESRT FIPVTSAKTGSFGVTA\TVVGDS NSNVNRSLSGDQDTFHPGGSH TTHGSESDGSHSGQEGGANNT SGPIRTPQIPEWLILASLLALAL LAVCIAVNSRRRCQKKKLVIN SGNGAVEDRKPSGLNGEASKS
17063	47431	A	17168	1	1980	

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17064	47432	A	17169	362	2551	EDFSTSATTPSSSPRELPSGGQL WLCWLELLPSFTRNGVVHTGP C*GLC*RWQLSPQSLPSNFGM KISDMATLITTPAA/FSSSDW NTPAPTQSPPEVRRLLHLCSTFM DMLKVGQGEAAAGLVQNP SGHALGCLDSAASGSDPSVAV LLENVPNQRGESLRCPVYLGQ WNCSEKGTGMDSGQFGEEKGAH DPSPTYHYHACLSQWWPSPESP YPQSPGPVQKEPRNPGKSISML CLWIRYHAAADSGSSRAKLPLEE RLRPFSPTHDCLAFPLPLEKRPE GNVGRCPSTGKLPEEGSGSNI CCSAIFPVLPPLV1PRQTRSGV DLQQTPTDLQRLDTRSSLP MEQSWIENDFELNRSRLQKA NKLENLEETDKFLDTYTLPRLN QEETESLNRPTTGEIEAIINNVP TKKSPGPDGVTAKFYQRYKEE LRTVNKNHMIISIDA EKAFDNIQ QPFMLKTLNKLGDATYLIIRA IDDKPTANIILNGKLEAFPLKT GTRQGCPLSPLFNIVLEVLR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI NNFSKVSGYKINVQKSQEFLYN NNRQTEINQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYNPLL NEIKKDTNKWKNIPCSWIGRINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPSEAAEQILPN
17065	47433	A	17170	1	483	
17066	47434	A	17171	52	321	
17067	47435	A	17172	274	393	
17068	47436	A	17173	304	415	
17069	47437	A	17174	321	796	
17070	47438	A	17175	1	198	
17071	47439	A	17176	2	454	CRVPVPAATNGRCFPATPRDPGP RMRRACAWGRSKGAGRCLRR ATTRDKMAKKESILDLSK\YID\ KTIRVKFQGGRR\ASGILKGFEP NLL\NLVLTVTI*YMRDPDDQY KLTED\TRQLG\LVVFRG\TSLVL MCPQDGMEAI\NPFIQQQDA
17072	47440	A	17177	1	1806	
17073	47441	A	17178	1215	2065	
17074	47442	A	17179	217	441	
17075	47443	A	17180	117	296	DWSDIQLG*SLSLSEIFQL*IV SPPALHPAKLLHRS*A*LVSPQIG RECQCGGWTAMC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17076	47444	A	17181	2	138	LRTAPEFPGRFRGCAAAAAAES VAALL*STPPCRSGDSLCKGSR
17077	47445	A	17182	222	760	
17078	47446	A	17183	192	244	YIQPVF*GWTLGCCQFF
17079	47447	A	17184	1	990	
17080	47448	A	17185	1	2196	
17081	47449	A	17186	459	1387	
17082	47450	A	17187	2	454	
17083	47451	A	17188	1	957	
17084	47452	A	17189	398	553	
17085	47453	A	17190	2	293	
17086	47454	B	17191	53	182	
17087	47455	A	17192	3	1114	
17088	47456	A	17193	1	1024	SVVEFIPSCAVVLWSSVLLSPVR LLSYLSGVPPGHMPEDSMMDM MSPLRPHNYLFGCELKAGQDY HFKVVDNDENEHQLSLRTVSLG/ AGAKDELHIVEAEAMYEGSP IKV/THLATLKMSVQPTVSLGG VFEITPPVVALRLKCGSGPVHISG QHLVAVEEDAEEDEEEEDVK/ LSLSISGKRSAP/GGGSKVQKE RKCTMLMKDDDD\DEEDGYD EDD\DDDDDDF\DEEAEEKAP SERNLRYDTPAKNAQKSNQNG KDSKPSSTPRSKGQESF/KKQEK TPKTPKGPSSVEDIKAKMQASI A/EKGGSLPKVEAKFINVVKNC FPMTDQDAIQDLWQWRKSL
17089	47457	A	17194	2	291	
17090	47458	A	17195	185	307	
17091	47459	A	17196	3	392	VRGGQAFRQRPAPPLPVTRSAH RGRRPTRASQPSLFHILLREGK MSESSKSSQPLASKQEKDGT KRGGRPRKQP/PVSPGTALVG SQKEPSEVPTPKRPRGRPKGSK/ NKLEKEEEEESQESSEEEQ
17092	47460	C	17197	76	378	
17093	47461	B	17198	1803	1905	
17094	47462	A	17199	1	416	
17095	47463	A	17200	30	407	
17096	47464	A	17201	1	993	
17097	47465	A	17202	1	1287	
17098	47466	A	17203	1	2004	
17099	47467	A	17204	1	1368	
17100	47468	B	17205	1	3035	
17101	47469	B	17206	1	981	
17102	47470	A	17207	1	2017	
17103	47471	A	17208	1	1069	
17104	47472	A	17209	1	2463	
17105	47473	A	17210	1	324	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
17106	47474	A	17211	51	1528	GREASKMAQTQGTTRRKVCYY YDGDVGNYY*GQGHMPKP/HR IRMTNHLNLLNYGLYRKMEIYRP HKANADEMTKYHSDDYIKFLR SI/RVPDNIVGSTSKQMQRFNVG EDFPSIPMACFEFCQLSTGGGVA KCL*NFNKQQTDIANWAGGL HHAKKSEASGFCYVNDIVLAIL ELLKYHQRVLYIDIDHHGDBGV EEAFYTTDRVMTVSFHKYGEY FPGTGDLRDIGAGKGKYAVN YPLRDGIDDES YEAIKPVMSK VMEMFQPSAVVLQCGSDSLG DRLGCFNLTIKGHAKCVEFVKS FNLPLMLLGGGGYTIRNVARC WTYETAVALDTEIPNELPYNDY FEYFGPDFKLHISPSNMTNQNT NEYLEKIKQRLFENLRMLPHAP GVQMQAIPEDAIPESGDEDED DPDKRISICSSDKRIACEEFSDS EEEGEGGRKNSSNFKKAKRVK TEDEKEKDPEEKKEVTEEEKTK EEKPEAKGVKEEVKLA
17107	47475	A	17212	1	492	
17108	47476	A	17213	1	1851	
17109	47477	A	17214	1	753	
17110	47478	B	17215	427	614	
17111	47479	B	17216	1	711	
17112	47480	A	17217	750	1173	
17113	47481	A	17218	1	1224	
17114	47482	A	17219	1242	1743	
17115	47483	A	17220	423	1739	
17116	47484	A	17221	117	1183	
17117	47485	A	17222	1	377	FRRGAW/VPLLTRWGFRPRGGC ISNDSPRRS/IHYRETKPEPPVRV CARGLQRTPSAGHRAVLRMPPR RGRTRPGAPQGGGAALGGPARD RECACAGRAQTALRKNCVC KMPSGRGRTCSKNFSYFPS
17118	47486	A	17223	331	1134	
17119	47487	A	17224	178	1200	
17120	47488	A	17225	1	367	
17121	47489	A	17226	85	3360	
17122	47490	A	17227	8	930	
17123	47491	A	17228	1	765	
17124	47492	B	17229	120	509	
17125	47493	A	17230	232	3187	
17126	47494	A	17231	1	999	
17127	47495	A	17232	1	325	
17128	47496	B	17233	1	535	
17129	47497	A	17234	271	634	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
17130	47498	B	17235	301	523	
17131	47499	A	17236	1	1185	
17132	47500	A	17237	178	497	LPVPAYELNGSQQLPLLLGAAA IGYLAYKRFYVKDHRNKAMIN LHIQKDNPKIRHAFDMEIDLGD KAVYVCRCWRSKKFPFCDGAHT KHNKEVTGDNVGLIHKKET
17133	47501	B	17238	184	395	
17134	47502	A	17239	1	103	PAWHEGQPQPESECPQRQCIC SHGRGTPARCGVSY*ART/PAG ESP*TQQDLRAS*LGTRANHSQ RASARHKDSASAVTGAGHQ RD AE
17135	47503	A	17240	447	667	HRPRRRFQIKPQSQVPEHAPLPL PTASDPP/AHSPRCPSERLSPGG QRLGFPSSVLNCSKCSWQLAAC MGFSF
17136	47504	A	17241	265	890	
17137	47505	A	17242	1	1374	
17138	47506	A	17243	1	6189	
17139	47507	A	17244	1	8277	
17140	47508	A	17245	178	1177	
17141	47509	A	17246	1	447	
17142	47510	A	17247	1	465	
17143	47511	A	17248	3	3910	
17144	47512	A	17249	2	1871	
17145	47513	A	17250	1	666	
17146	47514	A	17251	1	635	FPGRFRRAVWCTHCCAPTSPG PVLPHSAAMSFLKSFPFPGPAE GLLRQQPDTEAVLNGKGLGTG TLYIAESRLSWLDGSLGFSLE YPTISLHALSRDRSDCLGEHLY VMVNAKFEEESKEPVADEEEE DSDDDEVPITEFRFVPSDKSAF* FPSCSVEAMFTAMCECQALHPD PEDESDDYDGEEYDVEAHEQ GQGDIPTFYTYEEGLS
17147	47515	A	17252	1	2796	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in U.S.S.N. 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
17148	47516	A	17253	1	2393	MEIRGALDLRKRQVLIFLVLLG LSRAGTESAHYSVAEETEIGSFV ANLARDLGLGVEELSSREARV VSDDNKKYLHLDLLTGNLLLN EKLDRLDELCGSTEPCVLHFQVV LENPLQFFRFELCVKDINDHSPT FLDKEILIKISEGTTVGATFLME SAQDLVVGNSNLQNYTISPNSH FYIKIPDSSDRKIYPELVLDRAL DYEQEAELRLTLTAVDGGSPPK SGTTLVLIKVLINDINAPEFPQS LYEVQVPEDRLPSWIATISAK DLDAAGNYGKISYITFFHASEDIR KTFEINPISGEVNLRSPLDFEVIQ SYTINIQA TDGGGLSGKCTLLV KVMDINDNPPVEVTISSITKRIPE NASETLVALFSILDQDSDGNGR MICSIQDNL PFFLKPTFKNFFTL VSEKALDRESQAEYNITITVTDL GTPRLKTEYNITVLLSDVDNDA PTFTQTSYTLFVRENNSPALHIG SVSATDRDSDGTNAQVNYSLPP QDRHLPLASLV SINADNGHLFA LRSLDYEALQEFERVGATDRG SPALSSEALVRVLVDANDNL PFVLYPLQNGSAPCTELVPRAA EPGYLVTKVVAVDGDGSGQNA WLSYQLLKATEPGLFGVWAHN GEVRTARLLSERDAAKHRLVV LVKDNGEPPRSATATLHVLLVD GFSQPYLPPEAAPAQADALL TVVYLVALASVSSLFLLSVLLF
17149	47517	A	17254	89	1283	
17150	47518	A	17255	1	276	
17151	47519	A	17256	2	259	WQGGILGSDPTPPLTSPNLLQT ACFREERDV/RRERGQPLGDHS ALCLPRRGVPPCDGLLCWWG PPDAAEPLRGSPARAGPVLPG
17152	47520	A	17257	624	4055	
17153	47521	A	17258	3	1784	
17154	47522	A	17259	1	1272	
17155	47523	A	17260	3	576	
17156	47524	A	17261	1	1017	
17157	47525	A	17262	1	1107	
17158	47526	A	17263	256	634	
17159	47527	B	17264	76	1340	

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17160	47528	A	17265	1659	2107	NLLCCTCSPFSSPVSAPOCTCTSN CIAILVHQQQWLVSLLQKHFF LHLHIFLA/LVFNFSLSHSF*IFDF DPWKLPP*PISPTLSSLPSNRHIA LILPCSCMTEDFDKMPPAVAR YMTSPQAVHIIAVCPFKASRKV SHSSLKIWLKFSV
17161	47529	A	17266	248	540	KFFSLRMLNPNHCLLACRVSA ERSAVSLMGFPLCISRPFSLAAL NIFSFISTLVNLMHISLGVALLEE YLCGLCIS*IGMLACLARLGKF SWIIR
17162	47530	A	17267	4880	5121	
17163	47531	A	17268	468	602	CLQLCSFGLGLTW*CGLFFYST *TLK*FPIL*RMVVF*WGLH
17164	47532	A	17269	359	462	
17165	47533	A	17270	457	600	LWWFNALFLCWTSFLTTLLE LHECLPVWRD*TRRH.TGWSK GSCTN
17166	47534	A	17271	2405	2830	TPVFRFIALSYTFADSDGEYF*IL LSENPQRFKCCFNMRSNKIPW DTFANSIKGAEFSGKHFIETFISS SESESESESTRFRDFRGLETSSSL SLDSFSLGDDFLSFLSFTIDA VSSKRLSKEIRKARLCWRFPRI
17167	47535	A	17272	1	2172	
17168	47536	B	17273	446	625	
17169	47537	B	17274	1	2604	
17170	47538	A	17275	1	3039	
17171	47539	B	17276	1	1383	
17172	47540	A	17277	1	993	

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17173	47541	A	17278	3	2494	RSTRQKVNKDTQELNSALHQA DLIDYRTLHPKSTEYTFSSAPH HTYSKIDHIVGSKTLLSKCKRTE IITNYLSDHSAIKLELRKLNLTQS RSTTWKLNLLNDYVWHNE MKAIEIKMFFETNENKDDTTYQN LWDAFKAVCRGKFIALNAYKR KQERSKIDTLTSQLEKELEKQEQ THSKASRRQEITKIRAELEKEIET QKTLQKINESRSWFERINKIDR PLARLIKNNREKNQIDTIKNDK GDITNTPEITQTTIREYYKHLA NKLLENLEMDTFLDTYTLPRLN QEEVESLNRPTGSEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL VPFLKLFQSEIEGILPNSFYE ASIIIPKPGRDITTKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNHKS NVIQHINRAKDKNHMISDEEK AFDKIQQPFMLKTLNKLK/DKI PRNPTYKGCEGLQGLQTTAQ GNKRGHKQMEHSMMLGRKN QYHENGHTAQ/IL*IQCHPHQ ATNDFLHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT *LQTLQGYSNQNSMVLVPKQR YRSMQENRALRNNAAYLQLSD L*QP*EKQAMGKGFPI* MVLG KLASHM*KAETGSLPYTLKYN QFKMD*RFKR*T*NHKNPRKRP RHYHSGHRHGGQLHVQNTKSN
17174	47542	A	17279	285	502	
17175	47543	A	17280	1	3189	
17176	47544	B	17281	1	1235	
17177	47545	A	17282	1	3139	
17178	47546	B	17283	1	1779	
17179	47547	B	17284	1	3127	
17180	47548	A	17285	1	3325	
17181	47549	A	17286	1	3145	
17182	47550	A	17287	1	1095	MIMGDFNTPLSTLDRSTRQKVN KDIQELNSALHQAADLIDYRTLH PKSTEYTFSSASHTYSKIDHIV GSKALLSNCKRTEIITNYLSDHS AIKLELKIKKLTNNRSTTWKLN NLLNDYVWHNEMKAIEKMFF ETNENKDDTTYQNLDWTFKAEC RGKFIALNAHKRQERSKIDTL TSQLEKELEKQEQTHSKASRRQE ITKIRAELEKEMETQK/TLQK/INE SRG/WKKFLEKLCFIELS*ARRI

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17183	47551	A	17288	1	3229	
17184	47552	A	17289	1	1205	
17185	47553	A	17290	1	986	
17186	47554	A	17291	1	3170	MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDYRTLH PKSTEYTFPSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDGS AIKLELRINKLNTQNRSTTWKLN NLLNDYWVPNEMKAEIKMFF ETNENKDTTYQNLWDFKAV CRGKFIALNAHKKRQERP KIDT LTSQLEKEQEQTSHKASRRQ EITKIRAELEIETQKTLQKIN*S QSWFFERVKKIDRPLARLIKKK REKNQIDTIKND
17187	47555	B	17292	1	2148	
17188	47556	A	17293	1	1416	
17189	47557	A	17294	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLDIYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRINKLNTQNRSTTWKLN LLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKA VCR GKFIALNAHKKRQERSKIDTLT SQLKELEKEQEQTSHKASRRQEI TKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
17190	47558	A	17295	1	3345	
17191	47559	B	17296	1	3122	
17192	47560	A	17297	1	2118	
17193	47561	A	17298	965	4091	
17194	47562	B	17299	15	2762	
17195	47563	A	17300	1	3049	MTVKVRITVTSGKKPPWLIPRQ TGYGVDLWQPTDQLRLVLT RRKTNKQKGHPHQNPICTSPSS KTKDRSTRQKVNKDIEQLNSAL HQEDLDIYRTLHPKSTEYTFPS APHHTYSKIDHIVGSKALLSKW KRTEITANCLSDHSAIKLELRJK KLTONWSATWKLNNLLNDC WVHKEMKAEIKMFFETKENK\ DTTYQNLWDAFKA VCRGKFIA LNAHKKRQERSKIDTLTSQLE LEKQEQTSHKASRR

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17196	47564	A	17301	3	4101	PLSTLDRSTRQKVNKDIQELNS ALHQVDLIDYRTLHPKSTEYTF FSVPHHNYSKIDHIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTQNRSTTWKLNPNLND YVWHKEMKAEIKMFFETNENK DTTYQNLWDAFKAVCRGKFIA LNAHKRKQERSKIDTLTSQKKE LEKQEQTSHSKATRRQEITKTRA ELKKIETQKTLQKINESRWFFE KTNKIDRLLATLIKKKREKNQI GARKNDEGAITTN
17197	47565	A	17302	1	3234	MANKNNQCREVLKGPDELKT MAREPHDKCTSFSSQFDQLEER VSAMEDQMNMKREEKFREK RIKRNEQRLQEIWDYVYKRPNLC LIGVPESDGENGTKLENTLQDII QENFPNLRQANIQIQEIQRMP QRYSLRRTTPRHIIIVRFTKVEM KEKMLRAAREKGRVTHKGKPI RLTADLSAETLQARRESTRQKV NKDIQELNSAQHQADLTDNYR TLHPKSTEYTLFSAPHHTYSKID HIVGSKALLSKCKRTEI
17198	47566	A	17303	1	3390	MLTLNHNRLTDAILNISTCLSR HLDLNTGGKKRISYKRNLYME EHLEGLCSNEFTWENSTIMTDS QMLMHREEPGLPNIPILSIVFT NNRSKRQKVKNKDIQELNSALH QADLIDYRTLHPKSTEYTFESA PHHTYSKTRIVGSKALLSKCK RTEIITNCLSDHSAIKLELRKIKL TQNCSTTWKLNLLNDYVW HNEMKAEIKMFFETNENKDTT YQNLWDTFKAVCRGKFIALNA HKRKQERSKIDTLTS
17199	47567	B	17304	1	2427	
17200	47568	A	17305	1	4257	
17201	47569	A	17306	1	3726	MVVKTNARELRDECTSLSSPFN QLEERVSVMENQMNMKQEE KFREKRIKRNEQSLQEIWDYVK RPNLCIGVTESDGENGTKLEN TLQDITQENFPNLARKANIQIQE TQRTPORYSRRATLRHIIIVFT KVEMKEKMLRAAREKDFTPTK IKRDKEGHIYIMVKGSIQEEELTI LNIIYAPNTGAPRFIKQVLSDLQ RDLDSHTLIMGDFNTSLTLDR SMRQKVNKDQELNSSLHQAD LIDYRTLHPKSIE
17202	47570	A	17307	1	1059	

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17203	47571	A	17308	130	1092	
17204	47572	A	17309	1	924	
17205	47573	A	17310	1	1206	
17206	47574	B	17311	1	1257	
17207	47575	A	17312	1	685	MEIILRICKLTISKELLDGSSRL TMTHYKHHRYFSHSAEEQIIEEL NESEMICQHHHTAENDFDELRE EGFRRSVITNFSKLKEDVQTHF KEAKNLEKRLDEWLTRINSVEK TLNDLM*LKTVA*ELRDYTSF NSRFDQVEERVSVIEDQMNMEN EREKKEFREKRV*RNQSLQEIW NYVKRPNLHLIGVSEIDRENGT KLENTLQDIFQENFTYLARQAN IQIQEI
17208	47576	B	17313	70	1227	
17209	47577	B	17314	640	751	
17210	47578	A	17315	1	2328	MGVSGAQPGRSCWHRSSSTGSQ GLGPVPEPADCGGEAAGRARE EGTVSLTMTGADSDMAPEAP QHTHIDVHHQESALAKLLTTC CSALRPRTAQRGSSRLVASW VMQIVLGILSAVLGGFFYIRDY TLLVTSGAAIWTGAVAVLAGA AAFIYEKRGGTWALLRTLTLT AAFTAIAALKLWNEDFRYGYS YYNSACRISSSSDWNTAPTQSP EEVRRLLHLCTSFMDMLKVGGO GEGAAAGLVQNP SGHALGCLD SAASGISDPSVAVLLENVPNQR GESLRCPVYVLGQWNCSEKGT MDSGQFGEEKGAHDPSTTYH ACLSTQWWPSPSPYPQPSGPQ VKEPRNPGKSISMLCLWIRYHA ADSGSSRAKLPLEERLRPFSPTH DCLAFPLPLEKRPEGNVGSRCP SGTKLPEEGSGSNICCSAIFPVL QPPLVIPRQTRSGVDLQQTPTD LQLRDLTVRRKTNKQKQHPHQ NPMCTSPSSKTKELKEDVRTHH KEAKNLEKRLDKMVMNRINSVE KTLNDPMELKTQARELHDKCT SFSSRFQLEERVSVTEDQMNE MKREEKFREKRVKRNQSLQE IRDYVKRPNLCLTGVPESDGEN ETKLENTLQDNIQENFPNLARQ ANIQIQEIQRTPQRYSSRRATPR HIIVRFTKVEKEMKMLRAAGE KGQVTHKGKPIITLADLLAETL
17211	47579	A	17316	508	666	
17212	47580	A	17317	622	780	

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17213	47581	B	17318	1	777	
17214	47582	A	17319	1	508	MSGFEKQYKKIRLDKTLDSENE GLELPVPAKRSLGVRLYACC GLLLCPAYPQHFAHGYVDKIPG YPGRAGTLTGLHPMQVCRCR QAPCLKSNNALIVILGTVTLD VGIGLVMPVLPGLLRDIVHSDS ASHYGVLLALYALMQFLCAPK YKLPSNTTNTSMQIN
17215	47583	B	17320	310	1047	
17216	47584	A	17321	1	1101	
17217	47585	A	17322	577	735	
17218	47586	A	17323	337	642	
17219	47587	A	17324	2	653	
17220	47588	A	17325	2	935	
17221	47589	A	17326	532	729	
17222	47590	A	17327	1	675	
17223	47591	A	17328	1	684	
17224	47592	A	17329	2	641	
17225	47593	A	17330	1	808	
17226	47594	A	17331	562	675	
17227	47595	A	17332	2	1687	DTGNNEWKQQEGLSHNNWLG LGCLFGPETPIFYPATLGHSTSIY YERKKEDKNGMKEEHDTVA MFFTLFNFQISVENIRKGPV GESIAQSYLNVVQEIFRSRNHQ LLQDLTRDLCDNLKTCHTSHGS VMAETA VINHKKRKNSPRIVQS NDLTEAA YSLSRDQKRMLYLF VDQIRKSDGTQLQEHGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKQRSNLGVRLYAC CGLLCPAYPQHFAHGYVDKIP GYPGRAGTLTGLHPMQVCRCR RQAPCMKSNNALIVILGTVTLD AVGIGLVMPVLPGLLRDIVHSD SIASHYGVLLALYALMQFLCAP VLGALSDRFGRRPVLLASLLGA TIDYAIMATTVPVRGHSVLKKGKQ HKSVENLQPDNVIEKKIPFSGEK FKPAAEICKSNRELNVNHQDNG ENVSRA CQRLLQLPSQA WRF RRKNWFCGPGWSPFSVQSRD LVPCVPAAPALTKRGQGTQA VASEGSPKPWQLPHGVEPAG AQKSRAEVWEPPRFQKM
17228	47596	B	17333	12	60	
17229	47597	B	17334	253	2103	

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17230	47598	A	17335	469	2512	PTSAYERGQRFASRLQMNLEY FLRWLMKIFPQAPCMKSNNAL LIVILGTVTLDAVIGLVMFVL PGLLRDIVHSDSIASHYGVLLAL YALMQFLCAPVLGALSDFRGR RPVLLASLLGATIDYAIMATTP VLWIYPLVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTRDPHYVEDK GHKYLVEANTGTENGYQGEE SLFNKAYYGGGTNFFRKESQKL QQSACKRDAELANGALGIIELN NDYTLKKVMKPLITSNTVTDEI ERANVFKMNGKWYLFDSRGS KMTIDGIKLNDIYMLGFVSNSL TGPYKPLNKTGLVLQMVLPDN DVTFTNFYLPGPQAKANMWLL QAHDKKSFSSRIKGTFGPAL
17231	47599	A	17336	2393	2945	
17232	47600	A	17337	980	1732	

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17233	47601	A	17338	1	2400	GRFPFRPRLCQRRRLGGGRMK MTGDFEECLKDSRFRFAALEEV EGDVAEELKLDKLVKLGAMI DTGKAFCVANKQFMNGIRDLA QYSSNDAAVETSLTKFSDSLQE MINFHTIL/L*PNSINLRHSFSN FVKEDLRKFDAKKQFEKVSE EKENALVKNAQVQRNKQHEVE EATNILTATRKCFRIHALDYVL QINVLQSKRRSEILKSMLSFMV AHLAFFFHQGYDLFSELGPMYK DLGAQLDRLVGDAAKEKREME QKHSTIQKDFSRDSDSLKYNV DAANGIVMEGYLFKRASNAFK TWNRRWFSIQNNQVVYQKKFK DNPTVVVEDLRLCTVKHCEDIE RRFCFEVVSPTKSCMLQADSEK LRQAWIKAVQTSIATAYREKG DESEKLDKKSSPSTGSLDSGNE SKEKLLKGESALQVRVQCIPGNA SCDCGLADPRWASINLGITLCI ECSGIHRSGLGVHFSKVRSLTLD WEPELLKLMCELGNVDINRVY EANVEKMGIIKPQPGQREKE AYIRAKYVERKFDKYSISLSPP EQQKFVSKSSEKRLSISKFGP GDQVRASAQSSVRSNDSGIQQS SDDGRESLPSTVSANSLYEPEG ERQDSSMFLDSKHLNPLQLYR ASYEKNLPKMAEALAHGADV WANSEENKATPLIQAVLGGSLV TCEFLQNGANVNRQDVQGRG
17234	47602	A	17339	1	782	
17235	47603	A	17340	1	475	
17236	47604	A	17341	1	852	
17237	47605	A	17342	432	696	
17238	47606	A	17343	3	296	ETEIEALKEELLFLKKNQEEFV KGLQAQIAISGLTVEVDVPKSQ DLAKIMADIWAQ*DELEDGEDF SLRDALDSSNSMQTIRKTTTRPI VSGWQSGV
17239	47607	A	17344	2	292	SQKKGLVGALTNPPHFPCPHL *EVKGLQAQIASSGLTVEVDAP KSQDLAKIMADIRAQYDELAR KNREELDKYWSQQVREGKGM GCQGVGGRQTE
17240	47608	A	17345	1	908	

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17241	47609	A	17346	1	1452	TGPEFHDLRLVRRRPQSLSPVL LLSSPDMSFTTRSTFSTNYRSL GSVQAPSYGAGPRRAARPASY AGAGGSGSRISVSRSTSFRRGM GSGSLATG\IAGG\LAGMG\GIQ NEKETMQSLNDRLASYLDRVR SLET\ENRRL\ESKIRE\HLEKKG PQ\VRDWSHYFKINEDLRA\QIF ANTV\DNARIVL\Q\DNAPSCVR DDFR\VKY\ETELA\MRQSCWRT DIHGAPQGFDDTNYHTDLQL EKTEIRGSSRRELLFQ*RRNHEE /EKLKGLQAQIAQFLGLTRGRLL DCPQIFRDLRQDSDWADIRGPIID ELASEEPRGSLDKY\WSQQHEE STTVVTTQFAEVEAAETTLTE LRRTVQSL\ENDLDSMRNLKAS\ LENSLREG*RPAYALQMEQLN GILLHLESELAQTRAEGORQA QEYEAALLNIKVKLEAEIATYRR LLEDGEDFNGLDALDSSNSMQ TIQKTTTRRIVDGKVVSEINDTI
17242	47610	A	17347	467	843	
17243	47611	A	17348	114	1363	
17244	47612	A	17349	2	281	
17245	47613	A	17350	1	588	
17246	47614	A	17351	184	354	
17247	47615	C	17352	391	657	
17248	47616	A	17353	1	2010	
17249	47617	A	17354	2	443	VPDLPPSHRGFRAAQGGLPPKN KVAALPSWGSANQNSSARWEL VSPPIHRRGS*GPGETGDLGGSS IQRAVELRLVQAFVVPKSSLRD PSREGRGGWAG*VQTKGA*AR PTLLWAPKR/DRGGKAAPTSTW NSPKAGCPSARSSPAPP
17250	47618	A	17355	1	1359	
17251	47619	A	17356	260	380	
17252	47620	A	17357	153	273	
17253	47621	A	17358	270	484	AKYRGTSRRLKALGAHVVPKQ PIPAWQHKKDPSGGRPEEGVKL YREKEFSS*TL*/RI*TPGDWA YAWADAW
17254	47622	A	17359	2	941	
17255	47623	A	17360	1	615	
17256	47624	A	17361	911	1472	
17257	47625	A	17362	2	442	
17258	47626	B	17363	76	235	
17259	47627	A	17364	38	190	
17260	47628	A	17365	134	523	
17261	47629	B	17366	1	1776	

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17262	47630	A	17367	394	554	
17263	47631	A	17368	22	831	
17264	47632	C	17369	1	1191	
17265	47633	A	17370	199	647	PSVPTGSRNRTTAVAVEERQSDGSGSLSPGKIQTTTTGIIIPALLHITGAPVSSDFRLDWLIERPKGGRRAELSIKSLALPLPQHCGSDNDWIPQLRLLSRASFSHSDDDLFGGAYRRALHILCIHSSKEALELNTFQPVTFNLNAFSK
17266	47634	A	17371	1	2697	
17267	47635	B	17372	25	1698	
17268	47636	A	17373	2	218	ASLRSSPFSRSLRCQGNTPERSGLPKALFCTKPSR\ADLGPAGHRRPLPSVQPG*AIPGRVSRGEKNLTNR
17269	47637	A	17374	2	2543	
17270	47638	A	17375	198	403	PQALREHSPSV* TGRQDRQLLFKDCTCQRQRDDVDSVQGKRRLHISSPQGLNSFPAVSLKLEHNVKAE
17271	47639	A	17376	58	543	VLYRSSRMCKIRVLISRPFSIVKICERVLSTQSGRHDYAAAAVSKTGQKRIHSSGTRGSGAPHS PGWWEPSDRVGVSI CFLFSLK YRLFSSCLVQPCLG PVLGNNSC SPEGPREPSPPSHGLGFPMCT* TQVPASTTQSDNGQNHNP GCP MPISPDS
17272	47640	A	17377	14	701	
17273	47641	A	17378	91	309	GRKQFPHLATGKEGCVGGQRLPCVTVELIFPAPAGAAVPRRP*L PRTAPS*LHCLPVC RMPGEAPT ARHAAWV
17274	47642	A	17379	2	2625	
17275	47643	A	17380	1	1752	
17276	47644	A	17381	3257	3412	
17277	47645	A	17382	1	1091	
17278	47646	A	17383	233	1148	
17279	47647	A	17384	1	1716	
17280	47648	C	17385	162	356	

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17281	47649	A	17386	836	2106	AKKFRKRWPLEEQEQNPVDGG AAPVTALRKRVTSQRCSLEFLE DAVGCAPAQRYTPPSAPSSTTP LGLPLT/TCGARGSWEEKSDLC PLPCRTHKHTSGSPRHGGLKKT FIKNMRQYDTRNSRVLICAKR SLCAAFSVLPYGEGLRISDLRV DSQKQRHPSGGVSVSSEMVFEL EGVELGADGKVVSYAKFLYPT NALVTHKSDSHGLPTPRPSVP RTLPGSRHKPAPTCSAPASTEL GSDVGDITLEYNPLDDPQWP CGKHKRVLIFASYMTTVIEYVK PSDLKKDMNETFREKFPVKLT LSKIRSLKREMRSLSECSLEPV TVAMAYVYFEKLVQGLIKQ NRKLCAGACVLLAAKISSDLRK SGVTQLIDKLEERFRFNRRDLIG FEFTVLVALELALYLPENQVLP
17282	47650	A	17387	1	2531	
17283	47651	A	17388	1	1506	
17284	47652	A	17389	34	576	
17285	47653	A	17390	112	1840	EELRVREHVTGGICGGSQMMV DLLGATTELVAVAPWVMSAA AGGKNLKSHPKVEVDIINDFI LRWNRSDSVGNVTFSDYQK TGMNDNWIKSGCQNTSTKCNF SSLKLNVEEIKLRIRAEKENTS SWYEVDSFTFPRKAQIGPPEVH LEAEDKAIVIHISPGTKDSVMW ALDGLSFTYSLLIWKNSSGVVE RIENIYSRHKIYKLSPETTYCLK VKAALLTSWKIGVYSPVHCIT TVENELPPPENIEVSVQNQYV LKWDYTYANMTFQVQWLHAF LKRNPNGHLYKWKQIPDCENV KTTQCVFPQNVFQKGIYLLRVQ ASDGNNTSFWSSEIKFDEIQAQ LLPPVFNIRSLSDSFHIYIGAPKQ SGNTPVIQDYPLIYEHFWENTS NAERKIIKKTDVTPNKLPLT VYCVKARAHTMDEKLNKSSVF SDAVCEKTKPGNTSKIWLIVGI CIALFALFPVIAAKVFLRCINY VFFPSLKPSSSIDYFSEQPLKNL LLSTSEEQIEKCFIENISTIAIVE ETNQTDDEHKKYSSQTSQDSG NYSNEDESEKSTSEELQQDFV
17286	47654	A	17391	3	373	

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17287	47655	A	17392	1	432	LPRFVGQQPRPLGPLRSGSGEG CRAPGEAVRAPDYAFPIPGTRA S/PLNRFPLGGTAWPQAHPTNP KPAPAPGAQLDDPPRYSRHGLS RWGLPLQSLVLLPPLQRPMPLPQ AAAPNTPWPPWTLRAGRREN AHAQRKLHLWAGKVE
17288	47656	A	17393	98	376	
17289	47657	A	17394	1	364	
17290	47658	A	17395	1	1230	
17291	47659	A	17396	892	2004	RRMSFMSSEVLVGELMSPFDQS GLGAEESLGLDDYL/EVAKHF KPHGFSSDKAKAGLLPNGLA\/ DGLVSPSNNKSKE\DAFISGTDW DVGRK\WVLKEFDGCPCLGIE* PWETIARLTFLTTFGIDICDSELLP P*FQGRLIKAAPRRLNPIGHLP QKFLT\KPRPGLAPFTF\LQPLPL SPGVL\SSTPDSFPFSFRSWSG*K WDIH*KGD*/RKPDYTAIYVA\MI PQCIKE\EDTPSDND\SG\CMSP ES\YLGSPQHSPSTRGSPNRSPL SPGVLGCSARPKPYDPPGEKMY AAKVKGKLDKLLKKMEQNK TAATRYRQKKRAEQEALTGEC KELEKKNEALKERADSLAKEIQ Y\KDLIEEVKARGKKRVP
17292	47660	A	17397	43	1300	DSCCIQGTMLRSRTQQRPGVEG SLKQHQLHSNFSSINESVFIVS FSLNTIGSGGRGAEGER/GREPL SRPQPPAGPLGGALPAPP\SLMP QL*SE*GRLQLLYLLQ/PAVC SCSRCSAPRSRCVARPAARTGL PTPAPASSP/CSRSLSSSRSLSSSC RVSCCHSLSSCCRSLSCSRSSST SSRSSSTSSSLSLSSSLSCSSCRL SCSNSFSTSSSLSLSSSLSCSSC CLSCSNSFSTSSSLSLSSSLSCS SCRLSCSNSFSTSSSLSCPGSFS CSHSLSSCSRSLSSCSHSLSSCSR SLSSCSRSLSSCSRSLSSCSRSL SCSRSLSSCSRSLSSCSRSLSSCS CSLSSCSRSLSSCSRSLSSCSRSL SSCSRSLSSCSRSLSSCSRCLSSC SCSLSSCSRSLSSCCLFRRLNI
17293	47661	A	17398	288	574	

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17294	47662	A	17399	230	648	VIAPGLWMMAADIPRVTTPLSS LVQVPQEEEDRQEEVTTMILED DSWVQEA VLQEDGPESEFPFQS AGKGGPQEEVTRGPQALGRL REL CRRWLRPEVHTKEQMLTM LPKEIQAWLQEH RPESSEAAA LVEDLTQTL*DSWVQEA VLQ DGPESEFPFQSAGKGGPQEEVT RGPQALGRLREL CRRWLRPE VHTKEQMLTMLPKEIQAWLQ HRPESSEAAA LVEDLTQTL
17295	47663	A	17400	105	381	SSGFWPLRFPLDVIAVSTIAVH EKEESLWPRVAVFSTLAP/ESPP WGEAPQSAGR*SGVPEDHVL R YRGTL SLACSSRIHPPAQLS HYKN
17296	47664	A	17401	1023	1915	
17297	47665	A	17402	3	277	QVLLQGALLLLITVAQAGRVLK LGV SREFQDLILWGKETFR/C GPGCSPALHLPQGSSIP/SSQQL *YLA AEQPLHRGPPTAPV S GAE
17298	47666	A	17403	3	299	
17299	47667	C	17404	46	398	
17300	47668	A	17405	171	403	GKNSTLQQFNLLHYSSITVAV NNPTLGNVS VFLYILFTGIHQ LVKVILRKL GK*RFGL ELASLSL LFLPPVSLF
17301	47669	A	17406	291	467	
17302	47670	A	17407	2	395	DHAYVFLGRTACYLMKAYRK VNP RIVFSSNTIETHPKDLHSC DHPFAEKTQFTVSTLDDVKN SG SIRDNYCRTSEISA VHIDTECVS VMLQAGTPPLQVK*KKNFQQR KQG*KMKWDPSDISNSMAEVL
17303	47671	A	17408	1	149	EKEIPGPWLLGAMRFRFCGLD CPDWVLA EISTLAK/IPL*SCGCS AARY
17304	47672	A	17409	555	1156	QFYNKTPSRSECPNLLHMMRTE GPPGGVDQPDGHQAGWPPPEP AGQQRGRQSGCHLLQGGASPR PSCGTVHARACTPPASCPCHHR YRSHLQRGKWWPK/GLPQHTR LDHTEVLGAAEGSTVSAVP SAT RAARDHVRR LQTRKCFCKGAL LLLITAA RAGRVLFGQPQLLQF TGQGF AIDTVLGRGTGEDETHC HCLGHIA
17305	47673	A	17410	3	366	
17306	47674	A	17411	408	1702	
17307	47675	A	17412	1	2661	

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17308	47676	A	17413	2	2288	
17309	47677	A	17414	1	1992	MGDFNTPLSTLDRSMRQKVNK DIQELNSAVHQVLDLIDYRTLHP KSTEYTFFLAPHRTYSKIDHIVG SKALLSKCKRTEIIRNCLSDHSA IKLELRINKLTQNCSTTWKLN MLLNDYVWHNEMKAEIKMFF ETNENKDTTYKNLWDTFKA VCRGKFIALNAHKRQKERSKIDTL TSQFKELEKQEQTSHKASRRQE ITKIRAELEKEIETQKTLQKINESR SWFFEMISKIDRPLARLIKKKRE KNQIDTIKNDKGDIIIDPTEIQTT IREYYKHLIAIKLENLEEMDKF PYTNTLPRLNEEEIESLNRITITGS EIEAIIKSLPTKKSPGPDGFTAKF YQRYKEELVPFLKLLFQSIEKE GILPNSFYEASIIIPKP/DVGSSS QGNQAGERNKGYSFRRKGSQI VPVCR*YDCTFRKSHFLSPKSP* ADKQLQQLRIQNQC AKITSPI HHQQTNREPHE*TPIHNCFK E NKIPRNPTYKGC EGPLQGELQT TAQ*NKKGHKQMEEHSMLMD RKNQYRENGHTAQGNLQIQCH PHQATNDFLHRIGKNYFKVHM EPKKSPPHQDTPKQKE*SWRH HAT*LQITLQGYSNQNSMVLVP KQRYRPMQNRALRNNTTHLQ QSDL*QT*QKEEMGKGFPI**M VLGKLASHM*KAETGSLLYIL
17310	47678	A	17415	1	1677	

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17311	47679	A	17416	1	2178	MGDFNTPLSTLGRSTRQKVNK DTQELNSALHQADLDIYGTLLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNCLSDHR AIKLELRIKKLTQNRSTTWKLN NLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTSHSKASRRQE ITKIRAELEKEIETQKTLQKINESR SWFFERINKIDRPLARLIKEKRE KNQIDATKNDKGDITTDPTIEI TTIREYYKTLYANKLENLEEMD KLLDITYTLPRLNQEEVESLNRPI TGSEVVAINSLPTKNSPGPDGF TAKYYQRYKEELVPFLKLFQS TEKEGILPNSFYEAASILPKPGR DTTKENFRPISLMNVDAKILN KILANRIQQHIKKLIHHDQVGF PGMQGWFNICKSINVIQHINRT KDKNHMIIISIDAFAFDKIQPPF MLKTLNKLVLVLARAIRQEKE JGIGQLGKEEVKLSLFADDMIV YLENPIISAQNLLKLSNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRKYLGIQLTR DVKDLFKENYKPLLNEIKEDTN KWKNPSCSWIGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARITKSILSQKNK AGGITLPDLKLYYKAIVTKTA WYCYQNRDIDQWNRTEPSEIM
17312	47680	A	17417	1	1770	
17313	47681	A	17418	1	1101	
17314	47682	A	17419	1	1614	

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17315	47683	A	17420	1	1878	MVLALTGNKADLASKRPLEFQ EAQAYADDDSWLFMETSAGK AMNVNEIFMAIAEKLPKNKPN NAAGAPDRNQGYLSACEFSGR KLPKQTTHKHKQSLRTKLCGAS YASSNLIPRKL YEPLLVIPRKTG SGVDLQQTPTDLQLWVLTVRR KSNKQKGYPHQNPICMLPSSKT KDFKPTKIKRDKDGHYIMVKG SIQQEELTVLNINAPNTGAPRFI KQALRDLQRDLDSHTIIMGDFN TPLSTLDRSTRQKVNKDQELN SALHQADLDIYRTLHPRSKDY TFFSAPHHTYSKIDHIVGSKALL AKCKRTEITRNCLSDHSAIKLEL RIKKLTQKCSTTWKLNLLND YVWHNEMKAIEIKMFFETNENQ DDTTYQNLWDTFKAVCRGKFIA LNAHKRKQERSKIDILTSQKKE LEKQEQTTHSKASRRQEITKIRVE LKEIKTQKTLQKINESRSWLFE KINKIDRQLARLIKKKREKNQID AIKNDKGDIITDPTIEQTITREY YKHLAYAKKLENLEEMDKFLDT YTLPRLNQEEVESLNRPIGTSEI EAIHKSLLPAKSPGPDGFTAIFY QRCEKELAQFLRLFKSTEKEGI LPNSFYEDSIIILPKPGRDITK KENFRPISL
17316	47684	A	17421	1	1761	
17317	47685	A	17422	1	1875	
17318	47686	A	17423	1	1611	
17319	47687	A	17424	1	4539	
17320	47688	B	17425	1	6294	
17321	47689	A	17426	2	1913	
17322	47690	A	17427	1	1026	
17323	47691	A	17428	1	2112	

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17324	47692	A	17429	1	1884	MENGFDELREEGFRSSNYSELO EEIQTGKGEVKNIEKNLDECITR IPNTEKCLKKLMEKTKARELR EECISLRSCDQLEESVSMED EMHEMKREGKFREKRIKRNEQ SLQEIWDYVVKRPNLRLIGVPED RSMRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFSSAPH HTYSKIDHIVGSKALLSKCKRT EITNYLSDHSAIKLEKIKKLTQ NFSITWKLNNLLNDYVWHN KMKAEIKMFFETNENKDDTYQ NLWDTFKAVCRGKFIALNAYK RKQERSKIDLTSLQKLEKEQE QTHSKASRRQEITKIRAEKEIE TQKTLOKINESRSWFFERINKID RPLARLIKKKREKNQIDAINKD KGDITTDPTIEQTITREYYKHL TNKLENLEEMDKFLDTYTLPR NQEEVESLNRPTGSEIVAIHSL PTKSPGPDGFTAQFYQRYKEE L/RNKIPRNPYKGCCEPLQGE QTTAQGNKRGDKQMEHSML MGRKNQYRENGHTAQGNLQIQ CHPHQATNDFLHRIGKNYFKV HMEPKKSPHRQVNPKPKEQSW RHHAT*FQIILQGYSNQNSMVL VPKQRYRSMEQNRALRNATY LQLSDL*QT*EKQAI
17325	47693	A	17430	1	1695	
17326	47694	A	17431	1	3779	MELKTKARELREECRLSRSRN QLEERVSADEEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSSRRATPKHIVRFT KVENMKQMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQGEEL TILNIYAPNTGAPRFIKQVLSL QRDLDSHTLMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE
17327	47695	A	17432	1	735	
17328	47696	A	17433	1	2541	
17329	47697	A	17434	1	1461	

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17330	47698	A	17435	2	429	AACAAAMSLVPEKFQHLRLV NTNIDGRRKIAFAITASSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSVNLLSNGLYL/VKG VGRRYAHVVLKADIDLTKRA GELTEDEVERVITIMQNPRQYKI PDWFL
17331	47699	A	17436	1	615	
17332	47700	B	17437	264	556	
17333	47701	A	17438	1	406	FFFFFLQKVGIYLIHKITFQQHRL WVTSAAFLSLSSMAAVGTSSSL SENSGPGHGGKQTF*GP/EGTDI PEGRHHFSAQAFSVVAGRGT AALLHGSHVPQGR/SRIGSRSGG PPSHPDTCSSSHSAGRSCPHSC TG
17334	47702	A	17439	3	3484	
17335	47703	B	17440	42	367	
17336	47704	B	17441	203	382	
17337	47705	A	17442	22	266	YRDLPHLLNSDLIFNMSTSLRE TMILIRTLRVPL/PLHGVIPIS KIQGLVLNALNQVESIFQVSF NLFDPDAFQHVIRA
17338	47706	A	17443	1	1137	
17339	47707	A	17444	1218	1482	QSPWPSSLRGDVSITPNLIFSCL SIGWPFCLV/SFC*PKK*TFQGV GSEVYDVVKHFASCVLCHKQMN KLNLVFRNTYFVALLSTELFEN
17340	47708	A	17445	2	377	
17341	47709	A	17446	1	211	
17342	47710	A	17447	2	732	CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVVPNYTL LSQIPEEAESFTVLDLKDAFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPGGFRDSPHLFGQAQ DLVHFSSPGTLVVQYMDLL ATSEASCQATLDLLNFLANQ GCKRVGIALGVLQTQHTGTPQP VAYLSKETDVAAGPLTAILL LAFGPCIFNLLVKLVSSRDAIK LQMVLMQEPQMSSVTNNFYRGP

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17343	47711	A	17448	1	3003	MPGAQDLQPTMPEPPHPQWAP TWPEPPRRVPPPAPRRVPPLTA QGLSVDQSRGKGFSDDPDRYID VLQGLGQTFDLTWDRVMLLLD QTLAFNEKNAALAAAREFKDT WYLSQVNDRMATAERDKFPSPG QQA VPSMDPHWDLDSYGDW SHK YLLTCVLEGLRRIRKKPMN YSMMSTITQGKEENPAFLEQL WEALRK YIPLSPKSLEGQLIKD KFITQSAADIRGKLQKQLVPE QNLEALLNLATSVFYNRDQ
17344	47712	A	17449	5	624	IQPILAYPHPKTLKQLWGFLGIT /GFCPVWIPRCSKIAKSLYTLIKE TQRANTHLVEWEPEAETAFTK LKQALVQAPTLSLPTGENFSLY VTERAGIALGLVTQTRGTTQP VTYLDKGEPMKDCQCIIVQTY ATQDDLLEVPLANPDNLNYTD GSSFVENGIRRAGYAIVSDVTIL ESKPLPPGTSQAELVALTRA LELGKGE
17345	47713	A	17450	636	2628	SNDRTEDDCGKHHPFMSSPPTEP WVCLIEGQEIDFLDGTTFVS LIPCLGRLSSRSVTIQILGQPVT RYFSHLLSCNWETLLFSHAFV MPESPTPLLRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPIG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYLLSQVPEAEW FTVLDLKD
17346	47714	A	17451	2	568	CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVNPYTL LSQIPEEAESFTVLDLKD AFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPQGFRDSPHLFGQAQAQ DLVHFSSPGTLVVQYMDLL ATSEASCQQATLDLLNFLANQ GCKRVGIALGLVTQTHGTTQP VAYLSKETDVAAK

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17347	47715	A	17452	254	849	LQPESLEIAGILVQ*MIE*QPKK GTNSIPVSKPS/GVQKPNGQW RQVQDLRLISDAVIPLYPVAVSNP YTLLSQILEEAEWFTVLDLKDA FFCIPLRSDSQFLAFEDPTDHT SQLTWTVTQGFMDTPHLFGQ SLAQDLGHFSPGTLVLQYVDD LLAKQATLDLLNLANQGY KLSKLKAQLCELLVFSSCARMH
17348	47716	A	17453	1	369	
17349	47717	A	17454	1	1632	
17350	47718	A	17455	636	1837	SNDRTEDDCGKHPFMSSSP(TEP WVCLIEGQEIDFLDTGTTFSV LIPCLGRSSRSVTIQILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPPTLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPVQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLSSQVPEEAEW FTVLDLKDAFFCIPLHSDSQFL AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQDLGHFSSPG TLVLQYSEIAKTLTYLIKEMER ANTHLVEWEPEAETAFETLKQ ALVQAPALSLPTQGNFALYVIE RAGIALGVLTQTHRTTPQPVAY
17351	47719	A	17456	2	52	EISFVENGIQAGYATVSDVTVL ESKPLPGTSAQLAELVALTRA FELGKGRINANTDSKYAYLIL HALAAIWKEREFLISGGTPIKYH KEIMELLHAMQKPKEVAVLHC QSHQKG*EWDITKGRILCHS
17352	47720	A	17457	1625	2505	PGVQKPG/QWRLVQDLRLINEA VIPLYPVVPKPYTLFSQIPKEAE SFTVLDLKDAFFCIPLHSDSQFL FAFEDPTDHTSQLTWTVLPQRF RDSPHLFGQALVQDLGHFSSPG TLVLQFVDDLLAASSEASCQQ ATRDLLNLANQGYKASKSKA QLCLQVQVKYLGILARGTRALS KKRIQPILAYPRPKTLKQLRGFL GITSPCRILQIPGYSKMARPLYTL IKETQRANTHLVEWEPEAETAF KSLKQALVQAPALSLPTRQNF LYVRERAGIALEVLQTHGTTL QPVAKG
17353	47721	A	17458	1	2415	

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17354	47722	A	17459	2646	5167	KNSGHILGTCPGYRYAKGKET GKEIKGPQNPPGYRLCPLQAV GGGEFGPTQVHVPFSLDLKQI RVDLGKFSDDPDRQYPLRPEAH EGLQDILRYLKVQGLVRKCSSP CNTRILGVQPKPGQWRLVQDL RFINEAVIPLHSVVPNSYTLSSQI PEEVEWFTVLDKDAFFCIPLH SVCQFLFAFEDPTDIITSQFTWT VLPQGFDRDSPHLFGQILAQDLG HFSSPGTLVIQYVDDLLATSL EASCQATLDLNLNLANQGYK ASKPKAQLCLQQVKYLDLSLA RVTRALSKERIPILACPRKTL KQLRGFLGITNFCQLWIPGYSE MARPLYTLIKETQRANSHLVER EREAEATFKTLKQALVQALALS LPTGQNFSLYARERAGIALGILT QTHGTTQPVTYLRKLIYSFVE NGMRRAGYAIUSDVTVPESKPL PPGTSTQLAELVVLTALELRK KKRINVTNDSKYAYLILHAHAA IWKEREFLTSGGTPNKYHKEIM ELLHAVQKPKEVAVIPQSHQK GEEK/EAEGNRRADAEAKIAA RRNLPTIEMEGPLVWNNPVQE IKPQYSLTKTEWGLSQGHSFLP LGWLTTLEGKAGRATPNPRNV YFPLHLRGLRTGRLPLSQSTRA QEMTLVRPRPSSPPPEKAAEG RGRRCSETKLRRRLFRPLRTP LCATAPLAASVAAVLAAAPAA
17355	47723	B	17460	1	2208	
17356	47724	A	17461	2	168	
17357	47725	A	17462	890	1034	
17358	47726	A	17463	386	619	TFITGDCGLGKTN/HIFDGCGLVS EVGLVLDCSNQRFKAGPA*LCQ SPFKNIL*ESLPMCMCRQLEKH AHPQGLCHTQVT

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17359	47727	A	17464	123	2169	DLGHRGSRMASVALEDVAV NFTREEWALLGPCQKNLYKDV MQETIRNLDCVGMKWKDQNI DQYRYPRKNLRCRMLERFVES KDGTCQGETSSQIQDSIVTKNT LPGS/VGPYESRMSGVIMGHSS LNCYIRVGAGHKPHEYHECGE KPDTHKQGRKAFSYHNSFQTH ERLHTGKKPYDCKECKGSFSS GNLQRHMAVQRGDGPYKCKL CGKAFFWPSLLHMHERTHTGE KPYECKQCSKAFSYSSYL RHE RTHTEKPYECKQCSKAPFPYS SYLRHERHTHTGEKPYCKQCS KAFPDSSSLIHERHTHTGEKPYT CKQCGKAFSVSGSLQRIETHTS AEKPYACQCGKAFHHLGSFQ RHMIRHTGNPHKCKICGKGF DCPSSLQSHERTHTGEKPYECK QCGKALSHRSSFRSHMIMHTG DGPHKCKVCGKAFVYPSVFQR HERHTHTAEKPYCKQCGKAYR ISSSLRRHETHTHTGEKPYKCTLG KAFIDFCSPQNHKTHTHTGEKPY ECKECKGKAFSRFRYL SRHKRTH TGEKPYECKTCRKAFGHYDNL KVHERHSGEKPYECKECKGKAF SWLTCFLRHERIHMREKSYECP QCGKAFTHSRFLQGHEKHTGT ENPYECKECKGKAFASLSSLHRH KKTHWKKTHGTENPYECKECKG KAFASLSSLHRHKKTHWKKTH
17360	47728	A	17465	1	1317	
17361	47729	A	17466	1	336	
17362	47730	C	17467	51	353	
17363	47731	A	17468	190	348	YAIHIMDVHTVRSLYYFNCFRY *ACYCCHYLTDIPEITKLSGCSY GGTSLIWG
17364	47732	A	17469	1	1716	
17365	47733	A	17470	1	840	
17366	47734	A	17471	699	1283	LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTPPHCSFSICFV C/FKNVDLKGFEVDVRILLTKYS NSNGSQSPWMEEQIRDAGERV HSAFSLNWGKPLVFEKDRPYSV SVFIGLFLPMAEKTGPLKGNPG GEFLLFLRQIQLVWLPAAAGIMT EHYFPITATQALEINNAISTIMEI FPTVSFASQWITASFSV
17367	47735	A	17472	300	461	
17368	47736	A	17473	1	2451	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *~Stop codon, /~possible nucleotide deletion, ~possible nucleotide insertion)
17369	47737	A	17474	2	3542	
17370	47738	A	17475	1	1156	
17371	47739	A	17476	1	1176	
17372	47740	A	17477	1	257	
17373	47741	A	17478	295	1353	
17374	47742	A	17479	3	1772	
17375	47743	A	17480	2	284	
17376	47744	A	17481	1	141	
17377	47745	A	17482	1	506	PHSPLWKTLCPSSGVC CGFVT LFCNDRFACLFQLTPPPSPAWM TAAASLLASLLPALPPLNLQDA KFVEERRKQLQNYLRVTMKNV IQMVPEFAASP KETLIQLMPFF VMGLQVGM YGLFHFVGMMDQ PQPSLTRADESPCDRVLSPCAA HRKQRDCCLSWKAEPE*FLVK* KTLCPSSGVC CGFVT LFCNDR FACLFQLTPPPSPAWMTAAASL LASLLPALPPLNLQDAKFVEER RKQLQNYLRVTMKNV IQMVPE FAASP KETLIQLMPFFVMGLQ VGM YGLFHFVGMMDQPQPSLT RADESPCDRVLSPCAAHRKQR DCCLSWKAEPE
17378	47746	A	17483	1	741	
17379	47747	A	17484	1	993	
17380	47748	B	17485	277	416	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
17381	47749	A	17486	686	2400	TGMSVDEKPDSPMYVVESTVH CTNILLGLNDQRKKDILCDVTLI VERKEFRAHRAVLAAACSEYFW QALVGGQTKNDLVVSLPEEVT RGFGPLLQFAYTAKILLRENI REVIRCAEFLRMHNLEDSCFSF LQITLLNSEDGLFVCRKDAAC QRPHEDCENSAGEEEDDEETM DSETAKMACPRDQMLPEPISFE AAAIIPVAEKEEALLPEPDVPTD TKESSEKDALTYPRYKQYL ACTKNVYNASSHSTSGFASTFR EDNSSNSLKPGLARGQIKSEPPS EENEEESITLCLSGDEPDAKDR AGDVEMDRKQSPAPTPTAPA GLCLERSRS/GNYGQPH/VGQK EVSNFTMG/PLRGPGLALCK QEGELDRRSVIFSSACDQVSTS VHSYSGGARFLATEHQEPGLM GDGMYNQVRPQIKCEQSYGTN SSDESGFSFSEADSESCPVQDRG QETGSTDLRLSTKLQSCSGPM FKGPTATVAATESWGTVLQNIP LGCAGTGEEVYTNPPPRGRAA LVPRSPLTVYSSSLPEHQTSLKQ CAQAGPGVCLLVHNHWQLLEG
17382	47750	A	17487	1	1089	
17383	47751	C	17488	295	348	
17384	47752	A	17489	1	711	
17385	47753	A	17490	1	1248	
17386	47754	A	17491	135	259	
17387	47755	A	17492	434	506	
17388	47756	A	17493	3	227	
17389	47757	C	17494	3	236	
17390	47758	C	17495	25	153	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
17391	47759	A	17496	1	1557	MASPEAVASQDNDGFSQKPPPT PLFASRSVNRLLKSQRTPRGEVE SVTDGKTDGSGWRMTVDYCKL NQVVTPIAAAVPDVVSLLLEQIN TSPDITLVHYIDDIMLNGSSEQE VTNTLDLLVRHLCAWGWEINPT KIQGSSTSVKFLGVQWCGDCR DVPSKVKDKLLHAPPTTKKEA QHLTGLFGFRKYIPYLVLLC PIYQVTRKAAAFQWRPEQKAL QQVQAAMQAALPLGPYDPAGP MVLEIAVADTEAVVGH/WHSA SFPSPCHCPMGP*TKWP*WQG WRLCMGSATWTSTHGG*PGYG HQ*VPNLPAEETNTEPAI*HHS/ SRRSASYLVAG*LYWTSICMER AEHLLWIWVCLSCMQCFQCD YHPWTHGMPYPPLWYSTQLCL *PRHSLYH*RSVAVGSCSWNSL VLPCSPSS*SSRVDRIVERPFEIT TTMPTSQESRVQESRGSGSGGT THHHHP*STSNIFASCFYGITFC WSRGLSSRRGRNAATRRQNNISIK L*VKIATWTLWAPPTSKL
17392	47760	A	17497	2	1120	PSKVKEKLLHAPPTIKKEAQR LVGQLGFWRQHPIHLGALLWLI YQATQKAASFEGPEQEKALQ QQVQAVQAALPLGPYDPADPM VLEVSADRDVWVSLWQAPIG ESQQRPLGFWSKALPSSTDNYS/ CFRCAIHY*FMGCCQ*FGWIVRD LEEA*LENW*QRNLGKRYVDG PL*VVKNNWKDICIPECSPPTGDL SRGGF*SSG*DDPFCGHHSASF PSHPCCRPMGP*TKWPWWQE* RLCMDSATWTSTHQS*PDYSH C*VPNLPAEETNTETSIWHHFS G*SASYLLAG*LH*TSIMEKAE VSPHWNKIISLWIWVCLSSMQC FCQDYHPWTHSMYPPLSWYST QHCLSLQRERHSLYR*RSAAVVG ACS
17393	47761	A	17498	1	1908	
17394	47762	A	17499	1	915	
17395	47763	A	17500	2	670	
17396	47764	A	17501	1	1332	
17397	47765	A	17503	151	674	
17398	47766	A	17504	1	825	
17399	47767	A	17505	134	447	
17400	47768	A	17506	98	778	

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17401	47769	A	17507	1	830	MHCFFIFSAAWFCLWSISLHLV ERPDMAVLLFPFGLRLGLMLQ CPRGYWPVLLGAEWLLIYWLT QAVGLTHFPLLMIGSLLTLPLV ALISRYRHQRDWRLLLLQGAA LTAAALLQSLPWL RHGKESWN ALLLTGTG/EPDAGPDMSGVLA LSRQ*HLAAARSVTGFSANQLA RATSGLVLAACVYQSLAPVGIA GRTVALYAILSGAADYRAGLA LWLARGADCDVDERHRADRH QSWRDLPLWTYCSGDCDSRHGA QGQKARAPPKHDQFPFAIFRG
17402	47770	A	17508	2252	2772	RSKTTAFTPLRVRTSAHARPAG PAPIIATFLPVCFTPDISGRQPISN ALSLI*RSMLPMVTAPNSSFRV QEPS/SQTVLRADSSANFRQGV GLVRQFRFRKNTPLVGELQPV DVVVYRAFFLAVVVAARQAA VSLRFGLAFGKRLVFNKLNFA DLQRFLWRINALQVDKLITF
17403	47771	A	17509	539	1077	
17404	47772	C	17510	192	396	
17405	47773	C	17511	10	294	
17406	47774	A	17512	2	379	KRPGSGITEATSSRRQRPTRLQ GQLPGQEKRLVKATEGIANPS WGWGGAVSPLRASLTSLRHKI NNHYNTENWKLPIKDSVHLIPSP QAPSMFPPLANPPWAAPHREK MWNPQIQGTNCIWVCGP
17407	47775	A	17513	291	590	
17408	47776	A	17514	187	589	VLSFLIHRWEGDKDLSLGNFES QTPQPSRRFICAFPPWENPS*EPS YPSISDPGFLILLPSKGDVWIHL GPIFSKKPLYS*SSFLVIFYVPTP SFLFLGYKFPLAHAVFRVEPTLS LLIQNSHCHGCYTYPDGPE
17409	47777	A	17515	1509	1748	IGVVREGIPVLCFLFSKGMLPVF AHSV**YWLWVCHR*LLLF*DT HQYLIY*EFLA*SVVDFCQRPF HLVLDFFWLVS
17410	47778	A	17516	152	568	CQLELSCMKCPTFPVGRSLPVG CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSGDGSFV CKHPTGAVTFPSGMPLGSMITF KILILPIHEHGMFFSLSVSSFVSL

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17411	47779	A	17517	152	568	CQLELSCMKCPSTPVGRSLPVG CTRSQTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQDGSFV CKHPTGAVTFPSGMPGLSMTIF KILILPIHEHGMFFSLSVSSFVSL
17412	47780	A	17518	152	479	CQLELSCMKCPSTPVGRSLPVG CTRSQTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQDGSFV CKHPTGAVTFPSGCPHTLQA
17413	47781	A	17519	1	474	
17414	47782	A	17520	1326	1712	FLYVIKALGKKQLQFGQQLIPS IELLDYLINPGSGCVSLWKLNK PQCYLIHFSGLTLSWKVHTIL LEGHYEFLEYAADR*PICLFSW KERQLVSFLDYSLHLLGFSFY VFFFLLYLLVRLCWDL
17415	47783	A	17521	18	236	
17416	47784	A	17522	281	1005	TGWSPLQLSKATVARLPLWIPP LWAGHLGELWLASGEYPSGLK LPEEGTGSNLRCSAASAGDTQA NRVWSGPAANFSRPAEAPAF HALRGPSVHCSPLCVHEFSSFS LISENMQYLVFCSGVRFRLIMVI SSIHILCLVPKRTRVLGRSLSLC FRFLRGPKERITIPHSSAPPLGH VIAIPL*SFMKPSPEADAPMTG SFLKSPSEADTGATLPVQSVVPI PLSILPILEVGGVLF
17417	47785	A	17523	1	1524	
17418	47786	A	17524	881	1108	SRKMGAPNA**SAWSWSREGL AAP*SMFSSLSADSSADCKLPE GKVPASSTGLTARASKDLVFC CCFSISARAS
17419	47787	C	17525	1	867	
17420	47788	A	17526	203	514	SSSTARPSQTSSAEESPTSWYRG DNPSKPMDDLAVGVFGAIVGA ASVLGNAPLDGIETGCCAWSST NAEHTGLWLQILRKEGLKDL*N GTVPRLGRTWASPWM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
17421	47789	A	17527	1	1578	MAKKEQLLSAAPSKTNAEGQEI PSGVYTRALGFKHKTGQPFQ TPSPQEFILYTNDTWNASKTE PFTPLERGLKPGSQESSGWHLV GTPLGRSFQRKEQAAIFAVLQP PLVIPRQTGSGVDLQQTPTDLQ KRVLTVRRKTNININKDDHA KTTSGHQQQRPKVDKSTKMR KNQCKKATNSKNQNVSSPPKD HNSSTAKEQNWMEFDFKLTE VGFRSSQFDQVEERISDIEDKLN EIKHEDKIREKRMKKKEQSLQE IWEYVKRPNLRLIGVPESDGEN GTKLENTLQDTIQENFPNLARQ ANIQIEIQRTQRYSSRRATPR HII/E*IHQG*NEGKT VKGSQRE K*GQEI PSGVYTRALGFKHKT GQPFQTPSPQEFILYTNDTW NASKTEPFTPLERGLKPGSQESS GWHLVGTPLGRSFQRKEQAAIF AVLQPPPLVIPRQTGSGVDLQQT PTDLQKRVLTVRRKTNININK KDDHAKTTSKGHQQRPKVDK STKMRKNQCKKATNSKNQNVSS PPKDHNSTAKEQNWMEFDFKLTE VGFRSSQFDQVEERISDIEDKLN EIKHEDKIREKRMKKKEQSLQE IWEYVKRPNLRLIGVPESDGEN GTKLENTLQDTIQENFPNLARQ ANIQIEIQRTQRYSSRRATPR RATPRHIGRFTKVEMKEKRLR AVREKSRVTHKGKLRITADLS
17422	47790	A	17528	738	1323	ATGGHSNQRRS*KLSKKFRR MYN*NNQYREV LKAGDGAEN QGSRTTETLCM*RMQRSLQFD SDLVRHQKHSGEKPYECCEC GKAFRGSSELIRHRIHTGEKPY ECGEYSYECIACGAFGRSST LIENQRIHTGEKPYECNECGKSF NQSSALTQHQRHTGEKPYECS EKRKTFHRSGMLMQHQRTHTR
17423	47791	A	17529	1	656	MAGKPEYDKTISTIVLNALNA LGVSAEASGRNDLVVKTVEGD RKVSGSAYRETKDRGFHHGTL LLNADLSRLANYLNPDKKKLA AKGITSVRSRVTNLTLLPGITH EQVCEAITEAFFAHYGERVEAE IISPNKTPDLNFAETFAQSSW EWNFGQAPAFSHLLDERFTWG GVELHFDV/GKRPYHPRPGVYR QPQPRAAGSPRRRTTARLPFLSL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17424	47792	A	17530	1046	1401	LLDIRMLCHGKGVIIHVLRLQF LLGRPAPHRLHAALQLPLGLSLH GTLALGLWLQLRQLLLQLQPF GISGCGSGCDPEQDCV/DCGRG CWPRKCPQGSAPSRSRGAPHR PRPQQAAGRG
17425	47793	A	17531	112	1170	YPPFHLDISTDTVCVCTKFLCC VFQLHQVIYVLL*TGYSILFDAD DLWMGFLRGHPFC*CYCLFVFS FPSNSQAPLLQVCWSLLEVHSR PCSPGYHQRRQLNSKSDCCLLLP LEALSQSGTHQMPAGALLYEM SVNPCWEEHQTDLFTHESTFI RSKTQKKVPDKLLDSSVTPLF KITENIGCVMTGMTADSRSQVQ RARYEAAWYKYGYEIPVD MLCKRIADISQVYTRNAEMRPL GCCMILIGIDEEQGPQVCKCDP AGYYCGCKATAVGVKQTESTS FLEKKVKKKFDWTFEQTLETAI TCLSTVLSDFKPSEIEVGVTTV ENPKFRILTEAIDAHLVALAER
17426	47794	A	17532	2244	2432	DGQQLIALHRLALRELQQAAPH AGIAPAGENPV*WWFRNRQNP LIALRSLPAFQSGNLSQCLH
17427	47795	A	17533	251	546	SSISDILSSA*SIRLLILVYAS*SS RAVFFSTIRSFIFSKLVILVSPSC NLLSRFLASFHWVVRTCSFSSKEF VIITHLLPTSVNSSYSLSFSFVHF G
17428	47796	A	17534	597	1092	FTNQKESRTRWIHSRILPEVQG GTGTIPSETIPINRKRGNPP*LIL* GQRHSDTKAG/RDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIR K/CNKCNPAYKQSQRQK/HT*L SQ*MQKKPLTKFNNPSC*KLSIN *VLVGRISK
17429	47797	A	17535	1	2153	
17430	47798	A	17536	2164	2427	
17431	47799	A	17537	1	322	GPRWGRVVRHAPDPVRIPSSGP LLPPRFYPRYVLPAPPSASTSRPC QRTSASGRCPMPH/DTVKATM PIWV/DPPVPDHYEGEAHQGIL VTHPHHQRCPAGHRHRVVF
17432	47800	A	17538	1	627	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17433	47801	A	17539	583	1145	GNGRTVDTQVCQAPITQSLSER PADPNPGEQDAEAGPASRRDT EAERLRFQFQYHVASGPILA VGQLWTLCRQWLRPEARSEQ MLEVLVLEQFLGALPSKMRTW VQSQQPRSCREAAASLVEDLTQ MCQQEGLAAHPSHDTAIRGIPR LAASWETASAMEATADARQKR THTEKEAWLLEAPHELA
17434	47802	A	17540	1	1301	
17435	47803	A	17541	1	1232	
17436	47804	A	17542	1	549	MNTANVEKPYVQKYQTAFVLV MKHRQCQLASHLVQNYRS/IQL WAWELQIDPGTTCPSENTITQG SKKPYPDFVARLRDAAQNSITD ENARKVIVELMAYGNANPECC SATKPLKGVPTGSDVISDQKA VGVQAAKRRNRDTGLGRSAR KSGKGVTRMLPKHASMILDGG GPATSPSCCRFL
17437	47805	A	17543	146	510	SPYWNKGKSPGWLAES/FKRPV FRQGAKEPYPDFAAASLQDAAQ KSITNENARKVIVELMAYENAN PECQSAIKPLKGVVPVGSVDVISR GFQGGQPPLSQVLQGMGQLPQ YSNCPRPQAAVQQ
17438	47806	A	17544	2	828	
17439	47807	A	17545	1	420	
17440	47808	A	17546	1	1947	
17441	47809	A	17547	1	399	PLKVNIYPDSKYAFHILHHHER GFLTTOGSSIHNASLIKTLKAA LLPKEARVIHCKGHQRASDPIA QDNAHTDKIAKKAASIPITYPH FQFFSSSATPTYSPAETSTYQS LPTQGKWFLDKETYFLPASQ
17442	47810	A	17548	1	2382	

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17443	47811	A	17549	1	2194	MAPEQGRVSIQLTFIEYHGYSI FVVKGDLPCDADQLQMIRV QQMHRPKLIGEELAQKQKRV HKTDLERVLEANDGSGMLDED EEDLQRAIALSRQEIDMEDEEA DLRRAIQLSMQSSRNISQDMT QTSGTNL.TSEELRKRREAYFEK QQQKQQQQQQQQQGGDLGGQ SSHPCERPATSSGALGSDALLL TQSLFGSLFTWTRVTFGAEDPG QEDSFRRRVPCPCPHSVRRSTY DLGSSDQPAQGTSHFQIGLLL TRLSPVILPQPPVPHPIILSPPP HTVSGQLFSLVTSPLPAQQFLL KEVAGAEGLAKVITCPVPLLG QDILTKLSASLIIPGLQPHLIATL LPNPKPPSPPLPVSPNLPQVW DTSTPSLATDQTPITIPKPNHP YLAQCHYSIPQLALRGLKPVIT RLQHGLLKPINSSYNIPLPVQ KPDKSYRLPQDLDLINQIVLPIH PVASPHIIPDTTDPDHCISLIHL AFTPEPHTSFFPIPHDHTWFID GSSTWPNRHSPAKVGVAIVVSS TSILEATALPSTTSQQAELIALT RALALAKGLHVNIYTDKSYAF HILHHNAVIWAERGFLSTQRSSI IIASLIKTLKKAALLPKEAGVIH CKGHQKASDPPIAQGNAYADKS DNGLAFTSQI//HKQFLRLVFS GTFIPLTVLNLQERTGQYFYLLP FTELEPVLEKLQGTVHLNFYMD
17444	47812	A	17550	1	355	
17445	47813	C	17551	99	335	
17446	47814	A	17552	21	447	LGPLPFLSPCLLHCQGRKLCG HHEEARRRKNVSIPIKEAGIHC KGHQK/A/SDPIAQGNAYADKT KFLDLAFPPRLSFTCQITQAVS QALGIQWNHLTLTILNLQKRIR ACPDATGYSPFELLYGCSFLL GPSLIPDTSTPT
17447	47815	A	17553	119	239	TQKGQRAALFLICILSPSPPLPTL GKNFKN*IPALKPHNRI
17448	47816	A	17554	1	798	
17449	47817	B	17555	460	1059	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17450	47818	A	17556	3	1476	IP*TCPVPLLQGDILTKLSASLIIP GLQPHLIATLLPNPKPPSPPLV SPNLNPQVWDTSTPSLATDQTP ITIPLKPNHPYLAQCHYSIPQLA LRGLKPVITRLLQHGLLPINSS YNSPILPVQKPKSYRLPQDL LINQIVLPIHPVASPHIIPDTTDP HDCISLIHLAFTPFHTSFFPIPH DHTWFDGSSWPNRHSAPKV GYAIVVSSTILEATALPPSTTS QQAELIALTRALALAKGLHVNI YTDSKYAFHILHNAVIVWAER GFLSTQRSSIIASLIKTLLKAAL LPKEAGVIHCKGHQK\ASDP QDNAYADKLAKKAASVPTSVP HGISQAPPLPTHQARYWQIDF THMPVRVKLLYLLVWVDTFTG WVEAFPTGSKKATAVISLLSDI IPQFSLPTSIHSDSRLAFISQITQA VSQALGIQWNLHISYRPSQSSGK VEQTNGLLKTHLTKLSLQLKK DWTVLLPLALLRIRACP
17451	47819	A	17557	24	594	VGSGDLWPWEGNPLSSCSLLHEK DPPTSGPQTDQPKHELTNFKS GCSSPGPARSQFFLSRSL*SF YHLPSSHLVCLTVSFRD*PSPTC PAIDS*KGG/CELKA/RVKEHFC HDLPASSMQSNYPVHDSGHILT TGFSLFKPTLNIEYSTGHAPYHV RSACFPFAFCHDCQFPEASPEAE AAAILSVQPAEP
17452	47820	A	17558	1	1152	
17453	47821	C	17559	301	462	
17454	47822	A	17560	1	423	
17455	47823	A	17561	421	856	KLINLFSNFCYSRQFLSFSSTL YFVWVFCYNRCCFSK*RMIVHI TNRDINCQIAYARIEGDMIVCA AYAHELPKYGVKVGLTNYAAT YCTGLLLAHLRLNRFQMDKIC YLDAGLARITTTGNKVFGDLDG GLSIPQSTK*FPGYD

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17456	47824	A	17562	3	1082	GPLCIALALQEFGTRRRWACRS LSSSGRRSLFRRMGSVKAVKNK AYFKRYQVKFRRRREGKTDDY ARKRLVIQDKNKYNTPKYRMI VRVTNRDINCQMLYA/RRIEGD MIVCAAYCTPNLPKIWV*RVGL TNYAAAAYCTGLLLAARRLLP*/ RFGMDKIYEGQV\ELTGDEYNV ESIDGQPGCLPPAYL\ DAGPCSE PTHWPLKFFGAPEGKL WMGGL SIPSQYPNRFPGYDSEKQRNFN AEVHRKAHSWGQNCRCFTWR YFMEED\EDAYKK'QFS'QYIK\ NSVT\PDMMEEEMYKKAHAAI RENPVLWRRPK'KEV\KKRW NRPKMS\LAQ\KKDRVAQKKAS FLQSSRSGLLES\TPAIFP
17457	47825	A	17563	2	4967	
17458	47826	A	17564	56	284	RQTRRAAGIVRGDCPASSPTNC DLGQC/NSTS/LEPRFVQTVHLL CPWT/GGSSPLLAARGLSPVSL GPLKPMVSCAGR
17459	47827	A	17565	1	3525	
17460	47828	B	17566	35	3691	
17461	47829	B	17567	80	3787	
17462	47830	A	17568	225	507	
17463	47831	A	17569	2	2621	
17464	47832	A	17570	14	1658	
17465	47833	A	17571	1	3654	
17466	47834	B	17572	1	3570	
17467	47835	A	17573	1	3663	

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17468	47836	A	17574	485	2347	TEPKTKTT*LSQ*MQKRPLTKF NNTSC*KLSIN/IVLEVLAIRIQ EKEIKGQLGKEEVKVSFLADD MIVYLENPTVSAQNL.LKLIGNF SKVSGYKINVQKSQAFLYTNRR QTERQIMSELPFTIASKRJYLG QLTRDVKDLFKENNKPLLKEV KEDTNEWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRACIAKSI FSQKNKAGGITLPDFKLYYKAT VTKTAWYQWYQNRDIAQWNRT EPSEIMLHIYNYLIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KVKLDPLTPYTKMNSRWIKD LNVRPKTIKLEENLGI TIQDIG VGKDFMSKTPKAMATKAKIDK WDLIKLKSFACTAKETTIRVNRQ PTTWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDV NRHFSKEDIYAAKHKMKCSS SLAIREMQIKTMYRHLTPVRM AIKKSGNNRKIQ/GGIWCDRI L* R*TTCTCRVAKEIQSL*RRJ/WKRL QRTL SIPVLDAV*PPMF*ASVID TMTI*CFEARDTCFTLTLESFWD MHRCLAASKIGILL C*PLIWH MSLMGVKSPPFVFSCLWTS AV
17469	47837	B	17575	1	3354	
17470	47838	A	17576	1	3297	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17471	47839	A	17577	1	2563	MKAIEIKMFFETNENKDDTTNQNLWDAFKAAEEVESLNRPTTGAEIGAIHNSLPTKKSPGPDGFTAEFYQRYKEELVPFLLKLQFSIEKEEILPNSFYEAASILPKPGRDTTKKENFRPISLMNIDAKILNKILANRIQQHIKKLIHHDQVGFFPGMQGWFNIRKSINVIQHINRAKDKNHMIISIDAEKAFDKIQPFMLKTLNKLIGDGYFKIIRAIYDKPTANIILNGQKLEAFPLKTGTTRQGCPLSPLLFNILLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMMIVYLENPIVSAQNLLKLISNFSKVSQYKINVQKSQAFLYTSNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELEKTTLKFIWNQKRAHITKSILSQKNKAGGITLPDFKLYKATVTKTAWCYQNRDIDQWNRTEPSEITPHYTYNYLIFDKPEKNKQWGKDSLFNKWCWENWLAIWRKCLKDPFLTPYTKINSRWIKDLNVRPKTIKTEENLGITIQDIGMGKDFMSRTPKAMATKAKIDKWDLIKLSFCTAKETTIRVNRQPTTWEEKIFATYSSDKGLISRIYNELKQIYKKKTNNPIKKWEKDMNRHFSKEDIYAACKHMKKCSSLAIREMQIKTTMYHLTPVRMAIKKSGNN
17472	47840	A	17578	1	3514	MELKTKARELREECRSLRSRCDQLEERVSAEMEDEMNMKREGKFREKRIRNEQSLQEIWDYVKRPNLRLLIGVPESDVENGTKLENTLQDIIQENFPNLARQANIQIEIQRTPQRYSLRRATPRHIIVRFTKVEMKEKMLRAAREKDRSTRQVKNKDTQELNSALHQADLIDIYRTLHPKSTEYTFFSAPHHTYSKTDHIVGSKALLSKCKRTEIITNYLSDHSAIKLELRILKLTCSRSTTWKLNNLLNDYW
17473	47841	A	17579	1	3693	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17474	47842	A	17580	1577	3354	TEPKTKTT*LSQ*MQRKPLTKF NNLSC*KLSIN/IVLEVLAIRIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPVSAQNLLKLSNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELGKTALKFIWNQKRARITKSI LSQKNKAGGITLPDFQLYCKAT VTKTAWFPSGDVGLADFSPSH TLKTQFFSCLAEFAAASCFFQR MNGFGMAAMTTTTYSTGAESPL PSCSIDQGGDTKLHRRASPGRT FPAAAGIPAAAA PDGPPLSLH KLWFPVELGGRALPRAESHGE VAALGVMVVAQGGKNQGEAA RSTPWLRPTSHLPCSSSSA WW TEQTAHPLLLCLGIYLLNA LSNLSMVALVRSDGALRSPMY YFLGHLSLV DVCFTT VTPRLL AGLLHPGQAISFQACFAEMYFF VALGITESYLPAAMSYDRATAA CRPLRYGALVTPWALRLAARY DRLASVVYAVITPTLNPFINSLR NKEVKGALKRGLRWRAAPQE
17475	47843	A	17581	1	3042	
17476	47844	B	17582	1	3384	
17477	47845	B	17583	1	3264	
17478	47846	A	17584	1	3780	
17479	47847	A	17585	1	3165	
17480	47848	A	17586	1	3894	
17481	47849	A	17587	1	3345	
17482	47850	A	17588	523	3981	
17483	47851	A	17589	1	3429	
17484	47852	A	17590	1	3921	
17485	47853	B	17591	1	4797	
17486	47854	A	17592	1	6499	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEITINYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLEKEKQEQTHSKASRRQE ITKIRAEKIEIETQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,421,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
17487	47855	A	17593	1359	2520	IQCHPHQATNYFLHRJGKNYFK LHMEPNKSLHSQDNPKQKGTK LEV/CTLPDFKLYYKATVTKTA LYLYQ/NQRCRSMQNRALRN NATYIYNVLIQDKPEKNKQWG KDTL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRP KTIKLEENLGNTIQDIGMGKD FMSKTPKATATKAKIDKWDLIQ LKSFCTAKETTIRVNRQPTWE KIFGIYSSDKGLISRIYNELQQIY K K K T N N P I K K W V K D M N R Y F S K EDIYAAKRHMKKCSSSLAIREM QIKTTMRYYLTPLRMAIHKFG NNRQETVREMACLLSGTMDFR HRACFVLSKPDFSTRWPGADA QRPPVLVVVALDSSLFPQASG QRPPSLEDVDGGAGALVAPC
17488	47856	A	17594	1	1227	
17489	47857	A	17595	2	2774	NLCSLIPLREVTIVEKADSSSVL PSPLSISTRNRMTFLFANLKD RD FLVQRISDFLQQTTSKIY SKFE AGSYNSSDDEVYSRPSSLVSSSP QRSTSSDADGERQFNLNGNSVP TATQTLMTMYRRSPPEEFNPKL AKEFLKEQAWKIHFAEYGGGIC MYRTEKTRELVLKGIPESMRGE LWLLLSGAINEKATHPGYYEDL VEKSMGKYNLA TEEIERDLHRS LPEHPAFQNE MGIAALRRVLTA YA FRNPN I
17490	47858	A	17596	1	3472	
17491	47859	A	17597	1	900	
17492	47860	A	17598	1	1290	
17493	47861	A	17599	153	3834	
17494	47862	A	17600	299	1184	
17495	47863	A	17601	1	729	
17496	47864	A	17602	1	2232	
17497	47865	A	17603	36	224	TQWGPSVCWCLIPWPSFPDQ*P GF*AVLLPWRCQGFWPLLLAC APAGPATAAEPAVSSPAEP
17498	47866	A	17604	1	624	
17499	47867	A	17605	1	578	RDLDLFSLPQDITL/VHYVDGIM LIGSSEQEVASTDLLVRHLHA RGWEINLTKIQLATSVKFLGV QWYGACRDIPSKVKDKLLHLA PPTTKKEAQHLAASFEGPEQ KGLQQVQVAVQAALPLGLYDP ADPMVLEVSADRDVAVWSLW QAPIGESQWRPLGFQNKALPSA DNYSPFERQLLACYWALVETE

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17500	47868	A	17606	1	282	PIYRVSRRKAANFEWSPEQEKAL QQVQAAVQAAWPLGPYDPAD PMVLEVSVADRDADWSCWQA SI/GHKVGHAAQQHSIIKWKWYI RDWARADPEGT
17501	47869	A	17607	1	338	SIYLVTKAA/SSSWGPEQEKA LQEVQAAAVQAAALILEPYDPAGP VVLEVSLADRDADVWSLWQAPI GESQQRPLGFWSKALPSSA/DH KACHAQQHSIIKWKWYIHDRA RAGPEGT
17502	47870	A	17608	1	757	
17503	47871	A	17609	1	1317	
17504	47872	A	17610	2	24	LCQRLLAEPNEKPGSLGNVM AVARIEIGICEYYHEKTTEKALD SHGVLAGSTIKGVRSFQRNLEL KLPATERATANAIELLTVLDQA YENFAPQILPSTGSPSTQETAQF KANQNKPLVRGKGPHEAIRYI SAAHREWKPAILTSAIRSFCT WLVFTSKNFPKLVTHGSGTIAG NGQSSDETQVQGAAWKSDSRG TKRQIPTWILAEGNNAQAQLDI PGPTIPAPNCSLKVPSWSTTPS MPSSLGKAYWLLACYWALVET E/RLAMGHQVTM/KPELPVMN WVLSDPSSHKVGGAQQHSINK WKWYIRNRRARAGEGTS*LPAP LIG
17505	47873	A	17611	1	1815	
17506	47874	A	17612	875	1916	PGKQGLEWTPRKLQQTCKRGA GQLEEKLANKRQ*HQH*QKG*P /PQKLNAKDIIINSSPTREQNWTE NEFDELTEVGFRRWVITNSSEL KEHVLTKCKEAKNFDKRIEEL LIQITSLEKNISDLMELKNTARE/ LLEAYTSINSQIDQAEMDR*PD* *RRKERRIK*HNKK**RGYHN*S /QEIQTITIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVEP INRPTSSIEIAVINSLPNQKSPG QTNSQLTSTRDAEAKFNKIQHP FMLKTLNKLIDIGTYLKITRAI/ S*QTHSQCHTEWAKAGSIPFEN RHKTRMPSLTTPIQYSGNSGQ GNQEFWKLHLVEREW
17507	47875	B	17613	1	1158	

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17508	47876	A	17614	851	1344	HLKPSPSPLYPWKNCLPRNP SLVPRQTGSGVDIWQTAADLQQ RGLLEGKLTNRKE*YQHQQKR CPHQNP1*RSPTSNTKARE/QNW TENEFDELTEVGFRRWITNSSQ LKEHLLTQCKEAKNLEKRL EELTRITSLLEKNNDPME LKNATAEPHEAYTSINS
17509	47877	B	17615	99	716	
17510	47878	A	17616	1	588	
17511	47879	A	17617	1	1140	
17512	47880	A	17618	1	774	
17513	47881	A	17619	3	527	AENSKKQNAASSPPND/RNSS/EA QNWTENEFDELTEVGFRRWIV TNSSKLKEHVL TQCKEAKNLD KRLQELLTRITSLLEKNNDLMEL KNTARELREAFSTFCVNCEAVS LITSLREDSHWLEDKSGHRM/R RHQE*KCEYFHPPHGLQFYQL PESDSDHSDPLWPHGGSSFLSSVV
17514	47882	A	17620	1	1383	
17515	47883	A	17621	1	990	
17516	47884	B	17622	337	1515	
17517	47885	A	17623	153	474	QTKSNVNIKKQDVHTKTPSEG HQHQRPKIDHNSLPAREQNWIE NEFDELTEVGFRRWITNSSSEL KEHVL TQCKEAKNLEKRLQEL LTRITSLLEKNNDLMELKNTA
17518	47886	A	17624	1	771	MPFSDTERVITGPSTKVHSYPG GLQALLQLRLHSLMWRWSAA VAIGVHVRCDLLAVHPVLWAY PQWQEPKMLTLIPGRITATII GLYQHEGIRAYCDSRVYIYKPS SGIESVLTRPSTQDHNSSPAREQ NWTENEFDELTEVGFKKWWIT NSFELKEHVL TQWKEAKNLEK RLANLLTRITSLLEKNNDLMELK NTAQELHEAYASINSRINQSEER ISEIEDQLTEIEQVDKIREKRIK/R RNEQSL*EIWDYV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
17519	47887	A	17625	53	814	PGKQGLEWTPRKQLQQTCKRGA GQLEELKANRQK*HQH*QKG*P /PQKLNKADHNSSPTREQNWTE NEFDELTEVGFRRWVITNSSEL KEHVLQCKEAKNFDKRLEEL LIQITSLKKNISDLMELKNTARE/ LLEAYTSINSQIDQAEEMDR*PD* *RRKERRIK*HNKK**RKEQAAI FAVLQPPVLVITRQTGSGVDPQK TPADLQKRCRTVRRKTSQQKA VASTLTAKRIITQKLNKADHNSS PTREQNCTENEFDELTEVGFRR WVITNSSELKEHVLQCKEAKN FDKRLEELLIQITSLKKNISDLM ELKNTARERWKHTQVSIKSIK QKWTASQTNKEEKREESNSTIK NDKGDITDPTEIQTITREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEVEPLNRPITSSEIAVI NSLPNQKSPGQTNSQLTSTR
17520	47888	A	17626	1	1566	
17521	47889	B	17627	1	1005	
17522	47890	A	17628	1	2172	
17523	47891	A	17629	1	504	
17524	47892	A	17630	2	1601	
17525	47893	C	17631	132	278	
17526	47894	A	17632	380	828	EVLRVMIELNAVITYPYPKDTGC QPLV*HAAASLNSPEVMGATQ LKPLRPCKKCPKILEGGH*EW MEARHRNLGTLHGLPCSRTHF* TTTAQGEWLCCCHCGEHPQG GRHPCIC*HCYSCHTLAPPVQW TPNVAEPDNKAGAQQYKSPRV
17527	47895	A	17633	1	963	
17528	47896	A	17634	2	368	EFSDPIHHTFDHMRWTKHENE AGWLLSSVDKVMKENDELGD SISQLQKQILSLKSAKIALSESLI SCRERTEIVEK*I*ALIMLVADL Q*KVHAQPHHAQPRQVSTVKV RALIVLQEVTD
17529	47897	A	17635	1	1881	
17530	47898	A	17636	755	939	ARKNTRIISYSGVCKKNVETWR* MFCTLLGRQQGCATVGKGDRC GPLRYYSWVRKGDVQLQGD
17531	47899	A	17637	367	423	
17532	47900	A	17638	3	1925	
17533	47901	A	17639	1	1137	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17534	47902	A	17640	153	474	QTKSNVNIKKQDVHTKTPSEG HQHQRPKIDHNSLPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLQTCKEAKNLEKRLQEL LTRITSLEKNINDLMELKNTA
17535	47903	A	17641	1	1068	
17536	47904	B	17642	1	717	
17537	47905	A	17643	585	2302	VLQLLRQERLELFVPPGELVVS LASGVKLQTFAGGKAWLLQTH SDLGEQKLTTHIPISLSKVIFWC NWPEAKTAAVDGEQATCEPVL KAMFLADTHLLREFLGHWLDK LRREWQVERAFQATALWLLQPE VVFILEDVDFEGKWTSEAWV DDVEQFRKMFRHPSHVQLKV AGNHDGTFHYETNTYEVEWR NRNNSPFIMGSITPTDYALSKCH LPPEDEVLIYCGVKLPDRIVDS KAGLLKLPVKNVISTQLQFPSI MDQLLYNLFNETSPLVMCLD VMAMSNRGNHHLAATRLRKV LDHNSLPAREQNWTENEFDEL EVVFRRWVITSSSELKEC/DVLT QWKEAKNLEKRLDELLTRITSL QKNINDLIELKNTAQELHEAYT SINSQIDQVEERISEIEDQLNEIK CEDKIREKRMKRNKQTLQETW DYVKRPNPCWIGVPESDGENG TKLENTLQDIIQENFPNLAQA NIQIQEIQRTPQYSSRRATPRHI IVRFTKVEMKEKMLRAAGEKE DETNDNEFFLWSQKGKRACTL NDHVEESCPTTKNACLGTPIHC
17538	47906	A	17644	1	282	PIYRVSRKAANFEWSPQEKA QQVQAAVQAAWPLGPYPAD PMVLEVSADRDADWSCWQA SI/GHKVGHAQQHSIIKWKWYI RDWARADPEGT
17539	47907	A	17645	3	903	
17540	47908	A	17646	1	349	
17541	47909	A	17647	1	489	
17542	47910	A	17648	1	352	
17543	47911	A	17649	1	505	KTDGSRWMTVDYHKLNQVAT PVAAPVDPVSLLEQINTSLDT WYAAIDLGNVFFSIPVHKVHQK KFAFSWQQQYTFVTPLPQGYIN SPALCRHFVRRHLD/RFSLPQDI TVVHYIDDIMLVGPLIYRMTR KAAIFEWGPEQKALQQVQAAV QAALPLGPYPADPMRLR

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17544	47912	A	17650	1	1557	MASPEAVASQDNDGFSQKPPPT PLFASRSVNRLKSQRTPRGEVE SVTDGEKTDGWSRMTVVDYCKL NQVVTPIAAAAPDVVSLLEQIN TSPDITLVHYIDIMLNGSSEQE VTNTLDLLVRHLCATGWEINPT KIQGSSTS VKFLGVQWCGDCR DVPSKVKDKLLHLAPPTTKKEA QHLTGLFGFRKYIPYLVLLC PIYQVTRKAASFQWRPEQEKAL QQVQAAMQAAALPLGPYDPAGP MVLEIAVADTEAVWGH/WHSA SFPSPHCPCHMPG*TKWP*WQG WRLCMGSA TWTSTHEG*PGYG HQ*VPNLPAEATNTEPAI*HHS/ SRRSASYLVAG*LYWTSCIMER AEHLLWIWVCLSCMCQFCQD YHPWTHGMPYPPLWYSTQLCL *PRHSLYH*RSVAVGSCSWNSL VLPSPSS*SSRVDRTPVERPFEIT TTMPTSQESRVQESRGSGSGT THHHP**STSNIFASCFYGITFC WSRGLSSRGRNAATRRQNSIK L*VKIATWTLWAPPTSKL
17545	47913	B	17651	47	838	
17546	47914	A	17652	1	1566	
17547	47915	A	17653	1	981	MVAIAKVLIAYKEDSDSHNQPN TRMTVSKGPVSAVEGRRRGQD SDDCVEENDAVRTWPPSRILRT ESHPSPHTC SWRRHLLSSCPYT GMSFPIPPSSGNISSTHAVISFPPL SEEMNPMLPKATVMTSLEAAA RQNLKSRQAPRCEVESVTHIEEV YYTRKELFEFSNLYRKKSGEQI REWILRKTDGWSRITVDYRKL NQMVTPIAAAAAPDVV/VVSLLEQ INTSPGTWLCNLIWRDLDCFL LPQNITLVHYTDDIMQIGSSEQE VANTLDLLPALMASW/ENSP*SI DRGRED*SLVHKWFCTICRHP KVDSCSTTAPF*DIPEGQQL
17548	47916	B	17654	179	1219	
17549	47917	A	17655	1	2655	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17550	47918	A	17656	1	942	MVGKAKWKPLELPLRKIVNQ KQHHIPEGIAEIAATIKDLKDAG VVIPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHKPFPAFSW QG/QQYTFVTLPQDYINSLAL*H NLIWRDLDFYLLLDITLVHYI DDIMLIGSNDHKVGGAQQHSII KWKLYIHDQAQTGPEGTTTSVI AQWAHEQSGPGSRDGGYAWA QQHGLPLTKADLATTAECPVC QQQRPTLSPRYGTIPSLPLTKAL TLQLKKCSSGPMIMEFTGLAM FPILKQLD
17551	47919	A	17657	1	868	
17552	47920	A	17658	83	346	
17553	47921	A	17659	1	643	MVGKAKWKPLELPLRKIVNQ KQHHIPEGIAEIAATIKDLKDAG VVIPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHKPFPAFSW QG/QQYTFVTLPQDYINSLAL*H NLIWRDLDFYLLLDITLVHYI DDIMLIGSNDHKVGGAQQHSII KWKLYIHDQAQTGPEGT
17554	47922	C	17660	38	202	
17555	47923	A	17661	3	410	LKSRQAPRCEVESVTHEEYVYT RKELFEFSNLYRKKSGEQIREWI LRKTDGWSRITVDYRKLNQMV TPIAAAVPDVVVSLLLEQINTSP GTWLCHNLWRDLDCFLPQN ITLVHYTDDIMQISGEQEVAN TLDLL
17556	47924	A	17662	2	526	
17557	47925	A	17663	2	431	
17558	47926	B	17664	55	1506	
17559	47927	A	17665	1	753	
17560	47928	A	17666	73	310	QLAEPHWPDP*KAGGFEWGP EQKKALQ*VQAAVQALPLGP YDPADPMVLVVSVADKDAVWI FHLSGSDRWRRITYRCL
17561	47929	A	17667	323	687	KTDGWSR/TVDYRKLNQVVTPI AAAVPDVVSLEHINISPGIWIH HQKQFAFS*QQQQT/FTVL/PH GYINSLALCHNLIRRDLDHFSLP QDITLVHYIDIVLTGSSEQEVA GSLESTCRHTKV
17562	47930	A	17668	3	1363	
17563	47931	A	17669	1	1203	

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17564	47932	B	17670	130	1374	
17565	47933	A	17671	1	1063	
17566	47934	A	17672	3	239	
17567	47935	A	17673	231	368	NKHQEDSLKPPIPGPSSWTA/P KPTLGQKGTCCTEKKKKKKKK GRI
17568	47936	A	17674	1	1270	
17569	47937	C	17675	100	270	
17570	47938	A	17676	459	1978	
17571	47939	A	17677	35	347	VVRAWYPGWGQGSEKEWQW DQQEALGRVRSKVTGEWEGR AGPEGTGQNGEGPRGILEVGGT TAPFCLAEGEWGPGGHPHLLF PPSPPRPPPPPTTPEPPS*PPSP PRPPQPPTTPEPPS
17572	47940	A	17678	236	397	NWLQPCG*AHPTGSGFPAPKLC PASPGAFSNEILSEPGPTLAPM PT/GAPCRSHGAGHSGDPGWPS SSPTGEDTNSAGPGAARVQMG CGHCVSLVPR*/CCWTPGGA
17573	47941	A	17679	132	492	TDHRDRKDKHPPALPASAMDK KNA/GQEGRPASRGSSPMATA TTGPQGVMPGYH*CSLRPKGSS VGLW*MLPGLGLTLQDSGLPS GPRQVQNYCPGAKALNQQPQE PA*CKASNQRPSVYLPTRYPS EQHVTEKTNILLRYLHQWTK RTLPRRKTRSKQRKLTGYGYCH YRSTGSNARLPLMFIKTQGFES RLVVDAAWPGTHPSGQWAPF WPKAGPELLSRSQFESGTSRA RLMFYPTMAAPVPK
17574	47942	A	17680	618	755	
17575	47943	A	17681	796	1092	
17576	47944	A	17682	1	391	
17577	47945	A	17683	1	697	
17578	47946	A	17684	1	888	
17579	47947	A	17685	749	1667	
17580	47948	A	17686	1	2088	
17581	47949	A	17687	189	438	
17582	47950	A	17688	387	497	

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17583	47951	A	17689	1	728	MAQEIEGDRLEFRARLTRRVQGGKPGCGPLKAPLGMVPECHSVKPSRDTFDTKSFKALLSFLKIP AIDVHKPIDHPINFTFDPGHRA PARHRHSTAAAVTMSPSGP/PA AAPSPCSPIPRHG*GPLRATSYC PVSWKQKQNSVSNKQTNEQTK TAKAEGARSRGPRNKIPGLPPG PRSGRLRIWLPPPREGSGQFPTAR GHPQPPCSGKGTECQSIQNLA SRISPVGTS CGRTSRQTIRVRK
17584	47952	A	17690	1	819	
17585	47953	A	17691	1	2115	MSGYSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKQPLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSDHGKCLKLP GQLEGVEIKADLSQSALVISLPQ AYLEYTPWDWPPSRWDDGIS GIIADYSITAQTRHEENGDDDS NEISGNGTVGVNLGPWRMRAD WQNTYQHTRTQLALGEDYLSN DIFDGLNVYGGVSTDDQMLPP HLRGYAPDISGVAHTTAK
17586	47954	A	17692	1	1080	
17587	47955	A	17693	1	253	
17588	47956	B	17694	1	1069	
17589	47957	A	17695	1	764	
17590	47958	C	17696	136	990	
17591	47959	A	17697	1	1422	
17592	47960	A	17698	547	1017	
17593	47961	A	17699	176	431	
17594	47962	A	17700	1	846	
17595	47963	A	17701	1	1815	
17596	47964	A	17702	1	1578	
17597	47965	A	17703	1	1149	
17598	47966	A	17704	22	441	
17599	47967	A	17705	828	920	
17600	47968	A	17706	1	231	MESKRLDNA/CAGGGD*PQLH QCPR*TAVD*RRNQTAFA*RDA STYRHESGGNASPECHGLYQR QKNADGGGGQRR!
17601	47969	A	17707	1	563	
17602	47970	A	17708	19	372	
17603	47971	A	17709	134	491	
17604	47972	A	17710	1	969	
17605	47973	A	17711	59	839	
17606	47974	A	17712	186	725	
17607	47975	A	17713	1	251	
17608	47976	A	17714	1381	2217	
17609	47977	A	17715	357	804	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
17610	47978	B	17716	1	2361	
17611	47979	A	17717	1	2832	
17612	47980	A	17718	1	3477	
17613	47981	B	17719	143	3122	
17614	47982	A	17720	1	3018	
17615	47983	A	17721	1	4371	
17616	47984	B	17722	1	2010	
17617	47985	A	17723	1	2168	
17618	47986	A	17724	1	2067	MKEIEIQKSLPKINESRSWFFEKI HKIDRLRLARLIKKREKNQIDTI KNDKGDIITANPTAIQTITREYY KHLVANKLENLEEMDKFLDITY TLPRLNQEEAESLNTPTGSDIE AIINSLPTKKSPGPDGLTAEFYQ RYKEELKKEGILLSSFYASILLI PKPGRDITKKENFRPISLMNID AKILNKILANRIQQHIKKLIHHD QVGFIQMGQGFNICKSINVIQ HINRTKDKNHTIISIDAEKAFDK IQQPFMLKTLNKLIGDGYLKKI RAIYDKPTANIILNGQKLEAPPL KTGTROGCPVSPVFNTVLEVL AREIRQEKIKGILGKEEVKRS LFADDMIVYLENPVSAQNLLK LISNFSKVSGYKINQVKSQAFI YTNNRQTESQIMSELPFTIAPKR IKYLRQLTRDVKDLFKENYKL LLNEIKEDTNKWKNPSCSWVGR INIVKMAILPKGIHRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAR IAKSILSRKYKAGGSMPLPDFKL CYKATVTKKAWYWYQNRDID QWNRTEPSEIMPHIYNYLIDFKP EKNKQWKGDSLFNKWCWENW LTICRKLKLPFLTPYTEINSRW IKDLNVRPKTIKLEENLGNTIQ DIGMGKDFMSKTPKAMATKAK IDEWDLCLKSFCATKETTVR VNRQPTWETIFAIYSS
17619	47987	A	17725	1	3457	
17620	47988	A	17726	1	3630	
17621	47989	B	17727	1	3384	
17622	47990	B	17728	1	2199	
17623	47991	A	17729	1	3924	
17624	47992	A	17730	1	3345	
17625	47993	A	17731	1	2382	
17626	47994	A	17732	1	3720	
17627	47995	A	17733	1	3894	

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17628	47996	A	17734	1	2427	MGCVRQIPLGTHPVVHQLTSIP QNCQSPQKTRKDREIGQPRGAY GDMRSKCNVMLMMESWNRKR TLEIQTIREYYKHLYTNKLENL EEMDKFLDTYTLPRLNQEEVES LNRPIHSDIVTIINSLPTKKISPG PDRFTAKFYQRYKEELVPFLLK LFQSIEK/EGILPNSFYEASIIIPK LGRDITKKENFRPISLMNTDAK ILNKILANRIQQHIKKLIQHDQV GFIPGMQGWFNIRKSNIIQHIN RIKDKNHHIISIDAFAKFDKIQQ PFMLKTLNKLGIQDGTYLKIIIRAI YDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEALAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTS NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWNIPCSWIGRINIV KMAILHKALYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLPDFKLHY KATVTKTAWYQYQNRDIDQV NRTEPSEIIPPIYNLIFDKLDKN KKWGKDCFLFNKWCWQNLAI CRKLKLDPLLPYTKINSRWIK DLNVRPKTIKTLEENLGITQDI GMGKDFMSKTPKAMATKDKID KWDLIKLSFCTAKETTIRVNR QPTKWEKIFVTYSSDKGLISRIY
17629	47997	A	17735	1	3780	
17630	47998	A	17736	1	2808	
17631	47999	A	17737	1	4842	
17632	48000	B	17738	331	3282	
17633	48001	A	17739	1	2880	
17634	48002	A	17740	1	3213	

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17635	48003	A	17741	1	2561	MKAEIKTFFETNKNKDDTYQNL WDTFKA VCRGKFIALNAHRRK QERSKIDTLTSQLKELEKQEQT YSKASRRQETIKIRAELEKETQ KTLQKINESRSWFFEKINKIDRP LTRLIKKKREKNQDISIKNDKG DITDPTEIQTITREYYKHLNAN KLENLEEMDKFLDTYTLRLNQ EEVESLNRPTGSEIEAIIINSLPT KKSPGPDGFTAIFYQRYKEELV PFLKLLQFSIEKEGILPNSFYEAS IILITKPRHHTTKNFRPISLMNI GAKILNKILANRIQQHIKKLIHH DQVGFIPMGQGFNIRKSNINVI QHINITNDKNHMIISIDAENAFD KIQQRFMLKTLNKLGDGMYL KIIRAIYDKPTATQNLKKLIGNF SKVSGYKINVQKSQAFLYTNN QTESQIMTELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLSEIK EDTKGKNIPCSWVGRNIMK MDILPKVIYTFNAIPIKLPMTFFT EVEKTLKFCINQKRIAKSFL SQKNKAGGITPPDFKLYYKATV TKTACYWYQNRDIDQWNRTEP SEIMQHIYNYLIFDKPDKNKQW GKDSL FNKWCWENWLAICRKL KLDSFLTPTKINSRWIKDLNIR PKTIKTLEENLGSIIQDIGMGKD FMSKTPKAMATKAIIDEWDLIK LKSFTAKETTMVRNQPTW EKIFATYSSDIGLSIRYNELKQI
17636	48004	A	17742	1	5042	MTGSNSHITILTLLNGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDKFT KIKRDKEGHYIMVKGSIQQUEEL TILNIYAPNTGAPRFIKQVLSL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRJKNLTQS RSTTWKLNLL
17637	48005	A	17743	101	471	MLSRILASRNRMRF AVEVVRA VRE/RVGNDFIHYRLSMLDLVE DGGTFAETVELAQAVEAAGATI INTGIGWHEARIPITATPVPRGA FSWVTRKLLKGHVSLPLVTTNRI NDPQVADDILSSTH
17638	48006	A	17744	161	311	

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17639	48007	A	17745	221	799	
17640	48008	A	17746	20	346	
17641	48009	A	17747	431	1578	
17642	48010	A	17748	1	771	
17643	48011	A	17749	3	863	AVLRREMQRMEGAWLGS DLV DQGERLNRLGFFETVDTDTQ RV/PGSPDQVDVYK/IVSLGGR LFYNDFQADDADLSDYTNKKIE IIDSADYFHIDIMDGHFVPLNT LSPFFVSQVKKLATKPLDCHLM VTRPQDYIAQLARAGADFITLH PETINGQAFRLIDEIRRHDMKV GLILNPETPVEAMKYYIHKADK ITVMTVDPGFAGQPFIP EMLDK LAELKAWREREGLEYEIEVDGS CNQATY EKLMAGADVFI VGT SGLFNHAENIDEAWRVMTAQIL AAKSE
17644	48012	A	17750	2	893	
17645	48013	A	17751	139	2057	
17646	48014	A	17752	2	361	
17647	48015	A	17753	497	897	PRSAFSAWLAFCST/TKDSHPL LAQLLDGVENLDHRQHLLFTA GHGARPLIRAHADVEENDCHPF ILIVHPSIHPIYLSIHPSTIRGERL MTQIPLIKHFLAGVTGLKLTQQ MRFCENVCLPLIATAGNRQTH
17648	48016	A	17754	83	1038	PSRAGHLPPKIKSSMAGTTPCLS IMVRQRK/PLVPAPLYQGM RDG KIVRFEEITRTPLEVQDCLLASA LALGLALMGNAQAVTTIPFWH SMEGELGKEVDSL AQRFAEN PDYKIVPTYKGNYEQNLSAGIA AFRTGNAPTYFAGHIMQACGV ALSATYFIRRKVVSLSDQKLNI AMTFVGSMSGALLVQYVQAD VLRQILPILVICIGLYFLMLPKLG EEDRQRMYGLPFALIAGGCV GFYDGGFFGPAAGSFYALAVTL CGFNLA KATAHAKLLNATSNIG GLLLFILGGKVIWATGFVMLVG QFLGAPHGVPTCV
17649	48017	A	17755	571	1728	
17650	48018	A	17756	332	511	
17651	48019	A	17757	581	637	RALR*SLQDGS AKRGASVS
17652	48020	A	17758	1	1098	
17653	48021	A	17759	1	366	

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17654	48022	A	17760	321	611	GEGENYCDSSVMTWVAI*QN WQCHCCSLRCASLRQG*RQDV TDRGETIKREMARNVV/WRA RVINAGFSRGSLLRGPSIDHRRK RLSASIRQFYPRP
17655	48023	B	17761	95	645	
17656	48024	B	17762	1	3978	
17657	48025	A	17763	1	328	MLIAEGLMTAKNITVITNSLPA AFALSENKDITLVVCCGTVVRHK TRSMHGSIAERSLQDINADLMF VGADGIDAVNGITTFNEGYSIS GAMVTAANKVIAVLDSKFNRR RGFNQVLPIEKIDHITDDAVSEV DKLALQKTRDTSLVVYVLSLADF FRTASTIGERDGTQVEMILFAGF VYLVISLSASLLVLTDCSTEVK KGEVVVVCGPSGSGKSTLIKTV NGLEPVQQGEITVDGIVVNDKK TDLAKLRSRVGMVFQHFELFPH LSIHENLTAAQVKVLKRDKAPA REKALKLLERVGLSAHANKFP AHYSGGQQQRAIARALCMDD IAMLFDEPTSAIDPEMINEVLD VMVELANEGMTMMVVTHEM GFAVKWRIGSTQQGAQLHCNR WLHVRKHLLVAYYNLVGIKPG KESYMRLENEKALDDFCQSLVD YLSAGHFSIYERILHKLEGNGQ LARAANKIWPQLEANTQQIMDY YDSSLETAIDHDNYLEFQQVLS DIGEALAAAFVLEDKLILLVLD AAR*NLKLVIIIDGGGFQGTGI VVIIHNLISIGFELRPNLRGAREL PVAFQLMKNALINTEMSGRQVI DQALTKIIKGFV
17658	48026	A	17764	216	473	DALRVASGNGCYSALLPLFCRL L*AESA*VPVQRPCGETLMRSS VVCLGGTAPECSSLGCAEKSGR SWPRKV AHTLGSWTVPRES
17659	48027	B	17765	1	1570	
17660	48028	A	17766	1580	1764	PASSLVMR*CLNRIA'SRAHQPA VRAY*SASAPGIA*KENA*G*RL HHR*NPAGKPDPLGL
17661	48029	A	17767	1	1827	
17662	48030	B	17768	1	1281	
17663	48031	B	17769	72	1169	

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17664	48032	A	17770	20	552	SAGDA*DWFWHGGVAGGNG* RSP*A/VTSSALKCIHRAIVRAW LLRMKKV*ATCA*CVTMRLLKC CIK*/CPDNLRLMVQLFFPDPPWH KARHNKRRIQVPPFAELVKSCL QLGGVFHMMATDWEPIAEHML EVMSSIDGYKNLESNDYVPRP ASRPVTKFEQRGHLGHGVWD LMFERVK
17665	48033	A	17771	3287	3568	CAFQRNIWHAKLNASPTPVFVP **LLASLTIPMKPAAMPGGKMD WWRVCRASASRPCQK*SLCQT PASVNTLLTVTAVCCASMASTT TRLWKI
17666	48034	A	17772	1	3126	
17667	48035	A	17773	249	3943	
17668	48036	B	17774	1	2178	
17669	48037	A	17775	263	434	
17670	48038	A	17776	619	1184	MRTSCGSGFIKRRVMRIASGMV AENRAV**PSGICAIMVSTSSMK PMRSISSASSRTRPLSL/AEVQSA TFQVVQQTARSTDNDLRPLTQ GA*LVHVTILAAVQS/PHLRAC V*RNPSLLQQPVPPVGRGSPAP ESVVLSAQDDQDSATEVKRMLQ FFRSPSGPYPERRGHSADVEYT LPELEMVFRNPDR
17671	48039	A	17777	1	1485	
17672	48040	A	17778	497	1838	
17673	48041	A	17779	534	922	
17674	48042	A	17780	1	458	MQQLEEALKQLAQGSGSSQAL TQVRRWDSACQKLPDANLALI SVAGEYAAELANQALDRNLNV MMFSDNVLTLEDEIQLKTRARE KGLLVMPGDC/WYVDDCRHTA GFC*RDAGRQYWRHWRFRYR DSGAVFADCAGRGGNYSRDWP WRARPQP
17675	48043	A	17781	2	270	QAGKYYGGAVFAPVFGAIMGG VLRTMNIEPDALTSVDKNEFVI NHGEGTGGRS*FARPSCSVGAR RTFASTARDTRQCPCGGGRSL CS
17676	48044	A	17782	1	1437	
17677	48045	B	17783	63	201	
17678	48046	A	17784	1016	1263	
17679	48047	A	17785	1	933	
17680	48048	B	17786	1	1888	
17681	48049	A	17787	845	2220	
17682	48050	A	17788	110	581	
17683	48051	A	17789	696	989	

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17684	48052	A	17790	199	573	
17685	48053	A	17791	1	3270	
17686	48054	A	17792	1	3018	
17687	48055	B	17793	1	708	
17688	48056	A	17794	264	512	FLAQWLPELPLSRHLRQCTWCR RHRNRW*VRS�HRCWLADCRC PELRIRSHDL*SLAQRLYDRTR TPDRRQLRTVLHWLLC
17689	48057	A	17795	1	2109	
17690	48058	A	17796	1239	1854	YHDDRNPQDAGNPSNADSGPQ I*QATGSPRRLVRRRWKRVNR LLAGKLAIVIDDFGYRPHNENQ VLAMPISAISVAVLPDSPHAREM ATKAHNSGHEVLIHLPMAPLSK Q/TAGEKYATPGDEQRRN*AHY S*WVNNVPYAVGINNHMGSK MTSNLFGMQKVMQALERYNL YFLDSVTIGNTQAMRAAQGTG VKVITRKVFLDGFAG
17691	48059	B	17797	1	2243	
17692	48060	A	17798	74	295	TISVLWMLSLNNTSKKRLA*TG SIGFFGLHSFTPRNGLRGASGTA FFGGVEVSTCGSFSKLLAFTSV MSGGRL
17693	48061	A	17799	1	1872	MLRIHCMQHWYNLSDGAMED ALYEIASMRFLFARLSLDSALPD RTTIMNFRHLEQHQQLARQLFK TINRWLAEGVMMTQGTGLVD ATIEAPSSSTKNKEQQRDPETH QTKKGNQWHFGMKAHIGVDA KSGLTHSLVTTAAEHDLNLQ GNLLHGEEQFVSADAGYQGAP QREELAEDVDWLIAERPQKV RTLKQHPKRNRTGISIAYMTGSI RARVEHPFRIIKRQGFVTARYR GCLNTITNGDVFPLATWFGG
17694	48062	A	17800	1	1269	

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17695	48063	A	17801	1	1988	MNDSEFHRLADQLWLTIERLDDWDGSDIDCEINGGVLTTITFENGSKIINRQEPFLHQVWLATKQGGYHFDLKGDEWICDRSGETFWDLLEQAATQQAGETITGFRVYTLQLNAQLRLGFLRLPYSVNLATEYKSLTHYTKVPEATNPSSVVDVVKLSANRLKYPMMRKRLMKMWREAKALHSDPVEAWASIIEDADKAKSFKQARGRGGFVRSSWQEVNELIAASNVTIKNYGPDRVAGFSPIPAMSMVSYASGARVLSLIGGTCLSFYDWYCDLPPASPQTWGEQTDVPESADWYNSYIIAWGSNVPQTRTPDAHFFTEVRYKGTKTVAVTPDYAEIAKLCDLWLAPKQGTDAAMALAMGHVMLREFHLDNPSQYFTDYVRRYTDMPMLVMLEERDGYAAGRMLRAADLVDA LGQENNPEWKTVAFTNTGEMVAPNGSIGFRWGEKGKWNLESIA/RIENPHFRSVKHNPNVLVRQLPVKNLTLVDGNTCPVVSVDLVLANYGDLRGLEDENSAKDYAEIKPYTPAWGEQITRVPRQYIETIAREFADTAHKTHGRSMILGAGVNHWHYMDMNYRGMINMLIFCGCVGQSGGGWAHYVVGQEKLRPQTGWLPLAFALDWNRPPRQMNSTSFFYNHSSQWRYEKVSAQELLSPLA
17696	48064	A	17802	3854	5726	
17697	48065	B	17803	1	1869	
17698	48066	A	17804	391	1246	
17699	48067	A	17805	58	1353	
17700	48068	A	17806	872	2123	
17701	48069	A	17807	1	1422	
17702	48070	A	17808	217	509	
17703	48071	A	17809	76	422	
17704	48072	A	17810	2	288	
17705	48073	A	17811	1	1626	
17706	48074	A	17812	779	832	
17707	48075	A	17813	1	1818	
17708	48076	A	17814	1	645	
17709	48077	A	17815	157	293	ALVCSSPWPSEKCKSKPQ*DTISHQLEWQSLKSQETTGAGEDVEK
17710	48078	A	17816	1	1446	
17711	48079	A	17817	1	306	

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17712	48080	A	17818	71	513	TIRSLGLWSQMEMRNLGTGA KKYKLPSSENTINTSTQIN*KI*K KRINSSTHTLSQD*TRKKLNL*I DQ*QELKLWQ*SIAYQPKRVQD QMDSQ/REFYQRYKEELHINRA KDKNHMHISDAEKAFDKIQQR MLKTLNEVLMGRISK
17713	48081	A	17819	I	828	
17714	48082	B	17820	I	567	
17715	48083	A	17821	I	1224	
17716	48084	A	17822	I	897	
17717	48085	A	17823	207	547	NHFLQGLGPLLQFPTSSSSPSET TSAWTLCPHHYQAFGQSHSTSL *EV/HKLSHIFMSSSEPSKLFQPL PVTQFQSRFHIFRYLFSSIPLYW CQFTVLVHFPAAADKDISVTTIP
17718	48086	B	17824	I	1128	
17719	48087	A	17825	I	765	
17720	48088	A	17826	I	952	
17721	48089	A	17827	1570	2176	FLQSTHLTKG*YPESTMNSNKF TRKKQPNQRAKDMKRPFSEKED IDAANKHMKKCSSSLAIREMQI KTTMRYHFTPPVRMAIHKSSGNN RCWRGCGEIGTLHCWWDCKL IQPLWKSMMWFLKDLLEIPEFD PAIPLLGIYPKDYKSCCYKDTCT HMFIAALFTIAKTWNQPKCPTM IDWIKKMWHIYTMEEYGAIKR MSSCPL
17722	48090	A	17828	I	531	
17723	48091	A	17829	I	462	
17724	48092	A	17830	876	1111	
17725	48093	A	17831	2	276	LLPGFFCSNLAPVPPSGGHQHD LPYPSSA*NPGASGTGQARMGQ SHQWAFWLWRKDAHVRKESGY MYSLYDRAYGERTTGRGRGR GPIPRP
17726	48094	A	17832	I	1290	
17727	48095	A	17833	1293	1863	RSTPSMKE/QLATALPRHMTAE RMIRIANTEFRKVPALGNCDTM SFVSAIVQCQPLGLEPGSAGH AYLLPFGNKNKESGKKNVQLII GYRGMIDLARRSGQIASLSARV VREGDEFSEFGLDEKLHHRPGE NEDAPVTHVYAVARLKDGGTQ FEVMTRKQIELVRSLSKADTDI* PWMCPCPMKRKSAT
17728	48096	C	17834	I	786	

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17729	48097	A	17835	2	654	FCRQRQCQVYRRGRFTHAAFT GTHRDNLVQVQSKLRADGCAL EDYFSQSEQVLPSLEAFDEAPQ DVVNKKVFNILRTIMEGQSIVN VDEIHRAARFFYQARQRDLYG AGGSNAICADVQHKFLRIGVRC QAYPDAHIMMMSASLLQEGDV VLVVTHTSGRTSDVKAARELAK KNGAKIICITHSYHSPIAKLADY IICSPAPETPLLGRNASARILQLT LLDAFFVSVAQLNIEQANINMQ KTGAM*KRP*NWQKRTGQRLF V*PIATIHRRNWPILFAHQPRK RRY*VVMRQEYYN
17730	48098	A	17836	1	4806	
17731	48099	A	17837	1	466	
17732	48100	B	17838	193	1045	
17733	48101	A	17839	1196	2732	
17734	48102	B	17840	1	732	
17735	48103	A	17841	290	664	
17736	48104	A	17842	302	1716	
17737	48105	A	17843	249	909	
17738	48106	A	17844	36	340	
17739	48107	A	17845	902	1455	RRCVLRP/GLDIMRNLNRIRQQ QRLEQAAAYEMTALRAATIELGP LVRGLPHLRTHRQLYQDIFDW AGQRRITLNLHGFVPKSTTVVET NGPSDQSIAMRRPGQTISRHHV QKKLGIELTNCYEHSGLPDIKN VTGILICRQTHARPARLARLIFT ANKTNTINALVDIEVDDFFDTA CQIDCCFETGSHSVLARLGAS AQDLQLDATSASHGSK
17740	48108	A	17846	1	1668	
17741	48109	A	17847	1	1080	
17742	48110	A	17848	1	907	MRAGFTSNVLTFLTCTSHFLNT FRAADVAVQATATSNFRQIQVF EDITQYNGKYILAVEGNPPLGE QGMFCISSGRPFIEKLKRAAAG ASAIIAWGTCASWGCVCQAARP NPTQATPIDKVITDKPIIKVPGCP PIPDVMSAIIYMTVFDRLPDVD RMGRPLMFYQRIHDKCYRRA HFDAGEFVQSWDDDAAPKVT ACTKWAAGLPPITVPVHTLE* WVWSRLLAGGNGLDRGRFSGV DSSWISYSSAISVTMAPATTLN QTSKAALAAACIAISTLCNGWPA VILAQRHWMKWSGLAS
17743	48111	A	17849	239	899	

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17744	48112	A	17850	155	249	CMRRKLTALTGGEPDR*TAMR* HNKSPALTGS
17745	48113	A	17851	1	1326	
17746	48114	A	17852	1	1394	
17747	48115	A	17853	46	705	
17748	48116	A	17854	2	488	
17749	48117	A	17855	563	687	LLARTSRQ*KTSLNCVNKL*MP SGQWAVLLLPVCRCWVWLRT
17750	48118	A	17856	1	1429	
17751	48119	A	17857	1	1037	
17752	48120	A	17858	2	276	LLPGFFCSNLAPVPPSGGHQHD LPYPSSA*NPASGSGTQARMGQ SHQWAFI.WRKDAHVRESGY MYSLYDRAYGERTTGRGRGR GPIPRP
17753	48121	A	17859	1	1290	
17754	48122	A	17860	1293	1863	RSTPSMKE/QLATALPRHMTAE RMIRIANTEFRKVPALGNCDTM SFSVAIVQCPQLGLEPGSASGH AYLLPFGNKNEKSGKKNVQLII GYRGMDLARRSGQIASLSARV VREGDEFSFEGFLDEKLHPRGE NEDAPVTHYVAVARLKDGGTQ FEVMTKRQIELVRSLSKADTD* PWMCCPMKRKSAT
17755	48123	A	17861	207	210	QLSLLNLPDLSIHRLASSALK RVNDQVGAAPPRHQSPPRNA VSLAPRPVPEWESACKLLCLSC RVNCQD*GNKALTSIHFWGE GIVGKMWLFYCTEAHFVRDPS GYSN
17756	48124	A	17862	2	654	FCRQRQCQVYRRGRFTHAAFT GTHRDNLVQVQSKLRADGCAL EDYFSQSEQVLPSLAFDEAPQ DVVNKVFNTLRTIMEGQSIVN VDEIHRAARFFYQARQRLDYG AGGSNAICADVQHFKFLRIGVRC QAYPDAHIMMMSASLLQEGDV VLVTHSGRTSDVKAALVELAK KNGAKIICITHSYHSPIAKLADY IICSPAPETPLLGRNASARILQLT LLDAFFVSVAQLNIEQANINMQ KTGAM*KRP*NWQKRTGQRLF V*PIATHR*RNWPILFAHQPRK RRY*VVMPRQEYYN
17757	48125	A	17863	1	4806	
17758	48126	A	17864	1	466	
17759	48127	A	17865	214	907	
17760	48128	A	17866	1288	2757	
17761	48129	A	17867	705	839	AGRSRENNRYRAKQPRCKR*F *CVYRFYPSGRYAEPSSAPNYT

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17762	48130	A	17868	199	1628	
17763	48131	A	17869	746	1013	TRARRRFITALRFSSLVASAPCC NWAAAFSSYYFCQQIVR*PHFDR QEKRSVQNQPDGCGSSASQSVR QRPKSPQQPVQSANPSLLLCR
17764	48132	A	17870	2	331	
17765	48133	A	17871	1	591	
17766	48134	A	17872	1	1197	
17767	48135	A	17873	45	3402	NRFSHISVTSACGWYHIPVEE/Q PEY/PGNLELERRIRSAIRWNAI MTVLRASKKDLELGGHMASFQ SSATIYDVCFNHFFRARNEQDG GDLVYFQGHISPGVYARAFLEG RLTQEQLDNFRQEVHGNGLSS YPHPKLMPEFWQFPTVSMGLG PIGAIVQAKFLKYLEHRGLKDT SKQTVYAFLDGDEMDEPESKG AITIATREKLD/NLVFVINCNLQ RLDSP/RWDELLRKDTSGKLIQL MNETVDGDYQTFK
17768	48136	A	17874	452	1395	LAGATGTAIRLILHAPLLPIKM RLP/TVSEGKPDSPAAEKFAAE NKNTYGALASLELAQQFVDKN ELEKAAAQLQQGLADTSDENL KAVINLRLARVQVQLKQADAA LKTLDTIKGGWAAIVADLRGE ALLSKGDKQKGKHQRAENCEIQ GYIDMIKHLVAPLVFTSLILTGC QSPQGKFTPEQVAAMQSYGFT ESAGDWSLGLSDAILFAKNDY KLLPESQQIQTMAAKLASTGL THARMDGHTNDYGEDSYNEGL SLKRANVVADAWAMGGQIPRS NLTTQGLGKKYPIASNKTAQGR AENRRVAVVITTP
17769	48137	B	17875	1	1579	
17770	48138	A	17876	182	2069	

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17771	48139	A	17877	1	2017	MESGVATRPADFDVYIDKLTE FVYKTNLFMKPFSQARKAPKR VVLPEGEARVLHATQELVTLG LAKPILIGRPNVIEMRIQKLGQLI KAGVDFEIVNNESDPRFEYWT EYFQIMKRRGVGTQEQAQRALIS NPTVIGAIMVQRGEADAMICGT VG DYEHFHSVVKNVFGYRDGV HTAGAMNALLPSGNTFIADTY VNDEPDAAELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTVGPVLMGVAKP VHVLTPIASVRIVNMVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRQYHGVTTLRFSG CFFAFHRHINAVFFRNIQAVFV ALRPEVIAIMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIYQH VLQAEGFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTPLWAWLKLLW QRIDEDNMTTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFI FANFLPATGDDVIQRYIE QFVANSNKMTAVGAASLAISS YLLSLIANVLMMS*SVLRMS WNPKWAWSSIWYS
17772	48140	A	17878	31	312	RGTHGCALYRRAAARCAKITL TTFISLFSSYFVIYNILLIYLIFA ASFCLLVV*CHTVFITVCSAGD VSGMSATWCAFVAISVDHFTG FNRF
17773	48141	A	17879	1	1098	
17774	48142	A	17880	1	1015	
17775	48143	B	17881	1	1917	
17776	48144	A	17882	931	1773	
17777	48145	A	17883	785	956	KKWMHSAV*WRKRSIRRVSSL GY**TQAKDRRFALPELRRIVCS TVRRYVRRWRTNRT
17778	48146	A	17884	221	367	
17779	48147	B	17885	1	1318	

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17780	48148	A	17886	1190	1634	APSQTVSLPEVASSMSGVMAG VEAVSSPGPYAVCAGSLLPSGW LCVKTSVMIASAWSPAGAVS IKRSSAVSVRIWALCGA\QPECA VRSLPSYPAFRQVLAPVTHAL* PRRSSGCP*CDYSLQLLLQ*PAH *HLQGLLRKQLSCQR
17781	48149	A	17887	1	2499	
17782	48150	A	17888	454	1698	
17783	48151	A	17889	635	1665	KSIFWRAPADCEP/QVRQSAKV QFGDYQANGMMAVAKKLG APRQLAEQVLTHLDLNGIA EIAAGPGFINIFLDPFALEHV QALASDRLGVATPEKQTI VDYSAPNRGFFGGAPLGT TLQDLTRPTKEDGLQAKP ISFWASFALQFVNVKILY GVTALSTFVLPQTQAL SWVVGVSVLLAMIGTFG NVCWALAGHLFQRLFRQY GRQLNIVLALLVYCAAFS KGTSDNVALFRSQRVKAN CITGYTDGQLRIFFRMLN CIFSATQNVNVQVLTTFN ANFWHFYWNFTVFNVTQ FAYCNHFIFCITCFNDAT PFAFAVQQPERVHRKTA ILL
17784	48152	A	17890	73	212	
17785	48153	A	17891	2049	2445	VFPVFLRIYFVWKKPGMK VTNARNWQLKPLFTELPV LDPDTQLHYVAVMELYS PAE*ERIQAFVWVSWNI WLY*A*RLIQ*HIALTP VVRTGKTKLMSAILFN ITHRMKANMLSSPKRRL PPRNCGKK
17786	48154	A	17892	1	1476	
17787	48155	A	17893	332	572	RGGA*RQKHRTSALSLSL P*NMATAVHLHRFSTR RAVTSSSARKWNTNSG AMSGLNRAA\AVLRV* QSPEDGCCARIR
17788	48156	A	17894	80	405	PRNLKSGPPISDAISPTK P*TI TEPISAPSLLATY KAAGCGGITQCTAINA VHSGMASFNNEVLV FLAIEKARGINSTPTST NSVMPQIRPTSTIMTST ESQRQR
17789	48157	A	17895	1	1392	
17790	48158	A	17896	1	1374	
17791	48159	A	17897	1971	2306	
17792	48160	A	17898	209	449	
17793	48161	A	17899	1	240	
17794	48162	A	17900	1	456	
17795	48163	B	17901	222	3807	
17796	48164	A	17902	3140	3219	
17797	48165	A	17903	240	298	

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17798	48166	A	17904	1902	2047	NQPVYRSNGD/RIWRTGKLFPT TVFRLIRLTSPRAFPPTSYRRCS VAY
17799	48167	B	17905	1	1994	
17800	48168	A	17906	1	2151	
17801	48169	A	17907	3	1127	GTPYASQPVRPVEGSKPLIKQV LDIGAHTDKTIAQKLARVAR MHFARQLAAVATFACSAQNA IALMEEIAANFSYEMIRLTECIL GFTWNRLYQGINVHNAERVQR LAHDGHLELVYVPCRSHMDYL LLSYVLHQGLVPPHIAAGINL NFWPAGPIFRRLGAFFIRTFKG NKLYSTVFREYLGELFSRGYSV EYFVEGGRSR/TGRLLDPKTGM LRGGTRPITLPIYIGYEHVMEV GTYAKELRGATKEKESLPQML RGLSKLRNLGGYVNFGEPMMP LMTYLNQHVDPWRESIDPIEAV RPAWLTPVTNNIAADLMVRIN NAGAANAMNLCCTALLASRQR SLTREQLTEQLNCYLDLMRNV
17802	48170	A	17908	192	486	PVLVYLWVSFSWLCGRSLVCD AFGCVLCLFCWGCWGWGF SRCLVLRVLDCAVAVWCPL GVGIGLWV/RVLPGLVSAVPC CCDVLARFRVLDLWGW

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17803	48171	A	17909	1	2470	MFQPSDSGKSFIFNMSVGVNLE GIKQPPMQQFIDNMMDASDHP KFAQYRDITLNLKLLQDDAFLAR HGLQEKRESLQALPARIPSTSMV HGVTLSTMHGCPPHEIEAICRY MLEEKGLNTFVKLNPTLLGYA RVREILDVCGFGYIGLKEESFD HDLKLTQALEMLERLMALAKE KSLGFGVKLTNTLTGTINNKGA PGDSTSGVLRITYERLLTAWML TCPCADEHQGESVKKLATALT WWLRGSSQNRDEITKDGQFSNH AGGILGGISSGQIIAHMALKPT SSIDVPGRTINRFGEVEEMITKG RHDPCVGIRAVPIAEAMLAIVL MDHLLRQRAQNADVKTDIRC AQSIGSFNCGIVGADTLPIQSE HYQVMRTDQRRYFGHPDLVM FIQLRSSQVSNLGMGTVLIGDM GMPAGGRFNGGHASHQTGLDV DIFLQLPKTRWTSQALLRPQAL DLVSRDGGKHVSVTLWKPEIFSL IKLAAQDKDVTIRFVNPAIKQQ LCLDAGTIATGCAKCDPGVSIG AYAYLLTLRAQCLAHDLDPLE PLEIDGTLPRYVFIHGGPRVFT YYTPKEESIKLFHDYLDLHRNS PNLDVQMPVPSVMFGRAPGRE KGEVNPPLRMLNGVQKFFAVL WLGRDSFVRFSVSLRRMADE HGTDKTIAQKLARVARMHFA RQLRAAVGPRLPARQDLFNKL
17804	48172	A	17910	1	734	
17805	48173	A	17911	1	962	
17806	48174	A	17912	1630	2633	
17807	48175	A	17913	1360	1600	HSTGRWATTINVPITCGTKARH STSSICKTGMLLWANALKQHC LLSRNLP*KGESINVANSLISYP NLRPQCNQTRTQD
17808	48176	A	17914	1	816	
17809	48177	A	17915	703	1546	
17810	48178	A	17916	209	485	QVIRPTFIPSTSSNGAISLPASTR RDS*MANAS*RCSLA*RATMFP A*SATSIHARPGVEGT*IVRIV VIMLRLLSRRKVRGIRLPAAVLI
17811	48179	A	17917	619	1167	

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17812	48180	A	17918	1	764	DSGQQLDDVQLARYLLSGQNG PKSDRPYRVR*LTGAMLKILIT L/VEIGNVTLGHVRVKIGTGCVIK NSGDWR*LRNQSVYRCGRCS GSGLYHWARLPVCVLVLSCWK VLTSSLVPPD
17813	48181	A	17919	3	1462	
17814	48182	A	17920	122	983	
17815	48183	B	17921	1	1287	
17816	48184	A	17922	289	958	
17817	48185	A	17923	1	5079	
17818	48186	A	17924	1	255	
17819	48187	A	17925	1892	2448	TESRCADGAGSVDVGTPEVVP RVELVAKWPGSRAGGTGLGCS PWVGAGCVGLGPQARLSGPT ASTEASAKAASTLASLMWLRV RL*GACPFARTGATAPSSSKGP ELGVSGLRKATWMGRGSGCCT RGLGAGEWRAVPESCGLDESS EDSDRDHAVPFSSSSCRSMRL RPRRVARGLCRRRGV
17820	48188	B	17926	52	888	
17821	48189	A	17927	929	1148	TVWNGTCGLPFSSLMKCMVIM IMRAIQKKMMSKPDITLVGW N*RRASVFGQPRVEKVHSAEE NQVSRSSS
17822	48190	A	17928	125	937	RISMVFPWCFCSCSRSLATTPAP TVRPPSRIAKRRPSSIAIGWIRVT TILMLSPGITITPSGSSMVPVTS VVRK*NCGR*PLKNGV*RPSS LDRMYTSDSNLHGLRPAVSPVT NTPA/SDGYSHDGLAQVDLS ANYHEGQYTSAGLSLQGGATL TTHGGALHRTQNMGGTRLID ADGVADVPVEGNGAAVYTNM FGKAVVSDVNNYYRNQAYIDL NKLPEAEATQSVVQATLTEG AIGYRKFAVISGQKAMAVVNF AEGKVS LAVV
17823	48191	A	17929	3992	4213	VPAIQKFPRSWKLGGERPPKA FRLRLSAA*RKSV* AQRSLAD/ SGMPLRLEKCLDTF*QIV*SAF KIQREGS
17824	48192	A	17930	1	1636	
17825	48193	A	17931	1	900	
17826	48194	A	17932	1	939	
17827	48195	A	17933	427	1250	

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17828	48196	A	17934	521	805	LCPSTNTSPLSCLCDLVASTEM APMRVFQAPAPKVNA**LFA TIEP PYSVNKLKPY**PAWTKSLCL LAPSIWLRPAAKSYFDTPGCSIF GTAA
17829	48197	A	17935	1	2052	
17830	48198	B	17936	1	573	
17831	48199	A	17937	1	1278	
17832	48200	A	17938	161	659	
17833	48201	A	17939	1	588	
17834	48202	A	17940	695	1281	KLKPYSWAFSRQSGRSVILTPPR VTVVVVAGFGPIPVFGTVMVRP GWAAP*FLPVASVYFP*AGLAG FLKKNRGCCANPAPPPIRRPIMY PP/MQRLQEPADW/WACA/WFS GKD*WKKSPNCTRCA
17835	48203	A	17941	261	2045	
17836	48204	A	17942	1	637	
17837	48205	A	17943	31	280	
17838	48206	A	17944	1	582	
17839	48207	A	17945	1	2496	
17840	48208	A	17946	330	507	
17841	48209	A	17947	1087	1875	
17842	48210	A	17948	1	476	
17843	48211	A	17949	1	537	
17844	48212	A	17950	2	492	
17845	48213	A	17951	1	1101	
17846	48214	A	17952	2538	2833	TRRNWRPIQSSEESWRAAGSST PLTTQNRQQTAGIY*RSR*TAA RR*SPALPRRNRLATAG/WQY ATQTRQQRVYPQL*LSAPATRK NRLLANAWLTM
17847	48215	A	17953	125	1831	
17848	48216	A	17954	2	825	
17849	48217	A	17955	1	840	
17850	48218	A	17956	1	1725	
17851	48219	A	17957	463	1824	
17852	48220	A	17958	2	117	
17853	48221	A	17959	1	2640	
17854	48222	B	17960	223	1560	
17855	48223	A	17961	638	746	RIP*MT*WS*KPWHKNYMMHA QASVDNLKWKKGYYQ
17856	48224	A	17962	385	514	
17857	48225	A	17963	17	225	SSPSKFTVAFFASLVMASAVSL ALSRLSLTTLSI/CGLVLQEERT DDALVEQFSPIRRARGHAPQQE ATEM

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17858	48226	A	17964	1	521	LVFLVLFVGFSLCFKSTYTLTY GDSPSLCDGLLII*IIIRIDTNKPA DNSISGIRDVGWVAKSYQVA/V GERLHNRTPGTSHQSDTRFDF* LC*PGSACPVLVSEHERPQANM LVEASGLAA*YQNALSCSFGY GVGLVRRQDFSSLGRFLQSAFA SNRY*QVWVFEFQQVS
17859	48227	A	17965	267	554	LRFRTAVRGRIFHRDLVLVLL GCNRYGRRGGDHGLCSVLVPR SLRLGRLPGGDSAAADAQSRH REKCR*DGVLVCDQDQNRQTPV WKPHQEDVQV
17860	48228	A	17966	1	915	
17861	48229	A	17967	1226	1399	SDSNISICTCAQH*KHFRII*NCI L*EVEP*RLS*M*LQRKCVQGE SKVHSLWGI
17862	48230	A	17968	828	1070	SFFDYQTSALEHARR*LHCRT* NAGWLPHRTDRSSGYHGRCS AAGRCSSGDHSSYQQNPAAEK LPAGHPQRSQSPERTG
17863	48231	A	17969	45	1198	
17864	48232	A	17970	348	508	RLFRWCPM*S,WASYFPPEQS PDSYWLF*ECNLPTAYNSQNAII RESHAITS
17865	48233	A	17971	251	601	MAKKMSLSIAVFWRRLYAYY PHLR*KS*TNW/QWWSALS*A V*PNRS/IDRSWIIWSVLFGLM V/AT/ALAPAFWLRV*KKSFSA WNPTKSPRCLSNARPCCSLSKK ASLPWTIAARSR
17866	48234	A	17972	1	2121	
17867	48235	C	17973	1	1710	
17868	48236	A	17974	1	1335	
17869	48237	A	17975	1	1497	
17870	48238	A	17976	2	824	
17871	48239	A	17977	1	1965	
17872	48240	A	17978	1	3555	
17873	48241	B	17979	197	2021	
17874	48242	A	17980	1	348	
17875	48243	A	17981	1	891	
17876	48244	A	17982	1	679	

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17877	48245	A	17983	3	2502	EAIREVSNPIPQEEIWTHEREAVP PVQLLTGWCVTAKAPDISAIS ALTA VKHGNCSSLTPLLNPPTS DVI VCAEMDEQWGYVGA KSR QRWLFYAYDSL RKT VVAHVFG ERTMATLGRMLSLSPFDVVIW MTD GWPLYESRLKGK L HAILV TFEEKFQEEP VKKQIMVSISVS DTGGKKEPKLINLSSKTNGLQ NTTEAQLCETKSD FELSFGFN ISIDTEDMTGCCFQEQSVRR YFKATSSPRRLIITKLTTVRVDG YVADDP SRRYS GHGDL LWPNA GNSCVETT VGSLLCEVQAAPTP HTLEGKHGCRNK EKKRLTHSG ACTYTFSELGLELWAWNCGKT EVNLGAVGKGVGGRGFKKI AKSQFTCSVLYTFTIKQISLTL WSKVMHILEHLKENSQ L TSIC TRYQRVFGPTWLHETIFCKVAL TATLLAELEKTS LQTFLDKIWI LGAQQHTGSQEPSQALLTCDPA WKKALRKVTKGGAFFGVND LGSSLSPTDLL YEEQRLTSLSG SWFPICV MVELT L RAGSSPGGR LYVEFDQAVTKEP RFLQYKHY WDGAVAGSSILRQDSFVAEAST TITRIESPSVPSRSTFLDDFSITQ QHRRHAGLSVMLS LIISPPVRGL CQERTLRDRFRERL MYLDLEY QSGYCR LRTAGSEM QMPDVL IFAHRSGLAGLFPGLDRRLVNA
17878	48246	A	17984	10	211	GSQSTIFTFAARWNLWANENT DTSISPLGVGEQRHCSSP* RFPD SDRCS PWSPRSQQGNQSPQTW Q
17879	48247	A	17985	1	1725	
17880	48248	A	17986	1	379	
17881	48249	A	17987	3	273	
17882	48250	A	17988	3	1157	
17883	48251	A	17989	76	378	
17884	48252	A	17990	1527	2005	
17885	48253	A	17991	578	1312	
17886	48254	A	17992	1	1758	
17887	48255	A	17993	1	2433	

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17888	48256	A	17994	1	537	SQEELLQQALVAQLA/HSEQLE GVQLPEPDEPSARHALPANEPR VLNNGVVSNDRLNNLSWQ HIGYVSSSLHLDYRVSTTVRNV ILSGYFDSIGIYQAVSDRQQLV QQWLDILGIDKRTADAPFHSLS WGQQRLALIVRALVKHPTLLIL DEPLQGLDPLNRQLIRRFVDVLI
17889	48257	A	17995	1	536	
17890	48258	A	17996	1	1319	
17891	48259	C	17997	74	341	
17892	48260	A	17998	3	103	
17893	48261	A	17999	1	745	
17894	48262	A	18000	1	663	
17895	48263	A	18001	2	297	
17896	48264	A	18002	8	340	VPANLSAIALFRRESVTPLAAL AASPVCAGRFLVLLKNHRRDLP* ISVPVNSSNSARSLLVWHSGRQ QIAPDWSSKDDFMRLGKPNRFS VLLLATWIR*STVIRRSPTFS

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17897	48265	A	18003	1	1341	MVHRFGIRVRFVALGFYQDVL PVRAHRHEWHGYVHLCAISQR QIDVSFARDATSHSSCPVTGVR FWGYPFAANKVVIAGFELEGET MTRPGLICAEGGLVMIVSLRS ELYDSYHEFTIRQRTVEIVEKAA NHLPAVVEMMTLHRCAINRHN FVRRVGPAGISTFFASSPDGVN AGFSTFRVVFTRQSRPLQRHS HADVQTATLLNTVNLEQKQA NAILSGLSDMI PNSSPESAPEIQL LQSRMILGKTIAELNLRDIVEQK YFPVIVGRGWRLTKEKPGELAI SWMHIPQLNGQDQQLTLTVGE NGHYTLEGEEFTVNGMVGQRL EKDGVALTIADIKAKPGTQFVL SQRTELEAINALQETFTVSERSK ESGMLELTMTGDDPQLITRILN SIANNYLQQNIARQAAQDSQSL EFLQRQLP*TLKSNRPTPFSAA*/ DDMI PNSSPESAPEIQLLQSRMI LGKTIAELNLRDIVEQKYFPI/D GSRLGEINQRKTR*AGDQLDAY STTEWSGSATDTQVGENGHYT LEGEFTVNG/NGRPASGKRWR CADYRGH*GQDQQLTLTVGEN GHYTLEGEEFTVNGMVGQRL KDGVALTIADIKAKPGTQFVLS QRTELEAINALQETFTVSERSKE SGMLELTMTGDDPQLITRILNSI ANNYLQQNIARQAAQDSQSL FLQRQLPEVRSELDQRKKNSTFI
17898	48266	A	18004	414	893	VFAQHGLTVAAIAAHARDRWF VGRTAHANPPVRCSTDGSGRVP VTRYSGFVAAA VILLTASPRGG ECSREAPLCSVSEYLLQSAGE YAPAPRCVLRVCVPSVDEDFVPV VPD*APPVEVALFLRLTPVAR PADGGWLLAAIRPDALTSIAIV VLAAAR
17899	48267	A	18005	432	1108	
17900	48268	B	18006	1	753	
17901	48269	A	18007	46	282	
17902	48270	A	18008	1	1201	
17903	48271	A	18009	1	618	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
17904	48272	A	18010	1	1045	MLCTKWDLKLEKNAGKNKN AYKWWGPANAPDEPHIEQLV GECRVMRQLKRLISRIAPSSSV MVVGESGTAIPVVSHEFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDFGYLEFEGGANFSWGEM YGFDFWENFYNGRHNKPGSEQ RYTFKNTNRIYLGDTGFNLYLH AYGTYGSANRVNFHDDMFLA GFGQF*PAGGW/WGSPFFAK/ RYTRSKPYITGDNGYVAGWV AGYNFMLGSEKFTLTNWNVEYE FDRDATYAADFLPLYDVDCQD NGNLEYDTSYQPEWKHNLFDH YLA VLYRFKDESGKEQFSGAV VKTREATPGKEIEAITRRMLDFS PRLKKLA
17905	48273	A	18011	228	430	YPRQHRQRADGSDRHR**/CWS A*IWANPTSNLPPCRFALTTRK RPILCAPPSRQSYAAWCRWEIRI A
17906	48274	A	18012	296	1178	
17907	48275	A	18013	1	1395	MPSDISLASCLRLRATSRFLTDRH RQSDCMATNRIPIVDDDEDNVR RFETHCANNVRTALHLFADIHP DVVLMDIRMPMDGIKALKEM RSHETRTPVILMTAYAEVETAV EALRCGAFDYVIKPFDLDELNLI VQRALQLQSMKKKEIRHLHQL STSWQWGHILTNSPAMMDICK DTAKIALSQASVLISGESGTGKE LIARAIHYNRRRAKGAFIKVNC AALRESLLESELFGEHKLFR ANEGTLLLDIIGRM/PLVLQAIL RIHQEREFERIG/GHQTIK/VDIAS LLAPTRLQAMVKEGTFREDLFY RLNVIHLILPPLDRREDISLLA NHFLQKFSSNQDRIIDIDPMA MSLLTAWSPGNIRELSNVIER AVVMNSGPIIFSEDLPPQIRQPV CNAGEVKTAPVGERNLKEEIKR VEKRIMEVLEQQEGNRTAL MLGISRRALMYKLQFYGIDPAD
17908	48276	A	18014	1	771	
17909	48277	A	18015	1	2154	
17910	48278	A	18016	859	1014	IKTGETHPGIGPSVM*RHSKAD LTHRHCGGIPEPQSVSFGSQH GGGQFPPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
17911	48279	A	18017	1224	1520	SPLVNQ*GA*KFFSRGNLFPOG ETH*KTKGVPCWTRYPLDKRS DSAEIFKTPANASGRTSGLGC AAQLEKVAADGRDLDEKLAEG IGGSNKTSVWQG
17912	48280	B	18018	182	2392	
17913	48281	A	18019	72	266	
17914	48282	A	18020	600	914	PYRGSPRNHGQLCDHCSHRI.SE DPFVRYSNHCQSISNYRCDKPP VRPLSPLHQKTDKHHQRDPDRP FQWSAAPAHGRWRSGDS*ETP LHYAQPAGKLRWLWVNY
17915	48283	A	18021	1102	1171	LLGYGQQPPASNLLSEG*RSVV L*ISALRM*ALPPQKSSDAPNG WLPNRWPISSTHMR
17916	48284	A	18022	1	1279	
17917	48285	A	18023	1329	1403	
17918	48286	A	18024	442	918	
17919	48287	A	18025	3	1345	
17920	48288	B	18026	436	988	
17921	48289	A	18027	637	1086	
17922	48290	A	18028	1	321	
17923	48291	A	18029	1	845	
17924	48292	A	18030	298	581	GARAEARAGSGQGAGLVSSP VRWRGWSDKGAERPGGPLSPL REVSRAGPSG/HAARGQQPGRP RFPPPGPRPRRRCPCTRARPGG AAGGGPCL
17925	48293	C	18031	450	604	
17926	48294	A	18032	1279	2253	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
17927	48295	A	18033	1	1957	MAQFHVSHPPAEWPRHVLMLM ADSKNELQNMNTGQTCGRQT LKSKLQGWKNPGIQSDPGSQG HPRCLKTFPLVAQSQSTQERNHV MEKAVLKSQNWALIEEFITKIG WFPDYSKGKVKYLSPPKSSCTTV LQVTHFSLFFHPNPDELVSQIKV WSKHRLYQNNSEAFLEVOIPEP KCEVYSMRMTGRRQPGTAMD LNAGGSICNVPTLLHLTGESTF RDRQRVGAYLDIRGWYILVLV VDKEKLGIPGQKQNSKLLFGSE KLKQWVYVKNHAKESITQEAM GIWVGQQRKRQPLGYEERKLT NRKDIHIKNPSVCHHQRPKVD KTTKMGGKQSRKTGNSKNQST SPTLKESSSSPATEQSWTENDFD ELREEGFRSDYSELQEEVQNN GKEVKNFGKKLDEWITRITNAK KSLKDLMLKTKARELCDETS LSSQCNQLEERVSVMEDEMNIE KQEEKFREKIRKNEQSLQEIW DYMKRPNRLRIGVPESDGENGT KLENTLQDIIQENFPNLRQANI QIQEIQRTPQRYSLRRATPRHIIV RFTKVEMKEKMLRVAREKGRV THKGKPVRLTADLLAETLQAR RQDTHRLKIKDGGRTFKQMEN RKRQGLQS*SQIKQNLNQQRSK ETKAIT*W*RDQFNKKS
17928	48296	A	18034	1	2838	
17929	48297	A	18035	1	897	
17930	48298	A	18036	26	308	
17931	48299	A	18037	749	1020	
17932	48300	A	18038	1	1773	
17933	48301	A	18039	1	1890	
17934	48302	A	18040	1	756	
17935	48303	A	18041	399	660	CPPEAVMPRRHEPVWEMTGFF LPDVLSDSDTSEGRLHLET WAPFLCRCLSLRLIS*HHHQT GNSSPPVSASQHQSVDRDSL
17936	48304	A	18042	909	2005	
17937	48305	A	18043	1	490	
17938	48306	A	18044	104	775	
17939	48307	A	18045	170	451	
17940	48308	A	18046	1	207	

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17941	48309	A	18047	146	678	LGFLRLSEMPRKQGDYRTRIWK KFEDGLSNVLVIQLNKLIIICVM CLVRDCDVLKTYFHR*SGLLPI KDTSPFPTRVTQWGWKNDQ TFQGLLDTGSELTLPEDPKRHC GPPVKVGAYGGQVLHSHKWAPI YHFLSSHNCNGFCYISIANLPKK FGQNIKECLTNNRIVPFNCVQD
17942	48310	A	18048	270	1444	
17943	48311	A	18049	700	1062	
17944	48312	A	18050	3	1096	
17945	48313	A	18051	1	1500	
17946	48314	A	18052	1	6215	MEDNLISINKIKILLAVSDGEIDE TFSLKQLMFNSVPVQNEGDGSFN FEGVKAEFPGTQTQEYIKGME DSSSEVTVNREVTDDNPYTISVT NKTLSAIRIKMFMPRGVRIESN GDKNGVRVEYEVQAVDGGSF ETVLTDVIEGKTMSGYDRSRRV NLPFNFNQVIFRVVRKTPDSND SNVVDIAQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKA
17947	48315	A	18053	1325	1417	
17948	48316	A	18054	1	4971	
17949	48317	A	18055	251	1091	
17950	48318	A	18056	1	2277	
17951	48319	A	18057	2	448	KNDKGDIIVTTKSGGRGTSTVS FKLLKPEKI/GSKFSQKDEMLF HGMRA DFTSENFSAAWYLIEN HSNTSFEQLKMAVTNLKRQAN KKSEGLAYVKGGLSTFFEAQD ALSAIHQKLEADGTEKVEGSM TKLENVLNRSNTADTVYE
17952	48320	A	18058	124	984	

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17953	48321	A	18059	142	1393	DKKPGMVPPPPGEESSQTIVLPP GWQSYLSPQGRYYVNTTTNE TTWERPSSSPGIPASPGSHRSSLP PTVNGYHASGTPAHPPEAHM SGRKSTGDSQNLGSSSPSKKQS KENTITINCVTFFHPDTMPEQQL LKPTWESYCDYFWADKKDPQG NGTVAGFELLLOKQLKGKQMQ KEMSEFIRERIKIEEDYAKNLAK LSQNSLASQEEGSLGEAWAQV KKSLADEAEVHLKFSAKLHSEV EKPLMNFRENFKDKMKCDHH IADLRKQLASRYASVEKARKAL TERQRDLEMKTQQLEIKLSNKT EEDIKKARRKSTQAGDDLRC VDLYNQAQSKWFEEMVTTTLE LERLEVERVEMIRQHLQCYTQL RHETDMFNQSTVEPVDQLLRK VDPKADRELWVREHKTGNIRP VDMEI
17954	48322	A	18060	1	435	
17955	48323	A	18061	3	926	
17956	48324	A	18062	3	693	RPFLAYLRDGDARAGLNLQL AVLAMLSSRKMFCKKSGQSYS PSRVLITENDVKEGLQRSIILYD RAGEEHYNCSALHKS MRGSD QNASLYWLARMLEGGEDPLYV ARRLVRFA/SEDIGLADPSALTQ AVAAAYQGCHFCMPECEELLA QCVVYFARAPKSIIEVYSAYNN VKACLNRHQGLPPVPLHLRN APTRLMKDLGYGKGKYNPM YSEPDQEYLPPEELRGVD
17957	48325	B	18063	1	2020	
17958	48326	A	18064	19	404	
17959	48327	A	18065	1	407	FRATITSAKMGA YKIQLWR KKQADV MRLLRVRCWQYRQ LYALHRAPRPTRADKARRLGY NDKQGYVIYJRVRGRGRKRPD PKGATY GKPVHHGDNQLKIAR SLQSDAEFPAGRHCALREQSS Y*VGEHST
17960	48328	A	18066	53	431	AKKGAYNYIQLWRKKRADV MRFLLRVRCWQYRQLSALHRA PRPTRDPKARRLGYKAKQGYVI YKIRVRRGGRKRPVPGATYG KPVHGGANQLKSAQSLQTGVQ ERP GHP*YAMRVLKAYRAPD
17961	48329	A	18067	5	328	

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17962	48330	A	18068	93	836	AKMGAYKYIHLEWRKKQSDV MRLLRARCWQYPALHRRAGTE WQLSALHRAPRPTRPDKARRL GYKQAKQGYVIYRIRVRRYI*D SCSPWWLKTAAQFPKGCNFTGK PVHSWVFNQLKSFASKAFQFR WQEGGEAWDGTGGLLEEFNLN FFNWVWV/GKIST*QNFFEGLLIL I/VIPFHS*SEENPDTQWDQPN QSHKHRIEMRGLTSAPEKSRG L/GKKGHKFFHTIGG/SLRRAT WRRRNTLQAPPLPLI
17963	48331	A	18069	1495	2055	
17964	48332	B	18070	125	2530	
17965	48333	A	18071	345	800	RWRLQNLSCSSCSGSGSEGAT CFARGR*RPPGNSLNVSRMCTR SSYSCRRHSPAFLSWGKGRCHL CNKAHLLAGA*HYSFLSGSAPY *N*VNGQI**R*TAHRSTPDAPT GH*NCCS*L*CHSY*QRA*PGY RHD*CRMCC*CADCSHAC
17966	48334	A	18072	181	1687	
17967	48335	A	18074	205	1734	
17968	48336	A	18075	1	705	
17969	48337	A	18076	590	685	
17970	48338	B	18077	1	881	
17971	48339	A	18078	1043	1248	ITLGIMAIFTVLPIPIHEHGMVFH LFVSSFISLSSGL*FSLKRSFTSL VSWIPKYFILFEAVVNGSSL
17972	48340	B	18079	1	1977	
17973	48341	A	18080	805	1153	AWKVLPPFFVSFCFLSSGL*FSL KRSFTSLVSWIPRYFILFEAIVN GSSLMIWLSVCLLLVYKNACDF CTLILYPETLLKLLISLRRFELLF LSMFSASFSSCKAGLVVAESL
17974	48342	A	18081	471	1442	IWSFHIVPYFLEALFV*GVRKGS SFSFLHMAQFSQHHLLSRESF PHCLFFSGLSKTR
17975	48343	A	18082	188	355	
17976	48344	B	18083	1	1677	
17977	48345	C	18084	35	1816	
17978	48346	A	18085	557	724	
17979	48347	A	18086	179	346	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17980	48348	A	18087	135	1461	INRIYILLSTTSHLFQN*PHSWK*STPQQM*KNRNRYNKLRLRPQC NQTRTQDEETHSKSLNYMETE QPAPE*LLGT*QNEGRNKDVL* NQREQRHNIPESLGH1*SNC*QD **RRKERIK*MQ*KC*RCNKN AKGVITTDPTIEQTTIREYHKHL YANKLENLEDTKFLDTYTLPR LNQEEVESLNRPTGSEIEAIINS LPTKKRPGPDGFTAIFYQRYKE EQRIKYLGIQLTRDVKDLFKEN YKPLLNEIKEDTNKWNIPCSW IGRINIMKMAILPKVIYGFNAIPI KLPRTFFTELEKILKFIKNQKR ARIAKTILSKKNAGGIMLPDFK LYYKATVTKTAWYWFQNRDID QWNRTASEITPHIYNHLIFDKP EKNKKWGDLSFNKWCWENW LAICRKLKLDPLIPYTKINSRW IKDLNVRPKTIKSLLENLGPFR
17981	48349	B	18088	1	2016	
17982	48350	A	18089	659	826	
17983	48351	A	18090	3531	3878	
17984	48352	C	18091	1	2793	
17985	48353	A	18092	1607	1774	
17986	48354	B	18093	1	1666	
17987	48355	A	18094	1	1068	
17988	48356	B	18095	1	1549	
17989	48357	A	18096	557	623	KKWINYWTHTPSQD*TRKKLN P
17990	48358	B	18097	1	1231	
17991	48359	A	18098	263	1461	GGSSCYPSEWATIRTAKMVTLR KRTLKVLTLFVLFIPLTSFFLNY SHTM/VATTWFPKQMVLESEN LKRLIKHRPCTCTHCIGQRKLS AWFDERFNQTMQPLLTANAL LEDDTYRWWSLESVMFSVTM GFCLQRPFGDKQGTTPQVYINQ TGRDLTQQQLRQREKPKNNLN DTIKELFRVVPNGVDPMLEKRS VGCRRCAVVGNSGNLRESFYG PEIDSHDFVLRMNKAPTAGEA DVGTKTTHHLVYPESFRELGDN VSMILVPFKTIDLEWVVSATITG TISHTYIPVPAKIRVKQDKILYH PAFIKYVFDNWLQGHGRYPST GILSVIFSMHVCDEVLDLYGFGA DSKGNWHHYWENNPSAGAFR KTGVDHADFESNVTATLASINK IRIFKGR
17992	48360	B	18099	1	4855	

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17993	48361	A	18100	571	4189	FSLKRSSTSLVSWIPRYFILFEAI VNGSSLMIVLSV*AKILVQRA* VLAFFHP*LRFKDQVVVDMW HYF
17994	48362	A	18101	7449	7626	SFRSRLFSFHVVELF*VSFLILSS SLIALWSEKQSVIISVLLYFLRS AFLPTMWSILE
17995	48363	A	18102	63	329	SGQRRKEVPSPTLPAPPFILKKK EWPDPPRSFFSGGHWAKSSCPS DCSSQLMAC*/CKNAKHQKDN SCL/STHMKGNSEK*NSGYQ GLG
17996	48364	A	18103	2	618	GAFLLLEVATAAGLSAGLTRLGS QVGGAMRRSKADVERIASVQ GSTPTLQKSMKGFYFAKLYYE AKEYDLAKKYICTYINVQERDP KAHRFLGLLYELEENTEKAVEC YRRSVELNPTQKDLVLKIAKLL CKNDVTDGRAKYWVERAAKL FPGSPAIFYKLKN/DGWVRGQM VPKPDDEGVQVRGRSGRPDAG WRLNRRSSVGGSAW
17997	48365	A	18104	1	995	
17998	48366	A	18105	1	513	
17999	48367	A	18106	62	521	
18000	48368	A	18107	1	375	
18001	48369	A	18108	76	480	LVKVCCHCTYHHFLTGVVSLPR DGGKGAPCWGRARSPKSALLP YLAPGRG*VGTYEVQN/PNGTS PVQSPATDVGRSPALGNQEP/G T*SPGPQIGRGVITGTARPHGT SRDSWRRPPSFILNAVANIPKGN APIPKE
18002	48370	A	18109	445	1128	
18003	48371	A	18110	784	1189	IPLGKLLKVPVGAQPIERFPQIP VPLCSLSFPSPSSSSARS*VRQ ES*LGTGPGAPTGP/TSHHPSAS SPPHPSAKAAFLSFVCLCS*PPP SSCHPCGLGPGDPSPQKMMICT VAHLNQLSLIFTVVKVHLL
18004	48372	A	18111	1	2088	
18005	48373	C	18112	169	213	
18006	48374	A	18113	1145	1229	
18007	48375	A	18114	1	975	
18008	48376	A	18115	1	750	
18009	48377	A	18116	288	368	
18010	48378	A	18117	34	168	
18011	48379	A	18118	479	1579	
18012	48380	A	18119	2279	2398	SDCSCPL*GPPGRWHKRRKSG SPHLSTPEGTALTSQA
18013	48381	A	18120	21	190	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
18014	48382	A	18121	1	1773	
18015	48383	A	18122	18	290	VAGTWPNFLKKVGVGVKYGTR YGASLRKMKVKKIEISQHAKYTC SFCGITKMKRRAVGIWHCGSC MKTAVAGGAWTYK*V*FLVVF SVWTT
18016	48384	C	18123	325	486	
18017	48385	A	18124	1	498	
18018	48386	A	18125	3	306	RQEIDSIHQGVGYCLALVPANT LPKTPLGHHISQTKQLFLEGS HPCNLMCPHTCVTNLKPQRQK QP/WCRPFCRDGWESGCWKTY STSCWKGSGTNRRE
18019	48387	A	18126	1	1197	
18020	48388	A	18127	1	390	NSRVDDFVAPGLSEAGKLLGLE FPERQLAAAVG/CSPMSGVIS MSAPFPLGKIIDAIYTNPTVDYS DNLTRLCLGLSGVFLCGAAAN AIRVYLMTSRQRVVKRLRTSL FSSILQGEVAFSDKAGTGELI
18021	48389	A	18128	1	695	SGFMDHLEEKADLSELVEKEEL GFFQYYRERCHQKVYHPITKPG GSAKDAAPGGGHHQAGPGQG GDEGIRMMFCVSPNRAFTVVS VVPVLSIIDVIYGRYLRLTKVT QDSLAQATQLAEERIGNVK/TV RAFGKEMTEIEKYPSKVDHVM QKARKEAFARAEGVILNEKSFQ GALEFKNVHFAYPARPEVPIFQ DFLSLIPSGSVTALVGPSSGSKS TVLSLLRLLYDPAS
18022	48390	A	18129	1	2136	
18023	48391	A	18130	1	822	
18024	48392	A	18131	257	388	
18025	48393	A	18132	1	765	MVNALSLAARIHAEPVPADESPE MTEGYEGFYHLASMKGTVERA DMHYIIRDFDRKQFEARKRKM MEIAKKVGKGLHPDCYIELVIE DSYYNMREKVVEHPHILDIAQQ AMRDCDIEPELKPIRGGTDGAQ LSFMGLPCPNLFTGGYNYHA/P SPKFSAVSAMLLASASSAGRCG ESIFSPLA YTSSPIESDSCGPAL* RFLRH*/P/EIFLTQPVF/SENEAID IWN/SPTASVSPLMPSRQNAVRE LFLLTVRPRPTGTD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
18026	48394	A	18133	1	1166	LTHWVYHLYGIQRILIHIPSTSQ PNRVRGDIPPLQRIVVPTVIVQ PRLIMLLPWQTVRLVQVMRV LLIKLVAPFIILPAPRRJAVFADE RQRQAPVVAVVKMNFSSRCVF RLHLSGQLLHRQPALRKPRPAF TAHAVCPDFFLQPVPQQPHQFSR EHHAVAVLTPFLLERLCQAAPL RFFPLAVLCLDPDERREASRLV YRLDTGCVSLHRRQPVSVPAIS LALPMLAILVVQTFMALYAI VTWRMMGKNYDAVLAAGH CGFGLGATPTAIANMQAITERF GPSHMAFLVVPVMVGAFFIDIVN ALVIKLYLMLPIFAG*PMKRR* K/SPPQQRQMPDTRLSSVPSA SSVLGGLPVVGNVREYGVPGA ELPGSSPDRAVNPPL
18027	48395	A	18134	48	314	LVPMTWVIEASYSIMRKKVGE HPHFLDIAHQAMRDCDIEPELN PIRGGTGDAQLSFMGLPCPNLF TGGYNMVMMSL*LWKVWKK RCR
18028	48396	B	18135	83	3044	
18029	48397	A	18136	1	1080	
18030	48398	A	18137	3	979	DAWADAWSKKADVKEVNPID TKEKKPEAKKVDAGGKVKKG NLKA/KKPKKGK/HC/SRNP CKKEIGRNSRSGMYSRK/AM YK RKVYSAAKSK/VEKK/K KEVLA TVTKPGV/GDKNRR* PGVVKL PQKCPRYYP/SL EDVPRKACLSHGKKTP LVQHVEKNCEASIPRG PF*FILTGRHRGK/RVGF PESSL AKLAYLLC*L GPLVLKSEVPL/R RTHQKFCHLPLSTKINDIS N/VKI PKHLTGCLSR RKKLRK/PRHQ EGEIFDTEKEKYEN TEQRKIDQ KAVDSQIL PKIAIPQLGGYLR S VFALTNGIYP HKLVLVNLKNP
18031	48399	A	18138	858	1418	
18032	48400	A	18139	97	516	
18033	48401	A	18140	1	219	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
18034	48402	A	18141	110	768	NLFSGCVSTFRKQPAHQRRSR ARAETMQRRLLVQQWSVAVFL SYAVPSCGRSV EGLSRRL/LKLP MRPKNVHVPTKVTTYKRAVSE HQLLDHDKGKSIQDLRRRFFLHH LIAEIHTAEIRATSEVSPNSKPS NTKNHPVRFSGDDEGRYLTQE TNKVETIKEQPLKTPGKKKKG KPKGRKEQEKRRRTRSAWLD SGVTGSGLEGDHLDSTTSLE
18035	48403	A	18142	338	661	
18036	48404	A	18143	443	661	
18037	48405	A	18144	474	531	
18038	48406	A	18145	208	317	
18039	48407	A	18146	1	807	
18040	48408	A	18147	1	1122	
18041	48409	A	18148	283	2204	ASPMAPTSLCVPTLLPSLNQTSS SSTAPTGKASGWPMRLRPGL TTPWLSLTL*SRPTFTSSPC SFVVLASPSTSLKCWPLSEGA
18042	48410	A	18149	208	1212	
18043	48411	A	18150	202	1677	
18044	48412	A	18151	1	3285	
18045	48413	A	18152	3	2206	
18046	48414	A	18153	1	1041	
18047	48415	A	18154	2	1460	
18048	48416	A	18155	1	792	
18049	48417	A	18156	51	362	AHGAAWPSHRKDRESADLGSD GQNGQDLWDGGGCRCC*RC DVLWCWAPHTFRHSYAMHML YAGIPLKVLQSLLLGQAPCRG LGQNVGTALPLVSGGPMLFP
18050	48418	A	18157	609	690	
18051	48419	A	18158	1	2055	
18052	48420	A	18159	3	2236	
18053	48421	B	18160	406	454	
18054	48422	A	18161	1	2151	
18055	48423	B	18162	1	1215	
18056	48424	A	18163	1	594	
18057	48425	B	18164	1	1380	
18058	48426	A	18165	441	692	

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18059	48427	A	18166	2	1311	QHVRSTVTELWTGTFNFSIQTA FAAGIGWLITFCCKGGDCLTQS TRLRLSGMLFLNSLDAKEIYLE VIHNLDPDFELLSANTLEDRLAH HRWLLFFHFGKNENSNDPELK KLKTLKNDHIQVDRFGCSSAP DICSNLYVFQPSLAVFKGGQGTK EYEIHHGKKILYDILAFKESVN SHVITLGPQNFANDKEPWL DFFAPWCPPCRALPELRRASN LLYGQLKFGTLDCTVHEGLCN MYNIQAYPTTVFVFNQSNIEYE GHHSAEQILEFIKDLMNPSGGG LTPTTFIELVTQRKHTEVRI/V*F HCPGWPPWRLWPMACKPRNL LP*SSRPLNT*SSLFCSSNQPDLR GPLLHRPLSLPRRYRGAQVNP DFGHYSVSPSLIHGLHQCSHLFS HSPPPRVLRPPRILTTSTGLPPSP RRSATDVHTAYPPTAD
18060	48428	A	18167	1	924	
18061	48429	A	18168	10	1254	
18062	48430	A	18169	1	618	
18063	48431	A	18170	1	460	MAAPMTPAARPEDYEALNAA LADVPELARLLEIDPYLKPYAV DFQRRMFWMFLPFFTLAFSPSV LVRFHADKDIPETGQFTKGRG LLDLQFQVAEDASQSWQKLYL LPNCSGQPHQKLVPTAQKFYIT VEWGTFFSVPGQVVGSEGSQM SVTVEGSESEDDKMYMTCCS ALLDSFALC**RHT*DWAYKR KRFIGLTVPMWLMRPNHGRS CISCLIALANHTKNWFPQRRSFI SQWNGVLFSQCLAKLWALKEV RCQ
18064	48432	A	18171	1	582	
18065	48433	A	18172	1	1578	
18066	48434	A	18173	1	1293	

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18067	48435	A	18174	344	1358	EAQSVTNHKNRSDCTFKEDNSL PVRKPSFLITNPGSNQGPFRFAGS PLGHEFTSLVALLWTGHIHPSK EAQSLLEQIRHIDGDFEFETYYS LSCHNCPDVVQALNLM SVLNP RIKHTAIDGGTFQNEITDRNVM GVPAVFVNGKEFGQGRMTLTEI VAKIDTGAEKRAAEESARKGIR TGLMGERFGGQILDVTDIENYIS VPKTEGQKLAGALKVHVDEYD VDVIDSTGRSS/AISGFHFTYDS NSPTARCAPT*QNCAPSPSEY APGEKAMRRITLVWRHCDY/PL CNAGNFVSMISRATSNITATMII *GVCTDNTRLCLYALNCSGDIL SRTSCD
18068	48436	A	18175	I	1561	
18069	48437	A	18176	884	1171	PRRLNNEHKLRLMSWLHCLVP HHAKWLQRWQWSAKVV*FA *IRAVNFVTAIRAIHQQSRKQ HRYLRSACHGRSIIITVITQSPK SSATKMPEN
18070	48438	A	18177	274	416	QADDDADNQSQDGTDAAFGLI Y/CESDDLC*LPLPALCPLCVM WYQTM
18071	48439	C	18178	24	509	
18072	48440	A	18179	1	1932	
18073	48441	A	18180	1	2583	
18074	48442	A	18181	1	495	
18075	48443	A	18182	36	798	KQRHSCFWSCWFSRAG*LGE LV*NPEIA*RP RPQQQT VSGNG AWSGKAPRRRHSWHY/YTISFQ KLPLVECTNAGPIF*VAKAGRK CSIKPPLTSRSYITD*PVSLRSQ LTGR/AGNFVTGW/QQLDEEIR YTMRTTVNAQTRDRKGVQPP TTWIFNDTKDQLERRIARLETG MAWAEPPSRTRHLISNCQIS DIPNVFAVRVNYLLYRAQKER DETFYVGTFRFDKVRRLDDTG ASWNGNRTGSAGIISIT
18076	48444	A	18183	114	724	ARTRVPHFPFHETAGGAAAH HLSLLGQDPGNQTLPGGRGGI PGGRGGGGGGGGGGDGRRR ALRRQQVPVLCVQRAGPAMDA AAPRHSSPDRERPKDQEVHLRL PGHASHSPHLGRHAGQAPGA GLWQAPGLRHHLHAGIQPPE/V TNTTLTALT*TRRCPAFSSGTVK PLFIWNLAAGPPLLRKGAA ICSCSIFQR

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18077	48445	A	18184	1	2130	
18078	48446	A	18185	2	433	EMTLDSRVAAAGDLFVAVVGH QADGRRYIPQAIAGQVAAIIAE AKDEATDGEIREMHGVPVYVLS QLNERLSALAGRIFYHEPSDNLR LVGVGTGTNGKTTTQLLAQWS QLL/GRNQRGNGHRW*RPAGES DPDRKYNRFGSRCSA
18079	48447	A	18186	114	586	SYITALGQFSRSGIQLDLRLGNF GTGWPNFDRKRFGSTMRRTVN GQTR/GPPQRRPAADNLD**H QRPAGAAANRPSGNGHGLGRRRA AVTHPSLNQQLPDKRNRHPKRI CCAGKLSALSGTKRSAMKHS LERVSTKFVWKMTTGACWN GISSWIKR
18080	48448	B	18187	1	3577	
18081	48449	A	18188	2	861	YHSINAASACSAHPVAFILTILT CRTCSSSLVATTSTMRLPNTLP DLIISPVESILSTSCAVPAFIRE PVTTSAPTIGVMANSVAVETAL PGLQEIPTRVQPSWRAVSSPAIT YGVRLAAMP/SHHILCR*INIF QIINTAFPAIFRAHFRVLNGIFSA SNQTNHQTRFHAVCGRTFGDV GWVAKSYQVAEERGSITEHQV QGHQSDDTEHFGGEIERQQQ HYHRQRGDPVGEIGEPELSISR RHHVCHTGYNPAEPVSPAGEIS NGTANGNKLNMSVCEIAP
18082	48450	A	18189	560	2021	
18083	48451	A	18190	525	804	GG*CRNWCDDHYANGCRDTS LYDKLAELGPQGLSPR*NNWQ TARRNQSSGRNSCHLRREVE*R RLDKALRRIRQFSAPDEGAKCP WPGIICDSNHFAFLRCQYGRFL EVTSAGDEKPYPLVDHVGVLV VEQLRCIITAKVTRHFHYVLK SIHPAVAGLPAALRDCGELFNSV YCRKPATGPQLQADVMVVVAY GLILRKQCWCRCVLAVSTFMFT AATLARCCNTPLTRAGDAET GVTIMQMDVEIPVVRTTSWQ SLAHKAYHHVETIGRRHGETR VQDET LVTYAEKLSKEERVLTG HFRQHSLNAALRFQSMANELA
18084	48452	A	18191	1	266	SQYPLVAGHEVIGRVVALGSA AQDKGLQVGRVGIQWTRASC G/QLRRLY*R*SDQLRARC GDY YESRWLCREVACGLAMGDST ARKY

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18085	48453	A	18192	5	385	
18086	48454	A	18193	330	598	VMRFIVVTGPAYGTQQA SFAQALADGHESSVFFYREG VYNANQLTSPASDEFDLVRA/S ATTECATWCGAEYLRSGSITPW RC
18087	48455	A	18194	1	2652	
18088	48456	A	18195	1171	2091	
18089	48457	A	18196	486	837	
18090	48458	A	18197	1	2943	MAIYKQSQMHTEVVRRCPHHE RCSDDSLAPQHLIRVEGNLR VEYLDNRNTRFRHSVVVPYEPPE VGSDCTTIHYNYMCNSSCMGG MNRRPILTIITLEDSSGNLLGRN SFEVRVCACPRDRRTEENLR KKGEPHIELPPGSTKRALPNNT SSSPQPKKPLDGEYFTLQIRGR ERFEMFRELNEALELKDAQAG KEPGGSAHSHSLKSKKGQSRL GTRFLCQPAVTVIPVKIVRVGT DTVIRPHAEAVRVQLRVGQA VTCRVCGIRDADIQIRCGGVNA GQPAGGAVAVTPGLARAADAD EFAVVVPGQPFHGGQAVRYTA VRQPLRVGRMSGLMLAKTCFR LQVMHRLTLTVFSQKVFTESIE VVEALKVNLMRVFLRRMDLRQ HRKMIMIDNYIAYTGSMNMVD PRYFLRDALPHCPNLTGPTFA VLEKLGYPHTFVSTDFNTVALD VKTFGIKANDDKAKLKALGEIA HACVDAITIIYCKSPTVAGLVAR ELIKLGHGTPTENPHVYWSPL TVLACILARYRGHCSNTLATNS MLENCAFCSAPPRSLKESTLSL NTVVIYDNRDGTSLDKFNRFCI HAFPKIIRNAIYEVEQHT* RACRYQ* DVGWFNIIYQPGISLAASKH CSTSSR* RWI* LDWI/CASASLL DEATAAAEAMAMAKRVSKLK NANRFFVASDVHPQTLDLMSY
18091	48459	A	18198	643	776	
18092	48460	A	18199	1	1257	
18093	48461	A	18200	3	346	
18094	48462	A	18201	1120	1335	
18095	48463	A	18202	312	1108	
18096	48464	A	18203	1	744	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
18097	48465	A	18204	381	1112	GVEPSPTNPPTTAIPRATCVA AARAASPSPS*SHQPHPPPLAYD RCST*PTPTTTAGQDHDHGR WRSAPAPRSDHLSMDLQE/RSM SLLPLILSSSTRSGSNPLRSTFLSR SRSISKNCSEA*SV*SNNSAGVGTI STS/RSTYDINRADTQVRRAVN NYDIIHMSNSFNGQSEHQVWIG QQF/ILHQICPLTQFQYGAEPDR KE*COAPASKWALLHK*HRPFP QDRKAGECLLHEYEDLYPSVIH
18098	48466	A	18205	2	307	HPARHKFVKGSSSEHRKSPVKPP PIPSH*PP*PENTNPMRPLAPTD VTNLRSLMTGRQRFTPYNNVS RSDPSTTARSSSADRVNASEYP TSSEETSGRSSR
18099	48467	B	18206	1	723	
18100	48468	C	18207	127	1410	
18101	48469	A	18208	1	1773	MGKKQSRKTGNSKNQASPPPP KERSSSPAMEQSWTDNDFDEL REEGFRSNYSSY*EIRIT*WQ TSLKALKRN*MM/ILLASPSR TPISGPNCDPAGPKFVKAAT GKARQRFHPATTTFHGRTPAPP LAHPAPTSTPASTQHPARRHQ VARPDRSSTPLPARIALRVFCPT PSTAPPEHPRQNPAPQTDSA LPGADDVRVSTTDPERRHPHPT NTTTPGGRVLRKELNRPRRPI HHRRRRRFHVQRAWQLPVPHRH HHLDHTSHTRRRRLMTDVRLD RPQPQRPPRITITTVGGDQRLRL DRSYQPESPCDGLRQLQMAG RAPCSPLSMLVLEKCDNLKTCH TSHGSVMAETA VINHKKRKNS PRIVQSNDLTEAAYLSRDQKR MLYLFDVQIRKSDGTLQEHDI CEIHVAKYAEIFGLTSAEASKDI RQALKSFAGKEVVYRPEEDA GDEKQNAKNEIIGTSSLPQTQFK TDHMSQKDPHKEETSPKVP HLVQESQKDLHKEATNLKVP HHPGKPGQPPQEGNKQRPP PPGRPQGP PPPGNGPQQLPPPA GKPGQPPPPQGGRPHRPPQGG

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18102	48470	A	18209	944	1577	RLCCLEISSTGYPKSSISSSKYPQ IPRAGAQCQSQAV*SGSNPLRSTF LSRSRSISKNCSAEV*SNNSAGV GTISTS/GSTYDINRADTQVRRRA VNNYDIIVMCNSFNGQSEHQV WIGGQF/LHQICPLTQFYGAE PDRKE*QAPASK WALLHK*H RPFQDRKAGECLLHEYEDLVP IRDTRLRFPGGRYLPRAKHVAP SEPDPTHHAYD
18103	48471	A	18210	3	634	DRVFDSSGSKWRSEQDWAAAK AVGQCSENGDWCCGNGRYP ARGPAVPA*PSLCLHHPR*RCT CCMPVYR
18104	48472	A	18211	3	255	
18105	48473	A	18212	101	547	TSVELMDLCPRLCRTFSGIPAY SMCIA*EWRNVCGVTGTENVT PSAAAAATASPIQVLTVLSVTS QIRAFSVLPVRRLRRSMLSRLIN TCRTEYPRCAVVCLLWKDAVS CLSTTFCARLCGQNTWLPRPCR HVNRAASDASVSLSTVT
18106	48474	B	18213	1	1113	
18107	48475	B	18214	220	1173	
18108	48476	A	18215	1	509	MPNHKAILIKFKKTEIIPITLLDH STIKIEINIKKIAQNHITWKLNN LLNLYFWPLTVSLCEMCKDFYS LGIEFSRFLQELQNKDCALEK/ HSHWAQMWP*YCPAKHWWWS CRREHVLVVN/DCSTS*NSYWH FSD*LRAMKRNRNEQCKR*AIRS LSRSLPARQDLKLLS
18109	48477	A	18216	3	281	
18110	48478	A	18217	878	1135	
18111	48479	C	18218	1	1602	
18112	48480	A	18219	33	608	VDSLRFQSPSCSVYSTDR*ISE T**NKL*PPKPVIACPKMWQV GQKFRQKAAATP*KAR*SPRPIP SH*QP*PKIQTRCGPQPQIRSP QKPHDRQTALSHRTTTFHGPTP APPLAHAPTVSTPASTQHPAR RHQVARPDRSSTPLPARIALRVF CPTPSTAPPEHPRQNPAPQTD SALPGAVRG

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18113	48481	A	18220	3	893	NPRKRTEQGKAQNKVQVWLT RTPVMVQKRPTIVSLKSSPDSPL ETYSMFLFLGMWVGVGVEM/C SVKLEEFQVNTYHYQRILLGISS DNAILLEEESEGRPMHISTIKE PSPDSPILYLTNLKLLTSLILFH YGESWNLLRADQRLIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEAVAAAA ADGVTFSPVPTPHTFRHSYAM HMLYAGIPLKVLQSLMGHKSIS STEVTYKVFALDVAAARHVQF AMPESDAVAMLKQLS
18114	48482	A	18221	1	327	LISLRQRQQRTPGKPGKGPRPIP SPWPP*PENTNPMRPPSPTRSGH QPRSLMTGRQRFTTAQQRFTV RPQHHRSLIQRRCQQRQVPI QRGDIRSLVQIGHQRCLRG
18115	48483	B	18222	1	1419	
18116	48484	A	18223	1	2784	
18117	48485	A	18224	936	1157	RTSTGLSGCIRCG/CASEGGQAV FV/WPRGPPETPCSRCPAAEGSP G*SPPREDPSSGSPGKRQTCTQT SARSPS
18118	48486	B	18225	67	1314	
18119	48487	A	18226	302	1423	CRWRFRFIMPFVMSMSAECL MNYNSTAMSGKTGLQNDTLI ARPWVKPYLGLIIMRIVGN*PH LTWCFCPTMYIPLFSQLCCPV FGQCGAFRNPGHPPSPNPEFFLG PRRCNPSLGHKALVQEAASDTP GKS/PGKSPGPPIKPIGP*PGK HKPDAAAPSHRSGSPNPEAS*PE DSAFTHNNVFTVRPQHHRSLI QRRPCQQRVPIQRGDIRSLRF GCFARHHPRHHRNIHDRTRTRP RRLTRHSRGLFEDDVRVSTDP ERRHPHTNTTTPGPGVRLRKE LNRPRRPIHLRRRRFHVQRAWQ LPVPHRHHHLDHTSHTRRLR MTDVRILDRPQQRPARITITAV GGDQRLRLDRITKPRARP
18120	48488	A	18227	1731	2392	
18121	48489	B	18228	1	1422	
18122	48490	B	18229	298	1464	
18123	48491	B	18230	1	1800	

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18124	48492	A	18231	745	1250	HTQNQRSGRSQND*RRRKNIS ERSAVYR*RQLYIRRPYAERP SLR*RQRP*IPCIRSQHGNKRKIP RRRIFI*QSVLRRRHLLP*RKPE ASAERHKTRC*VSERRPRYHRV KYDYH*KSIYSR*AHGAA*PSH RKDRESADLGSDGQNGQDLDC RGGCQPLLLTV
18125	48493	A	18232	1	1661	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLF DQIRKSDGTLQEHGDCIEIHA KYAEIFGLTSAEASKDIRQALKS YAAKEVVLYRPEEDAGDEEGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIERYQLPQSYQRM PDFRRRFLQCINAGHEMTKAI AQFNDDSPFAKITRRWRIGEA ADLVGVSSQAIRDAEKAGRLPH PDMEIRGRVEQVRGYTIEQINH MRDVFGLTRRAEDVFPPVIGV AAHKGGVYKTSVSVHLAQDLA LKGLRVLLVEGNDPQGTASMY HGWWPDLHIHAEDTLFPYLYGE KDDVTYAIKPTCWPGLDIIPSC ALHRIETELMGKFDEGKLPTDP HLMRLAIETVAHDYDVVIDS APNLGIGTINVCAADVLIPTP AELFDYTSALQFFDMLRDLKLN VDLKGFEPPDVIFIRDKLMERRNR RTGRTEKARIWEVTDRTVRTWI GEAVAAAAADGVTFSVPVTPH TFRHSYAMHMLYAGIPLKVLQ SLMG*YVHCALWMDCAHV** TKEIHSLLHRRHPLQGDKEPL PSPRNSSMPAVYPYWLQRSIRI FQHI
18126	48494	A	18233	162	446	
18127	48495	B	18234	144	2537	
18128	48496	C	18235	1	873	
18129	48497	A	18236	700	1198	PFFGTDFFPWARWCILRHKFW SKGKQRTTKKAPVKPGGSPA DHP*PGKHKPDAAAPSPHRS GHQPKTSMTGRQRFHTAQPFH GPTPAPPLAHPAPTSTPASTQ HPARRHQVARPDRSSTPLPAR IALRVFCPTSTAPPEHPRQNP NPAQTDSALPGAARG

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18130	48498	A	18237	363	940	LQTVLQGYNSNENSMFVKQKGS PPGKPGKKKPCFWGAPKNGAD IPSQSWRPSGNPGTTPLPKPPSF FPGAPRMGQSQAWGHKGFWF KKGKPTPEPGKKARVKKPPGG QSPKAIGPTRGPGKPPKPDMDRA PKPPTDSGHQTKQPS*PADSAFT PHINVSRSDDPRTTARSSSADRVN ASEYPTSSEETSGRSSR
18131	48499	A	18238	861	1517	SLRPHLSGFYQARTL*DQRS*A DHE/DISKNCSAEV*SNNSAGV GTISTS/RSTYDINRADTQVRRV VNNYDIIVMSNSFNGQSEHQV WIGGQF/ILHQICPLTQFYGAE PDRKE*CAQASKWALLHK*H RPFQDRKAGECLLIEYEDLVP IRDTLRLFPGGRYLPRAKHVAP SEPDPEDQDEQLRFCKRHLYGQ QPRSPVEIRLQHVAIAYQTHHA
18132	48500	B	18239	1014	2337	
18133	48501	A	18240	1495	1947	IVTLCFPSYCLHCEAGP/LPCGH PWLWLC*VLGSPG*TRQTGSW AMPGVQASKPACG*KVAPAAR RVPHPLHMLPHSGHSAASGGA SCPLCRG*ATGSDQVLKHAFRK GRSSNCASNGTPPNADFLGQD VHPARHKLROKQSAPEPRKKAR
18134	48502	B	18241	1	2055	
18135	48503	A	18242	1	909	
18136	48504	B	18243	184	395	
18137	48505	A	18244	447	667	HRPRRRFIKPPQSQVPEHAPLPL PTASDPP/AHSRCPSESRLSPGG QRLGFSSVLNCSKCSWQLAAC MGFSF
18138	48506	A	18245	265	890	
18139	48507	B	18246	1	551	
18140	48508	A	18247	407	636	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR */ERDYISIMPKPDGLTAANKLA EAFEHYNECIRI
18141	48509	A	18248	1	1448	
18142	48510	A	18249	817	930	
18143	48511	B	18250	303	461	
18144	48512	A	18251	612	3359	
18145	48513	A	18252	1	462	

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18146	48514	A	18253	268	749	RGGIEYLLLVFILTTRTRFIQAV EHRNRGRRVAEKIVPELITHFM AEIRDLLQRTGVAL/W*HQSA YLPG*QICALA**IHPGVAAGEY QRRSIQENGKGVQESGQTAS*M RG*MSVESRSGIAARCPESDAQ SGVVHRSRWQSLPARFGAGR DYREAS
18147	48515	A	18254	1793	2193	TQRIPAAQKQGSRCIVDSSAE LSAALAIGNIELVKPSRTMS/DK AAQEIIVNSGKAKRVVSLGPQ GALGVDSENCIVVPPVKSQS TVGAGDSMVGMATLKLAE SLEEMVRFGVAAGSAATLNQ TRLCSH
18148	48516	B	18255	1	1557	
18149	48517	A	18256	606	1123	QRDNPSGTDGGRNRAFGAGNI HTRGAAQAVRLVDSFPAQEK DPGESTGRDLSLPSRPQKVAY PVHRNDRR/ERLWFAAPSSPSN ATWGNAEWTLNFSSDSVTGA SSER*NLFLRLATVRCITLPSVS ADGAIVAALATHIGEAELET QCGAWRATFSSTCSLLPLNPN
18150	48518	A	18257	110	318	TALKLPLMSTKVTRCLSNLLK PKFNLPPLVQPPKMLPRHLSR *APNTKTSRLVKKK*PIPIPTRR KT
18151	48519	A	18258	2	3062	
18152	48520	A	18259	4435	4954	
18153	48521	A	18260	1	1959	
18154	48522	A	18261	2	715	
18155	48523	A	18262	1	756	MIRRVSVASGNEYMPRPASYIR TAPITVPSSSPAGTWFAAGNAP SSCGFRDRYLIVCSHQTPHVP KREEVNYETGIYWLRYHYGTD YSRNAKQRLQRNNLAPILFTTT VPLGGRQYNNSQLPQRQSLE RIRHHTQAFTALIPHGAAGQGC GSGDLHYLSLEDVAVSSKATPD GSGVTRKASANLRVTIQIGGFQ LRTCGFGPSCRCGHPALQISRAL AVAAHQQAADNNMEFANYGP FELLQARQLIES
18156	48524	A	18263	1	799	
18157	48525	A	18264	1	270	
18158	48526	A	18265	2	188	LGFFFRPLFGGQELSKL*EQVL LAPEEVGHLGEHLFRHASEWP APRVQLLLLVVRVQDLQE

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18159	48527	A	18266	2791	3274	SKIFPRHDDLLWRSHRNGDDL RTAGMNAFKQRLTLGLFKITIL TANDYLEADGQ/RSVRKKYPQ AQVSRVAGADLWEELMARAG KE/GTPVFLVGGEPEVLAQTEA KLVRSSATSIAWPLLPICAISS WIRSTAFCCCSWVSEGGKPADRS PAPSRTWLRC
18160	48528	A	18267	202	627	
18161	48529	A	18268	1	2390	
18162	48530	A	18269	1081	1911	
18163	48531	A	18270	86	272	
18164	48532	A	18271	674	2808	FILKLRTRR*RHRLRPWELFQ TARNAEVMKA/LVRHLWLEVK GVDLGRFPERRYGSDDKDLRNP MELTDVADLLKSVEFAVFAGP ANDPKGRVAALRVPGGASLTK KQIDEYGNFVKIYGAKGLAYIK VNERAKGLEGINSPVAKFLNAE IIEDILDRTAAGDGMIFFGADN KKIVADAMGALRLKVGKDLGL TDESKWAPLWVIDFPMFEDDG EGGLTAMHHPFTSPKDMTAAE LKAAPENAVATLGDPLESPDDG LHNRISTHGCFFVLCGISTNIGV ESTARNAWELGFNLVIAEDACS AASAEQHNNNSINHIYPRIARRG RDPQVRVMYIGLPQWSHPKWV RLGITSLEEYARHFNCEVGNNT LYALPKPEVVLRWREQTTDDF RFCFKPATISHQAALRHCDL VTEFLTRMSPLAPRIGQYWLQL PATFGPRELPALWHFLDSLPGE FNYGVEVRHPQFFAKGEEQTL NRGLHQRGVNRVILDSHPVHA ARPHRKLGGTAVWEWEPEGA HWVGDEPGWFSSGDLKAEY WAQKAADSGDADACALLAQIK ITNPVSLDYPQAKVLAEKAAQA GSKEGEVTLAHILVNTQAGKPD YPKAISLLENASEDLENDASVD AQMLLGLIYANGVGIKADDDK ATWYFKRSSAISRTGYSEYWA GMMFLNGEEGFIEKNKQKALH
18165	48533	A	18272	532	2103	
18166	48534	B	18273	1	4401	
18167	48535	A	18274	343	765	
18168	48536	A	18275	447	709	

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18169	48537	A	18276	1	1571	MIEVKIILKTLQALRNCGSLAA AAATLHQQTQSALSHQFSDLEQR LGFRLLFVRKSQPLRFTTPQGEILL QLANQVLQJISQALQACNEPQQ TRLRIAIECHSCIQWLTPALENF HKNNWPQYSVIFKSGVTFDPHFF FQQGELDPERAFDDFGIKPMAS ASIAQVHSARFNSNGHEVVIK IRAETLPVIKADLKLIYRLARW DAAFAAGWSPPAANLSCAGST KIHRLMNRTCCRNLPPTFSFGA KPGLYLVEAMVGGYRATTVVV VSDTVALS KVS GIELLVWGAG KKQGEANAGSEILWTDGLGVVM TRGVTDSDGTLQLQHISPERSYI LGTLAMVQLREDMAKRQAAGI IAPRSGRRMHRTHQKPPMTTE MGPRAVLREDTIPFLEALKASG KQRILLTNAHPHNLAVKLEHTG LDAHLDLLSTHTFGYPKEDQR LWHAVA EATGLKAERTLFIDDS EGDAMKEKPAVEVRLDKWLW AAR/SL*NPRAG*ND*RR*GAL QRAAHEAEQNRRAECHASAP
18170	48538	A	18277	2080	2274	RFQVVYFDHEKPSLRHE*FALE EYTGTRN*GCVNLLDR*KPPF KFMERWLAFSPGTLLESSRG
18171	48539	B	18278	1	3126	
18172	48540	A	18279	1	341	MLDRLESEILADRVSEESRRWL ASGGLTVEQMOMQMDPVYTPA RKIHLHYCHDRGLPLALISKEG TTEWCAEYD/GMGQPAE*REPA SAAAAYPAGAAV**GVRPVL QPPPLL
18173	48541	A	18280	945	1484	
18174	48542	A	18281	965	1403	
18175	48543	A	18282	703	1149	
18176	48544	A	18283	161	476	LLPWRSCILRSDPLAAHPVI/LV P*ACIFIARNCYPRPSCDSACKL RRESCG*FG*TRMVSAQATFSIQ ITSA/LPFCHELPKGRSGDFDTG EDNALSGQRPEFRHG
18177	48545	A	18284	1	443	MLSEPALRELATAIAGVRKGEN DIAVENIIGANIFNIVVLGLPALI TPGEIDPLAYSRDYSVMMLQAG KEVLAIERECLAELDQYINQNF TLACEKMFWCCKGVVVMGMGM KS/RAILGEKWPRNVQHRJAN HENRDSIRKICCYHR
18178	48546	A	18285	3	550	

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18179	48547	A	18286	2157	2504	LVSLAGAAAYRSPQDPVPYMPIS PGLDWVRQIVCCVMASDAD** RVPRQNALLPVCTSGPYHALA TGCGRFRGQMLKTTVLPRHYK LYLGASSGMRYSTPATALMPLP LPHLAER
18180	48548	A	18287	1	621	
18181	48549	A	18288	1	423	
18182	48550	B	18289	1	1551	
18183	48551	A	18290	1171	2757	
18184	48552	A	18291	347	690	
18185	48553	B	18292	1	528	
18186	48554	A	18293	1	1417	
18187	48555	A	18294	292	699	
18188	48556	A	18295	859	1377	
18189	48557	A	18296	1	3036	
18190	48558	A	18297	1	942	
18191	48559	A	18298	1	2124	
18192	48560	A	18299	1955	2797	GGISIDRSGDH*GRGA VYHVAG R*NAGRTAELYFASRPTCG/RW LVAAVQGAATARISTIEMSVW AQL*QMCGRKIRAT/ISLPEATA QVISSGSGATKVEDGLGLDNKP VSNQNLVTGIDTPVYNAPSAGS APFGVLADNMRYPIHLKDKDR LNQTWYQIRIGDRLAYISALDA QPDNGLSVLTYHHILRDEENTR FRHTSTTTSVRAFNNQMAWL DRGYATLSMVQLEGYVKNKIN LPARAVVITFDDGLKSVSRVAY PVLKQYGMKATAFIVTTRIKRV
18193	48561	A	18300	1	1191	
18194	48562	A	18301	1	298	MPVVFTVFFLWFPGLVLYIV SNLPRYAEYLTVKDADGSVLD QGIALWFP/GPNSFTGEDVLELQ GHGGPVILDLLIRILTVCLRI ARPACSPRSL
18195	48563	A	18302	1	1011	
18196	48564	A	18303	1	1845	
18197	48565	A	18304	1	755	MSPVIDKMYVDAYQPFSEEEKIS MQEAELEKGAQPLREFMLRQTR EADLGLFARLANTGPLQGPEAV PMRILLPAYVTSELKTAFIGFT IFIFLIIDLVIASVLMALGMMM VPPATIALPFKMLFVLVDGWQ LLVALVTGLIISILQAATQINEM TISFIPKIAVFIAIIIGPWMLNL LLDYVRTLTFLNPPYIGRTMLQ VTSEQ/CAILVKPVLLAVTARA GADLHRADSSERTQRTKTGGGF CRYWAG

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18198	48566	A	18305	1	1977	
18199	48567	A	18306	1	630	
18200	48568	A	18307	1715	1996	LFRLLKLTGRRKRSNKS WITTCRGFWGTWCAGWSRP*VVQK CRIYTMWR*WQHAQR*VSPAT LNLGMLITISRKNPHTRK.GAGK HCPFSGPS
18201	48569	A	18308	517	675	
18202	48570	A	18309	480	626	
18203	48571	A	18310	757	1146	
18204	48572	A	18311	318	724	
18205	48573	A	18312	1	1743	
18206	48574	A	18313	1	1197	
18207	48575	A	18314	161	613	LLRQGFIVISAGGKRV EGQIKLVFPAKFEAGFRHGVIANLRLYPF PEEKIGEMATAPLSTSGDCRT* YALIGIQ/PTDGDARGSPRYKPA LALLPACVGS AKSTPHGRTPIPA IYVPSPT*FRALASDSVAQT*Y CRPASQTRRASPARSL
18208	48576	A	18315	177	425	SRYFSATSTWPLVMSIPVTC PFS PASWLST*QSLPLPLPRSKI QQFCRCSGITRPQP*YDPKSSS FVD AQGSPDHSNHLGLLLRVH FAR LPECAWGPALW
18209	48577	A	18316	1	576	ADSSKKIADIHSVIDGIAFQ TNILALNAAVEAARAGEQGRG FAVVAGEVRNLASRAQA AKEIKALIEDSVSRVDTGS VLVESAGETMNNIVNAVTR VTDIMGEIASASDEQSRGID QVALAVSEMDRVTQ QNASLVQESAAAAA ALEEQASRLTQAVPRSVWQ PAHSPINRK HHPVLPIATGALMPGCGS
18210	48578	A	18317	121	1819	
18211	48579	A	18318	1	2151	

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18212	48580	A	18319	3	1127	GTPYASQPVIRPVEGSKPLIKQV LDIGAHTDKTIAQKLARVAR MHFARQLAAVATFACSAQNA IALMEEIAANFSYEMIRLTECIL GFTWNRLYQGINVHNAERVRQ LAHDGHEL VYVPCRSHMDYL LLSYVL YHQGLVPPHIAAGINL NFWPAGPIFRRLGAFFIRRTFKG NKLYSTVFREYLGELFSRGYSV EYFVEGGRSR/GRLLDPKTGM LRGGTRPTLPIYIGYEHVMEV GTYAKELRGATKEKESLPQML RGLSKLRNLGGQYVNFGEPM LMTYLNQHVDPWRESIDPIEA V RPAWLTPTVNNIAADLMVRIN NAGAAANAMNLCTALLASRQR SLTREQLTEQLNCYLDLMRNVP
18213	48581	A	18320	1	2470	MFQPSDSGKSFIFNMSVGYNLE GIKQPPMQQFIDNMMDASDHP KFAQYRDTLNKLLQDDAFLAR HGLQEKRESLQALPARIPSTMV HGVTLSTMHGCPPEIEAICRY MLEEKGLNTFVKLNPTLLGYA RVREILDVCGFGYIGLKESFD HDLKLTQALEMLERLMALAKE KSLGFGVKLTNTLGTINNKAL PGDSTSGVLRTYERLLTAWML TCPCADEHQGESVKLATALT WWLRGSQNRDEITKDGFSNH AGGILGGISSGQQAIAHMAKPT SSIDVPGRTRNRFGEVEMITKG RHDPCVGIRAVPIAEAMLAIVL MDHLLRQRAQNAVKTIDIPRC AQSIGSFSGCIVGADTLPIQSE HYQVMRTDQRRYFGHPDLVM FIQRLSSQVSNLGMGTVLIGDM GMPAGGRFNGGHASHQTGLDV DIFLQPKTRWTSQAQLRPQAL DLVSRDGGKHVSTLWKPEIFSL IKLAAQDKDVTIRFVNPAIKQQ LCLDAGTIATGCAKCDPGVSGI AYAYLLTLRAQCLAHDLDPDPLE PLEIDGTLTPRYVFIHGGPRVFT YYTPKEESIKLFHDYLDLHRSN PNLDVQMVPVSVMFGRAPGRE KGEVNPPLRMLNGVQKFFAVL WLGRDSVRFVSPSVSLRRMADE HGTDKTIAQKLARVARMHFA RQRLAAVGPRLPARQDLFNKL
18214	48582	B	18321	1	1460	
18215	48583	A	18322	2	234	

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18216	48584	A	18323	282	422	
18217	48585	A	18324	1	1974	
18218	48586	A	18325	154	1944	
18219	48587	A	18326	18	386	KACEAVF*DQGLPLGPKVQGGQ WDWFFPGPALRHQQSVAHQA GGFRSLWGYSGVSGQCRHSD *SRPGREARRRRSVAG**SHAL HRQTALFGARSDADLPAAAPR YLLYRGLSAAHFRPQAG
18220	48588	A	18327	181	655	KARSPEDQGFRRPVHIDGGVW HLDVGSHPGAIEVGPKGMAVR HLKWAYASWV*NVVRQFGPYLP WALEN/WRGAAPSTRGHGVC/G ITVFGKSDGTT/SHDQY*TAPYG SPHPPGRWSLRHRYPAHLTSSA LAFSDARRNAARQPRRWNP GYSQVICLPW
18221	48589	A	18328	1	658	MDDGTSIAPDGDWAFIGDELK MGIPENDRIREQKQYLNRKSY LHDVTLRAEPYMYWIAGQVKK RNMPEMLVLLPIVESAFDPHAT SGANAAGIWQIIPSTGRNYGLK QTRNYDARRDVVASTTAALNM MQRLNKMFDGDWLLTVAAYN SGEGRVMKAIKTNKARGKSTD FWSLPLPQETKQYVPMKMLALS DILKNSKRYGVRLPTTDESRL ARVHLISPVKCARFSRFVFCPA VCRDSSGADERRTDSGDCQYA GGVKPESVMGAIEVEGFSHISV TSAWSRGDNPAPMAFSRLWL TVFSMVFKRRETVRSLSAVGA GELRGAAPSTRGPEWTHHWS GCHANGTARSADVPPDMPNPS EVKRRSADGSGVSP*RLITAAK VGS*RQLKRTKRVGNPRTSGRY RCRRKRSTCLCKWH*VIFSKT ASVMAYVCQRPMAKVLWRVC
18222	48590	A	18329	642	1343	LCLHLPLPTRFRLQL*EEGGPV QPAAMPQWRTLPGGPRPALPL PRRLRGSSRLRAPGRLRGPRLR* RRHVCGGRRRAPLLRAGLRRLP RLPRAGPVRRAPLCSRRPLLR PLLRPLRLRSRLHGSV*VPSA PRRRKRLARGPAGPQARGPSAL PFASGSGTARGRGRRRCALA GPRAPPWPLPGCWVSLAGWDP GAVSPRTPGCTQQPKDAGGFR GWSEAGVHDAQTV
18223	48591	A	18330	1	810	

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18224	48592	A	18331	236	717	ALPVGAAFSSTTGFSGFGAGG ASTFGLGGSTGFGGGATGAGS GSNSVLLAAIVAGSSDGAAASP ARTSSAAPSGGCD/QERRIVDFK RNKDGIPA VVERLEYDPNRSAN IALVLYKDGERRYILAPKGLKA GDQIQSGVDAAIKPGNTRLISYG QHREAWR
18225	48593	A	18332	49	291	
18226	48594	A	18333	75	839	
18227	48595	A	18334	1	579	
18228	48596	A	18335	223	563	
18229	48597	A	18336	1	1219	
18230	48598	A	18337	157	864	RGNRQLQQFPRHWRNRLDGL LLQIQQLILGGHTVERHLVVQI ALVNVNGHPGHADGMWILCIRV LLSLQONGFRVRVPSIGHWTGH* AATDQARLMLGGHINAQFAGI QRLEDLGTQLLHTTNGLVEVE ARRQILQLGLPLFLNLQTDVW AIPGVHVLRFVDVVGDRPS/EVLI DPRQNAAGLLWKVFATFRPEPTR PAVCCPRGGQSGDDRRAGCAC NHVELVARHRRSCPWHSDRH
18231	48599	A	18338	1	219	
18232	48600	A	18339	1	2226	
18233	48601	A	18340	46	228	
18234	48602	A	18341	382	1431	
18235	48603	B	18342	1	2400	
18236	48604	B	18343	1	912	
18237	48605	A	18344	2267	2539	
18238	48606	B	18345	1797	3411	
18239	48607	A	18346	1842	2560	
18240	48608	A	18347	1	1284	
18241	48609	A	18348	1	792	
18242	48610	A	18349	1	978	
18243	48611	A	18350	757	1011	LFGFRSNGFLIIVCQRLRQAVV NEQFLPETATLTHRGELLFHSP A*LPGVFRLAQM*RHAVIQVF RATGVPEPERCQRPPHER
18244	48612	A	18351	148	679	RMSDDKFDAIVVGAGVAGSVA ALVMARAGLDVLVIERGDSAG CKNMTGGRLYAHTLEAIIPGFA VSAPVERKV TREKISFLTEESAV TLDFHREQPDVPQHASVTVLRN RLDPWLMQAEQAGAQFIPGV RVDALVREGNKVTGVQAGDDI LEANVVILADGVNSMLGRSLG MVPAS
18245	48613	A	18352	1168	2241	
18246	48614	A	18353	1	1344	

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18247	48615	A	18354	440	886	
18248	48616	A	18355	1	2876	MAGVPGFEPGNAGIKNRCLTA WRYPIRITTLSEGWCGRRDLNSQ EATLQQPLLQAIDLKKHYPVKK GMFAPERLVKALDGVSFNLER GKTLAVVSGESGCVLACTLFA WNRNYFVLLFVGVLSSFGSTA NPQMFALEHADKTGREAV MFSSFLRAQVSLAWVIGPPLAY ALAMGFSFTVMYLSAAVAFIV CGVMVWVFLPSMRKELPLATG TIEAPRRNRDITLLFVICTLM WGSNSLYIINMPLFIINELH
18249	48617	A	18356	606	726	
18250	48618	A	18357	1271	1726	
18251	48619	B	18358	1	1633	
18252	48620	A	18359	1	407	
18253	48621	A	18360	427	2307	
18254	48622	A	18361	120	694	
18255	48623	A	18362	804	1087	KRQHLCTHSGAIRLRJAGVGSW KG/GRPNWRKMAVRWRVPASA VVSGLVRRWHCWVPVAMPSPAE SPRIRCGAGCCICRLPLFRGCC TPARLTISH
18256	48624	A	18363	216	436	
18257	48625	A	18364	476	577	FRRWYWGCCSTTRLSHCLTR* M*CMRWSLAVCC
18258	48626	A	18365	1159	3744	
18259	48627	B	18366	169	743	
18260	48628	A	18367	2811	3513	SLPRGWFOPEYGNLEIMEKTYN PQDIEQPLYEHLGPPRVGLRRE LKKAQESYWAGNSTREELLAV GRELRARHWDQKQAGIDLLP VGDFAWYDHLVLTSTLLGNVP ARHQNKGSDVIDTLFRIGRGR APTGEPA AAAEMTKWFNTNYH YMVPEFVKGGQFKLTWTQLLD EVDEALALGHKVKPVLAGPGT WLWLKGKVKSEQFYRLSLNDI LAGYQQGLAETGVGPDIVTA

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18261	48629	A	18368	1	2810	MKQTVYIASPESQQIHVWNLN HEGALTLTQVVDVPGQVQPMV VSPDKRYLYVGVPEFRVLA RIAPDDGALTFAAESALPGSPT HISTDHQQGFVFGVSYNAGNV VTRLEDGLPVGVVHVVDGLDR LARQLIKNLATLKAGNARVVN SNAMSFLAQKGTPHNIVFVDP FRGLLEETINLEDNGWLAD ALIYVESEVENGLPTVPANWS LHREKVAFAAGAPYHYLNHTL GFPRVGLRRELKKAQDSY
18262	48630	A	18369	2279	2563	MNFGASLNSPTPRSYLSLGG EKAPVWEHTLGVPSRRPAAG KKAPERYWGGEHPVKKWLG G*ARKCRPRPWETL*KSHLR RRPSLGPWAGGL
18263	48631	A	18370	481	1020	
18264	48632	A	18371	1	998	MNENFGTQICVNNRSLFTDC SGYVTRYDHRFGQVTAHVRE EGLSQYRAYDSRGQIAVKDT QHETRYEYNAAGDLTTVIAP DGSRNGTQYDAWGKAICTQGG LTRSMEDAGAGRVIRLTSENG SHTTFRYDVLDRLIQETGFG DRTQRYHHDLTGKLIRSEDE GLVTHWHYDEADRLTHRTV NGETAERWQYDERGWLTDI SHISERHRTVHYGYDSKGR LASEHLTVHHPQTNELLWQ HETRLAYKRTGLANRCIPD TCPPVNAYLGTACQHEICD TPWLSYRDPFTGKSWLSGR YELHKRIYGITAKERKD VDVWHPDVRFELYDENNEL RGSFYLDLYARENKRGGAW MDDCVGQMRKADGSLQK PVAYLTCNFNRPVNGKPA LFTHDEVITLFHEFGHGL HHMLTRIETAGVSGISGVP WDVELPSQFMENWCWEPE ALAFISGHYETGEPLPKEL LDKMLAAKNYQAALFILRQ LEFGFLDFRLHAEFRPDQ GAKILETLAEIKKLVA VVPSPSWGRFPFAFSHIF AGGYAAGYYSYLWADVLA ADAFSRFEEEGIFNRETGQ SFLDNISLRGGSEPMDFK FRFRGEPQL*HTVVELPR PFHREILAFRPL*I TQAYLRHHR*RA*RC*CLASGC

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18265	48633	A	18372	409	533	TGNDAPVPAQSAQYRYLQ*SV RNFRLSFRGLNLSLPHYVDD VIPLMAEGKILPYLDPLQHAS RILKLMKRP
18266	48634	A	18373	222	659	SAGSVKTRQSGANKQRRTRSR ASFC/ETLSSVFPARWKISFLIP VGLPISNNYVCSLNPVWCAMR LNMPPMSKSCWQKHWSKTVS RWITTRHSFVQTLISTACWRRSP VTQSSWRSFACSTGLLSHAPP LPIRCHTNITNVWY
18267	48635	B	18374	1	1527	
18268	48636	A	18375	1	1005	
18269	48637	A	18376	2	314	WVSYCSGSTLL/LRLAQECQR QQGPWASAGDPGEGAGERERL PQALASPLQVKPARQ/RDPGL RTDPDGDASPALNGHIFALPA GTAGDCFP RPGRKNSGT
18270	48638	A	18377	3	576	
18271	48639	A	18378	189	563	QGRGSSRPGCGHLDPGGEWL PQRPLQLCLCPAYILIFAGVL VMVTGLGFGAILWERKGLS TTTGDRFWKDRQFWTCR/WQT SHRNQSGAGGQWDRFRSHQGH RDHEGRTSNWGS GFPREVA
18272	48640	A	18379	1	531	
18273	48641	A	18380	1385	1673	AASDRAAETG**KTR/HRWFL SVKLRTSTPTAVSPKK*KRLAW TRCMTPPSKR*KKRVI TPSSPT SLTSTLPGATVATSPVMRVWN CSTAVCRS
18274	48642	A	18381	1	921	
18275	48643	A	18382	1	2115	
18276	48644	A	18383	2	149	ARRNESRRGR*HPCRPIT*GT VNQRPA GFRFAGPF RYSGKPG RERL
18277	48645	A	18384	482	1655	
18278	48646	A	18385	1	776	MENACVLLMGVLSTFLVSWLG KDAMAGVGLADNFNMVIMAF FAAIDL GTTVPGAFSLCKRDRR QARVATRQSLVIMTFLPVLLAP LIHHFGEQIDFVAGDATTEVKA LALTYLELTVLSYPAAAITLIGS GALRGAGNTKIPLLINGQVAML MQAPYYFQEAQIEAAIAAMDV APEYADIRQVESSTAVLYLFSE RFMTY GKA YGLCEWFEGSRLSI AHIPVTDNDNETQYHFRQSCQ HC/DRCSVHRLPDGGVVA

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18279	48647	A	18386	1017	9228	FGRGAGVQC*RGDRGQRRDEA GDGRLRLARL*ALYQTITHDLR YRHKNLVYRRKLASQRVTEHVN RAGLRYSYQYKEDCITITDSLA HNKVLHTQGEAGLKRUVKKK HADGSVTQSQFDAVGRRLAQ DAAGRTTEYSPDVVTGLITRIT PDGRASAFYNNHNNQLTSATG PDGLELRREYDELGRLIQETAP DGDITRYRYDNPNSDLPCATED ATGSRKTMWTSRYGQLLSFTD CSGYVTRYDHDREFGQMTAV
18280	48648	B	18387	1	1431	
18281	48649	A	18388	575	835	RQKPERYLTAFTITLPLRWMT LVRVMRPVTCRRSRILLSIS HLCKWRVSTKSPVILWTILSN* RLFWKSWR*NLQSKYQDG
18282	48650	A	18389	1207	2465	ASTAQHQHLLSPAKEETTGWRI FHSPDPWALGRSQGGAGLIQPP EVQKGSVRYRARFALLGPAMV AHRHTGRPEIRYRYDSDGRVTE QLNPAGLSYTYQYKEDRIITD SLDRREVLHTQGEAGLKRUVK KEHADGSVTQSQFDAVGRRLA QTDAAAGRTTEYSPDVVTGLITR ITTPDGRASAFYNNHNNQLTS TGPDGLELRREYDELGRLIQET APDGDITRYRYDNPNSDLPCA TEDATGSRKTMWTSRYGQLLS FTDCSGYVTRYDHDREFGQMTA VHREGLSQYRAYDSRQGLIGV KDTQGHETREYNIAGDLGGI APEGG/RNG/TQYDAWGRRRTT /QGGDADDRSAGGTRARKGHT SFRSVDGRTVSRHGYPGRNLR RMVRSSVPLYRLTASIAVPVQE YRFPHPQSEEVY
18283	48651	B	18390	1	2604	
18284	48652	A	18391	1	2640	
18285	48653	A	18392	1	549	
18286	48654	A	18393	290	389	HLGCPRTAR*ARFWHL*RAYG L*SGECRRAGSV
18287	48655	A	18394	1095	1268	HLGCPRTAR*ARFWHL*RAYG L*SGECRRAGSVAENARSACRC RRSAHAGRLFQTAS
18288	48656	A	18395	1056	2178	
18289	48657	A	18396	1	669	
18290	48658	A	18397	1628	1856	
18291	48659	A	18398	227	668	
18292	48660	A	18399	1	3186	
18293	48661	A	18400	291	631	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
18294	48662	A	18401	1	1437	
18295	48663	A	18402	345	727	
18296	48664	A	18403	870	1043	
18297	48665	A	18404	1	2175	
18298	48666	A	18405	1	1332	
18299	48667	A	18406	1	1566	
18300	48668	B	18407	1	921	
18301	48669	B	18408	1	2487	
18302	48670	B	18409	1	2919	
18303	48671	B	18410	1	2214	
18304	48672	A	18411	1714	1979	RLAWRLAGRWAGSWRTSTIP PAAACSRRLRCSPPSKFCSAWCR WCSTRACSSCCRSSTSSPMPAWR PSAGS*LTARRRAPPSALVLR
18305	48673	A	18412	1201	2118	PSRQADKENRHPGRGVYPARM MSGLTGTHITVTGWCTTRGHN MKSRWSKVAIFTRWGRVAK RVWRRERDLTGWMSLSRKPVQV TWYGDGDLRTTIQNDRTRIQ TIYQPGSFTPLIRIPVLGGDDTT MDCLRTSIRLNAASVTCAVRRD QISMPGSRKEVVNAREEGVEFQ FNFQPYIACDEDGRLTAVGLI RTAMGEPGPDGRRRPPPVAGSE FELPADVLIMAFGFQAHAMPW LQSGIKLKDWGLIQTGDVGY LPTQTHLKKVFAGGDAVHGAD LVVTAMAGRQAARDMLTLF DTK*PGTAGTATG*PQYRTTEP ASRRFISRGASRHSSEGS/SVLG GGDTT/MGLFADHPPQCRQRD UPYRRDQISMPGSRKEVVNAR EEGVEFQFNFQPYIACDEDGR LTAVGLIRTAMGEPGPDGRRRP PPVAGSEFELPADVLIMAFGFQ AHAMPWLQSGIKLKDVGWLIQ TGDVGYLPTQTHLKKVFAGGD AVHGADLVVTAMAGRQAAR DMLTLFDTKAS
18306	48674	B	18413	1615	1656	
18307	48675	A	18414	1287	5056	
18308	48676	A	18415	1	271	
18309	48677	A	18416	1	588	
18310	48678	A	18417	2150	2332	
18311	48679	A	18418	1	238	LEELGVIGAVLVGFSL*VLWAP LQLPKAGGRVKVAGIQLGEVEF WKVS/KSCSSPDPPPGVMAAKIS ISQALQPPQSTR
18312	48680	B	18419	1	2721	

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18313	48681	A	18420	712	1031	PVMRQRGVFRSLIKRSARCC QMIQPRVISHAMYSLSPPFALR RSTKSPKRFSMNNS*ASRSSGST SRDTS AIS*ARRSISRRLIRS LISLISLLVNVV
18314	48682	A	18421	1	1779	
18315	48683	A	18422	693	921	
18316	48684	A	18423	758	1183	ALTAASRSECAVIMMTGRTSCC DIVEKWIPARCCQMIQPRVISH AMYSLSPPFALRRSTKSPKRFS MNNS*ASRSSGSTSRDTS AIS*A RRSISRRLIGWRSWLYTILI NSIPTNRAKSMKPEPSPNACSK VKRCC
18317	48685	B	18424	1	708	
18318	48686	A	18425	1	2436	
18319	48687	A	18426	1382	1813	
18320	48688	A	18427	900	1028	AGYAAPGRTRDRSSPSG*GYRY SGCYQICRQPGRLGSRKSPV
18321	48689	A	18428	1	881	MTPSRFAKKNGLVKRCMPGI DAEVTMIKPIAARPKVSHSKVR SYMIRLSVSFSREPIQPFSAVEI QTRIRYGVSGFFLRVDTEHHP DRHAARALQYHITGSNRCDAIN AVQFDTAGGECTNRRMAEDHG RNVAVIQMLRLVIKQAFREVP SELWTRNRKQACPFDFDCGENS AIAANNYDWFNGMNVLTFLRD IGKHFSVNQMINKEAVKQLRN REDQGISFTEFSYNLLQGYDFA CLNKQYGVVLQIGGSDQWGN TSGIDL/NPSSASESGVWPDRSA DH*SRWHQIW
18322	48690	A	18429	1	3270	
18323	48691	A	18430	1	374	MKTCWQILEIESTTQIDIRQAY LARLPLCHPETDPQGFALRQA YEEALRLAVNPVEEADDEEKD AAAEHEILRAFRT/FTGFRK*SFS AFRLAEIYSAIKYLEHGGRCSIT LAAVCNHRHSAI

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18324	48692	A	18431	63	1272	LRSCNAVVCW*CVATCPSGE EDGIVLIDQDKCRGWRMCITGC PYKKIYFNWKSSEKCFICYP RIEAGQPTVCSETCVGRIRYLG VLLYDADAIERAASTENEKDL YQRQLDVFLDPNDPKVIEQAIKD GIPLSVIEAAQQSPVYKMA WKLALPLHPEYRTLPMVWYVP PLSPIQSAADAGELGSGNGLPDV ESLRIPVQYLANLLTAGDTKPV LRALKRMLAMRHYQRAETVD GKVDTRALEEVGLTEAAQEM YRYLAIANEYDRFVVPSSHREL AREAFPEKNGCGFTFGDGCHGS DTKFNLFNSRRIDAIDHQEMF EATAASKNLPKEDAHALGIFLR DLTTMDPLDAQYQSELFDGRG RATSLLLFEHVHGESRDRGQA MVDLLAQYEQHGLQ
18325	48693	A	18432	2	859	WPLRRSPYSIINGSGKSAASGSV MQVAQFNSHYQYDPKFERGM YLYEHRRCFNNIIDYCNLCYH AWLVAHKDDIERNYRGPLVQV VGWCDALFGAEELGISRAQFDQ FLRMMQGGAGQGGGYQQQTG GGGRPGGHFFEKRRLLRMVDR LNARFTGGVLVSFKGPLLEGFG PWQGLSPWVIGDLGLPG/CLG AWGAVSVCHCPWVCKTGSFR WVPHRRFHPPPG*KFPENWMG FCSSRTCSGLFSPHSPPTMAFKN FELGHGTPPRGTRNRPTMSSNT YRPHRFQ
18326	48694	A	18433	479	601	CWRPLPAEKRWYLAANWW RLAARFVFPMLCVRQ*PSSMIW TTPDADIAIGTWRSCCAVLGR KMPVSSITMRRRCY*CWRPLPA EKRWYLAANWWRLAARFVF PMLCVRQAAPYTK
18327	48695	A	18434	69	194	ATYENMLANPRN*KHDANRHY PPGLSCSLTVVSSRNSARV
18328	48696	A	18435	173	298	ATYENMLANPRN*KHDANRHY PPGLSCSLTVVSSRNSARV
18329	48697	A	18436	1	1734	

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18330	48698	A	18437	851	2202	RQKRLIFCCVKGKNWPP*WRWLNEKLPCSLMLLPTLPPSVLGIRLQNQLQRQFVRQGGVWMPGD EVKKVTCKNGVVNEIWRNHA DIPLRPRFAVLASGSFFSGGLVA ERNGIREPILGLDVLQTATRGE WYKGDFFAPQWPQGFVTTDE TYARHRQGKPLKTCLPSVRCW ADLIPSPRDAVFPVSVLYMP LNRLPNAQEANNE
18331	48699	B	18438	1	5301	
18332	48700	A	18439	710	889	
18333	48701	A	18440	1622	2615	
18334	48702	A	18441	1	1309	
18335	48703	A	18442	1	266	PRQCGFMKKRLENGDDYFAVN PRGRCLHCCWMTVLC*RRKRS YAVSCRQRPRPVLAPVNSISRS VSPYTPPEYKPTVRAQLEKNCN M
18336	48704	A	18443	267	395	
18337	48705	A	18444	1	3807	
18338	48706	A	18445	1	2193	
18339	48707	A	18446	1278	1846	SCRSA PRNRHQIPGTYRSRLPRH TTPPGYDHNKNPNLYISTRQK RDAFFAVQYHSLYYRQTLLPN DHNQSVDR*FVFR*NQNGYNS GRHLYWRYHSYNWL*LCH HPVYYRLYYIFLQPVQMMPQ CPSPLMPECSFSFSLILINA/SNI QRESPVENRKVFNLRLKIIYYR LIJLCKGNLLNL
18340	48708	A	18447	1	2106	
18341	48709	A	18448	881	1401	
18342	48710	A	18449	1	233	MMGFDGTVQYMASLGAPMPM LAA/MYCGSYGSARRDINRAW LFHPSAGGAVYFLHAGYGGDW SPLLGYDRRCGWAKYD
18343	48711	A	18450	1	1960	
18344	48712	A	18451	563	928	FSAIKSSPKAALWHVLYH*AV N*TNIFKTEKPIFNRGRFRPTP TRQLRECWIWVGSASCOLTKQ AVVARWTIILMRRRKGWHG RAIILMPGGPRLKQVPRQFCKPPA AAARLSKSMGR
18345	48713	A	18452	1	828	

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18346	48714	A	18453	1	1327	MMQKPATVDEEESPRETHRYS VRRRGELIVEAGGRAENTVVT GAGWLK VATGGIAKCTQYGN NGTLSVSDGAIATDIVQSEGGAI SLSTLATVNGRHPEGEFSVDKG YACGLLENGGNLRVLEGHRA EKIILDQEGGLLVNGTTSAVVV DEGGELLVYPGGEASNCIEINQG GVFMLAGKASDTLLAGGTMN NLGGEDSDTIVENGSIYRLGTD GLQLYSSGKTQNLNVNVGGRRA EVHAGEVTGDHVEITDASRQT LCNALKLQPDGEGSSRVPTCK ASRLRIDANFKRFVDEEVLPGT GLDAAAFWRNFDEIVHDLAPE NRQLLAERDRIQAALDEWHRS NPGPVKDKAAYKSFLRELGYL VPQPERVTVTETGIDSEITSQAG PQLVVPAMNARYALNAANAR WGSLYDALYGSDDIPQEGAMV SGYDPQREAMECP
18347	48715	B	18454	71	4995	
18348	48716	A	18455	1	3572	MARKRKRNRNSKIGHGAISRI RPNPPEPCRNRYAQKYLTLAL MGGAFFVLKGCSDSSDVNDND GDGTFYATVQDCIDDGNNA CARGWNNAKTAFYADVPKNM TQQNCQSKYENCYVDNVEQS WIPVVSGLLSRVIRKDRDEPFV YNSGGSSFASRPVVPSSIVIMS YGLASYVIAVAFLEDRDRIQAAL DEWHRSNPGPVKDKAAYKSFL RELGYLVPQPERVTVTETGIDS EITSQAGPQLVVPAMNAR
18349	48717	A	18456	485	1999	
18350	48718	A	18457	44	270	
18351	48719	A	18458	1	2223	
18352	48720	A	18459	290	756	
18353	48721	A	18460	8	314	
18354	48722	A	18461	2	686	
18355	48723	A	18462	1	732	
18356	48724	A	18463	1	780	
18357	48725	A	18464	101	435	
18358	48726	A	18465	805	993	
18359	48727	A	18466	452	2180	
18360	48728	A	18467	691	1443	
18361	48729	A	18468	1	320	DPRDCRLKVGKEMFTLFGPQF VRELQQRGFDIFLDLKFHDIPNT AAHAAAAADLVGMVNVNH ASGGARMMTAAREALVPFRPD APLLIAVPV*RSIKASDLVVPL

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18362	48730	A	18469	632	796	
18363	48731	A	18470	129	425	TDIITRQNGTGANIDAEIATKA STGLFVYQPRFARCPVMSSGY HTATRGSSGRTVRARVCHTA AGVYVGSSKQTQF*NRFCQRKCR RYPDGCRRRA
18364	48732	A	18471	1	1062	
18365	48733	A	18472	1	996	
18366	48734	A	18473	1	1004	MLRVYHSNRLDVLEALMEFIV ERERLDDPFPEMILVQSTGMA QWLQMTLSQKFGIAANIDFPLP ASFIWDMFVRVLPPIPKESAFN KQSMWSKMLMTLLPQLLEREDF TLLRHYLTDDSDKRKLFLQLSSK AADLFDHVSAGSVSSKVEQLR AQLNERILVLDGGMGTMIQSY RLNEADFRGERFADWPCDLKG NNDLLVLSKPEVIAAIHNAYFE AGADIETNTFNSTTIAMADYQ MESLSAEINFAAAKLARACADE WTARTPEKPRYVAGVLGPTNR TASISPDVNDPAFRNITFDGLVA AYRESTKALVAGIVLMPAIPAL WEAEPGGCA
18367	48735	A	18474	606	846	
18368	48736	A	18475	3042	3933	GPHPAPGPGA/CHYDVHQPYL RQRTERDRTRHYLAQSFAYSL RQWAFHFLLDNITPDIQIVIAH TRRTGGFTITASEAAIEMLLCFK RDFVALQHLFNQIDAPARAVQF IAQKLIGWACCEAARKNQLPH NTTKRSLMSILYEERLDGALP DVDRTSVLMALEHVPGLIILP TDEEIIYPQCDGLSA/YRTRPLL VLPKQMEQVTAIVACHRLRV PVMVFPGLRLSREAFLLTAEFG TQELRRPAQLRLQVYRLSTAG RHHPAQNSPIRVLEVDIDLLGG TQELWG WKETH
18369	48737	A	18476	869	1639	ICSRCKSTRTSPTCRKAIVIL VCFVIRELLVVAPELTIIG.PEG NWITVSKGMLAKSPVDSNSTQ LKEAEERLKAQYGLQLVES QNELQNQLDKCRNEMMTMT MQLRNKKRRRELGNLIKRRSG AESLPDAVVLTEEGGIFWCNG LAQQLGLRWPDENQGNILNLL RYP/EVYAISENA*FFSPAQSGA QHRAASGNSRHALYPQTVADG GA*CHANASTGRGA*LFQCQRE P*VTYAIRDVTGLPGDDE

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18370	48738	A	18477	388	2356	
18371	48739	A	18478	137	318	GGQLSSWAMDFCHL/PAFWNS MTWHLQRLWGACGYFWHAQ WERLLTTFEGNEWILIFIGGIL
18372	48740	A	18479	923	1149	
18373	48741	A	18480	1	373	
18374	48742	A	18481	168	360	
18375	48743	A	18482	1	147	
18376	48744	A	18483	161	440	
18377	48745	A	18484	277	2172	
18378	48746	A	18485	164	406	LFRREGSYDRYLLMDDYCRRK DDSYFYDRYRDSFDGRGPPGPES QSRAGKGVETVYSSYY**NTL QKREETNNQYPHLKKG
18379	48747	A	18486	405	999	
18380	48748	A	18487	64	288	
18381	48749	A	18488	159	550	CAVCHISFQDTPVLVSSNVTMQ FGSKPLFENISVKFGGNGRYGLA IGANGSGKSTFMKILGGDLIPT LGNGSLDPNERIGKLRQIDQFAF EEFTVLDTVMGHKELWEVKQ ERDRIYALPEMSEEDGYKVAD
18382	48750	A	18489	3	481	
18383	48751	A	18490	2	233	
18384	48752	A	18491	2	3026	SVPTIIFFLPVLRFWRPGIQA KKCHLFA GTQSRRTLRQRT AKGIPQQRMTAKREEISIGILHV TPQQRRECRGDNRFTRFRRTPT WRLLGHCVSAAVTGVLPAVAG SPLAYS DTEFYVPVAGGTMSQ HPLVAAQPGIWMAEKLSPLS AWSVAHYVELTGEVDSPLLAR AVVAGLAQADTLRMRFTE DNG EVWQWVDDALTFELPEIDLRT NIDPHGTAQALMQADLPQDLR VDSGEPLVFHQTTLGLFI
18385	48753	A	18492	2714	3079	RLIGLRMVREFVGLIRRASVAS GSWHCCMRMRKRLIRPKPSILQ SMLWSPSTRMFFTLVPFISIEE LPFTFRSLMMVTLSPSASRLPLA SLTISSSLSCAGSASFHS*AHSG QMYMPLSS
18386	48754	A	18493	1	888	
18387	48755	A	18494	1778	2025	
18388	48756	A	18495	1	1425	
18389	48757	A	18496	3	96	FVGRIRRLRRIRRY*FTPLTD*LS CAHQVP
18390	48758	A	18497	420	955	

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18391	48759	A	18498	533	1006	RPSIFACVSP*RINHSRIMPQTN AKNAKPNAQVMRGVISRRRR AMLFNSAITRPTTSFTMAITS ASSSPPAVKVSIKPHGINTPTNIC NTTSCFRLIPHMTPKPLPLYSE SGPSCSSCSASARNSGLPISIKV ANAQAQSASTSGMLWLSGQ
18392	48760	A	18499	3	418	EWHYLSADRRQCAFQGVSRKT ATVCHHPVDYYAGSLYRLYFT DRLRLARLAGHAAES/GTPASHA VFQLVLE*L*SPLFSPVSTSGGR TANSTVLIMKSCMSGAVEROPT NWQAILMFLIFVVTGLITYWA SNAYVLAG
18393	48761	C	18500	63	500	
18394	48762	A	18501	1	1107	
18395	48763	A	18502	1	153	
18396	48764	A	18503	88	510	
18397	48765	A	18504	204	654	
18398	48766	A	18505	241	771	
18399	48767	A	18506	1655	1909	
18400	48768	A	18507	2	48	
18401	48769	A	18508	1	585	
18402	48770	A	18509	1	723	LQPPGRRWAAPAV\SGLSRQV\ RCFSTSVVRPFA\KLVGPSVQV\ SVIEGRYATALYYAASRQNKL EQVEKG\LLRVAQILEGTPKWA ASVLESPMLKAFPLKVKKPKM TITAKVGGSLPLTYQTLINfall ENGSD*GNYPRESFSGFLTMD GVFHSRERV\CTV\TSGIFL*EG RPQFSEFKNCSRGLR\SRAKFL KLGA\TDPSILGGMIVRIG\K YVDMSVKTK\QKLG\RAMREI
18403	48771	A	18510	400	894	
18404	48772	A	18511	1	1023	
18405	48773	A	18512	73	424	RPGMWSTRSPNSTA WPLSLEPD PGMASACTTMHTTTTIAEPDPG MSGWPDGRMETSSPTMDIVVI *CAIAAAEAI\VLVSLFVMLRYM YRHMGT\YHTNEAKGTGVADS ADACPAAGDPA
18406	48774	A	18513	141	563	RPGMWSTRSPNSTA WPLSLEPD PGMASACTTMHTTTTIAEPDPG V\SLP\PDGRMETPTPHP*LTMV VIAGVIA\CLWPFVLSLPSSFVM VALTLLTGHKGARTTPNEAKG\ TEFAESIADAALQG\DPAL\QDA GDSSRK\EIFI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
18407	48775	A	18514	182	935	QAFELHCPCRPKFSTLPSAWPP RHTDLRKRGRRTAQ*YAGNES HPPSLPRYLRRSRH/SRMQAPSS TCSYSHTSLQCSPAPQNH/AQHP *PALEELACG/SPSVSSPYLVLSS CQEQPHHCCPPSTPRPSW/CPSS GDAICYSPGQ/CPRSRGPL/EDS SDSPPAEQVLPSSGSHNTLYLR CKRFSAFILNCEPPSK/C*KPGHR CRS*AGILTLPPG/ERG/ GDGP CSTGRQASAKTPPPSPHTGHS LWSEEK
18408	48776	A	18515	48	676	KARLTWQOTREESLCRETPPYK TIRSRETYSLPREQHGKDLPP*F NYLPPSPSHNTICPG*QDQGRFT QPLYLRCKRFSAFILNCEPPSK/ C*KPGHRCRS*AGILTLPPGGE AQHFVKVHPSIPL/REGGEVGIK PKKTSPTGTELLMQP/CHQPSPT CQAPRKSNNR/LGCLSPMKHS TLGYLLWLQKATWLKGFGTSG W*M*GRFHL
18409	48777	A	18516	86	92	TANAALHQPSRPTCQAPRKSNNR RQAA*ALNC
18410	48778	B	18517	1	2031	
18411	48779	A	18518	98	367	DLFLYLSWQHCHPYSHCHPNQ KPGRFLMKLSS/ETVTIELKNGT TRSHGTJHQVVDV/QMNTHL KAVKMTLKNREPVL/ETLSIR GNNIR/YFILPD/SVYPLDILLVD VDPKVKSKKREAVAGRRRRG RG/TRDVARGR*RGNNIR
18412	48780	A	18519	1	310	
18413	48781	A	18520	37	136	RRRPSSSWALPPSRGPSST*AER GAQHQQPVPA
18414	48782	A	18521	3	305	FTTLCQLWGLFSCSPICSGVGR YWA*VCLCFLQIEAIELPMDPK LNKRRGFVFTFKEEPPVKVL EKKFHTVSGSKVRCSQLCLASC AAGELALRGMG
18415	48783	B	18522	249	367	
18416	48784	A	18523	1	1008	
18417	48785	B	18524	17	835	

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18418	48786	A	18525	2	1188	SLIKLNSPPRGGGTARYGAWL LVGGFPCGGGQGGDTVGAAP WADWGEASAAASFVLAEEAC ARLSSLRVGDEAGSRGVIWRAR SPRLGLALSEAGVEEQPMETT GASENGHEAVPEIASRGRGCW TPLRRGLEARPRRPRAGIRTAPR D/QRINASKNEEDAGKMFVGGGL SWDTSKKDLKDYFTKFGGEVAV DCTIKMDPNTGSRGFGFILFK DASSV*KVLDQKEHRLDGRVI DPKKAMAMKKAPVKKIFVGG LNPEPTEEKIRESFGFGEIEAI ELPMDPKLNRGRGFVITFKEE EPVKKVLEKKFHTVSGSKCEIK VAQPKVEVYQQQYQSGGRGN RNRGNRGQ/GGGGGGG*GQGS TNYGKTQ/RRGGHQ\NNYKPIL EAGRQERPT
18419	48787	A	18526	3	784	PAMNGLSLSELCLFCCPPCPG RIAALAFLLPPEATYSLVPEPEP GPGGAGAAPLGLTLRASSGAPG RWKLHLTERADFQYSQREVRST IEVFPTKSARGNRVSCMYVRCV PGARYTVLFLSHGNAVLDGQMS SFYIGLGSRLHCNIFTYDSSGYG ASSGRPSERNLYADIDATWQAL RTR*GRPLVGRVRARWRPRLTL LRRRQVRHQPGQHPSCCTGRSIG HGAHRGTWPRATSVPRWCCTR RSTSGMRVAFPDQERPASTP FPYIRERCPRLTSPRAHHPTGTK DEVIDFLEAGWRSTRRCHQGG GAAVGGGGPGHNDIELYSQYL ERLASLSFSQELPSQRA
18420	48788	A	18527	3	1990	
18421	48789	A	18528	82	406	

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18422	48790	A	18529	2	1474	ARASGSGSSSGQGKMGQSIQRG GHGSGGGKKDDKDKKKKYEP VPTRVGKKKKKTGPDAAASK/L PLVTPHTQCRLKLLKLERIKDY LLMEEEFIRNQEQMKPLEEKQ EEFRSKVDDLKGGPRLSVGNL GKRFDNDNHAIIVSTPVGSEHY VSIL/SFVDKDLLEPGCSVLLNH KVHAVIGVLMGDTDPLVTVM KVEKAPQETYADIGGLDNQ/IQ EIKESVELPLTHPEYYEEMGIKP PKGVAILLVPPGTGKTFLPKAV ANQTSATFLRGGGSELIQKNLG DGPKT/LSRELFR/VSEELAPSLR FIDRILPPLGTRKY/DSNSGGE/R EFQRTMLELLNQLADGFD/SRG D/VKVMPTNR/IETLDPALIRPR PAFDRKYEFP/LCPDEK/TKKRIF QISHKS/RMTLADVGTPWTTLI MAKDDLGA*PSKAICT/EAGL MAL/RENRRMKVPNEDFKKS KENVLYKKQEGTPEGVVSMLN PWLVIKRMVGRFLNP
18423	48791	A	18530	2	274	WQDLICRMAASVKEQSTKPIPL PQSTPG/ESHSLSTSGKSEVRDL FVAERQFAKEQHTDGTLEKVG EDYQAIIPDSHLPVSEERWALD ALRN
18424	48792	A	18531	3	844	

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18425	48793	A	18532	261	2814	VRFNRLIRIVCNIKICAVSHCPP KVFKLNSLFFLHRFDSVAFGES QSEDEQFENDLETDPPNWQQL VSREVLLGLKPCIEIKRQFVINEL FYTERAHVRTLKVLDQVFYQR VSREGILSPSELRKIFSNLEDILQ LHIGLNEQMKAVRKRNETSVID QIGEDLLTWFSGPGEELKHAA ATFCSNQPFALMIKSRQKKDS RFQTFVQDAESNPLCRRLQLKD IIPQMQRLTKYPLLLDNIKYT EWPTEREKVKKAADHCRQILN FVNQAVKEAENKQRL/EEDYQ RRLDTSLLKLEYPNVE/RLRN MDLTKRKMIHEGPLVWKVNR DKTIDLYTLLEDILVLLQKQD DRLVLRCHSKILASTADSKHTF SPVIKLSLTVLRQVATDNKALF VISMDSNGAQIYELVAQTVSEK TVWQDLICRMAASVKEQSTKPI PLPQSTPGEGDNDEEDPSKLKE EQHGISVTGLQSPDRDLGLEST LISSKPQSHSLSTSGKSEVRDLF VAERQFAKEQHTDGTLEKVEGE DYQIAIPDSHLPVSKE/RRALDA LRNLGLLKQLLVHQLGLTEKSA LENWQHFFRYRTAFQGPQTDS VIQNSENIKAYHSGEGHMPFRT GTGDIATCYSPTSTESFAPRDS VGLAPQDSQASNILVMDHMIM TPEMPTMEPEGGLDSDGEHFFD AREAHSDENPSEGDGAVNKEE
18426	48794	A	18533	90	383	ILQLHSSGCPCLLWL*LSFRSLST TAVICQCCRPAADFHPSGSSRV AVLLIQ/HRRPLPLPIGLKACYFS ALSLQTSLTCLGLVVLDDPPE AASLDKV
18427	48795	A	18534	1	456	
18428	48796	A	18535	830	1092	

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18429	48797	A	18536	391	1824	GSGADASGFISDAGLIFKKAASK GPKRLEKFSDERAAYFRCYHKL FLLFSSLCYGTYHVVLPTLKP REDEDWISLCLRHCLMQK DTH SMLGECGERREGKKQKTGALG SSLSLEDAKHL LFPALPFSWN ALPQDL CNVFKLLWDYRIRVD PSPiAGTLIRRDTPQGESHVKT GRHWSDTIKSQRCCQLRQPPDR PIPILLMVKGQHVWPSQLDKAQ IQEVTELN NVKNVARLPKSTKK HAIGIYFNDDTSKTFACESDLEA DEWCKVLQMECVGTRINDISL G\EPDLLATGVE\REQSE\RFNV Y\MTSP*LRMLHG\ECALQV\T Y\EYICLWGRPRTQPQEFKLISWP LSALRRYGRGTPWFNYQAGR MCQTGEGLFIFQTRDGEAIYQK VHSAALAI AEQHERLLQSVKN SMLQMKMSERAASLSTMVPLP RSAYWQHITRQHSTGQLYRLQ DVSSPLKLHRTETFPSSLQDS
18430	48798	C	18537	22	620	
18431	48799	A	18538	48	413	EDSKSKTISHPWRDCGDYCHH QGLERCGRGDSHHTPVQLS*LA CAED\NKSWMRT\GIIVSLTKC* LQMQLLYQMWFHCLSKLTHLL GISTLQLCVTLFREILITFPLHKI SHWSITLMTLR
18432	48800	A	18539	23	124	QWVIISLTKW*LQLQLLYQMWF FHCLSKLTRLPL
18433	48801	A	18540	1	1860	
18434	48802	A	18541	209	3816	QGRPTFRFRKYREHHKDTPRE QLQDT*SSDSPKLK*KKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKREKNQIDTIKNDKGD ITTDPTIEQITIREYYKHL YANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPTGSEIEAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQMEKEGILPNSFYEASII LIPKPGRDITTKGNFRISPLMNI DAKIL
18435	48803	A	18542	1	1521	
18436	48804	B	18543	1	2265	
18437	48805	B	18544	1	1716	
18438	48806	A	18545	1	1704	
18439	48807	A	18546	1	3618	
18440	48808	A	18547	1	3087	

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18441	48809	A	18548	277	350	SPVEKELKLWKNRHKLLSC*W-LTC
18442	48810	A	18549	197	422	IVNKVVLPGGGPASPSLKGFVWYKLAQVWVKLEGP*PFIFIQISL LSI*PRSFLV*IK*ECSRLPISFTS SGR
18443	48811	A	18550	1	3171	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSLQRLDSDHTLI MGDFTNPLSTLDRSTROKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALISKCKRIEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKTEIKMFF ETNENKDJTYQNLWDAFKAVC RGFIALNAYKRKEERSKIDTL TSQLEKEKQEQRHSPSRREQ ITKMRAELKEIETQ
18444	48812	A	18551	209	2432	OGRPTFRFRKYREHHKDTPRE EQLQDT*SSDSPKLK*KKC*GQ PERKVKLPTKGSPPD*KRISRQ/ KTLQARRQSWFFKINKIDRQP ARLIKKKREKNQIDTIKNQKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRNPTGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPRDITTKGNFRPISLMNI DAKILNKILANQIQQHKKLIHH DQVGFIQMGQWLEVLARA/IR QEKEIKGIQLGKEEVKLSLFAD DMIVYLENPTVSAQNLLKLISN FSKVSGYKINVQKSAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLNE IKEDTNKWKNI PCSWIGRINIVK MAILPKVIYTFNAIPIKLPMTFFT ELEKTTLKFIWKQKRSHIAKSIL SQKNKAGDITLPDFKLHYKATV TKTAWYWYQNRDIDQWNTTE PSEIMLHIYNHLIFDKPDKNKQ WGNDSL FNKWCWENWLAICR KKLDPFLTSYTKINSRWIKDL NVRPKTIKLEENLGNITQDIG MGKDFMSKTPKAVATKAKIDK WDVIKLKSFTAKETTRVNRQ PTEWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAAKRHMKKCSSS
18445	48813	A	18552	1	3255	

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18446	48814	A	18553	1	3139	
18447	48815	A	18554	1	3210	MVKGSIQEEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRKLNLTQNRSTTWKLNLL LNDYVVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRQKERSKIDTLTSQ LELEKQEQTHSKASRRQEITKIR AELKEIETQ
18448	48816	A	18555	1	3345	
18449	48817	B	18556	1	3127	
18450	48818	A	18557	1	3325	
18451	48819	A	18558	1	3145	
18452	48820	A	18559	1	548	
18453	48821	A	18560	1	3229	
18454	48822	A	18561	1	3352	
18455	48823	A	18562	1	1965	MGDFNTPLSTSDRSTRQKVNK DTQEMNSALHQADLIDYRTRH PKSTEYTFLSAPHHTYSKTDHIL GSKALLSKCKRTEITNLYSDH SAIKLELRKLNLTQNCSTTWKL NNLLLNLDYVVHNEMKAERKM FFETIENKDDTTYQNLWDAFKAV CRGKFIALNAHKRQKERSKIDT LTSQLELEKQEKTHSKTIRRO EITKIRAELEKEIETQKTLQKINES RSWFFERINKIDRTLARLIKKKR EKNQIDRIKNDKGDITDDPTQIQ TTIREYYKHLANKPENLEEMD KFLDITYTLPRLNQEEVESLNRI SGSEIVAIINSLPIKSPGPDGFT AEFYQSYKKELVPLLLKLFQSI KEGILPNSFYEASILLPKRGRDT TKKENFRPISLMNIDAKILNKIL AKRIQHIKLIHHDQVGFIPG MQGIKYLGIQLTRDMKDLKE NYKQLLNEIKEDTNKWKNIPCS WVGRINIVKMAILP/KELEKTTL KFIWNQKRACIAKSILSQKKA GGITLPDFKLYYKATVTKTARL YTKHGTSICCGSGFELLPMQKA KRELAHHMAKAGARVKGQLG HVTQHQLGSIEWFNKYSLSYY TVDTKPFQFSHPTKDNKTGLTCR NRTTVGVLDLQAKGNLVVVKHLS SLQHCYEFICHI

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18456	48824	A	18563	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLQNRSTTWKLN LLLNDYWIHNEMKAEIKMFFET NENKDDTTYQNLWDAFKA VCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQE TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
18457	48825	A	18564	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTETITNYLSDH SAIKLELRIKNLQSRSTTWKLN NLLLNDYVWVHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKA VCR RGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
18458	48826	A	18565	1	3095	
18459	48827	A	18566	2	2678	

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18460	48828	A	18567	1	2478	MKAEIKMLFETKENKDDTTYQN LWDALKAVCRGKFIALNAHKR KQERSKIDTLTSQLKELEKQEQ TLKASRRQEITKIRAELEKET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDAINKDK GDITTDPTETIQTITREYYKHLA NKLLENLEEMDKFLDTYTLPRLN QEEVESLNRPIITGAEIVAINSLP TKKSPGPDGFTAIFYQRYKEEL VPFLLKLFQSIKEGILPNSFYE ASILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDNHMIISIDAEK AFDKIQPFMLKTLKLAIEIKYL GIQLTKDVKDFFKENYKPLLKE IKEDTNKWNIPCSWVGRINIV KMAILP/KELEKTTLKFIWNQK RACIAKILSQKNKAGGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRKTETSEITPHIYNYPFD KPEKNKQWQKDSL FNKWCWE NWLALCRKLKLDPLTPYTKIN SRWIKDLNVRPKTIKLEENLGI TIRDIGMGKDFMSKTSTAMAT KAKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAXKH MKKCSSSLAIREMQIKTTMRYP LTPVRMAIIKSGSNRTPTRPIQ
18461	48829	B	18568	1	3403	
18462	48830	A	18569	2	2976	APRFIKQVLSDLQRDLDSHTIIM GDFNPTLSTLDRSTRQKVHKDT QELNSALHQADLIDYRTLHPK STEYTCFSAPHHTYSKIDHIVGS KALLSKCKRSEIITNCLSDHSAI KLELRIKKLTQNRSTTWKLNLL LLNDYVWHNEMKAEIRMFET NENKDDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELEKETQKTLQKINE/SR SWFFERINK
18463	48831	A	18570	472	829	AIASESPKAWQLPCGAQQF AALPGLGNYKFLTLITGYGSN KSPP*GYLVFQTYSSLP LLRLPP GHFGFLLPLSQRLRRELQCWL G*LTQTIKMKSVYHSTTEVRKS MHGQIEIH

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18464	48832	B	18571	1	2293	
18465	48833	A	18572	1	3810	
18466	48834	B	18573	1	4107	
18467	48835	B	18574	87	3161	
18468	48836	A	18575	1	3192	
18469	48837	A	18576	1	1983	
18470	48838	A	18577	1	3156	
18471	48839	B	18578	1	3471	
18472	48840	B	18579	1	2337	
18473	48841	A	18580	1	3852	
18474	48842	A	18581	1	3057	
18475	48843	A	18582	1202	2004	SGIYMIGFEQVLKAQPLPSSPNG PMNKAIVATVVGMEVMHGLSNM DFHSRRLTWLRPLPGFTGPG/Y QGVKVEVAPLTIITPSDPLAKFL LLISATSTSLEVTVPGEMLPPR DTTKIATFGTGTGFLALQLADG LLWDLVIIPGKGKPSRDLVESPS PYSTYEGIDGWDFEPAPTATKP PVMPAPALPPDTRSGSKAPTVP TPYPQMEHHQVQLASNNNSNTE ALGHLSPQSSWVQTGPGQNSGP AIPNHLGKDMISPPQMAPAGVK WESQKY
18476	48844	A	18583	1	2832	
18477	48845	A	18584	1	3702	MQKKHDKIRNSFMIKTLKKLRT EGIYLNLIKATYKKPITNIILNGE NQKAFALRSGRFWILALCQM SRLRKLTNLYSDHSAIKLELRIK NPTQSRPTTWKLNLLNDYV VHNEMKAEIKMFFETNENKDT TYQNLWDAFKA VCRGKLIALN AHKRKQERSKIDTLTSQKLELE KQEQTHSKASRRQEITKIRAE KETETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTI KNDKGDITTDPT
18478	48846	A	18585	1	3139	
18479	48847	A	18586	2	2918	
18480	48848	B	18587	1	3242	
18481	48849	A	18588	1	3640	
18482	48850	A	18589	371	522	
18483	48851	B	18590	1	3918	
18484	48852	A	18591	1	3057	

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18485	48853	A	18592	1	3233	MGKKQSRKTANSKKQSTSPPP KEIHSSSPATEQSWTENDFDLRL EEGFRRSNYSELREDIQTGKGE VENFEKNLEECITITNTEKCLK ELMELKAKAQELREECRSLRSR CNQLEERVSAEMEMNEMKRE GKFKREKRIKRNQSLQEIWDYV KRPNLRLTGVPESDGNGTKLE NTLQDIIQENFPNLARQANIQQ EIQRMPQRYSSRRATPRHIVRF TKVEMKEKMLRAAREKDRSTR QKVNKNTQELNSA
18486	48854	A	18593	965	4165	TSWKGTTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEV/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKLNQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRQKERS KIDTLTSQLEKEQEQTHSKA SRRQEI/KIRAEK/EIETQKTLQ KINESRSWFFERKINIDRPLARLI KKKREENQID
18487	48855	A	18594	1	5093	MEGEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIEIQRTPQRYSS SRRATPRHIVRFTKVEKKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNTQNRSTTWKLNLLN DYVWHNEMKAEIKMFFETNEN KDTTYQNLWDTF
18488	48856	A	18595	1	131	
18489	48857	A	18596	5382	9269	RAKSPANIIMTGSNSHITLTNL VNLGNSPIKRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHCIKVK GSIQEEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLSTLDRSTRQKVNTDTQELN SALHQADLIDYRTLHPKSTEYT FFSAPHHTYSKIDHIVGSKALLS KCKRTEITNHLSDHSAIKLELRI KNLTQS
18490	48858	A	18597	1	312	

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18491	48859	A	18598	142	876	RKKGILPPKESLKELEEEAEEQ RILQQSVVKTIEDMTLEEDH EDEFNEEDECAIEMCRQRLAE WKATKLKNKFGVEISGKDY VQEVTKA/ERRALWVILHLYK QGIPLCAL/VNQHLSWTLPGSFP DVKFIKAISTTCIPNYTDRNLPT ILVYPGRRYQGLSLVLWCLAG MNPQEQMSWEWKLESGAIMT DLEENPKPIEDVLLVLSAALW SS*RGDSDEGDLRATASITCRT
18492	48860	A	18599	1	2310	LYNRRRRRCRSHCRHRCRLSS GLRKEEVISLGASLGRVFPVPCSP PTVSAARGPTGAPGGPNKPLCS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTSQVNLVEILP AIFSSFLNLQHVNLWFLAAM KAVTEQGHELSNEERNLLSVA YKNVVGARRSSWRVSSIEQKT ERNEKKQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKCRLSNYFRYLSVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFTLILRLGLALNFSVVF YEILNSPEKACSLAKTVRKTL DI*P*QNSACVINFILFLNLRDN LTVSTTSTGFIVSFLFTYLIHCH LQEGICTIKCSYSFKLLNLL
18493	48861	A	18600	3	1124	
18494	48862	A	18601	340	1323	AARPQKRHHNNHSSLLTGSHH WKRGRVQNIADVLQFCFLYLLT VLFVPCSPPTGMTMDKSELVQ KAKLAEQAERYDDMACSERH VTEQGHVLSNEEKSCSLVAY KINVIVGARRFLPGRVSSI*A*K QRRNEKKAADGQKSTREKIEG RTCRTFCN*CFWELLGQISLFPN ATQPRKVKVFYFEK*KGDYF/R YLF*KWQS*RQQTQPTCVGTSP ARAYPGSNLKI*LRKKMQP/TH PNSVLVLAPKFPQSFYIEILNSP VEKGLVSLGKNGHFD*SNLLNL DTLEWKSLLIKDSTSDSWQLLR DNLLTLWDIRKTRGDEGDAGEG
18495	48863	A	18602	33	89	
18496	48864	B	18603	167	232	

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18497	48865	A	18604	14	600	MAELAPASPSDIKASVNSGDTT LLCSRRQSCGMNEVRQVSLTY GSPAPSHSLPLQPRSGGLCP AW/PDPHQLFDDTSSAQSRG YGAQAPGGLSYPAASPTPHAAFL ADPVSNMAMAYGSSLAQGGK ELVDKNVSGRGWWEWGDA HRASDLSSASPDHFRFIPITKLKY YFAVDITMYVGRKLGLFFPYL
18498	48866	B	18605	1	1230	
18499	48867	B	18606	41	931	
18500	48868	A	18607	3	166	PRPFKSRLLPGIIGGEYDQRP NIPILGRGGFNDRFPRPSGR PRTDGRSLFM
18501	48869	A	18608	212	1881	CLRVLLKRTWPVEVPETGAR P/TGGILRSHVLRQSLTCTWGY SSNTRFTITLNYKDPDTGDE ETLASYGIVSGDLICILQDD IPAPNIPSTDSEHSLQNN EQPSLATSSNQTSMQDEQPS DSFQQAQSGVWDDSLMLG PSPQNFEAESIQD NAHMAEGTGFPYSPRTPC SW*LNPVEGQVPHISLETLY QLADCS\DANDALIVLIHLL MLESYIPQGTVEAKALSM PEKWKLSGVYKLQYMHPL CEGSSVTLTCTVPLG VNLIVVNATLKINNEVRK C*KGC SLLPESFVCKEKLGENV ANIYKDLQKLSRLFKDQ LAHPLLAFT RQALNLPDVFLVVLPLE KLRI FRLLDVRVSLSLAVCR DLFTA SNDPLLWRVYFICVNF RDNTV RVQADTDWERTVQGR RAHTKE KESPKGRVLWMLAIR QTH/TIP FYSQPLWHPRGHFP KLPAFPPI YSGGWNMDQR/PT FPYVGRTO SSSLNSWVLGETPK PSFLRPR FDPVWPHFPGP*P PSLPRARAGP NDQISPRFPQGSQ GLIGRLSIH
18502	48870	A	18609	1	1065	
18503	48871	A	18610	1	1513	
18504	48872	A	18611	1	2247	
18505	48873	A	18612	3	421	
18506	48874	A	18613	1	103	
18507	48875	A	18614	3	435	
18508	48876	A	18615	268	501	QLECIPTGWELWKEQER AMAGGGLKKIISATEK KLARMLLAP SASWCCSGP*VFHGS T*WGKPG PVSVSLLGVLGK

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18509	48877	A	18616	3	296	EAMEAVILTCDPATPAASYQW WMNGQSLPMTHRLQLSKTNRT LFIFGVTKYIAGPYECEIRNPS*V PAASDPVTLESPPLLFNGLATIE TLRKRGNP
18510	48878	A	18617	3	1464	GAVRTWGRGFQTEKQASLLN FWNPPTAQVTIEAEPKVKSG KDVLLLVHNLQNLAGYIWK GQMKDLYHYITSYVVDGQIIY GPAYSGRETVYSNASLLIQNVT REDAGSYTLHIVKRGDGTRGET GHFTFTLYLIPWTLTYL*RS LQVSHYETPGKTAPPCGSTA**L N*PPDLTFLSPVLFLKYVPVPG AFQYPKGLKTIGSSITHL*DV LKGSCRENIPRAAK*D*N*EDS STACSK*GPQVETPKPSISSNLY PREDMEAVSLTCDPETHDASYL WWWNGQSLPMTHSLQLSKNK RTLFLFGVTKYTAGPYECEIRN PVSASRSDPVTNLNLLPKLPKPY I TINNLNPRENKDVLAFTEPKS ENVTYIWWLNGQSLPGSVPR VKRPNENRVLIFTPCSRGIE TGPIYQCEINRDYGGHPQLPS HPGMSSITTKHSGLYACSVRNS ATGM ESSKSMTVKVSPAGSGTHLPGL
18511	48879	A	18618	79	1516	
18512	48880	B	18619	96	1730	
18513	48881	A	18620	9854	11033	ESLCFPKTEQEASQSLSP*IIII LS CDTCTSYWLSRTHVG*QVGDA NSE*RMPEESKVPHTIFCYPH SVKLPMPYITINNLNPREKKDVL AFTCEPKSRNYTYIWWLNGQS LPVSPRVKRPMENRILIPSVTRN ETGPYQCEINRDYGGIRSNPVT LNVLCYPLFLCGPHQLNSKRP EARPLSLSPVQV*TTLLDIRPG HDSLPEILGRHSLNQEYKGRG ALVMGH*GPTACNERNRGIPQ AWA**T*MGFGCHLRCLGSEG HCVPLRDQEHPLPDDITCGFIL FPPDGPDLPRIPSFYTYRSGEN LDLSCFADSNPPAEYSWTINGK FQLSGQKLFIPIQTTNHSGLYAC SVRNSATGKEISKSMIVKVS GKWIPASLAIGF

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18514	48882	A	18621	3	1350	GRTAQLTAVLRKLLDPRLISTE ENTQAAETMGPLSAPPCTHLIT WKGVLLTASLLNFWNPPTTAQ VTIEAQPPKVSEKGDVLLLVHN LPQNLAGYIWKQGMTYVYH YITSYVVDGQRIIYGPAYSGRER VYSNASLLIQNVTDAGSYTL HIIKRRDGTGGVTGHFTFTLHL ETPKPSISSNLPREAMEAVIL TCDPATPAASYQWWMNGQSLP MTHRLQLSKTNRTLFIGVTKY IAGPYECEIRNPVSASRSDPVT NLLPKLSKPYITINNLPRENKD VLTFTCEPKSENYTYIWWLNG QSLPVSPIVWKPIENRILILPNV TRNETGPYQCEIRDYGGIRSD PVTNLNLYGPDLPISYPSFTYYR SGENLYLSCFAESNPRAQYSWT INGKFQLSGQKLSIPQITTKHSG LYACSVRNSATGKESSKSITVK
18515	48883	A	18622	273	2271	CGSWLMTQFSMDKRQGRSRV TITNTAVTSLEWVPFHAFAPRS TLVSQQATSHTDNTQEMDSP GQEPGFAKEVEVEPGFQPLPQM TLLVPAMCLLLHGACSAKGFC AAPHFLLASPMGKGQVLPNFS FTLSEELDLPQSLKRNPKGCIA RAKPILAAERHKRLILHTSKEN TLLDNRVIECLTMEAVAKFNIM KEREFGSHQALSPPKARWHIL WQKLMFTASLLTFWEPPTTAR VTTEAMPFNATEEEEEFFLLA HNLQPNLRTATIWYKQGMHRH LYHYITSYVVDGEIHYGPAVSG RETAYSNASLLIQNVITREDAG SYTLHIIKRGDGTGGVTGRFTF TLYLETPKPSISSNFPNREATE AVILTCDPETHDASYLWWMNG QSLPMTHSLQLSKANRTLYLF GVTNYTAGPYECEIRNPVSAS RSDPVTNLNLLPKLPKYITINN LKPRNE*GCLRPPTCEPKE*GTT PYIWWVKRFRSLPSPGVKRP LKNRNLIPTPVTRKWKQGPYS MWNYGDRYGGIRSLPSSPWNV LLWVQDLPRILPHFTYYRSGR KSSYLSGSGGTLNPPAQSVD N*WKSQFLTRGQKLFYSGHITT KHSGLYVCISVRNSATGRESSK SMTVEVSDWDITLNSTSTNSIF
18516	48884	A	18623	1	1131	

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18517	48885	A	18624	1	603	MDIADPFSGFPMGMGGFTNMN FGRSRPAQEPTRKKQDPVPTH LRVSLLEEIVSGCTKKMYQED/KI SHKRLNPDGKSIRNEDKILTIEV KKGISLPEALCG/TTVNVPTLDG RTIPVVFKDAIRPGMRKKVRGE GLPLPKTPEKRGDLIIIELEVFPE RIPQTSRTILEQILSSYLSYLSSP GLTRDLRAQGLDLSTSCGP
18518	48886	A	18625	3	1228	WSAAEPVDGDSGAGRRRGW PKTTYHPWAVARGASEKEIKR AYRRQALRSHDPKNKEPGAEE KFKEIAEAYEVLDPKREIFD HYREEALKGSGSGG/SGGGAN ATSFSYTFHGEPLAMFAEFFGG RNPFDTFPGQRNGEEMDIDD PFGSGPMG/LWGGFTNVN/GRS RSAQEPARKK/QDSPVTHDLRV SLEGDLTAAPVRRCTKKMKISH KRL/NTPDGKSIRNGDKILTIRSE RRGWKEGTQITFP/KEGDQTSN N/PADI/VFVLKDKPHINIFKRDG SDVIYPARISLREA/LCVGCTV NCPHSGTGRTPVVFKECYQGL GMRKSSWENGLPLPQNTREN VGDLII*GFEVIFPERIPQ/TSRT VLEAGSFQYSYLEVPQGLTRGP FPFLKDFWDLFLPVVGP
18519	48887	A	18626	321	1121	GDVPSAPRRPSRRTPGCGSRG ALQPGPPRA/PPPEP/PPRGAAA AAPPAGPAAPAAQPPRRPPAQ PRSCPRRVRPPTA/WSPPGRRGP RRSRRRP/PGGPGPAAPLRLSRA HSPAPPGSPYRPHGAGTSVAP WTRPPAARGTEADPGRCVPSAP GTAPGQMRGRGSATQRLHRGH STAPGAGGRCGRRPGGSGRPG AGAGPRRSTAAPPCRRRSPTG PRSPRGPRSARPARGSVGGPRG TPGKQPGPRA*TSGP/PRCCG HARG
18520	48888	A	18628	191	653	KLEIQRLRLMTTECIRHTKQKK FGSPGLQPPLPGNAKSRADSTA LPALPAQKQKTKQEPGESS*E PGGSSPSRMERAEAPASQ/PA GGTGQGWGAPHLGPALARR VTGPPQHGSPGPRTRTPYPAR C/PSRPIFVPAIVWSRLRAPGLP
18521	48889	A	18629	141	319	

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18522	48890	A	18630	178	722	PLGNVSCSHRSFQATARVDYSLI YVLAWGQKKEVWELRNWQTH ALMKLKNKLREPRTSVNKD/SP KSLLYSCSYSYFDEPVELRSSF SSWDDSSDSEYETHLLHLKLV* PNLAVFNCRPTARRKPDYEPVE NTDEAQNSFCCTAHNLWSLTFP FPCLL*YETRARLESWSLSCLR YEHISSG
18523	48891	A	18631	2	367	QRYSSRRATPRHIVRFTKVERK ETMLRAAREKGRVTHKGKPIR LTVDLLAETLQARREWGPIFNI LNEKNFQPRISYPAKLSFISEGEI NPNQMLR/DFVTTTRPTLRDLLKE ALNMERNRNYLPGRPL
18524	48892	A	18632	1	381	
18525	48893	B	18633	1	846	VGSMTGEASGNLQSQRKAKRK EARLTCLEPVEEPGSGTHPPMC YLAPPMWKQKQKQKPEIKEGDR DHNSLPAREENQTENESDELTE AGFRRWVITNSSRLKEHVVTQC KEAKNFEKSLKELLTRITSLLEDN INYLMEPRNTAREHREAYSSIN SQIDQAEKKEIPEIEDQHNEIKRE DKIREKRMKRNKQSLQEIWYD VKRPNLSLAGVPESDEENGIKL KNTLQDIIQENFNLAKQANIQI QEIQRTPQRYSRLRATPRHIIVR FTKVEKMKMLRAAREKGRV THKGKPIRLTADLSAETLQAR/ RTEWGPFIKILKEKNFQPRISYP AKLSFISEGEIKYFTDKQMLRD FVTTTRPALKRAPGKEGT*TL EDNRNYQPLQKHAKL
18526	48894	A	18634	3	1170	

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18527	48895	A	18635	73	1504	QDLRLFLYKLDTFMSKLAHLQR FAVLSRGVHSSVASATSVAATKK TVQQPPTSDDIFEREYKYGAHN YHPLPVALAERKGILLMGM*E GRKYFDFLSSYSALSNQGVHC HPKIVKCSGRVKWDKIDL*HLE AFYNNGTLVNMRYYYY*TFST YHKVLPMNTGVEAGETA\CKL AIRKWGL/YTVKGIQKY\AKIV FAAGNFWGRTL\SAISSSTDPTS YDGFQPFYARDFDIIPY**SCPH MEQCSFKDPKGLAFHG*EPIQ G\EAQVIVVPDPGYLMGSAESS GTRDQVLFICLMEIQTGLARTW *DGLAVDYENVRPDI\LLGKAL SGGLYPVSAVLCDDIMLTIKP GEHGSTYGGNPLGCRVAIAAL EV\LEENLAENADKLGILLRNE LMKLTLPSMLVTARKKEKGIY LNAHLAIKGNQKIWDA/WGKV CLRLQDNGLLPKPTS\VALTSRF APP\LVIKEDELRESIEIINKTILS
18528	48896	A	18636	2	348	
18529	48897	A	18637	588	801	RTAYFCQYHTASVYSERAMPP GCPEPSQA*ELQETGHRQVALR RSGRPPKCAERPGAADTGAHCT STDGRL
18530	48898	A	18638	175	510	NSESGPLWWLSCDNP\AKDRIY STEADGLGLPDQSFVVHRAQL* CVAG*LGTHSRFQEWAV*D*SD LLKAQLHFKVGRCVWEAGGGL EWVLGGRRCRCRVPQPLETLIQ WGPW
18531	48899	A	18640	1	1431	
18532	48900	A	18641	202	994	RWQQQRLLDSNIRLVVVLPIR YSFTFFRRALIRHYVSILLAEERQ RSFTQGNKYLDSSSPNFEGRV/R FRGKLGNYIPKQSFQFGR/RRKFLF FPNPEDGIFS\KLLKREVVPSPM TDP\TMLTDMMKGNVT\NVLPM ILIGGWINMTFSGFVTTKV\PFPL VTLRF*A*WLQQGNRSYSPFRCI PG*/WFCIPGYFPQCILGFRSI/YT LWISGGKDN\GRWNQSRMM/DR SRMTGASHGPPWADSGRRFPN KRWEAL\ELTDHQWALDAAGE DAA
18533	48901	A	18642	97	224	LPTKSTWVAGKK*KKRSNIKD YSTPLTSYRSIRSHAFKIVAS

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18534	48902	A	18643	117	457	IWGDVEKGKVKVFL* ^R CSQCHTV*/ ^E RGGKHKTGPKSP* ^V SFGRRTGQAPWDTLYTAANK\NKGIIWG ^E DTLMEYLENPKKVHPLDTKMIFVRHLRKRERADLI ^A LSKKLLN
18535	48903	A	18644	411	1054	VTGAQRLVTCRMGKQNSK ^L LA ^P EVME ^D L ^V KSTEFNEHELKQWYKGLKDCPSGR ^L NLEEFQQLYVK ^F FPYGRRLPS ^F AQHAFPNLSTRMGDGT ^I DFREFICAL ^S ITSRG ^S FEQKL\NW ^A FNMYGPGWVMGKITRVEM ^L EIHRGLSYQNG* ^G TVIMMKMNEDGLT ^P EQRVGQDFSARWVRNKDDQ ^I YTGIDFKGSCQRADPFIV* ^L L ^Q CDIHK
18536	48904	A	18645	3	475	GAEGARGGSSYSEMAETVADTRRLITKPNLNDAYGPPSNFL ^E IDTNLPIFKLKESTVRR ^R YSDFEWLRSELERESKVVVPLPGKAF ^L RQLPFRGDDGIFDDNFIEGKKTRGWEQFINK/VSLGHPLAQNEPLFFHMF ^L QDEIIDKSYTPSKIR
18537	48905	A	18646	1	695	LRARSLRDRCARAPCPHGGQQRRRRRLNAEGAEGARGGGSSYSEMAETVADTRRLITKPNLNDAYGPPSNFL ^E IDVSNPQTGVGVRGRFTTYEIRVKTNLPCFQ ^S *KNLIVRR ^R YSDFEWLAKWNLERSK\VVVPLPGKAF ^L RQLPFRGDDGNILMDNFI* ^E EERKIRGWSSFLNKVAIGHPLAQN ^E ERCLHMFYQDEIIDKLLLP ^S KNKAMPWKFGPRKGAKNV ^D Y
18538	48906	C	18647	3	474	

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18539	48907	A	18648	156	1254	RPLHTLEVLRMRTRKRLVTKAA ASAARAQPAEPRDRKYDKHLS YLATWGRSAGRAGSPRGARGR ELARAPVSLPAGVPGRGSAA HSSEARTGPNKMGSSREPPT EKVPCPRGLSPTRVGHQVHGT LGAGPNELHPSGAPAGRCRPG REAKLGDAARSEASAHKFHII DSLSPWNPTAMEMLMPKKNR IAIYELLFK\EGVMVPKK\DVPI PKHPELAEQKCAPTFHVMK\A MQSLKSPRPT*KEQFAWRHFY WYL\TNEGQYLRDYL\HLPEI VPAHPYGRSPSRRLARPRPKV WKGEATLRDFTRGEADSLCH S\DSYRRSAVPP\GA\DKKAEAG GLGQKPNFQFRGGFVRGRGQP
18540	48908	B	18649	1	1053	
18541	48909	A	18650	1	529	MGRYMEREP\QGNHRRSGLSG ERCSHMGGLIERRELQETETK EGVVEWCWLEKVLATITKPV RGDKNGGTQVVKHRKMPRY PTEDVPQKLLSHG\KKPFSQH RKL\FLYRRHARNLSLPPQELI SDVK\IPRHPADA*LEEQLSEP E\HSEGSTY*RIPEKVLSPAIRP
18542	48910	B	18651	258	363	
18543	48911	A	18652	197	398	ARMSQEKDFHKVMSALKARTG HLHFFCGGMSSVKVGQGFSLLL *FFSYFRPSGCILPL*ELPEARCP
18544	48912	A	18653	215	932	GTQSCNQKVLNSANNLQELGIG PKFQMR\KQPLAPMQPNRGTS LGRSIPCPVLCMRKIHLRPQV LRPTSPRNISPILNRVSEVSDHA GTPALVLHP*RQVPLFWGRGK YPNPFSLCLYPFSAFLGGKKHP TPSPSP*VASPLF*RSKYPNLVSL CPSPLFPRPDLLSLWPNPLFRTPT TSYISVPQSLISMRLPLISAPQPLI STTQPLSRFSGRSLLQVPEIWPP GQGMPAARDSS
18545	48913	A	18654	1	378	
18546	48914	A	18655	14	380	
18547	48915	C	18656	228	260	
18548	48916	C	18657	99	335	
18549	48917	A	18658	55	474	RQVPLFWGRGKYPNPFSLCLYP FSAFLGGKKHPTSPSP*VASPL F*RSKYPNLVSLCPSPLFPRPDL LSLWPNPLFRTPTSYISVPQSLI SMRPLISAPQPLISTTQPLSRFS GRSLLQVPEIWPPGQGMPAAR

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18550	48918	A	18659	1	187	AELATGNVKEASGTPEEKAGSVLG*ACFAGP*ERCCWQNN*DGIISIQSYCLCNLGCFTQ
18551	48919	C	18660	1	357	
18552	48920	A	18661	3	148	
18553	48921	A	18662	1	312	
18554	48922	A	18663	149	457	
18555	48923	B	18664	1	675	
18556	48924	C	18665	110	928	
18557	48925	A	18666	495	817	LTSRSTRIIEKSCSSLPPL*DKPQPHLQHTRTSKRLNCSSQVFLQNLPEELATSSRNLATGPRNACSPGFLLSHIPSVWDPTGNRTVQLTWQPLPELELWPKAL
18558	48926	A	18667	228	3021	VFDRTQNVQGRIMEAPEYLDLDEIDFSDDISYSVTSKLTPELCRRCDITQNEADRSVSSSSWNCIGISTLITNTQKPTGIADVYSKFRPEKRVLPKIHQPETLENNESDDQKNQIVGEYQKGGESDLGPQPQELGPGDGVGGPPGKSSEPTSLGEL EHYDLMDDEILDVPIYKSSQQLASFTKVTSEKRILGLCTTINGLSGKACSTGSSSSSSNMAPPFCVLSPVKSPHLRKASAVIHDQHKLS TEETEISPL
18559	48927	A	18668	1440	1764	ERSTYNLRSSDQP/RPRNLTNFKS/VDKGDTFYPWTHNSGASHGLGR/RLPWC*ELATSARNLTPRPRTAGSPGFLLSHVPSVWDPTANRTVQLTWQPLPELELWPK
18560	48928	A	18669	1	3255	MLTLTGAGGESWIIRPGNLLLEQLGAETLGRRQEPGDEVTAHFL LQGVINMGVPVYPGAHSSNMPGSVSPILGHSVKLFEEYYPVGDPLMGSGRPHITPRKKIWSDLNAHSDLYLALDWTPLPEQSEPGPLAAWKPFQAEETYCKCAEGNE NTPFDLRKGTLPGRNLERARQAYMHIEEKFPFELTEQHICEFQSMCYVLVRVLGACQSQTWILEPDGVSGPSKGASEAIGQCQSSAAKPRRSKGESVREPWA

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18561	48929	A	18670	1	1442	CSEYEDSSPAPVPATDLSSTLSS SVPQPDGTGTSQQLHPLDPWHE LLRAQELQGATNHHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSAFAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGSDWLPSSSAC KCLMLGLHFFVIVGNICATLKEK YSSMLHLDVTMKNKEKERTRL QKRKKGMPHPA/S*GPKHSCH HSPCQCPSSAK/SASELQGSWT PFGGLLTRTRMKFGAKTRDL QGTSLGRSLPCPPTLCSMRKIHL RPQVLRPTSPRNISPISNPRQR QVLSMDPKLRHRSRTGK/DSL LVFNHCRDTSIIHPCFKGVPR RDACLGPSPLAASPAFLEKGGD LINLAFKVYNNRKKLQFLASTV RQTAATSPAHNKFNQPEPQRP GVPEPPPTGACYMCRKIWPLG QANARSPGFLSRVPSVRDPTG NRTVQLTWQPLPEALELWPKA
18562	48930	A	18671	140	327	
18563	48931	A	18672	95	115	IIRHLCND*TPREGCLPSP*PAW SDTFETWVNNQASLQ
18564	48932	A	18673	218	674	MPISRPTARFKRIKVYYHSPAT AWFSKAYKLPLQFPHTCPKTR QGLQVTSGSAPYQPNCFVYPPR VAKTKYSPILNTSLHNPLLCSGS QTCFLY/SFLCTFHPSLSLSLGL TLTPIRLSKLRGLYCHKASQTA PITSIKPKFLPHLLPISA
18565	48933	A	18674	1	268	
18566	48934	A	18675	1	458	
18567	48935	A	18676	3	461	LLLTQSLFGLFTRTRMKFGAV TRIGGPPLGNQSPSSCSLLHEKD PPTSGPQTDQPKKHLTNFKSA ARPTFLGQGVPLNPFSTLS/E QVLLS*AARTPQSLISTPQLISV PQSLISVPQPLLYFSGGQEP PPP LLCVSSLSFRLASFTM
18568	48936	C	18677	156	329	
18569	48937	A	18678	449	667	
18570	48938	A	18679	79	311	

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18571	48939	A	18680	1	693	MAPTNCKGSRKCGRPHEQMPPH PYLPLLTFLSDSARLHPGEINSR VPHTKPVWWSLHTDAYEIWYH DSDWGDLPWEINPLSSCSLLHE KDPPTTSGPQINQPKHELMNFK SGPHWKSDCPTRQPLPGLELW PKA/HLTDSFPDLLSLAAED*CC LIALEAPWITDAELWITLTVED SQLYEDTLAGRSVLIKNLTP*TL Q/PLDGLDPT*SSIVPQLPSACRI LPTGFTVPE
18572	48940	A	18681	328	865	
18573	48941	A	18682	451	1238	TALLTQSLFGGLFTQTRMKFG AVTRIGGPPLEGDQSPVLLFFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPI/ ASHSML*KD*SLSLACYSMAF *SL*TLLTIPPFYLS*NQRRFTG* FRICALSTKLFCLSTPWCQTHIL SYPQYLPQSLILFWISNVLSLLF LCTLHPSLSLGLTLTPRLS KLPLGYCRKASQTAPITSVKPK FLPYLLPISA
18574	48942	C	18683	870	1037	
18575	48943	A	18684	933	4323	AASHLCGTPLE/IGLSNSPGSHSQ SPWNSGPRLSDCFPDLLG*VAE D*HCPIASEASWTVTIELWVTLT VEVAATALLILEALKITSYAPLT LYSSHNFQNLFSSSHLLT/PYTFC PQ/GPFSYTHSLLSPQSPLLLA QTSIRPPTLFLPHLTPMTVSL*/ ILTFIFPHISFFPVPHDHTWFD GSSTRPNRHTPAKAGYAIVSST FIIEATALPPSTTSQQAKLIALTQ ALTAKGLLVNIYTD SKYAFHI
18576	48944	A	18685	849	1944	WQVPLFSGRGKYPNPFSCLYP FSAFPGKRQELATSARNLSDHQ AKECLQPRIPKPCPIFAGPHWK SDCSTSPGQPLPELELWPKA/H LTDSFPDLLGLAAIED*HCPIAS EAPETITDAELPVTLTVEGKSIP CLIDTGATHSTLPSFQGPVSLAP ITVVGIDGQASKPLKTPPLWCQ LGQHSFMHSFLVIPTCPLPLGR NILTKLSASLTIPGVQLHLIAAL LPNPKPPLCPLTSPQYHPLPQDL

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18577	48945	A	18686	2	377	KGATIVYALDTLFIMEMKHEFE EAKSWVEENLDFNVNAEISVFE VNIRFVGGLLSAYYLSGEEIFRK KAVELGVKLLPAFHTPSGIPWA LLNMKSGIGRNWAWASGGSSI LAFTGLHLLEFMHL
18578	48946	A	18687	215	1135	PITLRRHLFFSGIGRNWPWASG GSSILAFTGLHGMKIVF*/HFF GNILFSIKVMNIRTVLNKLEKH YLN*KLHNSKIHFPLPDHVS GGGDSFYEYLLKAWLSINLRR DYKMLKNKCFSQAIETHLRKS SSGLTYIAEWKGGLEHKGMGH LTCFAGGMFALGADAPEGMA QHYPVSTVQENNPYSFPCPLV MKLGPEAFRFDGGVEAJATRO NEKYIILRPEVMETMYMFRL SGSDFSSFLLLPPQASSCFQTLF DLFKVPDLSCLIFERRHSSRQP YSTDQPFYLVGKRILFCPLT
18579	48947	C	18688	304	400	
18580	48948	A	18689	16	450	
18581	48949	A	18690	1	777	GHSMDMRVPAQLLGLLLWLP GARCVIWMTQSPGTLSPGER ATLSCRASQRVNSNYLAWYQQ KPGKTPKLLIYGASNLETGVPS RFSGSGSGTDFTITISLSQSE DIA MYCYCQYNNWPHPS/TFGQGT KLEIKRTVAAPSVVHLPGPSD EQLKIWELPSACVPA*NNFY PQ SRPKVQWEGGITPLQ/SG*LP QE SVHRGRTRQGTAPYSPQAPW TVRQSRJTEETQSLTACEVTP S GALRFRPVHKGAFNRGESF
18582	48950	A	18691	3	688	HASADAWAANAEEHRHDP R GTLREYKVVGRCPLPTPK/CH T PPLLACEIFAPNHVVAKS/RA F WYFVSQKIKMKKVQGGKIGL LVGQVF*ESSPLR/V*KNFRG SW LAAMDSRERAPTNNMLPGN NRG P*PPAGGCSTQLLTRDNGVAP G TGAPKPHFHFRIERLEGRFAG QQSCRRP/ALVQSSFDKIKFP ACPNGVLRRQHKPRF/ITKRP N TFFLGAGPSSGVCPK
18583	48951	A	18692	1	784	

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18584	48952	A	18693	1	4713	MQGPYLLWLPDSLEEGKEGL YLGNCIHTCLTVVPEDAFFPHF LTQHSGLTHLPSSDIPSHFMNNS TGRLAQRILGTSTEAFLSPEVM VVFHARNATVRTAMSLIERAK NCGHIPFFFTQGHYVLAKEQ VQRSRNKQVRELFPDGFSIHHA GMLRQDRNLVENLFSNGHIK LVCTATLA WGVNLPAAHVIK TQIYAAKRGSFVDLGILDVMQI FGRAGRPFQDFKFGEGIIITTHDK LSHYLTLLTQRNP
18585	48953	A	18694	313	489	SSCFKLHFQQLFKNCNTQMRN QIGFLRF*NNLVMLSSSVTNQ LELQKKIILLTKMQ
18586	48954	A	18695	1	851	ACGWALAQRPARRAMVAGID AGRSILGVLVSVCLLHCFGISC FSQQIYGVVYGNVTFHVPSNV LKEVLWKKQDKVAELENSEF RAFSSFKNRVYLDTVSR*PSLST T*TSR*KMKYEMESAKIVTDIT MKFLPYV*VSFQSPITLTCAL NGSIEVQCMPEHYNSHRGLIM YSWDCPMEQCKRNSTSIYFK MENDLPQKIQICLSNP/LFNTT SSIILTTICPSSGHSRHRALIP LAVIPTCIVLYMEWVF*KARN PDRTLQLIGNRRMKTTA
18587	48955	C	18696	35	181	
18588	48956	A	18697	75	344	PQVLRPTSPRNISPILNRVSDHA GTPALVLHP*RVQVPLFWGRGK YPNPYLCAPIPYFRT/HNLISLR PNLPCHPDLVSLCPDPFPAFLE
18589	48957	A	18698	1	268	
18590	48958	A	18699	39	376	QYISELQFLASTVRQTPATSPA KNFQTPEPQQGPPEPPPGAC YKCWKSQGHQAKECLQGPGRK PRPISGSHSQSPLELWPKA/HLT DSFPDLLGLAAED*HCPIASEAL
18591	48959	A	18700	2	295	CQTTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHP*RVQVPLF WGRGNHISGTQELPNT*TAV/V QAF/LPEPPPTG/CLLHVPEIWPL GQGMPPAGQDSS
18592	48960	A	18701	81	402	VKFGPEIWCRRSDQGRGGVGT SLGRSIPCPALCSVRKIYLRPL VLRPTSPRNISPILNRDPTVQLT WQPLPEPLELWPKA/HLTDSFP DLLGLAAEDRCCPIASEAP

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18593	48961	A	18702	165	439	PPRQAKMQNLAAPGSHSQSPW/TLRPKAL*LTSPQIFSA*RLKTD TARSPRKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
18594	48962	A	18703	284	511	IILVVKWANGRLCLTSRHSFTH QSLPS/PLCPVQLVFN/SRLSPQS QPQASLSLSNLPFLQTHLTSFPL PRLLLARPK
18595	48963	C	18704	414	557	
18596	48964	A	18705	1	1284	MNFEGTETLHCNGHCKVIAMT LGNQEVDNRNFSTGTTGPMEG MWLLSSNSHHSLKYAGALAILS AFQYQERGSQAGHRDSWPETK ETHFICGPKTPALVTDWEGSLP L VFNHCRDASLIHPRFSGVRPR RDACLGPSPLAATPQTITDTEL WVTLTVEVWDIST/LFPGN*SH A/TLPSH*NLITLTP/NAN/AIPQ HALKGLKPVITRLLQHGLLKPI NSPYNPILPVQKLDKSYRLVQ NLRLINKIVSPHPVVPNPAPFAS QITQAVSQALGIQWNLHIPYHP QSSGKVERTNGLLKVHLTKLSL QLKKDWTVLLPALLRIRACPR DATGYSRFELLYGRTFLGPNLI PDTSPLGDYLPVLQQAQAAAN LLLPTPDQPHEDTLAGRSVLV KNLTPTQTLQPRWTGPHFIYSTP TAVCLQDPPH
18597	48965	B	18706	1	933	
18598	48966	A	18707	3	435	TKETGFHIGPKTPAPVTDWEGS LPLVFNHCRDTSIIHPCFKGVR PRRDACLGPSPLAASPAFLKQ QDLINLAFKVYNNRKKLQFLAS TVRQTAATSPAHKNFQMPPEQ RGVVPEPPPTG/CLLHVPEIWP LGQGMPAARDSS
18599	48967	A	18708	2	111	
18600	48968	B	18709	1	595	
18601	48969	C	18710	1	1344	
18602	48970	A	18711	227	385	VPILPQPLLLHPAIFLSPPLTPG PAYSFVP*LALPHLSPNLLKR WLEPKA
18603	48971	C	18712	148	258	
18604	48972	A	18713	215	693	
18605	48973	C	18714	1	816	
18606	48974	B	18715	1	513	
18607	48975	B	18716	1	1452	
18608	48976	A	18717	1137	1303	

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18609	48977	A	18718	2	2107	IDMIFTGPPSTPKHKKSQKGS AFTFPSSQSPRNEPYVARPSTSEI EDQSMMGKFVKVERQVQDMG KKLDFLVDMMQHMRLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTIICNYSETGPPPEPYSF HQTIDKVSYPYGFADHPVNL RGGPSSGKVQATPPSATTYVE RPTVLPLTLDSRVSCSHQADL QGYPYSDRISPRQRSITRSDTP LSLMSVNHHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDTDTPFTPSGSMPLSST GDGSDSTVPLFLSSEILQKQVG QSITSMGLFSLRGPSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFLSLVSYS SFAFHKFSVAVYNISNLKTVD AKFPTRYCYCLNNRTNDLSDF ALLVDHGNSTSYLTFIKSTSL SVNQSNESDCIFCYMTGKSGR NLSDFWEIEEKYPIINYFTTSG SGVLALLLTQSLFGGLFTRTRM KFGAVTRIGGPPLGNQSPSSCSL LHEKDPTTSGPQTQDQPKKHLT NFKSAARPTFLGQGQVPLNPF FTLS/EQVLLS*AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPLPPPLLCVSSLFSLASFTM GAFTHGTQTPSTKATAPRYPQ TGDLSAEWPFAGEEPVLVPRP
18610	48978	A	18719	828	1063	RHSQAAED*HCPALAE/VPQTID AELRVTLTVEGYSLPPGCLRGL MLSVSGFSRSTVQAVSGSTVLG SGGQWFSCASV

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18611	48979	A	18720	183	1140	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHILTNFKSG ETKEMHFIRGPKTPVPVTDWEG SLLLVFNHCRDGLSDHSATFQG CQT/MAGMPALVLHP*RVVPLF WGRSKLLLARLS*VPILPQPLLL HPIILLSPPLLTPGPAYSFV*LS MSIHQVVLRPDEQGPGEQEQPP LYVMEPGEINSFIAHTKPVWWS LHTDAHEIWCHDSRGTSLGRS IPCPALCSVRNIRLPQVLRPTS PRNISPILNQERQRRCLFVDPK LRCQSRGTGKAAFSWCLIIAGTA SLIIQPHFKGVRPCRDACLGSPS LAASPAFLGKEQAAPCQALGPG NSSASAPPPYNPFITSPHTRSG LQFRSVTSPPPAQQTLLKKVA GAKDIVKASLAPALAQGVPGTP QATASEGASLKSWECLCGVNL ATAQSARVKEACQEACQSLPRF QRMYEKA WVPKQKTAEVELS QRASTRVVLRGNVGLESPPSRVF SIALSSGAVGGVHCPSDHRMIE PAAFNL SMKNPQRQSCSLRA
18612	48980	A	18721	372	906	LRSA DLPWEINPLSSCSLLHEKD PPTSSGPOTDQPKHILTNFKSE KKETRFIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWSFTLSSKSHFSGG RGKSLQVPEIWPPGQGM PAA QDSS*AVPICAGPRWKSDCPH LAATPKAPGTLAQSLTPSQIFL
18613	48981	A	18722	983	1980	KFGLVQLTLGKPLPELELRPK A/HLTDSFPDLLGLAAED*HCPI ASEAA*TTDTLRLVTLVEVW DIST/LFPGN*SHA/TLPSH*NLIT LTPLNANI/AIPQHALKGLKPVIT RLQHGLLKPINSPYNPILPVQ KLDKSYRLVQNLRLINKIVSPIH PVVPNPAPFTSQITQAVSQALGI QWNLHIPYHPQSSGKVERTNGL LKVHLTKLSLQKKDWTVLLP LALLRIRACPRDATGYSRFELL YGRTFLLGPNLIPDTSPLGDYLP VLQARQAANLLPTPDPQPHE DTLAGRSVLVKNLTPQLQPR WTGPHFIYSTPTAVCLQDPPH
18614	48982	B	18723	1	271	

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18615	48983	A	18724	803	1158	CSWHDRFPDWKAGNLLSLAA* D*HCPAIEAP*TITDAELQVTL TVEGSGDLPWEINPPSSYTLCE KDPPTTSGPQTNPQPKHSHQFQ IRDKGDTFFYPWTHNSGASHGL GRQPSLGV
18616	48984	A	18725	1855	2506	GASPSVWDPTENRTVQLHLGS HSQSPWNTGQSRDLTSFPDLL GLAAED*HCPITSEAPLITTDAR AMG*LTSTVEGKVPFLINTEAT HATLPSFGQGPVSLASITVVGID GQAF*TSCLKLPNSWCQH*TIRR FKHSFLVIP/TCQVPLLG/EDTLT KLSASLTIPGLQLYLIATLLPNP KPPLCPLVYPHLNPQV*DISTP SLGDRSCTPYHLIKT
18617	48985	A	18726	2	979	TSTMAVGNKRLTKG/GKKGA KKKVVDPPFRKDWY*RRKHPL MFHVRNIEKDVGPSRTPRDPKL QSDGLKGSVCLKVSPAELPE*L KFAFRKK/LITEDVSGVKTCPD LTSHGAWDLYP*QNCSCMVQK MGRPMIEA/HVECSR/LDGYLL /RLFCVGFYLNKRNISDHGRPSY AQPPNRVR/QIR/KKMMEIHDPO RLQTNVP*KEVVNKLIPASIGK/ DIEKACQSIYPL/QNVFVKKV KMLK/KPKFELGKLMELHGE SSSGKATGDETGA/VERADGY GPPVQESVGFRLPIVGNRSGH CVKKEKQSSRRRDFGVSVHPRI
18618	48986	A	18727	1	615	ASTAAPRMLLLFQPRYRTLQPO RLMLPKKNR/IAIYELLFK/EGV MVPK/DVPIKHP/ELADRNVP NLHVMKAMQVSQSPRGVYVKE QFA/WKISYWCLTN*GYQGV ISSRDYLHLPP/IVPA/TPLRRS RPED/SGRPSA*KGLEG*SDLAR LHKNGEAGQLPYRR/SAVPPG/ ADKKAEAGLGQKPEF/QFRG GFVRGRGQPPQ
18619	48987	A	18728	3	395	SAEVGAAETTLTLRRTVQSLEI DLDSMRNLKASLENSL/GILLHL ESELAQTRAEGQRQAQYEAL LNIKVKLEAEIATYRRILEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH

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18620	48988	A	18729	323	1973	PCMWIGFAAVRKGLKSSSASC GCTRRVRGTWWQGLSRVCVA RNEEVRLWGLCWLGSSPPAGW NNVFYMLISADVLACLEPRAN KEAANELAGAVDLGWMANVR RNPDMVSTHGLTHFHLRKTTP PRGEKTCELASQQPLIEATTKT KSVAVSHILTYTPPTLNGVAAV SSRVHFSFWPPTLQTGLEQGS SFTICFTTSTNYQSLHSIQPHSHS VQFISSTAKVYA VLRGLGSRSTS VSFSTFSWGWGSGGLAAGMP GIDNARLAADDFRVKYKTEL MCLSVESNVRGLHKVTD DNTV TRLQLETFMEALKEELFMKK NQEKEVKGLQALIASSELTMEV NAPKSQLSNIMADLPAQYDEL A\RK N*EELDKYWSQED/IEEHT TVVTNTSLLEVWSC*DARLT ELRRTSPGLWRFDLDSMRNLK\AS LENSL/REVEAPYAL/QMEQL\N GILLHLESQGLQTPRTEAQQA Q/EYEALLNIKVKL/EAEIATLP GRLLGRMAKDFNL\GDS\LDER NSFQNL\QKNTNTPPGNV\DGKVV S\ETN\DTKVL RH
18621	48989	A	18730	1	897	MGHHRQSLSPVLSLYSPDSMS FTTRSTFTTNYQSLGSVQAPSY GARAVSSAASVYAGAGGSGSRJ SVSRSTSFRRGMGPGLAAGM AGGLAGMGGIQNKKTMSLN DRLAS YLDRVRSLETENRRL KIREHLENKGQPVKDWSHYCK TIEDLRAQIFANTVDNACIVLHI DNARLAADDFRVKYETQLAMR QSVENDIHGLRKL ETEIALREE LLFMKNHIEEVKGLQAQIASFR LTVEVDAPKSQLAKIMADIRA QYDDLAKGNREELDKYWPQFQ EENTTVVTQSAEVGAA
18622	48990	A	18731	3	423	SLSPVLSLSPDSMSFTTRSTFT NYRSLGSVQAPSYGARPVSSAA SVYAGAGGLATGIAGGLAGMG GIQNEKETMQSLNDRLASYLDR VRSLETENRRLKIREHLEKK GPQVRDWSHYFKIIEDLRAQIF ANTVDNAR

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18623	48991	A	18732	663	2089	AFTTRSTFSTNYRSLG\SVQAPS YGAGPGRAARPASYAGAGGSG SRISVSRSTSRFG\GMGSGGLGQ RELAGGLAG\MGGIQ\NEKETM A/QALNDRGLGLFTWDRVRS LG DRRTRKLGRAKFRHFGRKKG PQVR\DWSHYFK\IEDL\RAQIF RKYLLDNAPHPFLQDLTIAPSL LD*F*EFKY*GQSLAMRQFLWR NDIPLGSAKV\IDDTQYHTDLQ AWRQRFEAPQRRELALSMKKE PRRRKLKGLSSPRLPSSWG*PVE VRLPPNFQDLRQRLADIPGN MNELGSKKNPRRKLQSTWSQ QI*GRAPQLVTTTSLLEVGSLLK TTL/TQKLRTSPGPWKIRPWTS MKKS*KAQLGRNSP*REVGRPP YGPYKMEASFGRGSLHP*SQS W/QTRPGAEGTAPQAPRSYEGP C*NIRSKLEA*DRPPYPALLE D\GEDF*SLVDPLDSKQLHAKPI QKTTTPPG*VGLGKVVS
18624	48992	A	18733	53	1100	NFRVEAGVRGVQKQKTCFAFKV LES\GKFG\GLALAVAGGVVNSA LYNVDA\G\HRAVIFDRFRGVQ\ DIVV\GKGTH\ALIP\WVQETQLS FD\CRSRPRNVPSQSTG*AKDL QNVQHHTAASLFRACRQPSFPR IFTSIGEDYGWSVCLPSITTEVL KVSVGS\WMLGELITKRE\LV RQVSDDL\TERAA\TFGLLDDV SLTHLTFGK\DF*AVEAKQVA QQEA\EGQICWLEKAEQKK\ AAIISAEGDSKAAELIANSLATA GDGLIELRKL/E*AAEDIA\YQLS RSKNITYLPTGQSVLLQ\LPQLR GPPLPCTSRGLDLGPQRLILNN SLSFLLPTEINCEIFMIGLK
18625	48993	C	18734	222	458	

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18626	48994	A	18735	2104	2758	QFCPSRQKGLQKTRHFVAGH GGDFLFRSPTHAFFFCVPLFLP P/VTIVRPCPPFS*VLSSSPRNSQ NTIPRSPFLSPGTLRSRPA GSRDP GNPAPGSNTRLGPTAPVSR LAP VDIGFRSTDCWSLQPVVPVNG SRPAPTNP RSRSTPVDPGSNTRL GPTAPVSR LAPV/V*ALGPLTAG PYSRP/CPVNPGRPAPTNP RSR STPVDPGSNTRLGPTAPVSR LA PVDIGFRSTDCWSLQPVVPVNP GSRPAPTNP RSRSTPVDPGTRTT PEGL
18627	48995	A	18736	2	280	AMGFIVAPSLGCF/VGSRFVHG EGLRWYAGLQKPSWHPHWV LGPVWGTLYSAMGYGSYLVW KELGGFTGVSRASEVAPPEPPP GSSVLCFLHA
18628	48996	A	18737	331	972	TAAAAAMAPPWVPAMGFTLAP SLGCFVGSRFVHGEGLRWYAG LQKPSWHPHWVLGPVWGTLY SAMG*VGVHWPGDKPLQGE AWPRTE DTGQALNWA WPPIF FGARQMGGALVNLLV SIGAA GHTTLGGRGAS/QWLAARLLYP \YLGLAWPSTTTTQTTCVWR/D NHGWHGGRRLARVSARPTMG LQLHQAGAITLVMW WPSRFHD HWAC
18629	48997	A	18738	1	603	
18630	48998	A	18739	1	1782	
18631	48999	A	18740	237	876	CESFCWHHFFWDIFNLVTA PF LVHVDYQGFESVAKKYDVMN DMMSLGIHRVWEGFSCSGKMH PLPGDQLLDVAGGTGDI AFRFL NYVQSQHQRKQKRLRAQQN LSWEEIAKEYQNEEDSLGGSRV VVCDINKEMLKVGKQKALAQG YRAAHKSGVILDCLWFPPILHPI AQICQLYLQNTSGIWPSPYLY CYHLLVQATIPSYLDCNSL

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18632	49000	A	18741	112	995	VLGSLSQEKRAETHFGFETVS EEKGGKVYQVFESVAKKYDV MNDMMSLGIHRVWKKDLLWK MHPLPGTQLLDVAGGTGDIATR FLNYVSPASEKTEEAVKGPTR FILGKNLPKSTRMKKIPWAG/TR VVVCDINKEMLKVGKQKALA/ KDTRAGLAWLL*DAEELPFDD DKFDIYTIAGIRNVTHIDQALQ GSSFGCLKPGGRFLCLGFSQVE QSPILSRLYDLYSRSRVIPVLGEV IAGDWKSQYLYVESIRRFPSQE VKFKDMIEDAGFPQ/V*LTKV*H QGIVAIHSGFKL
18633	49001	A	18742	117	403	
18634	49002	C	18743	62	370	
18635	49003	A	18744	179	527	IQEPPV1**GLHMVHNFTIFVSS YFKFESTFAISFLKVNT/CFFSI* IKSLDEQCVVGKISKHWTGILR EAFDADNFGIQFPLDLVDKMK AVMKVGICGNLVKQGNFTMT HSN
18636	49004	A	18745	3	1242	AAPQAGLSVAIAAQLHLHS TQCSSPNTCCLPRRTRATIIYSR WSYHPLGSPV*SP*PFQEAS/AL TLPPACSFYGPLT*FQPK*GSFP LSQ*MEYTIGLYT*TFHCPGTSR RQIPSSYLNCDAFLPLL/SNPP QCRPFTGVGLVDVLTGFETNN KYEIKNSFGQRVYFAAEDTDCC TRNCCGPSRPFTRLRIIDNMQGE VITLERPLRCSCCCPCCLQEIKS LDEQCVVGKISKYWTGILREAF TDADNFGIQFPLDLVDKMKAV MIGACFLIDRNCSPAMEQSWM ENYFDEMTIEGFRRSVITNSEL KEHVLTHCKEANKNLDKMLDE WLTRKNSVEKTLNELMEVKTI NEKLTIGKISKYWSGFVNDVFT NADNFGIHPADLDVTVKAAM IGACFLFAFRLGSELHN
18637	49005	B	18746	277	2415	
18638	49006	A	18747	102	196	

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18639	49007	A	18748	897	1656	SNAGLRHVCTSCSQGRARSCCH VGLHTPWVS*VPWHPWGIWR GDPQKQSRKCCVPGGAP/QK GGDPEPQPSLSVSWNLGSCA GFRAVLPRKPQRKVLFASSA GTAATEPPR**LAWKADSGGDP WQQPQQSARPHA*TWTRGD GAPPGRVA/QGRGTAGGASAG VSSGRSRGSPQTGFQALQSCLE ASRRPPVVACNPHAPALPAAQ AGNRATLMTGSLQPMIMYEE AQLRLEELCTKARLNCQWFL
18640	49008	A	18749	756	884	CLQRLPPGFRROPSKYRRNRG KSGKG*RPSPVATWQPDYNI
18641	49009	A	18750	1826	2772	RRVLEAMGPSRAAKVLSVCVR SRIGPLICSQRHPATSKTKPQGR PPGEQGTPRDNRPRNNRPARSA TPRGA/PQGAAPRPGEFPNAPQT IDKGPPSPPSRGHTRRLARSGNQ PPERHTPAAGGKTRYVRQSVL HRARGGEPVMPRLPRIAEE/P APDRVECF*VVQSPAREMHSCQ ADSMCPVW*GRIWRSAGSC*SR SEKILVWIPQSLQAHAACPSEA HKMPGNPRDGGAGICKSSPGG KGERRKVEGGSTTRAGTSRDS VSKRHANTMGEQAQGEKHPRG TV*KTKRRGPKQGTGRGKAPEE ETSREPPCTGPI
18642	49010	A	18751	196	322	
18643	49011	C	18752	189	650	
18644	49012	A	18753	1	53	
18645	49013	A	18754	31	449	
18646	49014	A	18755	1	389	GMPTSTIASCSQDGRVFIWTC DASNTWSPKLLHKFNDV VWH VSWISITANILVSGGDNKVTEG QQNEQ*QDRWGLAPHPAPGL PLPGPTNQTTGKSPQLQDDYFP RRSYRCSHRLICLNVIGNAL
18647	49015	A	18756	1	1041	
18648	49016	B	18757	15	782	

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18649	49017	A	18758	1	1425	EVKKINNAHTIGCNVSWAPAVVPGLSDHPSGQKPNYIKRFASGGCDNLKILWKKEEDGQWKKEQKLEAHSWVRDVAWAPSIG/IWPPSTIASCSQDGRVFIWTL**CPQAITVPLNCLHKFNDVVLGMLNWGPSQPTSLAVSGGDNKNGTNTVCPTGWLQDSNTLVHLV TYKMPRSLGLGLWCQLLSPRKYREGTSPVSLWVGVEWFNP DWWGSIRVYHPSPGSGYRTHKP PLNNLSCDTSIIRELLGKKFLLFVSVPVPSTVLGRKKVSVINT VDTSHEDMIHDAQMDY YGTRL ATCSSDRSVKIFDVRNGGQILIA DLRGWPRASRYQQGHQDLFIL RSDLP SQVFIRDKLMERRNRRTGRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSPVPTPHTF RHSYAMHMLYAGIPLKVLQSLMGHKSSISTEVYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
18650	49018	B	18759	323	1583	
18651	49019	A	18760	3	419	PSASSSPARIPAAATRQGRSPRIPAPSNEAPRLPADREFLEQQPPRFKPTIQASGADRAVDCGILKLQKSPARLARPRWPRRPSKRFWSAAGSVEEQPKPRRRAKSPEQSPQLSVLPLVTITPQASGASFEMKN
18652	49020	A	18761	2	385	WGRGGGRGLLYGRRHFVRRRRRGGRSPGESALTVT*GAV/PSAFRESAQPGPRSSSAHISTSPKRTDGGRDS*PGLPRSSLTPSLPRPASFSTSPGRVSAFHRLPRHS/AGPGLSGSS*PQPYSDPT
18653	49021	A	18762	242	422	

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18654	49022	A	18763	2	992	AREKKQKTRRQNKNIPIRQINKT QRICCC*QSCLTMTQDFFWPLCQ GHSRGAPCLLVPPGLSLTCAPA QPAARPGVSQLTCAIACTHIQW FPSSCPPSEKNGDTLTVKTPSA SSSPARIPAAATRQGRSPRIPPAP SNEASPAAGRPRVPGAA PPRFP KPTIQASGADRAVDCGILKLQK SIPARLARPRWPRRPSKRFWSA AGSVEEQKPPKAP/PAKSPEQS PQLSVLPLATITPQAYGASFEEK MKNLKTTRRGRSRWHFFNVIP QAPSLK WGFQTS DASSAEVFH VDRLASHKMGPRRPSPLW APPFCEAAAARRQEPGVCIMVE
18655	49023	A	18764	292	348	
18656	49024	A	18765	2	466	LITVVKLLDTMVDTFQLKLV AGSYQRFTDCYKCFYQLQPAM TQRIYDKFIAQLQTSIREISDIK EEGNLEAVLNALDKIVEEGKVR KEPA/WQRDTLRRHVQKQEA NQQLADAVLAGRRQVEELQLQ VQAQQQAWQALHREQRELVA VLREPE
18657	49025	A	18766	2	511	FNMAEASSANLGSCEEKRHE GSSSESVPPGTTISRVLKLLDMV DTFLQKLVAAGS/YSTPSLGRK CWS RLPSGGQSVKQAFSWAAC RLPQGRKEEISDIKEEGNLEAVL NALDKIVEEGKVRKEPAWRPS GIPEKDLHSMAPYFLQQRDTL RCHVQKQEAENQQLADA
18658	49026	A	18767	224	748	NRPVGRRAGYHRGGSYQRFT DCYKCFYQLQPA MTQRIYD/K FIAQLQTSIREILFDNQKQEGE PRKLSWNALG*KFVGTKGKVR KEPAWRPSGIPEKDLHSMAP YFLQQRDTLRRHVQKQEAENQ QLADAVLAGRK/QVEELQLQV QAQQQAWQALHREQRELVA VLREPE
18659	49027	A	18768	1	421	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
18660	49028	A	18769	666	1445	AGITTIEAAKRTIQVLHLQAND AQERAVERSQREFREERRAREPG LRLK*SFNNRRIQLVEEELADRA QERLGHLPCKKL*RS*KKLAD SERRY*RLFENRALKRLKEKIG TSREIPTQKKLKHICRKEADRK YEEVARKLGDHLKEDLEPTEVE RAVELAESRC*EIDEQIRLIDQNL QCLSAEDKYSQKEDKWEEE MKILTNKLREAE TRA EFAERS VAKLKKTIDDLLEDKLKCTKEEH LCTQRMLDQTLIDLNEM
18661	49029	A	18770	2	158	SAAPGAVPPPEADSTSAGMSRR PCSCALRPPRCSCSASPSAVTAA GRPRPSDSCKEESSTLSVKMKC DFNCNHVHSGKLKLVKPDIGRL VSYNPAYLEGSCDKICKDYER LSCIGSPIVSPRIVQLETESKRLH NKENQHVQQTLLNSTNEIALET SRLYEDSGYSSFSLQSGLSEHEE GSLLEENFGDSLQSCLLQIQSPD QYPNKNLLPVLHFEKVVCSTLK KNAKRNPVKDREMILKEIARG NFRLLQNIIGRKMGLCEVDILSEL FRRLGRHVLATILAQSLDMDLI NVSKVSTTWKKILEDDKGAFQ LYSKAIQVRVTNNNKFSPHAST REYVMFRTPLASVQKSAQTSI KKDAQTKLSNQGDKGSGTYSR HNEFSEVAKTLKKNESLKACIR CNSPAKYDCYLQRATCKREGC GFDYCTKCLCNHYHTKDCSDG KLLKASCKUGPLPGTKKSKKNL *RLHVGWHEPAPLQRPATPL LLQRQRPQRSDSRRAPSTLG

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18662	49030	A	18771	4	1276	RKAASSYVSRMALPIIVKWGG QEYSVTTLSEDDTVLDLKQFLK TLTGVLPERQKLLGLKVKGKP AENDVKLGALKLKPNTKIMMM GTREESLEDVLGPPPDNDVVN DFDIEDE/R*FEVENREENLLKIS RRVKEYKVEILNPPREGKLLV LDVDYTLFDHRSCAETGVELM RPLYHEFLTSAYEDYDIVIWSA TNMKWIEAKMKVKPLGVIWG KFSEFYSKNTIMFDDIGRNFL MNPQNGLKIRPFMAHLNRDK DKELLKLTQYLKEIALLDDFLD LNHKYWERPRVRCHIFHGKED RYDPCPMGACCKTVCTTNLA LPALPLGSMKNGQPCRNVIQK GYALTVINSQPQGLFVRILLG LFIRDFFPAGCGARPFWNEGLM AYFQRRTLVGVMLVLSSSKSFK
18663	49031	C	18772	113	257	
18664	49032	A	18773	143	330	HHGPVPFPRGLIS*HSLHCPCT PGGKNVFFFCYEYFLKLAGIETT NCSADKRGGKVKCLIPR
18665	49033	A	18774	3	432	
18666	49034	C	18775	112	192	
18667	49035	A	18776	3	1015	SSRPVRPRPAARLSAMSSTQFN KGPSYGLSAQVKNRLLSKYD PQKEAELRTWIEGLTGLSIGPD FQKG/LKDG/TIL/CTLMNKLQP GASVVPKINRSMQN/WHQLENLS NFIKAMVSYGMNPVDLFEAN DLFESGNMT/QVQVSLLAGG KRPKTKGAEEGLDIGVYSE KQERNFDDATMKAGQCVIGL QMGTNKCAQSQSGMTAYGTRR HLYDPKNHILPPMDHSTISLQM GTNKCASQVG/MTA/PGTRRHI YEYQAGNPTSCDNFSM/SLQ/M GYTQGAQTQSGQVF/GPGRPDI *TPSTCPQGTIADGAPSGTGDC PDPGEVPEYPPYYQEEAGY
18668	49036	A	18777	2	110	
18669	49037	A	18778	74	289	

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18670	49038	A	18779	138	2039	GAAMAAAGRLPSSWALFSPLL AGVALLGVGPVPARALHNVT ELFGAEA WGTAAFGDLNSDK QTDLFV/LAGKK*LNR/LFGRPE CTRILNPK*RYLSRITVH**QV*S LGAYDGDGQMDVLLTYLPKNY AKWMN*ELSSGDKIKH*ILTI*P YSIGL/LQDEPLIMDFNGDLIPDI FGITNESNQPIQLGGD/CYHGI QH*PLQVKCEFH/PHAFIDLTE DFTADLFGATLNGTTSTFQFEI WENLDGNFSVSTILEKPNMM VVGQSAFADFDDGHMGSFTC QGCGR*K/CAKRVPSYLVRSGM KQWVPVLQDFSNKGT/WGFVP FVDEQQPTEIPITLHIGDYNM DGYPDALVILKNTSGSNQQAFL LENVPCNNASCEEARRMFKVY WGADRPKSN/SKGAMVATFFDI YEDGILDIVVLSKGYTKNDFAI HTLKNNFEADAYFVKVIVLSGL SISNDCRPKITPFGVNPGLTYH VYNCRCKWVSEK WIR/WPNSAQ SAHLALQLPYNVLGFRVGSANF LDHL/SLGIPRPSWRKIFYGKQE WTAIIPNSQLIVIPYPHNVPKL GVPCNCLYTKLILFWLTAIALIR CLCFQSLAINWHFTLGREKKAG WIEEKRTRKAHRFP/WMAW
18671	49039	A	18780	1	966	
18672	49040	A	18781	1	1035	RPFVPVPGVQKCLPTRGGHLHG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSVASGREM VVLSVPAEVT/VILLDMEGTTTP IAFVKG/DILFPYIERKMLK/EYL QTHWEEEEFQ/QDVSLFEGNK A/EEDAHL/DGA/VPIPGKHLGIG VDDLQQM/IQAVVDNVCWQM SLDRKTTAL/KQLQGH/MWRAA FTAGRMK/AEFFADVVPA/VR/K WREAG/MKVYIYSSGSVEAQKL LFGHSTEGDILELVDGHF/DTKI GHKRRRVKVKTRK/ADSGCST NKHVFVWTDVTSRRASAGLRE AGCCTLAVVVRPG/NAGINR*L RKTTYSLITSFQWNYLPSST

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18673	49041	A	18782	1	528	DNELLDYEDDEVETAAGSGMS/EAAPAKKDVKGVSFHSISGFRD/FLKPELLRAIVDCGFEPH/PSEV/QHECIPQAILGMDFLCQAKSGM/GKTAVFV/LATLQQLPEPVTGQV/SVLVMCHTRELAFQTR*KTRPF/WNVTVCPSGEDTRVGKTELL/PPPLTAPT/WLPSFASPLLNPH
18674	49042	A	18783	207	309	PPHSALLPFFTPFLPSPQLEIFVD/DETKLTLHGLQQYYVKLKDNE/KNRKFDLLDVLEFNQVS*TSS/RGMSIGALQL*QKPGY*VHFY
18675	49043	A	18784	85	348	
18676	49044	A	18785	1	930	CCCRHTRSPCLVMAENDVDNE/LLDYEDDEVETAAGDGAEAP/AKKDVKGSYSFHSISGFRD/FLKPELLRAIVDCGFEPH/PSEV/QHECIPQAILGMDVLCQAKSGGER/QAVFV/LATLQHLPEPVTGQGV/CAG*CCHTRELAFQISKEYERFS/KYMPNVK/VAVFFGGLSIKKDE/EVLKKNCPAYPSVGTGPRIL/AL/ARNKSLNLKHIFILDECCKM/LAEQLDM/RRDVQE/IFRMTPH/EKQVM/MFSA/LSKEIRPVC/RK/FMQDVNTLLPSLPPLPARCLLP/LALFLRLPCHSSAKKAACAQLG
18677	49045	A	18786	96	1618	LFTPCFHLFCENPSRSPFSPAG/PVMAENDVDNE/LLDYER*MR/WETAAGDGAEAPAKKDVKG/SYVS/LSHSSGFRD/FLKPELLR/A/VD/CGFEHPSEV/QHECIPQAI/LGMDVLCQCKSGM/GKTAVF/VLATLQQLPEPVTGQVS/VLVMCHTRELAFQISKE/YERFSKYMPN/VKVA/VFFGGLSIKKDE/EVLK/R/RNCPH/VVG/TPGRILS/LWVRN/KSLNLKHIFILDECCKMLEQ/LDMRRDVQE/IFRMTPH/PEKQV/MMFQCYLGAKAIRPVC/RK/FM/QDPMEIFR/VDDETKTLTLHGLQ/Q/YYVVKLKDNEKN/RKLFDLL/DVLEFNQVVIFVKSQ/RICAL/APAY*WEQNFPALAHNRGDAP/RKERLS/R*SSSFKDFPTNEILIG/YPTLFGRRHGTSEAGETIAF*FM/NMP*GILKTLPCR/VGPEQGRF/GHPRGLA/ITFVSDEE*LPRSCD/DVQGSALRVKFS/ELPDEIGHLP/PTLEQDTGRRLAHFNGVDR/LFL
18678	49046	A	18787	1	363	

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18679	49047	A	18788	78	714	GTTEGRQAEAVGYLCVLP LTTL PLVTRLPPQVADTMLPPMALPS VSWMLLSCLILLCQVQGEETQ KELPSRISCPKSGKAYGSPCYA LFLSPKSWMDADLACQKRPSE KLVSVLSGAEGSFASLLARSIS NSYSYIWIWGLHDPKKGSEPDG DG*EWSSTDVMNYFAWEKNPS TILNPGHCGSLSRSTGFLKWKD YNCDAKLPYVCKFKD
18680	49048	A	18789	52	186	QSEVHHGISYTTGQGENLSEPI WKSWQRSQDL*QENHPEIYSLT
18681	49049	A	18790	666	2732	KQLIKMICYFILLILLSSHIGKD KAIDKNGILVQYVQE*KLVEPF *KAIWPPCMETLNVDTPFPQPV CLGIYPNE*KLSK/CFKP*APKV YFHGCL*Y*NHWEPTETIPVK GWIK*ILF
18682	49050	A	18791	112	340	
18683	49051	A	18792	3	323	LSSLASMSFTTCSAFTNYWSPG SVQVPSYGTQPVSHAASVYAG LGGSGSRISVSHSPMAGGLAG MGGIQNEKETMQLSRDLASY LDRVRGLETENWKLESKIQEH
18684	49052	A	18793	1	994	APSYRA/RLVRSVASVYAGPGS SGSRISMSRSTSFQGGGSRSM AA/GMAGGLAGMGGIQNEKET MQSLNDRLASYLDRVRSLEMG NWKLESKIWEHLEKKGQVRD WGHYFKTIEEDLTQIFTSTVDN TCIILQIDNAHAADDPRVKYE TEPATCQSVENDIHGLHKVIDD TSVTQLQLETEIEALKEALLFLA KKNHEEES/WRHTVQALEIDLD WMKNLEASLENSLK/EGVEAC YTLQMEQLNGILLHLESELAQT WAEQGQQAQYQALPNIKVKL EAEIATYRRLLLEDGEDFNFGDA LDSSNSTQTQKTPTC/RTVDGK VVSETNDTKVL
18685	49053	A	18794	3	377	
18686	49054	B	18795	54	136	
18687	49055	A	18796	149	419	

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18688	49056	A	18797	83	1402	A EKAGGKKGEAPSYRA/RLVRS VASVYAGPGSSGSRISMSRSTSF QGGLGSRSMMAA/GMAGGLAG MGGIQNEKETMQSLNDRLASV LDRVRSLEMGNWKLESKIWEH LEKKG PQVRDWHYFKTIEED LTQIFTSTVDNTCILQIDNAHL AADD FRVKYETEPATCQSVEN DIHGLHKVIDDTSVTQLQLETEI EALKEALLFLKKNHGEEIKGL SRRQIASGVD PWRVDAPKSSG PSPKIMGRHPGPKYDELARKR TREE/LAKYSSQ/QIEEST/TQLV TNTSLL/GGLELAETNLHRS*TY KSRSLDSTLDSIEKS*KAQAW KKQPLKGSWKAPLRPLPDWSK LQTGILACTFESRAGNKTRARG TSAPGPQEL*GPLLKHQKVKAG GLRSP TLPARLLEDAEAL*SLV DPLDSKQLPCNTIQKTTTPPG*V
18689	49057	C	18798	140	283	
18690	49058	A	18799	2	783	VVQFARREKPPSSKVSQRHPCT EAVREVLHG/NQRKSPQRSWET VELQISLKNYDPQEGQSAFSGT RQALSP LPRPKFSCVCPGGTQQ H/CDEA/KARGISPPHGTFEGA* KNLNKE*KNWSKKAGPRKY*L RFFGPQKSLDQSKIPPNSPGPGF K*RAGKVFPFPWFTHNENMGG PKLDEGEVPPIQVFQMKERCLC L/AVAV/GHVKMTD/DELVYNI HLGCQLSWVSLKKEKNWQNV/ RALYIKSTHGQSPKRLIFKAHFE
18691	49059	C	18800	239	555	

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18692	49060	A	18801	401	3014	TRASSTMSKSFQSSLSRDSQG HGRDLSAAGIGLLAAATQSLSM PASLGRMNQGTARLASLMNLG MSSLLNQGAHSALSSASTSSH NSQSIFNIGSRGPLPLSSQHRGD ADQASNMLASFGLSARDSDELS RYPSDTITPENLRPILLQLKRRR TEEGPTLSYGRDGRSATREPPY RVPRDDWEEKRHFRRDSFDDR GPSLNPVLDYDHGSRSQESGY DRMDYEDDLRDGERCRDDSF FGETHNYHKDFSEYERMGRG PGLQERSLFKKRGAPPSSNIE DFHGLLPKGYPHLCSICDLVPH SNKEWSQHINGASHSRRCQLLL EIYPEWNPNDTGHMTGDPFM LQQSTNPAPGILGPPPPSFHLGG PAVGPRNLGAGNGNLQGPRH MQKGRVETSRVVHIMGFSTE GKTLRYQLQLVEPFGVHFKEFI *FLNKNLLRAFIEMATTEDCFK AAVIDYTTTPALVFGKPVV HLSQKYKRIKKPEGKPDQKFDQ KQELGRVHLSNLPHSGYSDSA VLKLAEPYGIKINILMRMKS QAFIEMETREDAMAMVDHCL KKALWFQGRVCVKDLSEKYK KLVLRIPNRGIDLLKKDKSRKR SYSPDGKESPSDKKSKTDGSQE AERSTVEGKEQEEKSGEDGEKD TKDDQTEQEPNMLLESEDELLV DEEEAAALLUESQFSGETSDL
18693	49061	A	18802	3	1013	NCRAAWRAKLEGCLSLRRNAC QCFLIWTQTPDREQSYSLDQLP REVLNQEEKSISWDIYLHLEM GNGLSDQTSILSNLPSFQSFHIVI LGLDCAWKRQLSYTRLQFQLN L*NTVPYPKGFNTEKI*/RVTLG NSKTVITFHFWDVGGQEKLRP LWKS YTRCTDGI V FVVDSDV ERMEEAKTELHKITRISANRGV PVLIVAN KQDLRNSLSLSEIEK LLAMGELSSSTPWHLQPTCAIIG DGLKEGLEKLHDMIIKRRKML RPTRKRKDEYQFPNIICVGVGF LWSDFDKNRRVSTAGVCLSAAPP WMLLKL CFVEQFRCPTRVALW KMSKCSAS
18694	49062	A	18803	3	1103	
18695	49063	B	18804	34	734	
18696	49064	A	18805	1	1741	

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18697	49065	A	18806	6460	6635	RTSTERSHLKTRYQRTSCSSNR* LNSSSSKTSFRCSLTSLFWRHT IFNMLLINRLL
18698	49066	A	18807	5567	5853	IGILEA*LLRNLPNDISIKALVDA *YKSLLSAVERCSFMVLFGPEM NKPPLAILRIQSGVNRPPVISIM ALIGPLVTPSASTYSGVTNADLS SATK
18699	49067	A	18808	664	992	SCADIHGYHRGNSSNDSNLIP KQTNRDCLNNGHQNHSCNG/D *PQPQR**QLTLQNLMQHQ*KQ QYPLPQHQQE*RTR
18700	49068	A	18809	3	1698	
18701	49069	B	18810	227	883	
18702	49070	A	18811	180	373	PDTLRSILPMLLEQLFCRTFGLL SP**RDTSLHLGHKTEQHT*LV MGSWFYLLASQQPRCCYAC
18703	49071	A	18812	495	701	
18704	49072	A	18813	138	418	AYRLLLCLVYSEGFMHLEFQ NRLYHQLVF*GRLWHFWKSIK RFSIY*FFWYRW*YICKLNKGR LQDVIGVINT*CHFLS*GLH*TI PIHRL
18705	49073	C	18814	62	175	
18706	49074	A	18815	644	828	
18707	49075	A	18816	1	1107	
18708	49076	B	18817	84	342	
18709	49077	A	18818	3	1399	
18710	49078	B	18819	1	1377	
18711	49079	A	18820	1	546	
18712	49080	A	18821	855	1099	VTLYSEYQHPSVREYGLYLTSH RIEPLCEVHRTL*PVLLSMQPSV LEYEQQGYEAET*LEQECHH QRTSSL*DLKQLLQ
18713	49081	A	18822	1	1680	
18714	49082	A	18823	1	3951	
18715	49083	A	18824	2	6446	
18716	49084	A	18825	2497	21785	SSPYPTFKQSSNNFVFDGNELF NSRDRLSQRFLYLQSSVHLINR Q/LEGYVQHHLNLAET*HHGLG KDAYIAAMYNDDGATFQMEI GGIHTNAALAAGDKLQCIWRY LDVNGNAPAAENEFVVSVEG FGTSNFSVKCKGMLPGKFIGCD AFYKGYLQTDGPIKQVDSVKW FTNLTVSGSGRKLQGRKYPQ VVMGMGMSTGFDGYNLTPE RQVKMAYGLGYRDWWTYIG MSHYWKLTAQDKETGELI
18717	49085	A	18826	31	479	

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18718	49086	A	18827	255	1002	SQFSLSQLVLVDSEEGSLAAAA ELAAQKREQLRKRFRELHLMR NEARKLHHQEVVEEDKRLKLP ANWEAKKARLEWELKEEEKK KECAARGEDYEKVKLLFISAED AERWERKKRKNPDLGFSDY AAAQLRQYHPV*PKQIKPDME TYERLREKHGEEFFPNSNLLH GTHVAFHRGKFDREVLRSGKN QFEKRD/KF*ARRRPYNDDADI DYINERNAQFNKKAERFY\GK YTAIEKQNLERGTA V
18719	49087	C	18828	91	225	
18720	49088	A	18829	3	212	
18721	49089	A	18830	88	239	
18722	49090	A	18831	865	1898	QQQQQQHRRYPRRRSPRAWC SHPRSPLLFLPSLAPWPDQLTEE QIAEFKEAFLFDKDG\DTITTT KELAGTVM\RLSLGQEPNKKLE\A QDMINESGMLMG\NGTHLTFPR IF*LMMARKMKDDTSEEGN/LR EAFRV\FAKDONGYISAELR\H VMTNLGEKTTFR/KKVDEMIRE A\DDGDDGVNYEEFVQMMTG KMEDLTFLQPFSPPLEESNWNL LLTFLQKKKKKKVHLFHSCFL YSKTECQKYL\LVH\THQNLHVL VGGPCPLKDKQATHQFYNTCT NLNDNGLLKR\SILLMINTL\GL ASFFHACSFDDWSTSQGLWYL KLENGKNQISKPIPNGLV\HVFV
18723	49091	A	18832	1	330	WVVLKNCVGVGLLIAT*MWFI SNKYL\VQRQSRDYDVEWGYAF DVHLNAFYPLL\VLHFIQLFFIN PLPFLKNTVILLYPFAPLILLYGL SLALGWNF\THLCSFYKYRVK
18724	49092	A	18833	1	534	VPSNSVNSLVQNGVNLNSRDA ARH\TAGAKRYKYLRRLFRFRQ MDFEFAAWQMLYLFTSPQRVY RNFHYRKQTKDQWARDPAFL VLLSIWLCVSTIGFGFVLDMGF FETIKLLWV\LDVGVGLLIA TLM\WHCHFVKQVILLYPFAP LILLYGLSLALGWNF\THLCSF YKYRVK
18725	49093	C	18834	295	570	

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18726	49094	A	18835	418	1567	SFTLNKNCVLQRVSSILPNTAEV DFPSWTTQSDWQQTRAQVLLQ ARARAALRLVLIIRLHDGASPP MRTRLSPATLATGSGASEAPV SGDRKPAATTSGGPRRKMLPST SVNSLVQGNVLSNRDAARHT AGAKRYKYLRLFRFRQMDFE FAAWQMLYLLTSP*RVYRNF HYRKQTKDQWARDDPAFLGF PFKYSGFCVSTIGGFVFLDMG\ FFETIKLLLWVGLID\CVGVGLL IATLMMWFISNKYLVRQSRD YDVEWGYAFDVHLNAFYPLL VILHFIQLFFINHVNLTDTFICY LVGNTLAWLVAVGYILR*LSL GYSVGLLFFSSIAHF*KNTVILL YPPA/PL*FLPTGFPLALGWNF THTLCSFYKYRVK
18727	49095	A	18836	1	888	MPGLLLLRGSQNLKQQAELCG LGLALVISAVKPLSKKFMLPNP TSMKPESDGIYSINLKRTEWKL LLAGHAIVVIENSADSVISSRN TGQKAMLKFAAATGATPIAGH FTPGTF/TNQIQAAYWEPRLLV VSDPRADHQSLEASCVNPPAI ALCNTDSPLCH/VDAITCNKNG APSVQGMW*MLAWEVLHMRG TISCN/SPWEVMSNLYFYRDPPEE TEKEEQAAAEKAVTKKEFQ GK WTVSAPEFTVTQPEVADWSEG MQICNLGKAQQGQLSSDAEDD FWSLESLDGYSHITVTR
18728	49096	A	18837	74	848	REIFINVRSLMACFVKEEDVL KFLAARNP/HVGGTNLDFQME QYIYIRKSDGIYIIRLKRTEWKL LLAARAIVAIENPADSVISSRN TGQRAVLKFAAATGATPIAGRF TPGTF/TNQIQAAFRE/PRLLVVT DPRADHQLTEASVNLPTIAL CNTDSPLRYVDIAIPCNNKGAH SVGLMWWMLAREVLRMRGTI SREHPWEVMPDLYFYRDPPEIE KEEQAAAEKAVTKKEFQGEWT APAPEFTAQPEVADWSEG
18729	49097	A	18838	72	528	DEACGVCCYSPGASPMPP*GRT RKEGRTAGKVRPKERPCTPVN\ KSGGQGPKRKNWSKRQKFRDK LNNLVLFDKAITYDKLCKEVP NYYKLITPSLWSPERLKIRGSLA KGKPFQEA*VKGLI/RNLVSKH RAPSNFTPGNYQGWEDAPSL

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18730	49098	B	18839	6	125	
18731	49099	B	18840	249	291	
18732	49100	A	18841	128	669	RPGHAQTI.GSPSLALGMAGQF RSYVWDPLLILSQVLMQTVYY GSLGLWLA/VVDGLLRISPSLD QMFD AEILGFS/TPFQGRLSMM SFILNALTALGFAVISSGEEKQ CLDFTVTVHFFHLLGLLGSNSS PFSPSGG*TLVGLGPKPVVALH SLAVIGEYLCMRTELKEIPLNSA
18733	49101	A	18842	1	818	MAELTVMRFHTEPQGSEGLRLP RISGSKPKQMHVWTWLEPLNGI CNGNTGNAQLLPPGVIFHKYP SHYVTAMLKSLKWPLQTELTS SSGQALWGLVGGGSPHRQAST EKLFEKVPKTAENFPCSELSCF HGENGFL*GVPCFHLRFPVRY AVRGGDFHTAINGTGGKSHPM GKKFEG*ETSSLKHTGPGDLVP WQNA GPNTNGSPVFLTSCTAQ ELSGLDGKPCGVLA KVKEIGM NIVEAMERFGSRNGKTSKKITI ADCGTTPNKV
18734	49102	A	18843	4	454	
18735	49103	A	18844	1	978	MRWACDFTKLLSSTWTLIQYPE NAMIARWALLADCEPKTKAL RTTEDGIVDAANFEQFLQERIK VNGKVGNLGGGVVTEIKSKSKI TVTSKG/PFNSM*/*GSASFVEK KRLLFE*KLLSSTWTLIQYPENA MIARWALLADCEPKTKALRTT EDGIVDAANFEQFLQERIKVNG KVGNLGGGVVTEIKSKSKITVT SKGHQFYVNLRSFLICGKEKA VGILEEIVLNLLIFSSIDILTVKG TCSGCGERGFLEIYDEVEDSSYD NHLKDDDPKREGPGAQALST PPCCPLEKRINDQTLIISWSGST NVIEEAGRHSVVQEGWGALGV LRTTLPSLPQTGGAGFVGSHLT DKLMMDGHEVTVDNFFTGR KRNV EHWIGHENFELINHDVVE PLYIEGRAENQLSHTVPGPVDL SDRIVNGYFLSL

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18736	49104	A	18845	167	1440	RDIWLSASAAAMVPPVRKLV/AE GGQKTKQVLRFTLGCTHPIEDG IIDAANFEQFLQERIKVNGKVG NLGGGVVTIEKSKSKITVTSKG PFNSM*J*GSASSFVEKKRLLEF *KAENLSKKNWNKTRMPTFTTL TQVAPNPITGYTSKGKISTLKR YLAFLCRLCCHGAREKACGEGG QKTKQVLRFTLGCTHPIEDGIID AANFEQFLQERIKVNGKVG NLGGGVVTIEKSKSKITVTSKG HFQFYVNLRIISFLICGKEKAVGILE EIVLNLIIIFSSIDILTVKGTCS SERGFFLEICDEVEDSSYDNHLK DEDPKREECRKRDAYAPLKDQ GNAEKRRHNVRKSWPLLSAKL LKIRTNLTGTTEEAEHLHANHIQ VPIKCLSYKLTERRKNGTQKHLH YALILHVKCDRRETSKFTKFG THPLTALFVPRAWGPPSALPE SELAVFLVAYEGNTLLHLFLSG AEQRGNSSSLKERAGRARFQSHQ KLNEQTIPPNDLTKSSVDLQSSF SAVHPNSQPTVWVDMPAHPLS QYLVPARKTVLPWYGNSCPD VIFGSLSDSKLSEGEFALPLKF
18737	49105	C	18846	713	831	
18738	49106	A	18847	2	303	
18739	49107	A	18848	97	233	RTVTCYHRNSRACHPQQITSCP *HRALPCLPLWSPKCPSPWPWF G
18740	49108	A	18849	229	359	MKWVYCSVTGMGKGQHRMP/ SKG*GWVQRYNRDGIQSPRVLE LF

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18741	49109	A	18850	1	1185	MSTIDDPR LQGRMCLMLRGT PEQKALVIGGEACMWGEYVDN TNLVPR L WLCPPSTQDLANE G REMTILHRH I PDRGKGVMRSCS FRTPRPFTLACGPEKSLMDPQS QSNSEGASSSLVVKLADTDRE R ALRRMQQMAGHLGAFHPAPLP LGACGAYTTAILQHQAALLAA AQGPGLGPVAAVAAQMQHVA AFSLVAAPLLPAAAANSPPGSG PGTLPGLPAPIGVNGFGPLTPQT NGQPAPTRSTITGSP L /SGWSQ SRPILRIMKYAEQRIPTLNEYCV VCDEQHVFNQGSMLKIQPD TII QVWREDIPVNYMKELELVTKA GFRALLSAPWYLNRI SYGPDW KDFYIVEPLSFEGTPEQKALVIG GEACMWGEYVDNTNLVPR L W AHRIQL
18742	49110	A	18851	231	416	
18743	49111	B	18852	184	594	

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18744	49112	A	18853	247	2296	PVYLSIFMSCVGENGGSHIENW HSILRNLVNASYTKLQDIKGQ FWNDDESEGDNESEEFLYGVQ GSCAADLYRHPQLDADIEAVK EIYSENSVSIREYGTIDVDIAL HINISFLADEEVSTAWKVLRT PIVLRRLRFFLSQYLDGPDPSIE VFQPSNKEGFGGLGLQKKILGM FTSQQWKHLASNDFLKTQKEKR HSWFKIASGVTIKKFRAGLQHSF SPIPKSPSPFPYS*QDSMAGKGK LGVPELRVGRMLNRSISCTMK NPKVEVFGYPPSPQAGLLCPQH VGLPPPARTSPLVSGHCKNIPTL EYGFVLQIMKYAEQRIPTLNEY CVVCDEQHVFPQNGSMLKPAVC TRELCVFSFYTLGVMSGAAEE VATGAEVVDLLVAMCRAALES PRKSIIFEPYPSVVDPTDKTLAF NPKKKNYERLQKALDSVMSA REMTQGSVLEIKKQMDKVWIP UAHPLQWIISSNRSHIVKLPL SRQLKFMHTSHQFLLSPPAK EARFRATKLYGSTFAFHGSHI ENWHSIL/RGNGLVQWHSYTK LQLHGAA YGKGIYLSPISSISFG YSGMGKGQHRMPSKDEL VQR YNRMNTIPQTRSIQS/RFLQSRN LNCIALC/EVITSKDLQKHGEH LGCCPVFRPMSCTRFLPL*YED G/QVGDAQHYIPHGQQRVHERE
18745	49113	C	18854	122	486	
18746	49114	A	18855	1	535	KNAAGNFISPT/ERLSPNAWKTI TDIVLNGTAFVTFLSITTYAET GSGFVVPASAKAGVEAMSKS LAAEWGKYGMRFNVIQPGPIK TKGAFSRLDPTGTFEKEMIGRIP CGRLGTVEELANLAFLCSDY ASWINGAVIKFDGGEEVLSIGEF NDLRKVKTEQWDTIEELIRKTK
18747	49115	A	18856	3	356	
18748	49116	A	18857	1	1581	

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18749	49117	A	18858	2	1242	RRLLGPSRPPIRRPRQRFRQPRELCSFCAPACPGTACGGFRPEFWRI NMKLPAKVFFTLGSRLPCGLAP RRFFSYGKILYQNTALQSKFF SPLQKAMLPNNSFQGVAFITG GGTGLGKGMITLLSSLAGAQC IASRKMDVLKATAEQISFSNW EIKVHAIQCDVRDPDMVQNTV SELIKVAGHPNIVINNAAGNFIS PTERLSP*CWKNQ/ITNIV*NGT AFVTLEMGKHLIKAQKGAFA SITTIYA/ETGSGFCRYPASAAQ SRVWEAHGASLLQLEWG*NM GLRIPVDSNQGPIKTKGALYPS GPPTGTGEGKMGKQKFCGSP WGLVEELRKSLPAFLCSDYA S WINGAVIKFDGGEEVLISGDF NDLRKVTKEQWDTEELIRKT KRFLRLWPSSWLQKRE
18750	49118	A	18859	8	432	NSKLPPVVTSSQMRFMY/DPQT DQHMKNFPEQLPLDEFQKTD KDPANYILHAVLVHSGDNHGG HYVVYLNPKGDGKWCCKFDD VVSRCCKEEAIEHNYGGHDDD LSVRHCTNAYMLVYIRESKLS ELQAVTDHDIQQL
18751	49119	A	18860	1	211	
18752	49120	A	18861	1	242	
18753	49121	A	18862	3	733	LVHSRDNHGRHYVVYLNPKGD GKWCCKFDDVVS/QLVERL*EE KRINAQKVDRIRQEVHLYMQA QVASEDQFCGHQGNMDYDEE KVKYTVFKVLKNSSLAEFVQN LSQIMEFPQDQQLWPMQARSN GTRKPAMLDNEADGNKAMIEV SDNENSWITFLETVDLELAASG VTLPKFDKAHDVMMFLKMYDP KMRSNLNYCGHIYTPISCEIRDLL PVMCNRAFIQDTSLLIYEEVK LNLTERIQD
18754	49122	A	18863	261	659	KHLFYLFT*EITLYPDKHGCV DLLEECKKAVELGEKASGKLR LLEIVSYKIGVHQEDELLECLS PATSRTRFRIEELPLDLEECKK AVELGEKASGKRLRLEIVSYKIG VHQEDELLECLSPATSRTRF
18755	49123	A	18864	107	407	CVFFADTWSRSEATFQFTVERF SRLSESLSPPCFVRNLPWKIM VMPRFYDPDRPHQK/SGVFFLQR NAESDSTEDSLNDATTNPHIVA FHYWKPNLNSLV

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18756	49124	A	18865	2	3698	YVVRVSLPPPPPAAGRPGAAVAD DAREEEEEAAPPPPPPPRLAA ARPPGSQLPPPAAGEAQAAD MNHQQQQQQKAGEQQLSEPE DMEMEAGDTPPRITQNPVIN GNVALSDGHNTAEEDMEDDTS WRSEATFQFTVERFSLSESLS PPCFVRNLPWKIMVMPRFYDPR PHQKISVGFFLQ/CNAESDSTSW SCHAQAVLKIIYRDDEKSFSS RISHLFFHKENDWGFNSFMAW SEVTDPEKGFIDDD
18757	49125	A	18866	16	450	
18758	49126	A	18867	3	26	QSGHSDMRVPAQLGLLLLR LRGARCIDIQMTQSPSSLSASVG DRVITTCRASLDIRWLAWFQL KPGIEVKLLIYAATLQSGVPS RFSGSGSGTDFTLTISSLQSEDA MYYCQQYNNW/SSAPYTFPGIG TKVEIKTKLWAA/PSVLHLPGPS DEAVENLGTAFCLCALLEKTSN PQSRPKSTSGRVDNALPNGGK LPQGECSQKQD*TAWT
18759	49127	A	18868	3	694	
18760	49128	A	18869	47	1712	FPTKMAAVGRVGSFGSSPPGLS STYTGGLPNEIASGNGGAAAG DDEDGQNLWSCILSEVSTRSRS KLPAG*NVLLLGEDGAGKTSLI RKIQGIEEYKKGGLYLYLN VHE*MTGNDQTRCN/VWILDG DLYHKGLLKFSLDVSLKDTL VMLVVDMSKPWTALDSLQKW ASVVREHVDKLKIPPEMKQM EQKLIREFQYVERGEDFPASP QRRNTASQEDKDDSVVPLGA DTLTHNLGIPVLVVTCKDAIS VLEKEHDYRDEHDFQSHIRK FCLRYGAALIYTSVKENKNIDL VYKYIVQKLYGFPYKIPAVVVE KDAVFIPAGW/DNDKKIGILHE NFQTFKRQEDNFWKDIITKPPV RKVFVHEKEIMAEDD/QVFLMKV QSLLSKSKPP/TTEAGRPVDAIS PKESQGGSPNTKIESVSS*CCQ ACHPIPCWGQKKIDPNMESWE LTSGRAFLGKFSFNSFV*VKRL GSPRRPLVVSQG*PCRVGLGGG SSGLLPASTKKVQAYKPVLDV HAELDRINR*PVIVS/PTPTISIP

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18761	49129	A	18870	3	885	LVCLVRELLGPRFFLKVFLLPT FPGV/PAPVLTATLPFFHPEGR YQVE/YAFKA/I*PGGPLPSLAV RGK/DWA/VIVTQKKST*PNYL DSSVTVTSLFPR*LKNIW/CVMT GMTS*PADSQVQAR/YEA/AN WKIQSMGYEIPVD/MLCKKNCP IFLQVYHTEMLKMKASLR/C/M IFNWVIDEEQGPSRYIRC/DPA/G YYCGV*KPTASGS*TKLRSTGF LEKKCKKKKFD/WTF*TRQWET AINTLPLTVPIQLDFKTFQEIEV GVVTVENPKPRILT/EAEIDAQL VAPSKRRD
18762	49130	A	18871	1	471	
18763	49131	A	18872	1	1524	
18764	49132	A	18873	2	719	RPQRAGPVRRAGVMAALLDLAL EGMAVFGFVLFVLVLMHFM AIHYTRLHLNKKATDKQPYSKL PGVSLKPLKGVDPNINNLET FFELDYPKPLFFSVAPMKRIEKT QM**P*CSTY*YEVLLCVQDHD DPAIDVCKKLLGKYPNVDARLF IGGKKVGINPKINNLMPGYEVA KYDLIWICDSGIRGTMEMPMML EQSYDPNVDRDPIYRNNGDADG QHLVLHDFYQQGSGPKCSLINA
18765	49133	A	18874	200	370	
18766	49134	B	18875	323	448	
18767	49135	A	18876	2	421	FVGPDPGDPPESETHKLVVVGG GGVGKSALTQIFIQ/ILDTAGQE EFGAMREQYMRAGHGFLLVFA INDRQSFNEVGKLFQILRVKD RDDFFVVLVGNKADLESQRQV PRSEASAFGASHHVAYFEASAK LRLNVDEAFE
18768	49136	A	18877	2	236	
18769	49137	A	18878	1	763	MTPHSALRARGKGGGTGGGSE GSSSGGDMSSGAASGTGRGRPR GGGPGDPPESETHKLVVVGG GGVGKSALTQIFIQSYFVSDYD PTIEDSYTKICSVDGIPARLDILD PAG/QEEFGAMREQYMRAG/HT GFLLVFAINDRQEFSTRWGKLF HADFCGFKDRD/DFP/VVVLVGN KADILESQRQVPRSEASAFGAS/ HHVAYFEPSAKMRFNVDEGF* RSWCGVVREIPRNKELPPSPPK CPPGRMGGGCPCVLL

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18770	49138	A	18879	2	403	RFLARRTNSTFNQVVLKRLFMS RTNRPPLSLSRMIRKMKLPGRE NKTA VVVGTTDDVRVQVEPK LKVCALRVTSRARSRLRAGGK ILTF/DEVYRHF GKAPGTPHSHT KPYVRSKGKRFERARGRRASR GYKN
18771	49139	A	18880	1	1006	PKLR*PEPSRNQVLLTRFQIAVH F/LLSRLLQFFRPARSRAFLSRK PKPGPGKKPMALIVEF IGELPTG VHARPPSHVETLCNTFSSQIEW HNLRTDRKGNAKSALALIGTDT LAGDNCQLLISGADDEQEAHQRL SQWLRDEFFHCDAPLAEVKSD ELEPLPVSLTNLNPQIIRARTVY SGRAGGIQTPISSLDLNALGNLP AAKGVDALQSALENGTLVLK NIEFRLLDS DGATS AILEAHRSL AGDTSLREHLLPVGQCANAASS TNHPFVTKKRQCFVFRQLA NGRNDSGWQTHAFWFRFHQ SRIMKYLYGFTARLKEHQPKLR
18772	49140	A	18881	1	716	VCCEFCRAERRHHGEWTRIRN KDRKSGGARDPKPEGFLL*RC CVKLYRFSGPEEPNSNIQRLW LKRLFMSRTNRPSPVPFSRDES GKMKASLARGKQDRPVVVG PLT*LMLRVSGRPKTERVVAL RRGSPGPQAALQGGGKIPS LFDQAWPLGLPLKGLLALVPGS SGSLGKGAREGGTRQFSAKAP KETPQKPHQNPYVRISKGRKFE RARGPTGPARGYKKLTLGSSYL
18773	49141	A	18882	3	168	
18774	49142	A	18883	23	2669	
18775	49143	A	18884	279	396	
18776	49144	C	18885	960	1250	
18777	49145	A	18886	52	925	EVLEPRLGVFSNGCFQGLSSVM ALGLKCFRMVHPTRFNLYAASI RPVSEVTLKT VHERQHGHRRQY MAYSAVPVRHFATKKAKAKG KGQSQTRVNNINAAALVEDIINLEE VNEEMKSVIEALQG*FQ*GLSI* GPHQDPIDKIAVVT A*REALL*T RFSQISMKSQPLNFG*IWASFPE CTAAAIKAJRESGMNLPNPEVEG TLIRVPHSPK*PESTEKCWVKL GQTEHQQGPKTLLREGFRTQLN EQAGRNP KD/NSLQEDTIRLTEK QISQMADDTVAELYRHLAVKT KELLG

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18778	49146	A	18887	2	389	DSGSHCHAPPTTARRAFPIPGS KSNMATLKDQLIYNLLKEEHTP QNKITAVRVGADGMACAITIL M/KDYNVTANSKLVITGGARQ QQGESRLNLVQRNVNIFKFIIPN VAKYSPNCKLLIRSNPVDI
18779	49147	B	18888	217	423	
18780	49148	A	18889	27	1217	ARRPTRPPDLIATRRPRPARRCI SRFPFGSKSNYWQPLKDQLIYN LLKEEQTP/QNKITVVGAVG MACAISILMKDLADE/LALVDVI EDKLKG/EMMDLQHGKPFSTR NTKVLSSGKRL* ^M LANSKAGS FITGWGHRQQEGKKAVLILVQ AVNVNIFKFIIPNVVKYSPNCK LLIVSNPVDILTYVAWKISGFP KNRVIGISGCNLDASAFR/YLML G/ERLGSSEH*ACHGWGPGWGEH GRFPVLPVMGVGLNVAGVSLE DFWHPDFRTDKD*E/QWKE/VH K/QVVE/SAVEVIKLG/GYTSLG LIGLSCKPD/LAESIMEESFRRV HPS/SSHHGLKGLYGNKRMNV LSVPCILGQNGISDLVKG/TLTS EGRGPVGSKSADNNSWGSTKK
18781	49149	A	18890	1	264	
18782	49150	A	18891	3	736	
18783	49151	A	18892	81	1065	GKGPVAAFIDQSNIFLTDPKIFL GQWREEPKMPLLLGETEPLKL ERDCRSPVDPWAAASPDALALA CLCHCQDLSSGAFFNRGVLGG VLFPTVEMVIKVFVATSSGSIAI RKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMRENV*REK Q/NGIPLPSQ/NFEE/QYCC/DFD SFSAKKENIISF/LGWAPLPDS KGSEKAEEG/GETEAQKEGSED VGNLPEAQEKNEEEGETATEET NEEIAMEGAEGEAEETAEAE EEPGEDDFLGLFMLHFFHFSQ KMEAMKQHSNVLSTNQTELEY FGLKPAHPRVTEIMLPDLIR
18784	49152	A	18893	19	445	

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18785	49153	A	18894	1	622	QAAWILKARALTEMVYIDEIDV DQEGIAEMMLDENAIAQVPRP GTSLLKPGTNQTGGPSQAVRP TSHSEKPTGFLRPSTQSGRPGT MEQAIRTPRTAYTARPITSSSGR FVRLGTASMLTSPDGPFIN*SRL NLTKYSQKPKMAKALPEYIFHH ENDVKTALELAALSTEHSQYK DWVWKVQIEKRYRRLGMYRE AEKQLISAMKQ
18786	49154	A	18895	1	1651	MKAIECKSRTVKDWHNHQKLG EGNKTDSPPPQSEGNTANTLIL DFWPLEMIACCWETFPQRLTAE LFMNPTRHWGKYKNQSVGAL RAPLGQGPSRRGLPGRVGRRLQ FTPRPPLSWSAGPSLAAPAAMS SEMEPLLLAWSYFRRRKFQLCA DLCTQMLEKSPYDQEPPELVP HQAAWILKARALTEMVYIDEID VDQEGIAEMMLDENAIA/PSSTP ITQAGRPTGFLRPSTQSGRPGT MEQAIRTPRTAYTARPITSSSGR FVRLGRLGMYREAEKQFKSAL KQQEMVDTFLYLAKVYVSLDQ PVTALNLFKQGLDKFPGEVTL CGIARIYEEMNMSSAAEYKE VLKQDNTHVEAICIGSNHFYS DQPEIALRFYRLLQMGIYNGQ LFNNLGLCCFYAQYDMTLTS FERALSLAENEEEAADVWYNL GHVAVGIGDTNLAHQCLRLAV VNSNNHAEAYNNLAVLGDAEG /RHVEQARALLQTASSISTPYV* TAFILQQLIRFGDLQRSYVAA QKSEAAFPDHDVTQHILKQLRQ HFAML
18787	49155	A	18896	2	295	
18788	49156	A	18897	1	4470	MLGLGLLRRLRQGSNAVTRCRP LPVRRREGRRDGSPPWRSVVCRY CRCSRQTGASVTTVSLPSSSSP GLDPRGPRQASVKKPAEANPV LRPLVRHGTPYRDSEEGKREGL SRLRAVCRAGPRGRGSFSPRD ARASPLRHLVA AVTTGAASRR QRGARVRQSPSSSRRRAKRLRE CERRSLHAPPAMDASYDGTEV TVVMEEIEEAYCYTSPGPPKKK KKYKIHGEKTKKPRSAYLYY YDIYLVQQLPHLPQS

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18789	49157	A	18898	89	810	QRRSGCVLRMTIEWETAAIPAG GQRTDPDIKALWGSAGPDDVAR SMNLSLQDYIAS*RRKLCPSYLP VHSCQGGYAAKNLSRKAQ(CPI) VERLNTNSPMMHRRPQQPARK LMTVRIVQA/HAFEIITPCSQAE NPLQVLGEPPSINSGBPREDST HLGAAGTVRRQAVDVVSPLRRV EPGPFVWVACCTRRLVKGALFPFG TFKTIG*VAWAD/ELI/NACQGA PSNSYCL*EEGRVAFLEHVAKS NR
18790	49158	A	18899	1	365	DTHFK/DSHRTSTAHL/LSLQ GPSPPNPLPLGVPSIGMGLGPRG EGRANPIPTVLKRDQEGLYRS APQPRVTHFPWDTRAVAGRE RPPRVATLSWREERRREEKDRA WERDLRTYMNLEF
18791	49159	A	18900	203	427	
18792	49160	A	18901	95	482	ALQSPKLWGYFSGRKVFLNYFF SSQQVSEAVVATGSPRAWLTC LILPLPGIIFSVLPKAMSRLITF TPATDPSDLWKDQGGQQPQPEK PESTLDGLAAKLFYEALIGDES SAPDSQRSQTETPARERKR
18793	49161	A	18902	348	1660	GVTHLFLFCRKLRLNGIAGRIK GPGWIFFSYCRSLRLWLTGSP LSLALPCLILPLPGIIFLKFSQKAI VPGPLITFTPATDPSDLWKIDG QQQPQPEKPESTLDGAAARAF YEALINGDESSAPDSQRSQT* WPEERKRKRGLLKAPAAEAL AEGVASGRPVQGRSLEADDPMT YRLTSAQEGDLP*LMRLLEPH EAGGAGGNINARDAFWWTPL MCAARAGQGAASVYLLGPGVA AWVGVCESGRDAAQLAEEA GFPEVARMVRESHGETRSPENR SPTPSLQYCENCDFHQD/SNHR VTSTVHLLSLSQGPQPPLPLGV PISTPRF*ILLGGVGSPPGMGLG PRGEGRANPHQPLILK*GPRKG LG/YKISTPSPEVTHFFSFGIPRA VAGRERPPRVA/TLNWKE/ERR RREEKDRAWERDLRTYMNLEF
18794	49162	C	18903	135	299	

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18795	49163	A	18904	3	2074	ERSRPVALRAAVPRMNPSTPSY PTASLYVGDLPDVTTEAMLYE KFSPAGPILSIRICRDLITSGSSN YAYVNFQHTKDAEHAIDTMNF DVIKGPVRIMWSQRDPSLRKS GVGNIFVKNI.DKSINNKALEYDT VSAFGNTLSCKVVCDENGSKG YGFVHFETHAEAERAIEKMNG MLLNDRKVFVGRFSKRKERE ELGARAKEFTNVYKNGFEDM DADGRLK\DLFGKF\GPALCKEK LMTDESGSKGFGFVS\FERHE DAQKAVDEMNGKELNGKQIY VGRAQKKV\ERQTELKRKFEQ MKQDRITRYQGVNL\YVKNLD DGVDDERLRKEFSPFGTIQLVP KVMDDGLVAAGLGFVCFSSP EAEATKAVTEMNFRIVATEPLY VALAQRKEERQAHLTNQYYG RGMASVTEAVPNPV\IQPLPGQ APPRFTFMGRFSHRFRNRA\AY Y\PSQIAQTKTKFLRWGTGGGA RT\HPFQNMPCGYCQALAPRP I*GTM\RPASSQ\VPR\VMPTQR\ VANTSNTDKWVPRSCSLQAAA AYVLARPAPFPQYKYAAGVRNS \QQLH\NAQPQVTMQPCCSMV PRVQGTLWTCLPMVGHLPSPSR SKSQMLGWNGLFPSYKPMIHP YSLLVKSLG\MLLEIDNSEL\H MLVESPESLP*RVDEAVAGTTS PPQAKRGLAQKAG*QVPTGV P
18796	49164	A	18905	1	988	MAEDGEEAEFFAALYISGQW PRLRADTDLQRLGSSAMAPSRK FFVGGNWKMNGR\KRRLGELI GTLNAAKV PADTEVVCAPPTA YIDFARQKLDPKIAVAAQNCY K\TNAGFTGEISPG\MIKDCGQ PWVV\LGHSERRHVF\GESDEL\I GQKVA\HALAEGLGVIRLHLG RS*DERGSLGITTEKVVFE\QTKV IRR*T*KDWKQ\VVVLGLMSPV WGLWLLARLATPQQA\QEVHR RSSRGWLKSNVS\DAVASEPPV TIYGGSV\TGATLQRLAKPSP DVDGLPLWGGASLQARNSWDI IQCHNNEPPSHLPLRLCQAQG LKQTQKPK

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18797	49165	A	18906	46	468	TGPTHASAILVPRSLHKMPGE ATETVPATEQELPQPQAEATGSG TESDS/GKSPASDTYIVFGEAKIE DLSQQAQLAAAEKFKVQGEAV SNIQENTQTPTVQEESEEEVDE TGVEVKDIELVMSQANVSR AVRALKNNS
18798	49166	A	18907	1	360	
18799	49167	A	18908	52	513	QLGPHGHRQPGGPAVPHPRG LVPLPALLPSGPRRGRTQAPR HSGPAL*GHPASDTYIVFGEAKI EDLSQQAQLAAAEKFKVQGEA VSNIQDINTQTPTVQEESEEEV DETGVEVKDIELVMSQANVSR AKAVRALKNNSNDIVNAIMEL
18800	49168	A	18909	1	422	RSLCQTGLRQVVTG/VTKVTIGN LENLFVI/TKPDVYKSPASDTYI VFGEAKIEDLSQQAQLAAAEKF KVQGEAVSNIQENTQTPTVQEE SEEEVDETGVEVKDIELVMSQ ANVSRAKAVRALKNNSNDIVN AIMVSVQAFVP
18801	49169	B	18910	427	529	
18802	49170	A	18911	122	252	
18803	49171	A	18912	44	189	SKLDYKSSKRHRKPVSNFITSF QIWD*FLFFF*LKCQLQPRVFSQ PN
18804	49172	A	18913	2	609	PFLPEALHGNKQCNCNSTSGI CRVSVKVCPPWVHAKLCAPT LMSRDVTLDPAPVKKPCGEGG AKKKKQVLKFTLDCTHPVED GUMDAAQF*ASFKERIKVING KAGNLVGGGVDDPSKGARGKIT VTSEVPFSKRVF*KYL/TPKKY LKNNLR*PGLPRSLPNQPKKEK LPNFRYFQINQGRKEGGRGF KFPLSGKILL
18805	49173	A	18914	107	524	AGTHLPPFLPVAVRQPMALRY PIAVGLKQGPTKVTQEP*ASPR HHVRRGRLTKHTKFVRDMIRE VCGFSPYVRRAMELLKVSKD KIRALKFIKKRVGTHIRAKRRR EELEQQYWPAIEEKLACQERLE PLPLPSPLK
18806	49174	A	18915	39	465	

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18807	49175	A	18916	439	1586	TWGP PARRLPSGSHVPSA/ASSR LPSPHREEPQLQPAPVTITATM SSEAE TQPPAAP/GAPALSA DTKPGTTGSGAGSGPGGLTSA APAGGDKKVIATKVLGTIVKW FNVNRNGYGFNRNDTKEDV FV HQTAIKKNPQKYLRSVGDGE TVEF DV VEGEKGA E\AANVTG\ PGGV PQGSKYAADR NHYRR YPRRRGPPRHYPQ\NYQNS\ESG EKNRGIGRVLPEGQAQQRRPY\ RRRRFPYYMRPYG\RRPQY\ NPPVQGEVMEGADNQGA\GEQ GRPV RQNM YRGYRPR\RRG\ PRQKTA*ERAAMEEDK\ENQGV WDPRFGSPQ\RRYRRNF\NYR\ RRRPQKTPK\QDQGRPKAAG SHPA*EFVPLPEAE\QGGAE
18808	49176	A	18917	1	651	MTAFNSGKVDIVAINDPFIDLN YMVYMF LYDSTHGKFHGT VK AENGTLVINGNPIT\IFDQDPS KIKWAP/LAKVIHDNFIIIEGFM TTVHTITATQTINGPSG\INCHVM AAGLSRTSSLSLLA/LAKPVGK VIPELNGKLTGMAFHVPTANVS VADLTCRLEKPA/KYDDIK\NT HSSTFDAGAAIVLKDHSVKLIS WYDNEFGYSNRV\VHMAHNA
18809	49177	A	18918	2	5264	

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18810	49178	A	18919	3	1466	PRSAPRAASWLEDPREVRVSLR SAPPVRQSAIIFCVASRATSLR TPMGKVKVGVNGFGRIGILVT RAAFNNGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFHCTVVK AENGKLVINGNPITIFQERDPSK IKWGDAGAAYVVESTGVFNQ PWRKAGAHLQGGAKRVMSAP SG*MPPMFVMGVNHEEV*QTA FKIIISN\ASCTNQLA*QPLAKG*F HDNFG*SWEGLMTTVVPWPSLG NPRKTV\DGPSRG\NCGPWMGR GGFSRNIFLCY\WALPRAVGKG HP*A*TGKLTG\MAFPVSPSTAN VVSGWTLTCRFRKNLPKY\DDI KEGW*KQAFGGAPSKGIPGLQL SHQV\SSDFNSDT\HSFHPFDA GA\GIA\NDHFVKLISWYDNE FGYSNRVVDLIGPHGLQGSKTP WTTEPQARSKKGKERPSLLGSP CHTQTPTTLNLPSSQLPCRPLEE GRGLWEPHVMYPSN\KVS LCS TKKKKKKKKK
18811	49179	A	18920	3	364	STVINIHSETSVPDHV/VLVPVQ HPLLE\RCCLGFIAFAYS\VKSRD RKMVG\DV\TGAQ/\ALCLHRQVP EHLGPD\SGHPHDH\WIHPVTGIR LCDSLPY\YVTDNTGKTGLLVA AHS\QLPHSTVQCW
18812	49180	A	18921	41	696	PDRRWSSLGHHESHCPNHSSLL STVASPPNYEDAQGR*SR/EVA VLGAPHNP\APPTSTV\IHIRQSR PPWPDHV\VWSRVQHP\Q*TPA CLGFI\AFAYS\KSRGQGRWLG DV\TGAQGLMPPPAKV\PETIWG PDFW\GILNDHF\VIRHPQWLIFP GHGIDQGRHHWRPGAL\PI/VTC IPRL\LP\TISIPRPAPRSKSCISPYI LTRFSTMAFNKSARVSGKKKK

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18813	49181	A	18922	127	1016	SNLILRLNLCFPHLALASSAFDKC QEEETVEKTELLAERRGLTENH PGNPITAGHHEPHCANLLSCQQ RRLPNYEMLKKEEQEVAAMLGA PQKPCLECPPIVHPQARPPWP DHVRLGPCFNNPLQ*TTCCPGL SLGISAYFRGSFRGTGKMV/GD VEPGQGLMPPTAQVAP*TSGA PDFLGSLEPHLAHQSSPPKCW VVPGAIDQEAASLRPA/LPVT CUPRTLSSPSLPPEARELLPFD LYSTSTFHSSPCPHSRVLHQPF ILTRFSTMAFNKYVMFLVKKK KKKKKKV
18814	49182	A	18923	115	652	VSESTDLVSGRLVTRA/AFNSG KVDIVAINDPFIDLNYMVYMF/ QYDSTHGKFHGTVAENGKLV INGNPITIFQ/ERDPSKIKWGDA GAEVYVVS/TLGVFTTMEKA GGSFRCGGAKRVIHLLPPLA*C PPCFVMGVNHEKDDN/TLKIIS N/ASCTTN/CLAPL/ASTGAAGKC GQGHPEA
18815	49183	A	18924	91	399	
18816	49184	A	18925	26	304	
18817	49185	A	18926	18	203	
18818	49186	A	18927	23	355	
18819	49187	A	18928	1	211	RLLRVRGPPSPRPPGTPAGRQA RHTAPVPARASPSTPPRKLKER APALASPERGSHSAEGRAPQ VPPK
18820	49188	A	18929	2	800	
18821	49189	A	18930	1098	1560	VSCPFTVIIFCYNFCRGGFSTTA VMARAKSMFLMLKKGAGPDF GIRFTASSGWFT*FEDRYALHN VNMNAESVGVADVKAAE/DFGS LIMEEYLP/QFFNMEEPSLFWK QMPERTFVICPKGFFPDHCNKE RPWHFCKRKS/LDTRVATPCG
18822	49190	A	18931	33	211	
18823	49191	A	18932	110	624	CHLSKMLRSPQELARLPGGQRQ LTRW*QRWPLWTIALVLVLWR VKSGP*S*RVSPSP/PVEPVWT LNMAGAPHGNAFPFGGPPHP VPQPGYGCQPLGPYPYPYPPPA PGIPPVNP LAPGMVGA/VIVDK KMQKMKKKAHKMKHKQKH HKYHKHDKHSSSSSSSSSDSD

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18824	49192	A	18933	2	664	CEPLRISGRPTRPGERSKPRRLR ER*WGWRTLNMWNPNAQGQ GPNPYPPNIGCPGGSNPAHPPPI NPPFPFGCPPPPGA/PHGNPAFP TGGPPHPVPQMGYPG/CQPLGP YPPPYPPAPG/PPVNPAPG/M VGTKQLISRQEDCRRKLKAS* KRCHKA/HQKHHK/VHKHGHK FLFFPPSFQAVISGLEAYRALDP SLKSHQFCSPK/LQMPCCGTGGM
18825	49193	A	18934	3	409	QTQVVIDAG/ALA VFPSSLTNP TNIQKEATWTMSNITASR/QDQI QQVYNHGLVPFLVSDLS/KDFE TQKEAVWA/GGTVEQIVLVH CGIIEPLMNLLPAKDKIILVILD AISNIFQAAEKLGETEKLIMIEE CGGV
18826	49194	A	18935	133	400	VLGPHGLGDHLGQFHSCQSRA EPPIAGEDIHAGLDEPDCLTKDF LRI*LQLSTQLHAGQEEEDQNV VPETTSEGYTFQVQDGA PGTFN
18827	49195	A	18936	218	863	
18828	49196	A	18937	106	1879	TQSALQPLIPASPSPWKAQARF GAFSLCLITMSTNENANTPACP VVHRFKNKGKDSSTEMR/RRRIE VNVELRKAKKDDQMLKRERL *AHFLDDATSPLEN/RNNQG/T LLNWSVDDIVK/GINSNVENQ LQATQAAR/KLLSREKOPPIDNII RAGLIPKFVSFLGR/DCSP/IOF ESAWALTNIASGTSGQTKAVV DGGAIAPAFISGWASSHAHISEQ AVWALGNIAGDGSVFRDLVIK YGA VDP/LALLASS**CQSLAC GYLR/NL/TWLSNLC/RNKNPA PP/IDAVEQILPT/LVRLHHDDP GSRVQDT/CWGYFFPTLLDGSK WNGIGHGW/VKQGVVPQLVK LLGASELP/IVTPA/LKSP*GNNW HLGTDQEQVVD/IDAGALA/V FPSLLTNPKTNIQK/EATWTMSN ITAGRQDQIQQV/V*NHGLVPF PLSVFLSKADFKTQKEA/VWAV TNYTSGGTS*TEL VYL/VHCG/II EPLMNLFYCKRLPRIILLILDAN FKISFQPAENLVIDLEKPSINLE/ ECGGLRPKLKALPKPMKMEVS YKASVKA*FEKYFPCRGKEGRI KTVVPE/TTSEGYTFSSRMGPP

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18829	49197	A	18938	2	251	KVTNVKDGTTHTQTSLELFMYL NEVAGKHGVRIDIVENRFIGM KSR/GMNVQGDYEPDTATGFIN INSLRLKEYHRFQSKVTVK
18830	49198	A	18939	1	888	MSSKGSVMVLAYSGLNTSCILV WLKEQGYDVTAYLANTGQKE DFEEARKKALKLGAKKVFIEDV SREFVEEFWAAIQSSALYEDH YLLGTSLTRPCIAHKKVTETVQR VGAKYEGPWRAPWRMPFYN WFKGRSDLMEYAKQHGPILVT PKNLWSIDKNLMHISYKAGILE NPKNQVPPGLYTKIQDPKAPN TPDLKIQFKKGVPRVTSVKD GTTHTQTSLELFMYLNEVAGKH GVG/YIAIVENIFTRQRP/PECEP VRPCIAKSQEP/PEGKVVQVPVK GQVYILGWESPLSLYNEELMSV NVQGDYEPIDDTGFININSLRLK EYHCLQSLLEFAGCRLQTLFAW VSPAGAAEQRLLPVPSSGNFIP EGHLPDASWSSPV
18831	49199	A	18940	1	1155	
18832	49200	A	18941	1	993	MSSKGSVVLAYSGLDTSCLV WLKEQGYDVIAVLGQAVKGN QLLPVSLVKRKTTPGAQYANR LSRVPGRFINAAGTTGFPTGKR AGNDQVRFELSCYSLAPQIKEM GSLKVRNE/LQEVSTVMPAST QLPADTQCKLAE/LSAPVKK*T LGLSKT*QTQVMSQSSADSMR AWYRN*LFTNPTVRRLGNSPVT GSSLPRLPG/RGIYETPAGTILYH AHLDEAFTMDREVRKIKQGLG LKFAELVYTGAECKLLVASVPE PWRGRGGVEEGRDIKEVQEH GSDSAESSTHPPASRPGEGLA CIFCGKWRHLNTPLCERYPRH SRDHRPH
18833	49201	B	18942	324	1035	

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18834	49202	A	18943	29	1516	KQIPDAGNSRLQSQTLSSKGS VVLA YISGGLDTSCLVWLKEQ GYDVIA YLANIGQKEDFEARK KALKLGAKKVFIEDVSRFEVVE FIWPAIQVAHLYEDRYLPGH LSLPGPCIARKQVGNPSGRGA KYVVPTGATGKGNEQVRFEL SICYSLAPQIKVIAPWRMPEFY NR/FKGRNDLMEYGKATLGFFI PVTPKNPWMDENLMHISYE AGILENPKNOAPPGLYTKTQGP SOKPPTLDILDSSFFKKGVPVE GGPTFKDGTTHQTFLAELFMY LNEVAGKHGRRAVFDI/VENRF IGN*SPRGILRRTPAGHHSFYH AHLDIRGLSPWDRGSGKIKQG PGAWKFAELVYTGFPQAPE/ CEFCPTGTIAKVPRKPSGKGKV QVVRSEFGPQVYI/LSGREIPHC LLLTMRVLVKHGTCGDYWRP IDGHRGSSKHQIPFKAEGNYHR LPRAKVTQIDPVYNEELGPPQ FSGSPQVTGANCDDNL
18835	49203	A	18944	1	560	GRARTPANMALRVVRSVRALL CSLRALWAPAVPCLPRPWQLG AGAIWTLTGPVLLWVCKFTE KHEWITTENGIGTVGINNFANE ALGDVVYCSLSEVGTKI*TKPS WSLVLLE/SVKAASEL/FSPLSG EVPDFNEALAE/NPGLVTKSRY EDGWLKMTLSNPFRT*MHL MSEEA YEKYK/SIEE
18836	49204	A	18945	3	108	
18837	49205	A	18946	1	845	MAIPGIPYERRLLIMADPRDKA LQDYRKLLLEHKEIDGRLELR EQLKELTKQYEKSENDLKALQS VGQIVGEVLKQLTEEFIVKAT NG/PRYVVGCRQRQVIELPLTNPE LFQRVGIIPPGCLLYGPPGTGK TLARAVASQLDCNFKVVS IVDKYIGESARLIREMFNYARD HQPCIIIFMDEIDAIDILPNEQA RLDILKIHAGPITKHGEIDYEA1 VKLSDFGNGADLRNVCTEAGM FAIRADHDFVQEDFMKAVRK VADSKKLESKLDYKPV

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18838	49206	A	18947	3	1181	LLIMADPRDKALQDYRKLLLE HKEIDGRIKELREQLKELTKQY EKSENDLKALQSVGGQIVGEVL KQLTAEKFIVKATNGPRYVVG CRRQL*QKVSCLKPGVTRVALD MTLTLTMMEDILPRVEVDPLVYN MSHEDPGDVSYSEIGGLSEQI RGI*GEVIGLPLYKPSYFQVRVG IIPPKIGCLLYGPPGTGKNT/LLA RAVASQLDCNFLKVVSISIVDK YIGESARLIREMFNYARDHQPCI IFMDEIDAIGGRRFSEGTSADR EIQRTLMELLNQMDGFDTLHR VKMIMATNRPDTLGPALLRPG RLDRKIHIDL PNEQARLDILAKIH AGPITKIHGEIDFESNC*SFRMG FNGADLRNVCT*SQACSPIRAD P*FC*YREDFWKA/VRKVA
18839	49207	A	18948	1	220	VNMRDRFGQIMENLRRRQCEL AGVETCKSLES/RIESLEFLDEM */LLEQLM/RHYCLCWATKGGN ELGLKEITY
18840	49208	A	18949	1	645	
18841	49209	A	18950	10	1226	AAPAEPRALPSSVAFSLWLAP SPAARRPRFVPGGAQLPGTVH ARWPARQRRESSITSCSTSSCD ADDEGVRGTCEDASLCKRFV SIGYVWHDPYIQL/VRLSKQR/ KAPEINRGYFARVHGCSVQLIK/ AFLR/KTECHCSNCSNLGGQGM GSPPFWRDKDEDLSSQVNIFEV DFPMIVTRKLHSIKWLAFLPSS PILELHSEDTLQMASDCIC/DGH ILDSKRYAVIGADLRDLSELEE KLKKCNMNTQLPTP*IAECLV VYMTPE/QSANLLKWA/INSFE RAMFYYYQQVNMGDLFGQIMI ENLRGRPV/CDLAGVET/CKSLE SQKERLLS/NGWENKHPVRT* LEFVPPGLPSKLG*SRIESLE/LD ENWELLEQLIPHYCL/CWATQR RK*SLGLKEITY
18842	49210	A	18951	3	502	TEANTLN*RLQNME/ARLAE/ RKFM/NPFNMPNLYQKLESD/P RTRTLLSDPTYRELIEQLRNKPS DLGTLKQDPRIMTTLVLLGVD LGSMDEEEIATPPPLPSSMS LSPAPSCCLGCSPIVGFFIWGS GHVMGRGGGSSSLRSQLSHV YSASPSPIKQASWAWL
18843	49211	B	18952	1	1071	

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18844	49212	B	18953	67	1026	
18845	49213	A	18954	2	1910	PVASSMFQKAARAVGNAERTD SIQRCSGPRCAMEQVNELKEKG IKALSVGNIDDALQ/CYSEAI*/R LDPHNHVLVSNRISAA YAKKG DYQKAYEDGCKTVDLKVPDW GKGYSRKA AALEFLYRFEEAK RTYEEGLKHEANNPQLKEGLQ NMEARLAKIRKFMNPFNMPNL YQKLESDPRTITLLSDPTYRELI EQLRNKPSDLGTLKLDPRIMTT LSDLLGVDLGSMDDEEEIATPA PPPPAKKETKPEPMEEDLPENK KQALKEKELGNDAYKKKDFDT ALKHYDKAKELDPTNMTYITN QAAVWFKEGDYNKCRELCEK AIEVGRESIREDYRQIAKAYARI GNSYFKEEKYKDSIHFYNKSL AEHRTPDVLKKCQAEKILKEQ ERLAYINPDALAEKNKGNECF QKGDYPQAMKHYTEANKRNP KDAKLIYSIRAACYTKLLEFQL ALKDWEEWYQLEPTFIKGYTR KAAALEAMKDYTKAMDVYQ KALDLDFSCKEAADGYQRCIM AQYNRHDSPEDEVKRRAMADP EVQQFMSDPAIMRFILKQMOK DPAQALSE/HL*RNPLLPREIQKL MDVGSDCCKFGDDLFIAPFLCPS CGKRSWDRGEQAARSGRESST ERKGEQGERRPSSPYIYT
18846	49214	A	18955	2	293	
18847	49215	B	18956	53	182	
18848	49216	A	18957	2	403	
18849	49217	A	18958	3	1646	
18850	49218	A	18959	3	408	
18851	49219	A	18960	1	2458	

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18852	49220	A	18961	88	1511	LWPLGMA SNSSSCPTPGGGHL NGYPVPPYAFFFPMLGGLSPP GALTTLQHQLPVSGYSTPSPATI ETQSSSSEIIVSPSPSPPLPRIYK PCFVCQDKSSGYHYGVSA CEGCKGFRRSIQKNM VYTCHRD KNCIINKVTRNRCQYCR LQKCFE VGMSKESVRNDRNKKKKEVPK PECSesyTLTPevGELIEKVRKA HQAETFPALCQLGKYTTNNS/SE QRV\SLDIDLWDKFSELSTKCI KNGEGRQGRLPGFTTLTADQI TLLKVAACLDILILRICTRYTPE AGTP*PSWDGLTLNR/TQMHN A G/FGPL/TDLVFAFANQLPLAE MDD/ARETGLLSAICLICGDRQ DLEQPD RVDM LQEPLLEALKV YVRKRRPSRPHMFPKMLMKIT DLRSISAKGAERVITLKMEIPGS MPPLIQEMLENSEGLDTLSGQP GGGGRDGGGLAPPPG/SCSPSL SPSSNRSSPATHSP

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18853	49221	A	18962	143	2159	LTHSSTWLGRSCNHDRRQMGSKVMSYVVVAGRGTCAQETPIYTIRYLEDKQYGGSLGVDSVLA RLFSGASVLFISGPPFSSYLSGVPPGHPMEDSDMDMDMSPLRPQNYLFGCELKADKDYHFKVDNDENEHQLSLRVTNLLGGLVAKG*VAHLLKAEATFEASPNLK VTTWATLKMISVPAQRVFPPLG LLLKITPTRWVLKGLKVWVQG PVHISGTAL**LWEGRCQSPED EEDVNRVLFMKPKGRGLKH MFGDLVCSWKLAAIETQSSSE EIVPSPSPPLPRIYKPCFCQCD KSSGYHYGVSACEGCKGFRRS IQKNMYYTCHRDKNCIINKVTR NRCQYCRQLQCFEVGMSKESV RNDNRKKKKEVPKPECSESYTL TPEVGELIEKVRKAHQETFPAL CQLGKYTTNNSSEQRVSLDIDL WDKFSELSTKCIKTVEFAKQLP GFTTLTIADQITLLKAACLDLIL RICTRYTPEQDTMTFSDGLTN RTQMHNAGFGPLTDLVFAFAN QLLPLEMDDAETGLLSAICLCG DRQDLEQPDPRVMDLQEPLEA LKVVYRKRPRPHMFPKMLM KITDLRSISAKGAERVITLKMEI PGSMPLIQEMLENSEGLDTLS GQPGGGGRDGGGLAPPGSCSP SLSPSSNRSSPATHSP
18854	49222	A	18963	748	1075	ILPTSLFFLCFVFVFC*DRVLL LSPGWSA VARSWLYCNLSLRG FKFGSCLSLSNWDYRCTPLRS ANFVFL/CRDRVSPCWPTSVSNS *PQVIHPPWPKVLGITRV
18855	49223	A	18964	3	674	GRRRLRDAEGPEETVRLWPA ARAAMDAAEVFLAEKELVTII PNFSLDKITLIGGDLGPFNPG/LP VEVPLWL/ARLNLKQRQK/CR LPPPEWMDVEKLEKMRDHE/RK EETFTVPMPPKFTTWELTKLL/ NHA/SDNIPKGRTEFRDPGSRVF WGHYSY*AKFRVFGDSFVRRQ EAHAKLD*LGPWMGDQQA V TFLTQA/LNPHVTNSTRINPPSPL E STSVLRTS

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18856	49224	A	18965	261	876	VAQKIDMPEYQGEPEISIQKC QEA VRQVQGPFVLVEDTCLSFN ALGGLPGYIKV/WFLEKLKPIE GLHQLLA/GFIEDKSA/YALCTF CTQAPGDPSPQPVRLVSGGRDL RGRIRWHPEGCQDFGWDAPCF QPDGVEQTYAEMP*GGRRNA VSHRFRAPCWEPA REYFWQV WPSLTASWKEGSPRPGDLGK GLAPKPSPHRGRAPP
18857	49225	A	18966	2	181	TAEKMAVLAPLIALVYSVPRLS RWLAQPYLLSALLSAAFLVLR KFPPCLHGLPTQREDGNPCDFD WREVEILMFLSAILMMKNRRSS TK*AHPTRRR
18858	49226	A	18967	5331	5454	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18859	49227	A	18968	5186	5308	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18860	49228	A	18969	4570	4691	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18861	49229	A	18970	5666	5788	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18862	49230	A	18971	5630	5752	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18863	49231	A	18972	224	456	
18864	49232	A	18973	5543	5665	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18865	49233	A	18974	4602	4725	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18866	49234	A	18975	3	313	
18867	49235	A	18976	5480	5602	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18868	49236	A	18977	269	394	
18869	49237	A	18978	5322	5445	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18870	49238	A	18979	164	434	
18871	49239	A	18980	5364	5487	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18872	49240	B	18981	18	1904	
18873	49241	A	18982	1296	1973	RILPGGQQNSSWNFS EDTVISIL NTINEVIAENLEAAKKLRETQGI EKLVLINKSGNRSEKEVRAAAL VLQTIWGYKELRKPLEKEGWK KSDFQVNLNNASRSQSSHSYDD STLPLI*PGPKNQIRNLIGKKFR* AIWDQTONH*IT/DYSTPNERGD HNRTLDRSGDLGDMPEPLKGT PLMQDEGQESLEELDVLVLD DEGGQVSYSPMVCPSTPKIVL EEGGS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
18874	49242	A	18983	5844	5967	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLK YNT
18875	49243	A	18984	5781	5904	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLK YNT
18876	49244	B	18985	1	1477	
18877	49245	A	18986	152	1539	
18878	49246	A	18987	5571	5694	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLK YNT
18879	49247	A	18988	4551	4674	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLK YNT
18880	49248	A	18989	2	1043	GVRLRYSPIAVVMVGEAGRDL RRRRRAVAVTAEMAVLAPLI/S LSVYSVPRLSRWLAQPPYLLS A\LLSAFLLVRKLPLCHGLP TQ\REDGNPCDFDWR\VEILM FLSAIVMMKNRRSITVEQHIGN IFMFK/SK\AVNTILFFRLDIRMG LLYITLCIVFLMTCKPP/LSPYM GPEYIKYFN\DKPFDEELERDNR VNW/ILLEFFGNWSNDWQSFAP IYADLSLKYNCTGLNFGKVVDV GRYTDVSTRYKVSTSLP\TK\QLP TL\ILFQGGGGQCGRPQI*QGK GR/ALFSWDL*GT*KEGQENVI REFNLNELYQRAKKLSKAGDNI P\EEQPVASTPTT\TSDG\ENKDD
18881	49249	A	18990	1	1105	MESTGEDAVNIVEMVTEDLVY RLVVLKSLQVWVSPGDFMGSE GTECMLIGPWVAMGRPSESTLS SHSGPRSPHGTGSPAPRLQAVH VLKCPKSRGVQGGWGLASQCL PEHRHTQLSCDSTQAWPQLCSA QSLRHNRSQGAGAVTSEPAG AGGLPRPRTQGCLGAES/PAG QLHSQQRGGPEEGRLLSDVDHP DLSSSQQRGPEGP/QVAGGWCV SAAWSS\THLAGPQQRWDQEEA RQWEQIPLSLLMMGDPPGYSR APGDGPQGPQRQLQLCLGSSH PTNS*GAELPPVPGSAECAALT VLPSLHLQVWQVGRPGPT*V DPRVGLPGQQAPEQRVYSLTHP EQLPVLQVPLLIYRYSSTYNGV
18882	49250	C	18991	105	393	
18883	49251	A	18992	38	230	LYWQKRKGKLLNNLTQGVAD PVR*KKFHFCKPSNCPKIHNTES AYA\VSFMKYSAHVLGSLYEM
18884	49252	A	18993	487	747	
18885	49253	C	18994	179	649	
18886	49254	A	18995	3	3187	
18887	49255	A	18996	274	423	

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18888	49256	A	18997	1333	2243	RCWRPRTLGFASPPTRPCSPTH APGCEMTPRDWRHVLFSFASPLR IEEIFQGYDKTFGLKNKKGAKQ QKFIKAVTHQVKFGQ/SKSTSGS TE*SWKRKLKKDDKKKELQEL NELFKPVVAAQKI/RVKGADPK SVVCAFFKQGQCTKGDCKCKFS HDLTLGKMEKRSVYIDARDE ELEKETKSSLIQADTMDNWDE KKLEEVVNKKHGEAEKKKPKT QIVCKHFLAEIENNKYGFVWV CPGGGDICMYRHALLPPGFVLK KDKKKKEKEDEISLEDLIERERS ALGPNVTKITLESFLAWKKRRR
18889	49257	A	18998	1	322	
18890	49258	A	18999	1	822	MGKAKEEVFLADELVHAKTNR NKECDYSVTANSKIVVVTAGV RQQEGESRLNLVQRNVNVFKFI IPQIVKYSPDCIII VVSNPVDILT YVTWKLSGLPKHRVIGSGCNL DSARFRLMAEKLGIHPSSCHG WILGEHGDSSDHPGRPRPHVPPI KPPETLPGRDTSSWTSRGAHWR RNTQAAGRREHIDRHQQAIDR WNNVGFGRGGQRRARLLSDLT PTGKPPSSYSVLLAPPSSAEYFH SIKPCIHSPS*CMQRPKEKN/RD YSVTANSKIVVVTAGVRQQEG ESRLNLVQRNVNVFKFIIPQIVK YSPDCIII VVSNPVDILTYVTWK LSGLPKHRVIGSGCNLDSARFR YLMAEKLGIHPSSCHGWILGEH GDSSDHPGRPRPHVPPIKPPETL PGRDTSWTSRGAHWRNTQA AGRREHIDRHQQAIDRWNNVG FGRGGQRRARLLSDLTPTGKPS SYSVLLAPPSSAEYFHSIKPCIH SPSPREIQFFGYTKARNPRVQK

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18891	49259	A	19000	1	1337	MEKPKRLRWLWGPAPSSLLAE PAPEETHAADVFVSARLLQRSP EPSLSWGGRALAEQKAEGSSC GSAERLVAFAAKTRPYLSLCK MATLKEKLIAPVAEEEEATVPNN KITVVGVGQVGMACAIISLGKS RAMEHTTAGAPYTPRQQTCCQ NMMSLADELALVDVLEDKLG EMMDLQHGSFLQTPKIVADK DYSVTANSKIVVVTAGVRQQE GESRLNLVQRNVNVFKFIIPQIV KYSPOCIIVVSNPRDALTGTW KLSGLPKHRVIGSGCNLDSARF RYLMAEKLGIHPSSCHGWILGE HGDSSVAVWSGVNVAGVSLQE LNPEMGTDNDSENWKEVHKM VVESAYEVIKLKGYTNAIGLS VADLIESMLKNLSRIHPVSTMV KGMYGIEVEVFLSLPCILNARG LTSVINQKLKDDEVAQLKKA DTLWDIQKDLKDL
18892	49260	C	19001	462	728	
18893	49261	A	19002	1	1033	MSGSLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLGRNLTKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTFPRWTVWEEPP PPGLVGKACARWWGKGEPD RKAPAPPPPPPGTEKVDQTSE/E RGTLIQRPPAPALPGWVRKTGR P/PPPA/TGRLQQVPLLGASTQPE /PPGRGV/PPGVSPGLGEDVE/N DGMSLSYLAEPQATSQRAP*G ENTVALSGRLGRNSSSYTCRPA GERNFHPRGGPSSTAALHLRK MPGTPQCEGRRVAPRALPET*M LQPGGTTR*T/PPGPLAFSPSSP TGPQKVKSLGNSSARTILPPKW
18894	49262	A	19003	2	212	
18895	49263	A	19004	1	425	PTRPAAVAEDGGLKKCKISSYC RSQPPARLISGEEHFSSKKCLA WFYFYAGPDEVVVGPEGMEKFC EDIGVEPEN\CDCTEKLQNKDFD LRSQLNDISSFKNIYRYAFDFAR DKDQRLSDIDTAKSMALLGR TWPLFSVYF

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18896	49264	A	19005	229	1028	GASKRTGTPFPFPAHPAREGR KMPVKKKRKSPPGVAAVAED GGLKKCKISSYCRSQPPARLISG EEHFSSKKCLAWFYEYAGPDE VVGPEGMEKFCEDIGVEPENII MLVLAWKLEAESMGFFTKEEW VKGWMTSLQCNLHRKGYPNF DFFAAHS*IDISSFKNIYR\AFDF ARDKDQR\SLDNDTAKS\MLAL LLGEGHGPLF\VFYQVPGGQS KYRVMNKD\QWYNVSEFSRTV\ HADLSNYDEDGAWPVL\DEF VEWQKVRQTS
18897	49265	A	19006	3	373	
18898	49266	A	19007	3	418	GRAGSRKWLTLTGSLASTSPSL LSGQGPWAPLQRAMKPPGGES SNLFGFPEEATPSSRPNRMSSNI FGPTEEPQNLKRTNPPGV*GSG IFDESTPVQTRQHLNPPG\GKTS DIFGSPVTATSR\LAHPNPKPDH VFLM
18899	49267	A	19008	1	684	
18900	49268	A	19009	3	81	
18901	49269	A	19010	1	465	
18902	49270	A	19011	120	344	
18903	49271	A	19012	3	1334	SPOLISSASRPVVRNSRHDATRP VVFQIMSGGSADYNSREHGGPE GMDPDGVIESNWNIEVDNF/D VTMNLKESLLARGIYAYGFKEP SPIQQA\IIPC\KGY*CGLLKLQ SGTGKTATF/SLISLQPVGRLSF KETQSTSYWAPTRELAQQIQK VILALGDYMGATCHACIG\GTN VRNEMQKLQAEAPHIVVGTGP RVFDMNLNRRYLSPKW\IKMFVL DEADEMLSRGFKD\QIYE\FOKL NTSIQVVFASATMPTDVLEVTK KFMRDP\IRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITQAVIFLNTRRKVDWLTEKM HARDFTVSALHGDMDOKERDV IMREFRSGSSRLVITTDLLARGI DVQQVSLVINYDLPTNRENYIH RIGRGGFRGKGVAINFVTEED KRFLRDIETFYNTTVEEMP MN
18904	49272	A	19013	75	540	

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18905	49273	A	19014	774	1529	RWGERILLTWKRQLQVPPSAL EAGGSSGLEDVLP LLQQADELH RGDEQKGREGFQLLL/TQQAW CMEAGRITFLWRLARAYSDMCE LTEEVSEKKSYALDGKEEAEEA LEKGDFEE/SLTCHI.WYAGALW SAG*AMRASRRRIQELALTFKE HCGQKPFALQPKTPMAHFLLG RWCYQVSHLSWLEKKTATALL ESPLSATVEDALQSFLKCYREL GKNSEARWWMKLALLELPDVT KEDLAIQKDLEELEVLIRD
18906	49274	A	19015	97	452	GTERRTGKLPALLTPNLVQLRR LLFPGIQTI*VPAQGRGHLLQRP AAA/RPRTSAPPAAAAAPPQV EARPP*LQPTRQEEAAELQTAR AGLWELWAGPQSPRDLNSLESI RITCSPTP
18907	49275	A	19016	1299	1800	FWGGRSGTVGYGADMGKFKN NTTNNQS*K*YRNTSRNPDHND *FLKGMDPKFPKNMHFA*KHN EKGLEKMQDNNMRAEAIKA/L PKPMEVQPRVPKSASRKLD/LA YTAHPKAGKHARAHIATGLRL CWPKAKAKDQTKAQASASAA APASVLAPAQASKGAQAPMKA LE
18908	49276	A	19017	410	1323	RQEGTLIGVFIPAAAAAAVAA AAAAAAAVAAAAAAV AAAAAAVAAAAVAAAAV AV/GTSFSKPHLMEKHEKPS KDSREHKS AFKEPSRDHINKSSK ESSKKPKENKPLKEEKIVPKMA FKEPKMSKEPKPDSNLLTITSG QDKKAPSKRPPISDSEELSAKK RKKSSEALFKSFSSAPPLILTCS ADKKQIKDKSHVMGKV KIES ETSEKKKSTLPPFDDIVDPNDS VEENISSKSDSVPGQSPVTNIF TSSSTPTILKSYQLDNDSDQGA QEASDKQIEGYFSGEVPAYRQG ELILVASRQ

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18909	49277	A	19018	91	890	GAERLPEPGPKRMVFRFRFEV GRVAYVVSFGPHARK/MWVAIV DVF*SEQGLLVE*PCTQVR/RQA \MPFRQMQLN*FHPSRFPNSAQ ESMFRQA WQK\ADI\NTK WGSP HDGAKKIEAQRKKGPKDDQIF D\RFKVM EGQKKMREQE*SKE* S*RSFKRAALLEKLSPKKKHLG T*GYCCLLLLLAAAAAAAAA AACCLLACCLKVPSKKRSPAAS KKAPAQKVPAQK\ATG\QKAAP APKAQKGQKAPAKAPAPKAS QGESISGNHKK
18910	49278	A	19019	280	1249	SLNEGIMYAQP\VTNTKEVK\W QKVLYERQPFSLDKLW\WDRRF LGRSSGKNIHAPENTQY\WGCG *FESSVVIQQLCSVCVFVIR\W YMDEGLLAPHWL\VTGLASSL IGYVLFDLIDGGEGRKKS\QTR WADL*ELP*SFITFTYG\FSPVLK TLTEFCSALTPIYAMSVFMLLR HLIFFDYG\ANAIV\SSTL\LVN MAIFAS\VCWASRL\PRS\LHAFI MVA\FAIQIFCPGGPML\QKKLK \ACT\PRS\YVGVT\LF\AFSAVG GLLSISAVG\VLL\LLMSISC LC\PFYLHFACSLFKENI/HMGP WDEA\EI\KEDLS\PGSL
18911	49279	A	19020	1	310	
18912	49280	A	19021	2	411	
18913	49281	A	19022	374	1275	VLTRLIRKRRRKAQSQRERCR CVLAKDFLAGGVTAISKMAV APTE/RVKLLQVQSAASKQITAD KQYTGVVDCMVRIPKE/QGVLS LWHIGIQFHHKFAAGSLASGAP GATSLCFVYPLDFARTRLAAD VGKAGAEREFRGLG*PAGLRiy KSDGK/LRGLYQGFNVSVQGIH YRAAYFGIYD\TAKG\MLPDP\Q NTHIVISWMIAQT\VTAVARVDF PIPFDTVRRRNE*MQSRAPKEL TIHVHQA RFDCWAEGLLRDEG GKAFFKG\AWVPMLR\RGHVG AFCALSLYGWKSKEGTHKLIS
18914	49282	A	19023	461	705	TERKKKGILPGNGNGFMSLRRT IRVWRNTPNYLG\TN\AVSP\RD *IGKKGVCQRKQAGPCPPSNQ GILEWRK\HRIS\ETKP
18915	49283	A	19024	2	408	

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18916	49284	A	19025	1	885	MTQHAGKRDELSELPVIVQDTET VPSVMDGKEYQAGRFARGRLRL QCFRRRRRRRRTRRRRRKEEEE EEEEEEEEEEEEVEEEGKKKEE EGRRRRKKKKKKAEEEEKKK KEEEEKKRRRREPPRPND ARRRRKEEEEGRRRSM/LGKRD SELPVIVQDTETVPSVMDGKEY QAGRFARGRLRLQCFRRRRRR RTRRRRRKEEEEEEEEEEEEE EVEEEGKKKEEGRRRRKKKK KKAEEEEKKKEEEKKRRR REEPPRPNDDDARRRRKEEEE GRRRSMKKEEEEEEEEEEEEE EEEEEEEEKKRRRGPAKMM GGFEELRRGLNVGPTMAIFFLQ SAALAPAILYFCPSLKSNSKCN FQFLMFCQLLGRVTIPFLVSQRS RIEVGRHSLSTLNAETAHEL YLGRTEPDECGKTAGLTGLDLK
18917	49285	A	19026	1	378	
18918	49286	A	19027	36	3415	ESAANAQVLAAPSPCSFAFTL SKVNMSLKNEPRVNTSALQKIA ADMSNIENLDTRELHFEGEEV DYDVSPSPDKIQEVYIPFSAIYN TQGFKEPNITQYLSGCPKIAQVL EVERFTSTTRVPSINLYTIELTH GEFKWQVKRKFHFQEFHREL LKYKAFIRIPITRRHTFRQRNV REEPREMPSLPRSSNMIREEQF LORRKQLEDYLTILKMPMYR NYHATTEFLDISQLSPIHDLGPK GIEGIMMKR
18919	49287	B	19028	37	147	
18920	49288	B	19029	10	264	

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18921	49289	A	19030	3	1255	HASGGRAANMAADRGAVQQQ SQDMMEVDRRVESEESGDEEG KKHSSGIVADLSEQSLKDGEEP GAEDPEEEHELPPVDMETINLAD RDAEDFADLNHYRIGKIEGFEVL EES*RLSCLRQNLKCL\ENLGR ELPESFRELDLYDNQIKKLENLE ALTEILDISFNLLRNIEGVDK LTRLKKLFLVNNKISKIENL\SN LHQLARMLGAGDLNRIRGQFSK YPTTLATNL\ESWFLGKKTITN FQNPGCASPNTVLMSQSNRLT KIEGLQNLVNLRELYFSHNGIE VIEGLENN\NKLTM\LDIASNRIK KI*KISAHLTEL\QEFWDGTTIPL KSWSDLDELEGEPEGALEDSVP WGGNPLARRTPKYRRK\VMLA\I LPSVRQDRCPRSVRFLKSFLGSL MWSLSSEELPSHGVPNPCCS
18922	49290	A	19031	138	564	YREVMVSES*ETPAGARGRPYY FSAPGTA\PAINVHPPPSLSAT PHPPQPQPPPHQHNAKARVAT IRTKRTSNCRIRSRKVRKSPPEK WVGFNRRPKASCSPPGAARV DVGGETERREQAAAPGEMGK WARPGEEYFHS
18923	49291	A	19032	1404	1586	ENESRFSDRNQASAGLGYLSDS L*QWIVGNNGHATDLWQNCSTS SSGNVHHCFSSSPNGSG
18924	49292	A	19033	187	701	AELAARMLLLLLSIIVLHVAAL VLLFVSTIVSQWIVGNNGHATDL WQNCSTSSSGN\VHHCFSSSPNE WLQSCSRGTMDPVDSSFSILSL FLFFCQLFTLTGGG\RFYITGIFQ ILAGLCVMSAAAIYTVRHP\EW NLNSGY\S*RFA*ILAWVAFPL\I ALLSGVIYVILRKRE
18925	49293	A	19034	1	493	
18926	49294	A	19035	105	307	
18927	49295	A	19036	32	302	
18928	49296	B	19037	119	641	
18929	49297	A	19038	496	653	
18930	49298	C	19039	568	747	
18931	49299	A	19040	522	656	ESSQSHGKNFYMGKRIKLSLY WNVWRMLNSKSETTNCPLIRH RLSKRVGAPFLPAVLVLTKITIY QT*KFQIRNHKLPSNKTSAI

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18932	49300	A	19041	111	277	RHVAVVLGDVGRSPRMQYH ALSLAMHGFSVTLGFCNSKPH DELLQNNRIQIVGLTELQSLAV GPRVFQYGVKVVLLQAMYLLW KLMWREPGAYIFLQNPGLPSI AVCVWFVGLCGSKLVIDWHNY GYSIMGLVHGPNNHPLVLLAKW YEKFFGRLSHLNLCTVNTAMRE DLADNWHIRAVTVYDKPASFF KETPLD\RTHRLFTKLTNMHSPF RARSEPEDPVTERTSAFTERDAG SGLVTRLRERPAALLVSST\SWTE DEDFSI\LALESRV*TTDS\SIG HNLPSLVCVITGKPPREYYSR LIHQKHQFQHQVCTPWLEAEDY PR\ILGSVDLGVCLHTSCSGLDL PMKVVDVMFGCLPVCVAVNFK WQEQNPNLSGDSFTDPLRRKQ CRASCQP*GPAPGLHELVKHEE NGLVFEDSEELAAQLQVLFNSF PDPAGKLNQFRKNLRESQQLR WD*SWGATPNPMMSSCRTTE
18933	49301	B	19042	110	2294	
18934	49302	B	19043	81	1538	
18935	49303	A	19044	21	1158	AVVAALPTSSSSRHSLTQKPGS RRLRIESLLPPSSCEIFLIFSIFR LCEKPYHQTRSASNVNTKTDPR SMNS\RVFIGNLNTLV\VKKSDV EAFISKIYKGK\VGCSVHKGLCLS VQVMLMRRNAPGLL*QGE\DG RMI\ALGVLDINLAAEPK\VN REKSSVKRSAAEMYG/SQ*QNT LLRPLYFSSSFDLDYDFQRDY DRMYSYPARVPPPPPIARAVVP SKRQRVSGNTS\RSGRGFNSKE WNSGVSSKFWKR*KGDDLQ\AI KEELTQINQK\VDSSLLENLEKIE KATGANKQLEMK\ND\KSEEEQ SSSSREGKMRTNVKDG*GGV PDDSAEGGGPTWMNDDNVKS GGMTSWEL\KDDEKEAEE\GE DD\RD\ANGGG
18936	49304	B	19045	93	303	
18937	49305	A	19046	1	246	
18938	49306	B	19047	123	487	

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18939	49307	A	19048	584	1664	SGLFLFLFFYSEIFLIFSIFYRLCE KPYHQTRSASNV TNKTDPRSM NSRVFIGNLNTLVVKKSDVEA IFSKYVGKIVG/CSCFIKGFAPFK *C*EEMPRACCSGRRVGRIDLL GQVLDI*PGLAEPK/VNPREKPG VETILPAGDVRGQ*QNTLLRPL YFSSFDLDYDFQRDY YDRMY SYPARVPPPIIARA VVPSKRQR VSGNTSRRGK/SGFNSKEWNSG VSSKFWRK*KGDDLQAIKEEL TQINQKWDLSLENLEKIEKAT GANKQLEMKINDK/SEEQSSSS REGKMRNTNVKDG*GGVPDDSD AEEGGPTWMNDDNVKSGGMT SWEL/KDDIEKEAEE/GEDDKR QGPMARND
18940	49308	A	19049	158	1001	KRLGSSAISMSKYKLIMLR/HGE GAWNKENRFCSWVDQ/KLNSE GMEEARNCGQK/LALNFEDFL VFTSVLNRAPITARI/ILAEELGQ EWVPVSSWRLNERHYGALN GLNREQ/MA/LNHGE/EQVRL/W RRSYNVTPPIIE/SHPY/YQEIY NRPGGIK VCDVPL/DQLPRSES/ LKDVLIERFLPYWNERIAPEVL RGKTLISAHGK*AVGALLKHL GRYPSGLKTSINIYSFLLGVPIIL VELD/ENLRAVGPH/QFLGDQEA/ QAAIKKVEDQGKVKQAKK
18941	49309	A	19050	1	521	SASWVGAMASRVLSAYVSRL PARFAP*PRVRMLA VARHLST ALCSEGQTQLGTLPALVLA/ QVPW*ELHMLCRQYSDMP/PRL TLEGIQ/DRVRLA*LKTLSDKVD PREAFQ*ILIIFMKDLGLDSLDP KWKIIMALEDEFGFEIP/DIDA EKLMTPPRKLVDLHCQDKKD
18942	49310	A	19051	1	516	IRALTMWRRALLAGTRLVWS RSGSAGWLDRAAGLR/DCG/TA ASGMESNTSSLENLATAPVNVQ IQETISDNCVVFISKTSCTM AKK/LFHDM/VNVYKVVELDL LEYGM/QFDASLQK*LVERTV PRIFVNGTFIGGATDTHRLHKE GKLLPLVHQCYLKK/SKRKEFQ
18943	49311	A	19052	825	1080	KRKIHQNFHKLKSLKKAIEKDYS ESGSSVNYKKIRPTDNVVIKQ YWPGAVAHTCNSSTSVGQGR WIT*GQEFETSLANVVKPHLY
18944	49312	A	19053	80	429	

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18945	49313	A	19054	3	752	FKNAVGNLAMEGGGIPLET LKESQSRHVLPAFSEVNSLQKS NWGFLTLGLVGGTLVAVYAVA TPFVTPALRKVCLPFVPATTK QIENVVKMLRCRRRDPLWDIGS GGRDGIVHRLRRKGFTAVGF MEFKPMG*FWVFPRYRAWRE GVHGSAKFYISDLWKVTFSSQYS NVVIFGVPMMLQLEKKLERE LEDDARVIACRFPFPHWTPDHV TGKGIDTVWAYDASTFRGREK RPCTSMHFQLPIQA
18946	49314	A	19055	157	829	TWKGDDPKKPRGKMSSYAFFV QTCRGGHKKKHPDASVNFSEF SKKCSERWKTMSA*R/EKGKFE DMAKA\DKARYEREMKTYIPP QRGRQKRKFQDSQLHPRRPPSG LLSSSCSEYRPKIK\GEHP\GL\SI GDVAKKLGRDVGINTAAD\DK QPIYEKK\AAKLKEKYEDIA\A YRA\KGKPDAAKKG\VVKAES KKKKEEEEDEDEDEEEEEDE EDEDEDEDDG
18947	49315	A	19056	85	267	GHLSHA WCGTYKPWPSPKEQS RAWKKGDLFPFPP/PLFPTGLK VRGRESF*SVELIRPQG
18948	49316	A	19057	1	1158	
18949	49317	A	19058	452	517	
18950	49318	A	19059	93	1069	YEGVTTSLPELPRGCLVLQEQ ELVQMSGMEATVTIPIWQNK HGC/SLRSVVRIGTNLPLKPCA RASFETLPNISDLCKRCAPSSL PWL\AWLGLAE*KGSQKARV\ RSDTRPLRHTWKPSPLIVMQRN ASVPNLRGSEERLLALKKPA/L ASPKAALLSCRTS*ATLRTKICK DSGKLMQLRLH*RQISYLQEVQ MSLLPLPCFGSSFHSTTSFCH**/ PSPRRQRWRSLSFHQSPCFVLP ALNVANQNTKLPAVRLKRMTA SLCPRPAALQDMMGILKGLFTG MKQSQDLNRSLLKEEDPAVLIS EVLRRKFALKEEDISRKGN

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18951	49319	A	19060	162	1410	GQASCPPLPGLQQTTPASSYTVQ IQTYAPSSPHPRQGGPGQSSDPR GLRGAIIPRGRQGGV*QGGPRC RPPSPVLPHIPQLSCCGHDGRD PEEGLGILELTLHHAHPWSPN SW*KDSVSPHGEPFAHSEPHSR DQTSMAATTKHEVQPLPQASLS QPSLGGCLVDWLRQLRTTQGS /PQDAAQDSTWERP*DAS/GKP WLL*PGVPTPGPCQAKERKPP FMGNCLP*SRVPWPSRLPEEL/P AMPLAPPVAGEAAGPASSHQSL SPSQDPTPLPGADRREKERGGE EGSSWPQTPLTTHTTSPPEKQ QQIESPPIRLSSFKTGHLASSGH SYAIKPNSTKAKEVGQVRVPR SHITIREQRQGRPGEHHRRTER DAKPGQGEEDHQATVVSQKLGT DRRLIKKQRTSVLSATAES
18952	49320	A	19061	1	340	GSVSGTTLNLQGFWSPPGTS LEPPCPWLDHIFVPWKDVA FGEGVCLPPGAPQPRRICPRR QQEFQGEPEETIPERTPADPGV LPPAFPGICLPRLRAPDPGPA A*AVPPVADA*GSVSGTTLNQ LGFWSPPGTSLEPPCPWLDHI FPVPWKDVAFGEGVCLPPGAP QPRRICPRRQGEPEETIP PERTPADPGVLPAPFGICLPRL LRAPPDPGPA
18953	49321	A	19062	3	396	IPLASLHLALPGHQRGPPPGRLP SCSSQGTVPPRAGPYQAGCPG TAPAPAAPASAPWSAPQASATG GTAHAAGPGSGGARSLPPARA HPPARCWQGRPLRSLLL*PSSVP ETGGPEKARLVKALSPNTAP
18954	49322	A	19063	563	1269	LEESTGRITHFKATLHCTMSNN LA WGGTKWLQESRVFFHIRRLP SDASAGPGCVYRVVPDGGSQ RPQGAPP*AAQA/GTPRGRPP/P GAPSALLPPPSGTSVGPGLQ QRRPPTGGQEDSPTEPGFWKPR WRSHLATSLATRCTMQGEPA AHPGGRGPAASEERHQRGPPP GGCFAALRYCATPRPDLGRCP GTAPAPAAPASAPWTRLRHQPL AAQLMQPGQVWWGPAASW

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18955	49323	A	19064	1	1158	MELKAKARELREECERSLRSCD QLEERVSMENEMNEMKREG KFREKRKRNEQSLQEIWDYVK RPNLHLIGVPESDGENGTLEN TLQDIIQENFPNLRQANIQIEI QRTPTQYSSRRATPRHIIVRITK VEMKEKMLRAAREKGRVPHK GKPIRLTADLSSETLQARREWG PIFNILKRIFSPQRGGTGGRRM VKLTAEIEQAAQYTSAVRDRE LDLRGYKIPVIENLGATLDQFD AIDFSDNEIRKLDGFLLRLRLKT LLVN/NNRIC/VLDFQKVK/LK ERQEAEMFKGKRGQAQAKDI ARRSKTFNPGAGLPTDKKKGG PSPGDVEAIKNAIANASTLAEV ERLKGLLQSGQIPGRERRLGPT DDGEEEMEEDTVTNGS
18956	49324	A	19065	2	431	RKLDGFPLRLRLKTLLVNNRI CRIGEGLDQALPCLTELILTNNS LVELGDLPLASLKSILYSLIR NPVTNKKHYRLYVIYKVPQVR VLDFQKVKLKFNPAGLPTDK KKGGPSPGDVEAIKNAIANAST LAEVERLKGLL
18957	49325	A	19066	92	303	NCFLVFSPARSTVGEFASMSSE ECI*MHVVFLFPLTLCVVSLEYR QEAEKMFKGKRGQAQAKDIAR RSKT
18958	49326	A	19067	208	293	LLLLWWFPLGPTDDGEEEMEE\ DTVNTGS
18959	49327	A	19068	22	904	ARNPSTHASGWREATGFPQR GGTAGCTMGKLTAEIEQAAQ YTNAVRDRELDLRGYKIPVIEN LGATLDQFDAIDFSDNEIRKLD GFPLRLRLKTLLVDTRICGIGE GLDQAILPCLTELILTNNSLVEL GDLPLASLKSVAIYLYLRNP VTHKKHYRLYAIYKAPHVRL DFQNVKLKERQKAEKMSK GK RGAQAKDIAARRSKTF*FPGA GLPN*PKRKGSP/SLPGDVEAIQ ECP*QNAFNSGLKVERLKGVCC KSGQIPGRERRSGPTDDGEE MEEDTSHQTGS
18960	49328	A	19069	1	395	AINYNEKIYELRVMETKPKDKA VSIIEDCMNVDFDAP/LGYKEPE RQVQHEESTEGEADHSGYAGE/ LGFRAFSGSGNRLDGKKKGVE PSPSPKPGDIKRGIPNYEFKL\G EAGGRFVAFSGEGQSLRKKGR

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18961	49329	A	19070	1	1108	
18962	49330	A	19071	353	693	GSLFLVKRREP/R/VQHEELTE GEADHSGYAGELGFRFSGSG NRLDGKKEPSPIKPGDIKRGIP NHIEFKLGKTFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
18963	49331	A	19072	2	1112	RLGAAAAAAGRAVGGVSSL HCPERSGVCQVVSI MFSFNMF HPIPRVFQNRFTQYRCFSLSM LAGPNDR/SSIGKEGKIIMPLG PGTKLSRL*HYRIPMLFK/LTNK NSGPHGRHCGVAGSLWA**GA SAYLPHWDDGRYSLGRKAA WVQGGRSVNLSSGPLISNFQPP SPDFL/DITNP/KAVFEN\ALRNF ALS*PPGDV\AINYNEKILRNCV VMETQTPTRPVSHH*SVNH*TV EL*LLPPGATKEPRKDQVQP*G VRTEGESRPHSGYAWKSLGFP RFSRSGSNRLDGGKKGVPEP SPIKPGDIKRGIPNYEFKLGKIT F/VSRNSRPLVKKVEEDEAGGR FVAFSGEGQSLRKKGRKP
18964	49332	A	19073	1	415	SGGGRNRSATGSWVGT MAGIT TIEAVKRKIQLVQQQADDAEER AERLQREVEGERRARE/RGMK VIENRALKDEEKMELEIQLKE AKHIAEEADRYEEVARKLVII EGDLERTEEPSLSWQESKCSLE EELKNVT
18965	49333	A	19074	1	421	
18966	49334	A	19075	3	388	
18967	49335	A	19076	1	1332	
18968	49336	A	19077	49	483	
18969	49337	A	19078	227	1030	AVSWVGT MAGIT TIEAVKRKIQ VLQQQADDAEERA/ERSQREFR EERRARE/QA/EAEVASLN/RRIQ LVVEELADRAQERLGHCPCKKL *RS*KKLADESERY*RLFEN/R ALKRLKEKIGTSREIPTS KKP HCRKEAD/RKYEEVARKLGDH LKEDLERTEERA/ELAESRC*EI DEQIRLIDQNLQCLSAEEDKYS QKEDK/WEEEMKILTDNLKEAE THAELAERSVAKLEKTIDDDLE KLCKTKEHLCTQRMLDQTL DLNEM
18970	49338	A	19079	50	864	
18971	49339	A	19080	1	1014	

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18972	49340	A	19081	1	1650	MGFHHVVGQAALLLTSGFQSQT QELQKFLFLFLVYVTTIVGN LLIMVTVTFDCRLHTPMYFLLR NLALIDLCTSTVSPKMLVDL HETKTISYQGCMAQIFFHLLG GGTVFFLSVMAYDRYIAISQPL RYVTIMNTQLCVGLVVAWV GGFVHSIVQLALILPLFCGPNIL DNFYCDVPQVLRLA CTDTSLLE FLMISNSGLVHWFLLLSYTV ILVMLRSHSGKARRKAASTCTT HIIVSMIFIPCIYIYTWFPFPL MDKAVSISYVTMTPLNPMIY TLRNQDMKAAMRRLGKCLKG PAVA VGP GPGDAEAAAEEER RVKVSSL PYSVDALVSDKKPPK EASVPVAKSASSGATLRLLLP GHGAREAHSPGLIKPFETASV KWENSQDGAAWMQEPC*YSP PPRHK\HKTNPKPRTAFTTSQLL ALEGKLLQKQYLSIAEGADFSS SPNL TETQVKILFQNRRAKTKR LQSELEKLKMAAKPMLPSSFS LPFPISPLQAASIY AASYPFHRP VLPPIPVGLYATPVGYGMYHLS
18973	49341	B	19082	62	440	
18974	49342	A	19083	1	902	METEALMPGLGVAVAGAQVTL GFLALETQLPFTGHKRILRFFS SPRDPPHVPSKGLKRKGWARR GRTFALREAEPQRLPSLSRAFQ TLARPYARLVPRGNPVVPFPLA GSAEAAARAATCERQARTCPM PGVTVKDVNQEFVRALAAFL KKS*VGKLVPEWVDTVKLA KHKELAPYDENWFFYTRAAS AQAPCTIRGGAGVGSMTKIY GRQRN/GVMP/SHFS/SGKS/VA RRVPPKWRG*KMVEKGTKN GPQNLTPSRDKRDFGTEFAGQV AAANKALEQIHCFGLIKLAHS
18975	49343	A	19084	1	673	AGPDAAESERVPEGAAPGAGP SRPLEPRPRASGRPGHGRCLGV TVKIDVNVQQEVRRHELWAAFLS KSLR/LRVS*TVPEWLDTVQAG QAQKSLLPYDENWFFYHAELAS TAIRHL YHPSALGVGSMTKIY GGTSETASMPKLSARGFQEI WARRVLQSPGRGLKMGGRKD QELRAAKLDTFGQKRFWDRI RRNRLAVAYKEALEQTMAGV NKLQPFVKKKKK

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18976	49344	A	19085	1	427	HPVRFVHRGPH/VDFSLEVV QWYELVFTASMEIYGSVAD KLDNSRSILKRRYYRQHCTLEL GSYIKDLSVVHSDLSIVILDNS PGAYRSHPDNAPIKSWFSDPSD TALLNLLPMLDALRFTADVRSV LSRNLHQHRL
18977	49345	A	19086	2	832	WNSAELGRGGPGAGGAGVIGM MRTQCLLGLRTVFAAALWS FFIYLLRRQIRTVIQQYQTVRYDI LPLSPVSRNRLAQVKRKILVLD LDETLHSHHDGVLRLPTVRPGT PPDFILKVVIDKHPVRFVHKRP HVDFFLEVVVSQWYELVVF/TA SM/EIYGSAVGRNLNWDNSRSIL *GGRYVYRQHCTLELGSYIKDP LLWFHSDLSIGIVLIDNSPGAYR SHPGYGR/DNAIPIKSWVSVTP ANTAILNLLPMLDALRFTADVRSV LSRNLHQHRLW
18978	49346	C	19087	69	206	
18979	49347	A	19088	312	438	
18980	49348	A	19089	635	826	QWISLWKCYKPEESGGQYLI KKSIFNDEFHVKNP*AS*GKEK* TPLQTSNC*GILSPGPLP
18981	49349	C	19090	1	390	
18982	49350	A	19091	336	551	ARPLGSLASAPFPAPM*NVYPT GP*YNADCPNVTAPVCA SNHG TFQNECFECVEQREFHYRKFE KYGKCD
18983	49351	A	19092	76	309	KGRFVIALTFTT*HSNLEKSCSK ICKIKNKSIVCKHQQLAKSIQSPS **WNGMNN*FTTLFICCHNTEK TFIHCGKRP
18984	49352	A	19093	181	447	NKYQTDNIKLSNDNL TIGHQTG NTTAHC/RYIMLFRSFQQA/IT ILS*YRKNIYPLWKETLTKRMWQ RHREKVGSEKVNIDKILFHHW
18985	49353	B	19094	1	639	
18986	49354	A	19095	1	160	NLHSQLMWNQIR*LTSV*LEL LCKNPNRVATRDQLLCLSGHL GMGRILEGG
18987	49355	A	19096	2	456	YKNTITDYEHLYAHKLENLEE MNKRRASTICTETIPKKLRRRD SSLTHSMRARRLSVDVQPDORS RGPSECTIFRAGVPEGTRGALW LPHFQTESDPGSKPATLLVIHP DELQIYVRTKTC/T/RMFIAALFI IAKT*KQPRYPSCLITST

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18988	49356	A	19097	138	1193	LCFFGQHAPIYCSLRHSLLSVTR PASLICCLPGSHRYLEFVLLLLK HHR LHEDLNHCPIGSRSGRDVR SQTTEQEHVIAMPFLRKLEPL HSGLYSHSCSRYLAWLALA TGGAARSPPAISILQPQEPSVTPS DTQRACGRSTEAFESKEQKASV RVETTVSFSCSIKVDGGLLEPKR ADTGWHGHHCRPASITPAGWV PARYLLYVFFSRQCVLMSVCGP QYTRGEIPGAVLKEECLPSLLT GRFDLSGRARRLSVDVKPQDRS RGPSECTIFRAGVPEGTRGV LW LPHFQTESDPGSKPATLLVIHP DELQIYVRTKCT/RMFIAALFI IAKT*KQPRYPSANTLLL
18989	49357	A	19098	3	247	
18990	49358	A	19099	1	1048	MQLKPMELNPEVSARCTATRRR RGRGRGSRVADRFGAFFFAFA FQMLNKVLSRLGVAGQWRVF DVVLGLEEESLGSPAPACALP ACLPLTAQHENFRKKQIEEL KGQEVSPKVYFMKQTIGNSCG TIGLIHVAQ*SKTNLGFEDGS VLKQFLSETKKNVPLKDRACK FIEKNEAIQAA\HECRGTRKGQ CRVDDK\WNHFHYSG*PTVDGP PSMNLGD/RMPFPRGPMAPSQ GDTLLEGRFPRSCRRISPRREQR RSPASSARGFSCKGSLNALWGG TWLISPLSPQHENILPPHASLKC FSTCETQAVLLFCQTRPSQPHP RHLSTSRVHSCPLGHCGVSFRW
18991	49359	A	19100	57	450	VGDCLTSRGMWVQATLLAR/ ALCRAWGGT/CRGALTGTSISQ VPRLAP/RGLHCSA/ASVSSEQS LVPSPPPEPRQR/PPGGERDKASF LQTVQKFADTSVVDSGHIDFIY LALRKMREYGVGERDLAVYNQL LNIFP
18992	49360	B	19101	307	390	

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18993	49361	A	19102	431	1267	SGTRITSTAARTSRTWRS*TPLL ACTPRPCGSAKLATATSRTCIRP *SPSATQTLTVTKVPLPKDSTG AADPPQPHIV/GAQGMVYVTPG IQSPDQQAALARHNPAPRVFVE GPFSLWLRNKCVYYHILRADLL PPEEREVEETPEEWNLYYPMQL DLEYVRSWGDNYEFDINEGKE QHVFI/LCSSGEC*ILRRQNVR LLDW/LAGKALTSTPCAPKITC VPLALPTPYCSGQNLNSSCSMT SVSDHLSVPVPTLLSTISKAHGTP PPNTKVTVKTVTRQ
18994	49362	B	19103	49	691	
18995	49363	A	19104	89	95	VGDCLTSRGMWVQATLLARG LCRAWGGTCGAAL/SQEPPLSLR SLASLPRGLHCSAAHSSEQSL VPSPPPEPRQRAHQGSWCPLR/VP VLGGQAGLGERGQGGAFL/LD GCRNLRTTTSVRKRGPV/VDLFY LALRKMREYGVVERG/DLAVYN QLLNIFPKVEVFRPNIIQIRIFVHY PRQCEGIAVLEQMENHGVMP NKETEFLLIQIFGRKSYPMCLKLV RLKLWFRPFMNVNPFVPRDLP QDPVELAMFGLRHMEPDLSAR VTIYQVPLPKDSTGASKIPPKPH IVGI/QRSPDQARPLARHNPSR PVFVIEGPFSLWLRNKVCV/Y HILRVADLLPPEERVRA*SKACV GAGEWAGTTLRVHGRGWRE TERALASDPACTPHLG/EEVEET PEEWNLYYPMQLDLEYVRSW DNYEFDINEVEEGPVFAMCMA GAHDQVATMAKWIQGLQETNP TLAQIPRGLSAFAGSTRKLQTS SAGLEPP/HCPRTTKEEDNLQ RQSRAS*SPCAGIRAQQDRA GLESAAGRVSR

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18996	49364	A	19105	1	1199	EFGALRRTRLGSSFFRRRDSSA MESYDVIANQPVVINDGSGVIK AGFAGDQIPKYCFPNYVGRPKH VVRVMAGALEGDIFIGPKAAEHR GLLSIRYPMEHGIVKDWNDME RIWQYVYSKDQLQTFSEHPVL LTEAPLNPRKNRERAAEVFFET FNVPALFISMQAVLSLYATGRT TGVVLDSGDGVTHAVPIYEGFA MPHSIMRIDIAGRDVSRFLRLYL RKEGYDFHSSEFEIVKAIKERA CYL/SINPQKDETLETEKAQYYL PDG/STIETGPSRFRAPELLFRPD LIGEESEGIHEVLVFAIQKSDMD LRRTLFSNIVLSGGSTLFGFGGD RLLC/VKKLAPKDGRIISAPQ ERLYSTWIGGSILASLDTFKKM WVSKKEYEEDGARSIRKTF
18997	49365	A	19106	1	3288	MPSSGGDQSPPPPPPPAAAASD EEEEDDGEAEDAAPAESPTPQI QQRFDLCSRLNMDEAARAEA WDSYRSMSESYTL/EGSGLWLP RGLFGHPGCTGLLLLRSGCV RSQPSDRACR*EK'CHSSHLEFF NKMKKWEDMANLPPHFRERTE RLERNFTVSAVIFKKYEPIFQDI FKYPQEEQPRQQRGRKQRROP CTVSEIFHFCVWLFYAKGNFP MISDDLVSYHLLLCALDLVY GNALQCSNRKELV
18998	49366	A	19107	56	3552	GPAAQGCAMPSSGGDQSPPPPP PPAAAASDEEEEDDGEAEDAAP /PAESPTPQIQQRFDLCSRLNM DEAAARAEAWDSYRSMSESYTL EGNDLHLWALACALYVACRKSV TVSKGTVEGNYVSLTRILKCSE QSLIEFFNKMKKWEDMANLPP HFRERTERLERNFTVSAVIFKK YEPIFQDIFKYPQEEQPRQQRGR KQRROPCTVS*NFSIFCVWLFIC AKGNFPH*LSDDLVSYHLLLG ALDLVYGNALQCS

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18999	49367	A	19108	1	1193	GRRRRFWWRKRIGGGGGGMA MPAEAPWMASFFNGFLSLPPG WLLLPSPDRNPPLQPSSRPPLC VRMWMNAFTPLISLFFWASLV SSGARRLHPIQPQPCREQAPMP APGAARSVAASMSDCTVAGP CTGSHTPCHSTSDSQSP/CGGVG SSLVV*AERSCAQCRMSPRKGH VCCCCCCCCCCCC/SCCCYCHYC CCYCCCCCCCCCCCCCCCCC CCCCCCCCCCCCCYCCRCYCCC CCYCCCCCCCCCCCCCCCCC CC*HYCCCCCCC/GCCCCRYC CCCRYRRCYFCFCCCCCYCY CCC*RTAHAWPSMNKSQCVLP/ CICKVPLGR LAVTTGCPGFG*G GCWEDCMFFPAKGPSIRLEQWFS TTAILLPSGPGDFWQYLGTLLV VTTREEVLLSEGG
19000	49368	A	19109	1	762	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLFLRLPL FADRVPKASQKIFVALS/TGEKG FWL*GVPCFHLRFP/GFYVSRGG DFHTAINGTG/KSILWGENLK DENFRLKHTGPGILSMANAGP NTNGSPVFLTSCTA/KTEWLDG K/HVVFG/KVKEGMNIVEAMER SLGPRMGKT/SNKFTIADCGQL RIKFDLVFYL
19001	49369	A	19110	95	240	LHSEITVCL*GSEHHFFENGTYI PHRSCHDPLEARAEDFL
19002	49370	A	19111	1	1644	
19003	49371	A	19112	237	632	AIGFPSYSSMQLVNIFGLLNLFSI ISSFRHQG*HS*ELPYPLEPGA EDFLR*GP/LAGHGHTGSQPFPC RVSEA/CGSHLVNSSRAALKRW AGV*RKIWPRGSPETPRNLKDL SVLEYENTPDTSGKKALED

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19004	49372	A	19113	274	2704	GISVLHGGCYRFQPRGMAAPGP FSEKPVPGCDAGDLQTPALSSW TQTFIISHEQGIKFLNQRWSCWS KERNHGHCRVRGHVTAACQCDL FGNGLKHNLDLHHDRNDASK NVKKSTNYGKMSFYTYCECTP TGEKLWDHNQHRKIIGYPASS QDQKIYSGEKSYECAEFGKSFT WKSQFKVHLKVPTGEKLYVCI ECGRAFVQKPEFITHQKTHMRE KPYKCNCEGKSFFQVSSLFRHH RIHTGEKLYECSECGKGFPYNS DLSIHEKIHTGERHHECTDCGK AFTQKSTLKIHKIHTGERSYIC IECGQAFIQKTQLIAHRRHSGE KPYECNCGKSFISKSQLQVHQ RVHTRVPKYICTEYGVFSNNS NLITHEKIQSREKSSICTCGKA FTYRSELIIHQRIHTGEKPYECS DCGRAFTQKSALTIVHQRIHTGE KSYICMCKGLAFIRKAHLITHQI IHTGEKPYKCGHCGKLFTSKSQ LHVHKKRIHTGEKPYMCNCKGK AFTNRSNLITHQKTHTGIEKIFI CSKCGKAFTQRSDLITHQRIHT GEKPYECNTCGKAFTQKSNLNI HQKIHTGERQYECHECGKAFN QKSILIVHQKIHTGEKPYVCTEC GRAFIRKSNFITHQRIHTGEKPY ECSDCGKSFTSKSQMTVEH*AV HSG*KPYVCAECGKAFFSRSN LSKHQKTHTGKPYICSECGKT
19005	49373	A	19114	3	180	
19006	49374	A	19115	95	433	PVLRTHPGPQSLPRVPGVPCGG LLEPLSRAEVSRLGLRRDLG GMAPSGSSTVFLLALTIASTW ALTPHTYLTKHDVERLKAASLDR PFTNLSEAFYSIVGLSSSLGAQVP
19007	49375	A	19116	196	706	ISISNETKDLLAAVSEDSVTOI YHAVAALSFGFLPLASQEALSA LTARLSKEETVLATVQALQTAS HLSQQAADLRISVIEEDLVARL DELGGVYLVQEEGLAETALFV AATYKLMMDHVGTPEISKEDQV IQLMNAIFSKKNFEVSLSEAFSV ASAAA VLSHNRHYH

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19008	49376	A	19117	275	2192	MVVSPQGSSTVFLALTIASWT ALTPTHYLTKHDVERLKASLDR PFTKRLCFSWFTTCVTT*H*LFP TV*KACTYIRSKSLPCLPQIAKT CSKTLCLPILS*ISISNETKDILL AAVSEDSSTVQIYHA VAALSGF GQVREGVSG*NKCTHSLGFYSL PSRTVDSGSCISFLL.LLDIQHISV LLWQDLVARDELGGVYLQFE EGLETSTAVALPPSQQRKRNSCI SHFFQDQVIQLMNAIFSKKNFE SLSEAFSVASAAAVLSHNRHPR NKILCSCSLCCNK*FFIYFQLQV TNVLSQPLTQATVVKLLFVISM T/R*TLAKPIVILNRDVFELNF MNVKFYICM*IPHEPPIDLATVF SIFL*LRVKISTDIFSACSQRYPD PL*RLTLYASFRVTYPKAKAGT FIADRDSMLGPGRILKLSDERL YYSSI*TFVRLHNQKTGQEVVF VAEPDNKNVYKFELDTSEKIE FDSANII*VSPSTSLPCFYRLSL FF*ADVVINPGIHGCPYWEHGIL KSSWCVFQRHLFREPEKSWHG LCCFPFK*CLFNFLPIIQWILT FLNRRASLCFI*LDVMTPLAA MLGLMYVYWTQLNMFQTLKS LAILG/SVTFLAGN/RMLAQQA
19009	49377	A	19118	3	413	PRKEAPSTFLSQ/NLFTPKQEIQ/ HLFREPEKR/PPTVV/SNTFTALI LSPALLLFALWIRIGANVSNFT FGLPSTNIFHWGHAAMLG/LSM YVY*TTQAQPCSQTLVWPWILG QCDRFLAGQSGMLAQRATVQE NQHN
19010	49378	A	19119	2	535	GRVDPKAKKEAPAP*SLPKPA *AFKGRKAVLKGVHSPQKA GRSRTSTPPFRAGRKTADSR PAPKILRKSRVPGGNKLD/HYA IIKFPADH*SASAVKKIEDNNT L/VFIVD/VLKANKH/QIKQGCE RSLYDIDVGQGGHPWIRPD/GE KKAYCSTWILDYDGGGMFAN QNWGSI

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19011	49379	A	19120	159	801	GAAGRRRLPEGEDEASAWR RLARCLMPKKNRIAYELLFKE GVVMVAKKDVMHPKHPLEAE VKNVPQPFMVMKGGHAGLSSPR GIYVKGTSFAWRHFLTGLTQ* GVSQYSPWITLHLAPGRFVPCP PLRPVARPRRMGRPRPKKVLG GVEATWRGFHKRGEVDRGYL TRRSACQQLGAIDKKSRGWGL GSSNPNFQFRG/GF/GCGRGQ/PP
19012	49380	A	19121	334	989	EPPAETLPVAARDPTGLSPTVLS SHKHEKFQQRHFVPLVGYPIA SSGASPEVRQRRITFFRFRPGES LCGDMKLLTHNLLSSHVPAGG SLPFSGGMVGRGPVLA*TP/LAL QATEGRICPVEINPQLRGRVMI P*KWKWSIAFLAEGPDKLAV*1 PGARKPG*GDMRENEEFS*GP WHHLACWEVGSD*EGTLQVP GNLGRYFSPFKPRGSPNMLAE
19013	49381	C	19122	61	177	
19014	49382	A	19123	4	191	
19015	49383	A	19124	1902	2187	
19016	49384	A	19125	55	340	GELVLKALSAFIRAFRCPAEGS DPVGRAADPSPAPRGISQGGG ACGSPFLPGPITESLPLPGLGSG SELPSTLYLSGIYGGVRRGPPA RLEA
19017	49385	A	19126	1228	2447	TSQGSSPPAHIGRWSSNHKKGL GSSFSQSCCKAEALVKNAWPPT QA*VSICCFEQDLGRGQKQKGS GGKWQKTAESREAVTECPACY RAARCRAAGDRGLRAEGAAAG HTASPSAYRVRGGRGHRDMHS ASARLSHPGETNMLGLAEPSV TSH*SHPFQGS*LP*QAGP**EM/ PLPPSARDSSDLCSG/SPSHDLLP LPNTVIFWGPSSPDWQPLPLSP FCVSQAAGSPCSPLLQGLEPGGI STSCPPGPAPYIDFGAVSAGQS AAQRGAHFPAAMAERPSAGTS GSSGISGAIAATVVSWSVAEGEQ AVKCLAEGSTRTQTQPSRRAPS RGCPAGAPPGRGAAPPQAPPA PAAGGGRGPPAAPRAPRPFQ QGAPRPVSPCRGTGAAPPPTLV WGLSSEAG

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19018	49386	A	19127	164	563	CEAALKGDSGGSPWPDEKPKPE GVKTENNDHINLKVDGAEMVT VVQFKIKRHTPL**T*LKAYL* TDRGLSMRQIRFRI*PGNPIN*K QTHLHQLGNGRIEDYNLMCFQ QARPGGVYLLKKGCTCFYFSKNS VSF
19019	49387	B	19128	166	426	
19020	49388	C	19129	76	285	
19021	49389	A	19130	3	179	
19022	49390	A	19131	93	172	
19023	49391	A	19132	1	2742	
19024	49392	A	19133	1287	2571	ILRQWLLASPEEKTGRPALASG SAETLSWLRAQGREPRGPA*SA VGAEHRTRTAPGSDPRCGILPS GRSPSP/PARLFLASVPATI*AM TPSPTRLPAWPPPCRG/PDASPE VVRKGGKAGQPRGSPQWRSG AEEIVEVGLLPLTPRALLFPQVP TALPAVYHFLAACEGICPHSCA APSMIELWDFLIQHQPEKAVA CTTTHIPGLRISALNKHRAWGG TDDDDVAASEMPLGAAGAEPW D/VE*LLPAALKIPTGHTATTTSW GAGP*SPQGSCKG/SGVSGGAT ADLLAPTAGVGTSTRACGGGT QFMSEGA PGVMNNGSPDWSST QFMSEGA PGVMNNGSPDWSSN LSQPQPMHLLYLTTWFLERPM CCPDTTALTQTLPVPFSFYPVCT SHIRQNPHLHFLAPSPHYTTA CSFEPQRFEQQQDLL
19025	49393	A	19134	31	202	ILITYIILKLNQADFSTP*FMSHLI VSSRIILCTEKNWFHFPFHF*D*Q QTFCTLQFL
19026	49394	A	19135	410	867	LLTLSRTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRVWTAS*SFICLSDPQKVQ IQSAFNRKAWCLVILVVVSHSS TPFSWQKVMKWIKISFRVFAA GQGLLGGYSNPRYSFSF

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19027	49395	A	19136	111	743	VITILTPMLADRTTRRIERPPKKK GTTSLGQRKWLTTQDWPSVYP VAHPFKPSAVPLPVRMGYVP KKGRAHGDRGNLELLKISQFF WILTSCSNLKSTCEALKDFCTG VGQPHWDSGRKKMLKKHFSN WKFGQHLDLCFHQGPSGSGNP RARVVVLKSKAFLV*/*HDHAK KTLITLVGERYCKTPDVLTIKQ NRWPLRSQITIMPVYL
19028	49396	A	19137	305	2291	YLDAEKMGGQKASQQLALKDSK EVPVCEVVSEAIHVAHQKLKE YLGFEYPPSKLCPAANTLNEIFL IHFIITCQEKGVDEWLTTTKMT KHQAFLFGADWIWTFWGSNKQ IKLQLAVQTLQMSSPPPVESKP CDLSNPESRVEESSWKSRLF LEEFCLIGEDCLGLFIIFGMPG KPKDIRGVVLDVSKSQMVRSH LPGGKAVAQFVLETEDEVFIKE LLRNCLSKKDLREGGASPGSL RLAAGPPLTLNAACPLRLAVL AAMAAAAALPAWLSLQSRARTL RAFSTAVYSATPVPTPSLRVDD LHLTEIVGMLDSVLTPESSGK YRFISGEVLCRITGCTGVRVEA KDLFGGCCSNPNEMVMTWIKVI VEKEVWLYLRYILKALPPRTEK MAVDQDWPSVYPVAAPFKPSA VPLPVRMGYPVK*GVPMAKEG NLELLKIPNHLTLTPAIIKHCE ALKDFCTEWPALDSDEKCEK HFPIEDSTDYVSSGPSVRNPRA RVVVLRVKLSSLNDDHAKKK LIKLVGERYCKTTDVLTIKTR CPLRRQNYDYAVYLLTVLYHE SWE/TEE WGKK*D*SRHGKSIY GENSSSERKYPGERFSR*KLLR KNMGN*LKKSS/CGTKEIEEYK KSVVSLKNEEENENSISQYKES
19029	49397	A	19138	3	233	
19030	49398	A	19139	1	256	
19031	49399	C	19140	5	114	
19032	49400	A	19141	8	444	TTDKEQ*EL*LLLDTE*GSYTK CHTDSLRY*TSSTSAEDRDDSL LRRSGSYRDL*E*IPYSCRLDKD DSTDICIKLYEQILAE*NDKLKAQ LHDTNMELTDKLQLEKATQR QERFADRSLEMEKRERTALQR RISEMEERLQM
19033	49401	A	19142	1	287	

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19034	49402	A	19143	211	346	
19035	49403	A	19144	175	3381	EDPAAGEGMMKADAKHKRNE QLKRWIGSETDLEPPVVKRQKT KVKFDDGAVFLAACSSGDTDE VLKLLHRGADINYANVDG/LSH ALHQAACIDDNVDMAKLLVDNG ANINQPVNDGWIPLHAAPSCGY LDIAEFLNGQGAHVGAVNSEG DTPLDIAEEEEAMEELLQNEVNR QGVDEIARKEEERIMLRDARQ WLNNSGHINDVRHAKSGGTALH VAAAKGYTEVLKLLIQAG/YDV NIKDYDGWTPPLHA'AAH'W
19036	49404	A	19145	1	2406	
19037	49405	A	19146	1154	1365	
19038	49406	A	19147	1	293	MGVSVLDFSHSDKCEVASRFAS GMPEPTNIVLPKLEVADTLGGC TTIPESDLERSVEQDSTELFTN HRHLTAETPR/PW*RLDGLHKQ VSPLOQVSE
19039	49407	A	19148	3	1290	VSQATDVEVGTDLVPSVTVKV TLQNRVILQKAKLSVYVQPPLE LTCQDFTFEMNRPDGIPIRVQ CKFRLPLKLCIPGQPSKTASHK ITIDTNKSPVLSLLSPFGFASQSD DDQVNVMGFHLGGARITVLA SKTSQRYRIQSEQFEDLWLITNE LILRLQEYFEKQGVKDFACFSFS GSIPLQEYFELIDHIFELRNGE KLEELLSERAVQFRAIQRLLA RFKDKTPAPLQHLDTLLDGTYK QVIALADAVEENQGNLFQSFTR LKSAATHLVILLIALWQKLSADQ VAILEAAFLPLQEDTQELGWEE TVDAASHLLKTCLSKSSKEQA LNLNSQLNIPKDTSQLKKHITLL CDRLSKGGRLCLSTDAAAPQT MVMPGGCTTIPESDL*ERSVEQ DSTELFTNHRHLTVETPRPEVSP
19040	49408	A	19149	48	642	WNSALREPLNGADMAKSKN HTTNQSRKWPRNGIKKPRSP KIRILLKGVAPPSFLARNMRFQ ESPNNKGP*RLQANKLPRA ATLPRAIKALVKPQGGSPKIP KGVSSRKLDSTCLTFAQPQALG SVARCP*LPRGPRLCPPKAKAK AKAKPRPKPRPRAKDQNGPG LQPQASVPAQAPKRTQAP/TKA SE

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19041	49409	A	19150	1953	2447	WTPQYMDTEYKNGPWMMKEK KVWLDLP/NETNEIPNANFRQQIR KLIKDGLILRHRKPVTVHSRAQ CWKSTLARRKGRHLGIESKKID RHMVHSLYLKLGKGNVFKHKRI LTEHSHKLKADKARKKPLADQ AEARGSKTKEARKLREHLQT KKEEIIKTLSQEEKAKK
19042	49410	A	19151	1	693	MAVMEKLYVWNREESYASLR VHLPCNATTMSMLSLQKRLAS SVLRCCGKKVWLDLPKETSEIAN ANSHQWIRKLIKDLIIHKPVT HS/*ARYR/KNTLACQKGRHMG I*KATANARMPEKIMWMR/RM RILCOLLRRCDSKKIDHHMYH RRYHESKKVDRHMYHSLYLKV KGNVFNKRILMEHIHNLKAD KACKLLADQAEATRRSRIKEAR KHREHLQAKKEEIIKTLV
19043	49411	A	19152	34	280	EVIHAAIGEEKGSY/NA**PWVE EQLTRQPLIHHQPASLHVSRY/ RYHSLYLKVKGNVFNKRILM EHIHKLKADKARKKLLA
19044	49412	A	19153	2	625	HEAMSMRLQLKRLASSVLRG KKKVWLDLPNETNEIANANSRQ QIRKLIKDGLIIRKPVTVHSRLR CRKNTLAR/*KGRHMGIGKRK VPANA/RMP/EKVTWMRENEG FCRRLASEDTRES/KKIDRPHVV TALYL/EVKGKGNVFNKRIL/ME HIHKLKADKARKKLLAD/QAE ARRSKTEATKRREERLP/ARPR KREII*TLSCKEETKK
19045	49413	C	19154	154	291	
19046	49414	A	19155	3	253	
19047	49415	A	19156	2	474	FKDKQNKPTGFGALSGIEGRVAI HYINPPNP*V*LCQLADFTGLFL TKEDLHEPLSFSKADNFTFKCH RSNGTNTSAPQDIYAVNGIAFH PVHGTLATVGSDDGRFSFWDKD ARTKLKTSQQLDQPIACCFFNH NGNFI/AYASSYDWSKGHEFYNN PQKKK

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19048	49416	A	19157	97	1728	IRGFFRGSGQSFYRRLKEASGS WDFCPRSWPSSLRLRSGSQTP ETLLLPAGVFRSETPMFKMSLF GTTSRFGTSGTIMGSA TVDNH NPIEGY*K*HSFSLMDSIG/CSCL FSPPTLPGNFLIAGSW/ANDVRC WAEVQDSGQTIPKAQQMHTGP VL/DVCWE/SDGGSKVFT/ASCG /KTAKMWDLRQ*PRRLQIAQH/ DAPV/KTIHW/KAPNYSCVMTG SWDKTLKFWDTRSSNPMMVL QLP/ERCYCADVIYPM/VVATA /ERGLI/VLIQL/ERIQPSEFRRIESP L/KHQH/RCAIF/KDKQNKPTG F/ALESIQGRVAIHYNPPNPA/K DTFTFK/CHRSNGTNTSAPQ/DI YAVNGH/AFHPV/HGHPNCNGD LDGRFSFWD/DARTKLKNFRE QLDQP/LSSAC/CFNH/NGKHILP YAS/SDWVWKGDH/EFYNP/QK KKFTFFPA*MQAEELKAPGNKE VVAGR TLGSAQSLFLLHSGLI S VRIWAPNLVGVVSPW/TMEFQP PGENDVIVQQLSPRRPAGDLP VFSIPTGLVAEVFSGKPKGGLK
19049	49417	A	19158	1	1254	
19050	49418	A	19159	1	921	
19051	49419	A	19160	1	1386	
19052	49420	A	19161	49	731	

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19053	49421	A	19162	61	1533	PLKAKMGKEKTHINIVVIGHV DSGKSTTTGHLIYKCGGIDKRTI EKFEKEAAEMGKDSFKFAWV LDKLKAERERGITTIDSLWKFET SKYYVTIIDAPGHRDFIKNMITG VTSQADCAVLIVAAAGVGEFEAG ISKNGQVTRHALLAYTLGVVE QLIVGVNKM DSTEPYSSQKRY EEMWLEEVSTFNKKIWLQPPPTQ *HFVPISWFGIDNMLEPSA/N MPWFKGWVKVTRKDGNSAGTT LLEALDCILPPTRTDKPLR/LPL QGVHKLGGIGTVSSAPMETGF SNPGMVVTFAP/STVTTESKIL SKMHP*SFEVKLLPGDQCGPSM SKNVFCQGMFRRGKRLLDGQQ KMTPPNGKAAAGLHWSRVLUN HPRPK*GAGPMPLYLDC/HTGS HLHAKFAELKEKIDRR/SGKKL EDGLKFLKSGDAAIVDIVPGRP MCVESFSYPLGRFAVRDMR QTVAVGV/ISKAVDKKGCWEL GKVTKVWPRKAPEG
19054	49422	A	19163	1	514	EFGTRAKKEAPAPP*SLKPKRK AFKGPRKAVLKGVS/HSHQKEE DPARSPTFPGGPKTLRLRRQPK YPRKSRVPGETRLDHLCLSNF PLTH*VLPMKKIEDNNTLVFIV DVKANKH/QIKQAVKKLY/D/D VAKVNT/LWIRPDGEK/KAYVR L/APDLPIAFGMFANKIWGFI
19055	49423	A	19164	433	1015	GLISLNDMASRGAS*PTGPDGT NKICQFKLSTSGSPAVCKSSLV LRFVKGQVHEFQESTIGAAFLT QTVCLDDTTEKFEIWDTAGQE RYHSLAPMYRYGAQAIVVY DITNEESFARAKNWVKELQEQ ASPNIIVIALSGNKADLANRAV DFQEAQSYADDNSLFMETSA NTSMNVNEIFMAIGKINISF
19056	49424	B	19165	1	2511	
19057	49425	A	19166	2	360	

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19058	49426	A	19167	125	211	FRPGSPRQPRAQPISAPDCTRA MVGRRALIVLAHSERTSFNYA MKEAAAAALKKKGWEVVE/S DLYAMNFNPIISRKIDITGKLE GPLRTFQYPGRSLFLAYKIEGHL EP/EIICGLNKKKLEAADLVIFQ FPLAVGLEVPAILKGWFEPVH KESFA*HFTAGHVMDKGPFFG VKKAVAFPFITGGISGSMYSC QGINHGDMNVILWPVQSGVLPF LGLPKSLDPQLTYSIWPLPAR RPEFSILEGWKKRLE/NIWDET PLYFAPSSLFDLNFQAGFLMK KEVQDEEENKKF/GLSVG/HHL GKSIPTD\NQIQS*KRECTVHYT RDSHKVAAGAAQLTESLVPAR VAPATTS PANQRPLGHQSHGR
19059	49427	A	19168	2	331	WVDSQQKRYVPVKGDHVGIV TAKSGDIFKVDVGGSEPAISY LSFEGATKRNRPNVQVGDLYG QFVVANKDMEPEMVCIDSCGR ANGMGVIGQDGLLFKVTGLIR
19060	49428	A	19169	145	350	QEFHLSSEPSIRLGRSLYHIHHL FASKKVLD*QWLDQSL*VCSW EHMRRSQ*GIFSRLANRGFQNG DC

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19061	49429	A	19170	1	1863	MAVAIRLSADTQWEDSPGKSIL ELHMSCTKIPERCEADKKESTS SWCTRKIRFRMDLEKECKVLLS GGGSRMRMSQKGDGVRWSSP RVGLPSSQTLRLPPPTDFHIAPL SKARQHLLVSVVLFCSAPLD VQPLKVLDECQNQRACHLLVN SRVFGDLCPGSSKYLVSFKC QPKQMFTQQGPGVLSIGETQV STSSVTRSSSPVGPDIHCEFHIN MCKIPDELKKNKTCVEDQELKL HCHESKFLNIYSATYGRRTQER DICSSKAERLPPFVFTRYCYFLY APVSSIANPVKGCFFHLGKKQDC LSYSALQVLSRRCYGKQRCII VNNHHFGSPCLPGVKKYLTVT YACATLSSMGPIAEVPPPEAKK VTLSLSDSSSGRMEDGRDGTG HTEVPVTSGLFIRVLNKKQNF LQIRCSFGRGPGKLRHCWAGA. AIALGTEYILVKGDQVTGIVTA KSGDIFRVDVGGSEPVSLSYLS FEGATKRNRPNVQVGDLYGQF VVANKDMEPEMVCIDSCGRAN GMGVIGQDGLLFKVTGLN*E SLLASQICE/ISIQEVGKLLPLEI VFGMNGRIWG*GQKTHPSQTLI LA/NI/LACEHMTSDQRKTDLP
19062	49430	B	19171	29	82	
19063	49431	A	19172	1	427	

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19064	49432	A	19173	1	1548	MTMAAAAVVARGAGARAATA AALRGGCGTAARGRPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGTKKYTTSLNARHY YTHFTEENEDEINSSSYASQKK TFEINPRHPLJRDMLLRKKEDED DKTVLDDLAVLVFETATLRSGYL LPDTKAYGDRJERMLRLSLNID PDAKVEEEPEEPEETAEDITE DTEPDEDEEMDVGTDEEETG KESDDPMAYIHFTAEGETFKS ILFVPTSAPRGLFDEYGSKKSDY IKLYVRRVFITDDFHDMMPKYL NFVKGVYIRKKLVKTLDMIK KIA DDKYNDTFWKEFGTNIKLG VIEDHSNRTRLAKLSRFQSSHH PTDITSLDQYVERMKEKQDKIY FMAGSSRKEASSPFVERLLKK GYEVIYLTPEVDEYCIQALPEFD GKRFPQVAKEGVKFDESEKTK ESREAVEKEFEPLLNW MKDKA LKDKI*K/ALWVSSAALTESPV LLVAQPVRDWS/GQHWERIMK AQAYQTGKDISTNYYA
19065	49433	A	19174	37	266	WADRAAGGVRILTQGCVGGG GSCDRRGLETSPARTPVRLWV LG\LCVLLTFGSV/READDEVD VDGTVEEDLG*KYEKDQVTD EVDVQEEEAQLDGLNASQIRE LAREKSENFPPQAEVNRMIETLF IQFHCIKNKEIFLERLISNSSCAL DRLSLISLT DENALSGNEELTV K\KCDKEKNLLHVQHTGVGM TREELVKNLGTIA\KSGTKRVF *TKRPEA/QEDGPSQPS*IDWPS LGVRF
19066	49434	A	19175	233	664	RAPEQSSGVSAAEQERVNAG WPCSVAPTCPSPRAEPARCT* GKEEGG/CEDSDRADSGSPFQE PRYPSSGFFPIPQASFFPCPLLVL GIRGHSTLQYRGQEHHLVFTG RCLLDVPTLLVLVVSXKSPNAA RDQPARYPGRPL

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19067	49435	A	19176	1	672	MAEAGPKPQRTLMWAWESVL SQRKPREAGRLSEGCVKATGTP FGFWQARPDQKEHRLDGRVID PKDRHGLVKDTEPRLNFQSLCG GLNPEATEEKIREYLASLGRRR PVKKVLEKKFHTVSGS/KCGPQ VPPSWSETYRTRA*SGDQLGTP AAPNPRWPMME*EQEIEAQRSA HSGARAPWPPWPPRPDGPNGP GPKFMVSLSCWNISSLRAGLLY AGCGCSP
19068	49436	A	19177	3	684	RHASARKKYNPPSWFHRGLPPP EDQEDEMVSSELE/PITLTPSSA LKPSDRMTMSSLGERACCRDY QRLGLGTLSSSLSRKSEPFRRIS PVNRMYAICRSYPGLLIVPQSV QDNALQVRSRCYRQNRFPVVC WRSGRSKAVLLRSGGLHGKGV VGLFKAQNAPSPGQSQADSSSL EQEKYLQAVVSSMPRYADASG RNTLSGFSASHMGSHGKWGSV RTSGRSSGLG
19069	49437	A	19178	1	341	
19070	49438	A	19179	1	3710	MVSGARAAAAAAAAAAAAAER TRGVPGHPDSTGRLPAAHQQLQ RGLLFRQLGITNVLSLVCATLM EHEVLFLSRSYQQLTDACRSLL ALLFPLRYSFYVPIPAQLLEA LSTPTPFJIGVNAAFQAEQELL DVIVADLDGETVTIPECVHIPPL LEPLQSQTHSVLRMVLDPELEL VDLAFPPPM/HDKELRLFHQLL QGYLWCLHVVICIHEPVIRFH KAAFLGQCGLVEDNFLMNVLE GMAFALFVLECCGPV
19071	49439	A	19180	1	303	
19072	49440	A	19181	14	942	TKLTGSRG*LA*NPCM/HNNCE SCVDLLFVRGAGNCPECGTPLR KSNFRVQLFEDPTV/DKEVEIRK KVLKIYNKREEDFPSLREYNDF LEEVEEIVFNLTNNVDLNTKK KMEIYQKENKDVIQKNKLKLT REQEELEEALEVERQENEQRRL FIQKEEQQLKILKRKNKQAFLD ELESSDLPVALLLAQHDKRSTQ LEMQLEKPKPKVPTFTSGIKM SVGITLCPAEHEFTFNDERSFNLS SSWSKFNKPPSTLPFKVLDEER LVELKVNTLITKLVPFAISPCS EAIQDHPAILLAYKKTPFWRLQ
19073	49441	B	19182	49	456	

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19074	49442	B	19183	53	333	
19075	49443	A	19184	2	208	VYPELQITNVVEANQPVTIQNW CKRGRKQCKTIPHL*FPYRCLG EPAGRGAGVDWGPGLGRKRG CSC
19076	49444	B	19185	51	300	
19077	49445	B	19186	148	3568	
19078	49446	A	19187	1	3411	
19079	49447	A	19188	2	2416	NSRGAACAGPRETAAVAARAE QGRGGSHSHSALGAPRRVAM LPGLALLLLAAWTARALEVPT DGNAGLLAEPQIAMFCGRLLNM HMNVQNGKWDSDPSGTCTCID TKEGILQYCEVYPELQITNVV EANQPVTIQNWCKRGRKQCKT HPHFVIPYRCLVGEFVSDALLV PDKCKFLHQERMDVCETHLHW HTVAKETCSEKSTNLHDYGML LPCGIDKFRGVEFVCCPLAEE DNVDSADAEEDDSVWVWAG ADTDYADGSEDKVVEVAEEEE VAEVEEEEEAD*LTRTDEDGDE VEEEA\EEPYQEATERTTSIATT TTTTTSEVVEVREVCSEAET GAVPSNDLPLVL*CD*REVCPI LRRMWRQPEQL*HRRVLHGRV WQR\PTTAASTPDA\VDKYLET PGDENEHAHFQKAKERLEAKH RERMSQVMREWEAE\ROAK NLPKADKKA\IQHFQ\EKVESL *QEAANE\RQQLVETHMARVE AMLNDRRLALENYITALQAV PPRPRHVFNMLKKYVRAEQKD RQHTLKHFHVVRMVDPKKAAQ IRSQVMTHLRVIYERMNQLSL LYNVPAVAEEIQDEVELLOKE QNYSDVLANMISEPRISYGND ALMPSLTETKTTVELLPVNGEF SLDDLQPWHSFGADSVPANTE NEVE\PDARPAADRLTTRPG

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19080	49448	A	19189	1	2355	MKSIFTSEISSVLIFVNPEGRVVSFLGSGRREHAEEARAGPRETA AVAAARAEQGRGGSHSSALG APRRVAMLPLGALLLLAAWTV WAL\EVPTDGNAGLLAEPQIAM FCGRI.NMHHMNVQNVKWDSDP SVGTKCIDTKEGILQYCEVYP ELQITNVVEANQPVVTIQNWCKR GRKIQCKTHPHFVIPRYCLVGEF VSDALLVDPKCKFLHQERMGC FAETHLHWHTAAKETLQ*RRS TNLHDYGMLLPCGIDKLRGVEF VCCPLAESDNVDSADAEDDS DVWVGADTDYADGSEDKVV EVAEEEEVAEEEEADDED DEGDVEVEEAKEPYEEATERT TSIATTTTTTTESVEEVVRVPTT AASTPDADVCKYLETPGDENEH AHFQKAKERLEAKHRERMSQV MREWEAEERQAKN\LPKADKK AVFQHFPAEKVESLEQEAANER QQLVETHMARVEAMLNDPRRL ALEWNYTALQAVIPPRPRHVF NMLKKYVRARTEGLVSTSL*HF EHR\MVDPKKAQIRSQVM\T HLRVIYERMNQSLSLLYNVPA VAEEIQDEVDELLQKDANYS** RLWPTMISEPRI\SYG\NDAL\MP SLTETKTTRGSSVPVNEE\FSLD\ DLEPVHFFWWLTSVPANTENE VEVPVDARPAADRGLTTR\PGSG LTNIKTEISE\VKMDAEFRHDS
19081	49449	A	19190	103	463	PLLYAMSTGKRWL\SFSGMIPPV AICASNKRIPWPFMSMSSLFMAW NKEMMFVPSGSLYPVTARSAD RSFSLNSMPTRPILL*ASSTGNLKL LLTGSTIKPVAAWASSNSRAVP GRTKPIFMAS
19082	49450	A	19191	1	182	
19083	49451	A	19192	3	437	MVHAEISDEGFFLSAPIALTOA WLNIPKTRRTFCKKCGKHQPH KIVTQYKKGKDS\LYAQGKRRY DRKQSGYGGQN*KPIFRKKAKT TKKIVL\KALSAL\PTCRSKSKC WLFKR\CKHF*TGEEIRKRGQ VDPVLKCHLLFMEGH
19084	49452	C	19193	341	421	

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19085	49453	A	19194	15	1066	VLACTVEASVIGGQKREMNMG SIVREGFMEEAGPRIGFNLSPFI QSTVTGSSSVGSTQLQPLSLPPA TAGQEPRGTTGPLGSHNSCPAPE PVSYGRINDPPATTHPGSFTRF HSKPLTSSCWDSMEGCVSNL MVCNLAFLNVSTNPCAFFPW YFYLLLL*AGWSPLHIAASAG RDEIVKALLGKGGVLNVYNT DRFLHCFLLSSPSQIAVMLLEG GANPDAKDHYEATAMHRAAA KGNLLARNPNHYIELVVINWSL VVPDFRHLACDEERVVEAKLL VSQGASIIYENKEEKTPLQV\AK GGLGF*YSREWVGRFKQLGFIL YFVLLCLLSPVSYKLMYLCTRH
19086	49454	A	19195	1597	1923	
19087	49455	A	19196	551	747	
19088	49456	A	19197	1059	1296	
19089	49457	B	19198	1	1281	
19090	49458	A	19199	3	565	LPGRLLLLNFRQRQIDRPSMN DTRNLSRTVRKFHAPTRPTSEEN KWVIDVLPAGRPVTP*DOQKFR EK\LA\KMYQAPHDPV\ILVFGF\ RT\HFGGGKTTGFG\MIYDSPWI MQRKNEP\KHLAR\HGLYEKK KDLKKATEKERQEPCLKVQG GLAKGPLLGAGQKEEMKCLAV ELEIGSQPKELKVQ
19091	49459	A	19200	2	476	

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19092	49460	A	19201	1	2448	M R G S I L K E C G S K E R A S Q V D L E Y S R G N T A S F A M C F H D R A R I M K G S Q R S R K L T G G E G R E E G E R V E N K D F I D L H G Q I Q V R L V V K T A S L L S R V T Y I A E V E G R E T D A G W R N E L Q V G R L D S G P D I L V V S I S T D H T L V D T H L E A V G G H S H E F P Y F K N H L A C H V E S E L Q R D R N G H R D A G W R N M R H G I T D K E M Q D S Q G S S D N H V L G S I R S W S A R A A P A I P G L P E E A F V E M S T E G G F G G T S R S D A Q Q S L K S F W L R P R F I T E L T L R A W I H T E D N N C R T Y V A M A I T K F D Q L D F L I D I V L R D E L K P P K C Q E E V L Q S V T P A E P V Q Y Y F T L A Q Q P T A / V Q V Q G Q Q Q G Q T T A S S M T T M Q P G Q I I I A Q L Q Q G Q T T P V T T Q V G E G Q Q V Q I V Q A Q P G Q Q A Q * A Q S G T G W T V Q G Q I Q T L A T S A Q P I T Q T E V Q Q R Q Q * F S Q F T D G Q Q L Y Q I Q V S I P A G Q D L A Q P M F I Q S A N Q P S D G Q A P R S H E V I A A P A A R R E R E R E L A G R G P C P P P A G N V R A L K S R R C L P G E R R E R A R K K K P E G G A A A S E R G E T D S H P G A S G Q G P R D S G R V P L G M W S R R G L G V S R A P L H L L I G V S T S F P L P L T P L I P T T A V V N P L K P L K N R I K A P H R R M P L V P G G S Q N L G T V R A R I S T R Q S H A E P S T D N E R V L S M T Q D I H S I F L N L K N I T W I C T L Q S C G F L L S N L C K D I V H K A G S G E A R T R W S P R A Q A G T H E D
19093	49461	C	19202	124	369	
19094	49462	B	19203	739	870	
19095	49463	C	19204	787	969	
19096	49464	A	19205	101	331	
19097	49465	A	19206	137	415	
19098	49466	A	19207	86	221	
19099	49467	A	19208	1	1347	
19100	49468	A	19209	120	899	F G A R G N L K K A Y S T R S K M A E L N T H V N V K E K I Y A V R S V V P N K S N N E I V L V L Q Q F D F N V D K A V Q A F V D G S A I Q V L K E W N M T G K K K N N K R K R S K S K Q H Q G N K I D A K D K V E R P D A C P L Q P P P Q I Q N G P M N G C E K D S S T D S A N E K P A L I P R E K K I S I L E E P S K A L R G V T G P N I E K S A K D L Q R C T V S L T R Y R V M I K E E V D S S V K K I T A A F A E L H N C I I D K E A S L M A E M D K G I E E A M E I L T A R Q R K A E A L K R L T D L A S Q M A E

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19101	49469	A	19210	211	2150	ADTKPERGVSSAVFASGSEGRRLGCVLLSSSETRLLSGTLWIPRAYSTRSKMAELNTHVNVKEKJY AARSVVPNKSNEIVLVQQQFDNFVDKAVQAFVDGSAIQVLKEWNMTGNKNKYKRIRSKSKQHQQNKDAKDKVERPEAGLPQPQPPQIQNGPMNGCEKDDSSSTD SAN EKPALIPREKKISILEEPSKALRGVTEGNRLQQKLSLGGNPKPIHGTTERTSDGLQWSAEQPCNPSKPKAKTSPVKSNTPAAHLEIKPDELAAKRGPNIEKSS/VKDLQRL/CTVFF*LEYRVMN*RERKWDSSGERRSKLPFAE\LNCHIEQKEV\SLMGRKWD*SLKEGRPWEILDWLVRKSKKKLRLTDLGQSRMAEMQLGPKLRAEIKHFVSEAVNYDEELGKSCPGFSCDIEQLKAQIHALPGKITHPKNNYFLKELPCSSLLPLLNARSKPLGKTEVTFSRKSSSTHNKPSSEGAANPKMVSSLPSTADPSHQTM PANKQNGSSNQRRRFNPQ\YHN\NRLN\GPAKSGQSGNEAEPLGKGNSRHGTQEGQPH/NRFGFRPKNKGRCQKIQEASLGIEGPPRAPAHFLKRPRAKGSHAADTFGRARAFSGVS/GSVRGSCNLFPTRI EVSTDAAVLSVPGCDRWVA
19102	49470	A	19211	93	180	
19103	49471	A	19212	3	39	
19104	49472	B	19213	1	888	
19105	49473	A	19214	863	1509	GCAGPCLVNQMFTSSILCKSHCHSLVSNQGHNAPWKAAG/PLPLKAGYQ/QSFPCDSLKYGSWD EKDLTVPQPDTRKASVLRWISQRGKPLAVDMEEG\HCL/CLPPGN*NVLGCKTPIVHLFNSELGRKAALWREARHVG/SNAALLFFTPLRCLGGEKHKSGLHAHPGIVP/SLELNYDIDSFAHVFVFAVELPLIITLLPYCIPLCCNNEK
19106	49474	C	19215	289	510	
19107	49475	B	19216	534	1686	
19108	49476	B	19217	1	1062	
19109	49477	B	19218	1	1878	
19110	49478	B	19219	1	747	
19111	49479	B	19220	230	786	
19112	49480	B	19221	67	6011	
19113	49481	B	19222	1	3455	

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19114	49482	B	19223	1	4763	
19115	49483	B	19224	65	4534	
19116	49484	B	19225	512	4782	
19117	49485	B	19226	345	2194	
19118	49486	B	19227	267	7391	
19119	49487	A	19228	578	739	
19120	49488	A	19229	419	1410	KQRQARERHLPRIQLSAVVTE TL*RK*RNFAELKIS/RLRKFFA HKMLQKARRKLIYEKVKHCHK EYRQMYRTEIQMATMARKAG NFFVHPKPKLAFVIRISAISGVSP KWKNNKQLCPNLNVFGLGMGD LRAFGLADGTGPGGEITGMRD LRGPLSVRAPSAAGVAEIPRHLIV FEDVNVNGKFLQTSRCEISGSKN KVVQTLKKNKRERQRLPTGFG RLADQRAYGEAKNNCGVGL VETLWERHLLRIGVYIATSSLA VPTLSSNYNGLAHDQSCSDTVQ RSTGAPEAWDRGYCVGRGAQG IPIFFLDRPLTSLFDEARGSSAS
19121	49489	A	19230	3	307	AGTMEGVEEKKEVPAVPETL KKKRRNFAELKIKRLKKKFAQ KMLRKARRKLIYEKAKHYHKE YRQMYRTEIRMARMARKAGN FYVPAEPKLAFFVIRIRGI
19122	49490	A	19231	3	160	GRVLL*DKTSRGTIRQQQLLFT NICCSAASA/G*YPGKQGLEWT SSRLQQTCS
19123	49491	A	19232	303	570	GLCIRHVLVPSAAGLLEFAGGP LQTLFAWVSAEAEQIIVVN SKCC/CPDRSSGSFVSEYLA GVGLTLSSASLMLGAVDWS HSA
19124	49492	A	19233	1	176	MQYVQQKPKLKFQVHCAYRK TVLQPLLIPRQT/VVWSGPPA NSNRPAAGGADC*KEN

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19125	49493	A	19234	1	1977	MFAVLQAPLVIPROT/VVWSGP PANSNRPA AEGPDC*KEN*RQT GSGV DLQQTPTDLQLRLIVRR KTNEQKGHPHNPIC TSPSSK T KVDTTTNMGEKQSRKTENSKN QSASPPPNLKKREKNQIDA IK NDKGDITTDPTETIQT TIREYK H LYSNKLENLEEMGKFLDTYNLP GLNQEEVESLNRPI TGEIEV IIN SLPTKKS PGDGTAEFYQRTK DKNHMIISIDE EKAFDKIQQPFM LKTNLKL GIDGTYLKIRAIYDK PTANIILNGQKLEAFPLKAGTR QGCPLSPLL FNIVLEVLAREIRQ EKEIKGIQVGKEEVKLYLFADD MIVYLENPIISAQNL LKLISNFSK VSGYKIN VQKSQAFLYTSNRQT ESQIMSEL PVTIASKRIKYLGIQL TRGVKNLFKENYKPLL NKIKED TNKWKNI PCSWIGRINIMKMAI VPKVYIRFNAIPKLPMTTFTEL EKTTLKCIWNQKRAHIVKSILS QKNKAGGIMLPDFKLYYKATV TKTAWY WYQNRHIDQWNRTE PSEIMPHIYSYLIFDKPDKTRNG ERIPYLIRWCWCQWNWLAICR KLKLDPF LTSYTKINSRWIKDL NVRPKTIKLEENLGITIDIGM GKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQ PTEWENISAIYSSDKGLISRIY
19126	49494	A	19235	206	456	
19127	49495	A	19236	2	385	NLCCSAASAGDTQANRVWSGT PTNSSRPEVSSGAMDGEGWGL PVDPLTPGHQDALPWQRCYHP CSSSSVPPRQACASPCSSSAA WTSASTGPWHS GCGSSCGSCC CWGSPSASVGVGAGAIRSRTV
19128	49496	B	19237	1	642	
19129	49497	A	19238	128	584	
19130	49498	A	19239	4054	4578	QSGPSAAGLLEFAGGPLQTLFA WVSA AEAQRI LVNSRCCCL I VPRKFC LRGVASHVRCQSAPY DVFC HGITLAKCWCSALGLPSL QSCEPNALFFINYPVCGI/TAPCC KVEGTMGVGP KSPQLSYNV L GSDNNGVLLGSM AIFTILILLIH EHGMFFHLFVSSFISLSSGL

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19131	49499	A	19240	1	948	MVLEKAREEVDPPSLIPPVTQ CGQLPRSQCPQPTLSRMLTLEV GISLGIIVLMISLWPDTVKEYQS REALSFKKYNKNPGLLKFAAGDP LQTLFAWVSPAEEAEQQISALC FLWKLPRGPATRCQPLLSTYTR CLSAPAGSFVYTMRGKPIQAS VMADASPTKIEHPRITSDCCV ASKNFKPVDSLSCSMGVGSAE LDHWATWLQSPFQGSERFCLA GVPGTTGV*KETPAASSVSAQM AAQFCA*N/HRTLTV*APKGIL WVCGLRPWKRSICAGVHHS SWHSPSWLPLARGSSSTPCTS WVRRCP TLHL
19132	49500	A	19241	171	1345	YCPKEGTLDFNFANMTAVNV ALIRDTKWLTLVEVCREFRGTC SRADADCKFAHPPRVCHVENG RVVACFDLSKSVTAVPFLFMA GLSREPETVPASMVQTFSLGVG GGAGSV*PDENCKYLHPPHLK TQLEINGRNLIQKQTAAMFMA QQMQLMLQNAQMSSLSGFPM PSIPANPPM/SFESLRYHILGMG LVPAELVPNTVLPGLKPTSLQL PGSCLGPKLMAFQINWEVLP RQNGNC/SRGENDICRY/AHPTD ASMIEASDNTVTICMGYIKGRR TVGVWGIKAKSSQRLDTKGS HQGNSFVRGTDYLPICTNMSK AKGTAFLKWMQKLVYNGSSG QCSAPFFCCAWEHSEKAGRA SGAKCNRHRTNPVFLMREGA IS
19133	49501	A	19242	61	544	KFNPIFVTSRPRARIRKRAFNP SHIPKGRLLSFPLSPKSLRPEG TNRADSHAPIKRMIESSRLYR GHL*GSAKLAKVVPFRTRKKY VIYIER/VQREKA\NGTTVHVGI HPSKQVITKAKTGTTRKKIP PNRKAQSRQVGKEG/KYKER TUEKMQE
19134	49502	A	19243	652	1042	TPLSSCFLSREKATQLLFPVVA VPMVLSAMGFTAAGIASSIAA KMMSAAAANGGGVAVSGSLVA TLQS/LG*VSWRGLPTVLPTEL RQACPTLSTLCFFPGATGLSGLT KFILGSIGSAIAAVIARFY
19135	49503	A	19244	48	397	

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19136	49504	A	19245	42	296	GCVGVRLHPATSTASGSASP TLARAMASVSELACIYALILH DDEVTVTEDKINA/APAEKKV EAKKEESEESDDMGFLFD
19137	49505	A	19246	172	519	LGPSFLHDEVTVTEDKIQMPLI KAAGVNVPEFPWPG/LCFAKAL GKRSTLGLSLAMLGGPVGPGS QPAGCLQPAAGSCPPSTCCWF QLEGEKEWEAKERKIPREF*LID MGFLFD
19138	49506	A	19247	3	175	
19139	49507	A	19248	2	390	GWDWNCVWEPHHWLCQSL/N SVTQAGVQCLNLSLQPLPLGF KQFSCLSLSSWDYRNSLKKQ LFSYAILGFALSEAMGLFCLMV AFLISLPCGAVSTSHSSPASG WPRVFLFLYLPRQPGERGWL
19140	49508	B	19249	139	13320	
19141	49509	A	19250	28	450	TNDFNLQNPFGSCFSPACPAVG SERLPVLGWVFGNRSFPPPPQST LSVLGKRLGRNGAIAAGVFGA LFIGYCIYFDRKRLK*PQLKDAE AVQKFFLEEI*LIGEEILAKGVD HLTNPSAFFG/QPNHFPLQMDSF GPFLRFQA
19142	49510	A	19251	164	420	
19143	49511	A	19252	1	329	STHTTYWEGCRTTSAGLLRKH EPGEEAF/FYHSTSKKPGIAGLI KVNVPQFVRMMKRSIPWAEINP YHQAHKATGGPLKNMVLFTRO RLSIQPLTQEEFDFVLSLEEKEP
19144	49512	B	19253	39	368	
19145	49513	A	19254	1014	1290	
19146	49514	A	19255	122	680	LARITRIVRTKVPCSVTMSRPRK RLAGTSGSDKGLSGKRTKTENS GEALAKVEDSNPQKTSATKNC LKNLSHSLWMKSEPEERLEKG VDVKFSIEDLTAQAKQTTCWD GVRNYQAS/RNFLRAMKLGEE AFFYP*QLAKKPGIAGLMKIVK EAYPDHTQF*EKNPHYDPSSKE DNPKWSMKSLILF

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19147	49515	A	19256	2	1005	RISTSTLCPPKKLIAPPGRAGL ASMGLNEEQKEFQKVAADF ^{AA} REMAPNMAEWDQKDRKADGK GGAVTQEVQAQLLVKHGQKL VSRFQLSSFSYVDSVRTTQSKQ EHLQTDKGLSGKRTKTENSGE ALAKVEDSNPQKTSATKNCLK NLSSHWMKSEPE ^{SR} LEKGVD VKFSIEDLK ^{AA} QPQ ^Q TT ^W EWEG VRNY ^Q ARNFLRAMKLGEE ^{AF} FYH ^S SNCKEPIAGLMKIVK ^{EA} VYPDHTQFEKKQPP ^{PL} *PPS* ^{QR} GTPPKWPHGWMV/QVWFGMM KRFHSP ^{LA} E/LKS/HHQA ^{HA} K ^{AS} GGPLKNMVLFTR/QRLSNQ ^{PL} T VQEEFDV ^{LS} LEEK ^{EPS}
19148	49516	A	19257	3	727	VRLQFLTPTLRAARTMAAPPQL RALLVVVNALLRKRRYHAALA VLKGF ^R NGAVYGAKIRGPSRR WVMTFLFREWAASREKLWAIL QATYIHSWNL ^{AR} FVHLTRV FRCPAVPYITRARTYPAHAFPG AGLSFGGILVFG ^R KQ*TFNSQI\ NMYLLSTRPCLP*SR ^{LA} VRRK GLHP*NPRWD ^{PFP} /VCLTAVVW GLVLWLF ^{EY} HRSTLQPSLQSSM TYLYEDSNV ^{WHD} ISDFLVY ^{NK} SRPSN
19149	49517	A	19258	1	849	MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSIVSSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIAA ^{AF} REPRLLVVTD ^{PRA} DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHS/DPEEIE KEEQAAAEKAVTKEEFQGEWT APAPEFTATQPEVADLSEGVQV PSVPIQQFP ^{TD} WSTQPATENW SAAPTAQATEWKM ^Q QSTILE AE ^{SS} PHQTPNLPA ^P WSKTSQ ^{PP} E

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19150	49518	A	19259	1	1309	GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLMKEEDVL KFLAA/GTHLGGTQFLLSRGHG YFYKGKS/DGLSFIINPKRAREE\ LLLPARQIVPHKTPSDVSVISSG NTGQVCGTVRA/VCLKFAAAAT GATPIAGRFTPTGFH*PRSKA AFIREPRLLVVT*PPGADPPALS RSASYVNLPHYLRGCGNTDS\QL RYVDIAIPCNKGAHSGVGLMW WMLARGSFCAAMRGTTISREHPW EVMPDLIFYRYRDPREEKEEQ AA*/E/RQVTKEEFQGEWTAPAP EFTATQPEVADWSEGVQGAPL VPYSAIPTEDWSSQPAMEDWS AAPTATQTEWCSRTSLRQNPSPD TELKKEGLYSARSISKTHVSKT ELPNQGTKKCSRTSHRQNPST ELKKEGLYLARSIGKTHISKTEL
19151	49519	A	19260	965	2495	AFTTRSTFSTNYRSLGSVQAPS YGARPRQAARPAASYAGAGGSG SRISVSRSTSFRGGMGSGGLAT GTPSGVMAGMGIGQNEKETM QS\LNDRLASYLGGQ*RSLEDR RTRKLGRAKFREHFGRKKGPQ VRDWSHYFYKINEDLEGFRFFR KILVGQCPASVSARFDNAPSL LD*F*EFKY*GQSWPMCPVLL NDIPLGSAKV\DDTNYHTDLQL VETEIRGSSRRELLFQ*RRNHEE\ EVKGLQAQIASGLTVE\VDIAP KSQDLAK\IMADIR\AQYD\ELA RKEPEKEA*TKYWSSADLREST TVGHPHKSA*GWKLAEDDASQ KLRRTVQSLEDRPWTSMRKSE RPALENSP*GEVEAPLRPLQDW SQLQTGIPACHLWSQELGTRHR AQRGQRPGPQGV*GPLLNHQG SSLEAEICHLTRPPSWKIGEDFN LGD\SLDERNSMQTIQK\TTPP G*VGLGKVVS*DQLTPKVLKAL SQQEA\VPFVGSRRPKISFRVQ KKKKEKESF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
19152	49520	A	19261	387	1125	CCRPCATPYALRSLR*PACPPP RWRPSSMPTSRPPVSPAASPTC GTCMLSPCPAEHLLHLPAAQ QDPALLQPCHPAPPLRPRALHA AHHVGVWPAHQPLLPPVLCPC GGAGRGGG*RCWWRGPSSSPG PTLIAGQDPGAAQ*TWQ/PTL TSVSATSPKAPLPLAAAVPGA PAEGCCPLLRLQALPAGQLPPGG RRATSAPPAVPGD/PPAQPTM PGSMSCWALAPRCPGPGRCW AWRS
19153	49521	A	19262	3	1097	RGNSRLRYSHDELQPLRLPEL FGNCRQLLEEVATDPAGFR/ IVQEKVFKGLDLE/RAEML/ SQSTLFGRECRFWKDLSPTHLIT FWGPAFQGALTMKQVNPSPKR LRSFCSGAREHFTNYLTQCH/C YHVQGSFEL/PKTMNNSAENH TANSSMAYPSLVAMIASQRQA KIQRKYKQKKEHLRLSAMKSA VESGQADDERVRGYYLLHLQR WVDISLEEIESIDQEIKILRERDS SREASTSNSSRQERPPVKPFHS HFGTWLHSQSTFGAGYSKGW TYGR*VSWYEQHRKLWSTYP DQGNMPRAAPEGISEKAAQQQ EDQEEKEEEDDEPNFHRARE WDDWK/DTHP/RGYGNRQNM
19154	49522	A	19263	2	262	
19155	49523	A	19264	3	1062	GRTAENPARAVSSPNFYAHRKT EVLFPCLTQPLARGPKKHLK/R VAAPKH/WMLDKLTRVFAPI/P STG/PHKLRECLSRJIF/LRNRLK YAL/TGDEVKK/CMQR/IFK/ID GQGSELDINLPLLGFMGCPSAF DKTGEENFRLDLIDTQGVRF WYIRI*PPWRKAKLQVWCQK* GKILCGPTKRESPPSLGTH*CPA PHPAYPIPPHPR*NGYPIPD*IE DLAKINLISIQSEHW*TLCMGD LEGA*P*GRNWVLIPTERGH GIFLTVGSR*KDANGQAFGHF GLFQHFVIGKGNKTHGSLPR GKGIRLHHLLEERDKRLA/AKQ SQWGEMLGLVDIVQIFWYRN
19156	49524	A	19265	62	298	

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19157	49525	A	19266	1	555	MAWQMMQLLLLALVTAAGSA QPR SARARTDLLNVCMNAKHH KTQPSPEDELYGQ/SP/WMCKG SCRKTKSWNI/HRKSKCEVGLA/ WEACSVSAGTGRGPGCGRWV GAPQGP/CPKCKSSG*PTW/VQR SQNMEEMAVNVNQSWRKERILN VPLCKEDCERWVEDCRTSYTC KSNWHKGWNWTSAPSAVCDP LL
19158	49526	A	19267	216	974	MDMAWQMMQLLLLALVTAAGSA QPR SARARTDLLNVCMNAKHH KTQPSPEDELYGQCSA WKK\NACCTAS\TSQELHKDTS RLYNFNW\DHCG*KWNPTCKR PLYPQDSC\YECLTPTLGPWIR QFNQSWRKERFLN\PLCKEDC ERWVEDCRTSYTCKSNWHKG WNWTS\GINKGRPGAF*STFES YFPTPAALCEGLWSHFKVSNY SRGSGRCIQMWFDASQGNPNE EVAKFYAAAMNAGAPSRGIIDS
19159	49527	A	19268	345	2138	QRLTATSSWTTMAKNRRDRNS WGGFSEKTYEWSSEEEPPVKK AGPVQVLIVKDDHSEFDELTA NRILLSEAVRDKEVVAVSAG AFRKGKSFMLDMFLRYMYNQE SVDVWVG DYNEPLTGF SWRGG ERETTGIIQWSEIFL INKPDGKK VAVLLMDTQGTDSQSTLRDS ATVFALRHNDPASIQVYNLSQN VQEDDLQ\HLQFT\YEGQDW AMGKGHFLEAIFRSLDYFFVRD WSFPYEFSGADGGAKFLEKR LKVSGNQHEELQNVRKHIHSCF TNISCFLLPIHGLK\ VATNPNFD GK\LEIDDEFHQKL* KYLIPWA YFRS RGA*Di*RRSNGGLKINTC RGLVEYFKAYIKIYQGEELPHP KSMQLQATAEANNLAAVATAK DTYNKKMEEICGGDKPFLAPN DLQTKHLAT*GRNLWKLFGRV KKMGGEESRRYLQLESEIDE LYTNISSHNDSKINTFCSSYPQ PTLFCSHPLITYVIAGVTGFIGL DIIASLCNMIMGLTLITLCTWAY IRYSGEYRELGA VIGPRWLQLC GTREVMQMRPWNKLYQCQAT PTDILYPSKPFPLHPKVGNLTEQ IQRRKKMVMMPKF

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19160	49528	A	19269	351	509	VVPLPLPLDSWTCESWLRSHI LTGESENPDHKRI*PYTSDLPEG PGPWATD
19161	49529	A	19270	781	4324	ESVREKVLCLGIQQTIVTVC/W SGTYIFAVLLVCVVFHSGAQEK NYTIREIPEENVLIGNLLKDLNL SLIPNKSLLTTMQFKLVYKTGD VPLIRIEEDTGEIFTTGARIDREK LCAGIPRDEHCFYEVEVAILPDE IFRLVKIRFLIEDINDNAPLPFAT VINISIPENSAINSKYTLPAAVDP DVGINGVQNYELIKSQNIFGLD VIETPGGDKMPQLIVQKELDRE EKDTYVMKVKVEDGGFPQRSS
19162	49530	A	19271	3	644	FRSLPRCLPRWQPSSFLGHHG PPFRPPCEAPKIVKKENPRKFIR APSGTGYAKLSVNWRTPEAI DNVRVRRRFKGGILMPANIGYG SNKKTKHMLPSGFRKFLVHN VKEPEIAADVATNLTVPRSLTM FPPNRKAIIRGKACPIGPRSS PNPIARVAQLKEN*VRQLMCN KSYCAEIAHNVSSKNRKAIVER AAQLAIRVTNPNARAQ
19163	49531	B	19272	27	161	
19164	49532	A	19273	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19165	49533	A	19274	482	832	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19166	49534	A	19275	121	201	SMYMDEN*RLLELTL*FSSMYM DHSL
19167	49535	B	19276	1	1147	
19168	49536	A	19277	305	442	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
19169	49537	A	19278	133	527	GFLERPRILIKVTLSIKQKSTSIF VGGQFSKFRFLTVLAWKCLSQP CF*A*TPASQHVS*SIRAISMSIS KRSELLVRLWRRPSP*AGLFKS RKVSSICIRFE*ILTSCLGVRIST GKLVARTHGSFADAE
19170	49538	A	19279	531	669	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE

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19171	49539	A	19280	80	428	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
19172	49540	A	19281	10	426	
19173	49541	A	19282	1	900	
19174	49542	A	19283	314	451	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
19175	49543	A	19284	1	1139	MWVGISRTPIYNKILVYSSPEVS CEKPKYVKSQTSTHTGFESHKR YIFYRLRVGKNLHVSAAGLGK SQERRKALKSQPPQPADSFPS LPTVEGLTTSGEVAAGFWLSGE ALSSC*LLSASVHLLACLGMG KCCSCGFWLYF
19176	49544	A	19285	1	864	
19177	49545	A	19286	306	444	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
19178	49546	A	19287	189	1089	HHTAHQ*CWL*/SDHGINPLRS WVG*G*/V/GVRGKVQYADLGA ENWKPSINLHDMSSSHSKTLGY KRLTKSNPISCQILLYKRSRGR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHRSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNGSLLTNWPSPVP TIKEEENSEEELAAATTSKEQEP IGTDLDAVRTPELEFPKREDQ EGSPPETSLPYKVVVEAANLLI PAVGSSLSALDLIES
19179	49547	A	19288	1	549	
19180	49548	A	19289	80	430	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
19181	49549	A	19290	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCPL LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMNTNF
19182	49550	A	19291	773	1015	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADASF STDLYHGTLKPASLTMSGVVLL GRMLARSARNWS

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19183	49551	B	19292	1	1488	
19184	49552	A	19293	2	133	YAQTDDNRRNLINGTPLRRVK VLVFDIEYP**KVYGYNSTLA
19185	49553	B	19294	1	879	
19186	49554	A	19295	80	428	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGILFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMNTNF
19187	49555	B	19296	1	1575	
19188	49556	C	19297	1	2187	
19189	49557	A	19298	473	613	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADADT
19190	49558	A	19299	410	547	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
19191	49559	A	19300	876	1005	
19192	49560	A	19301	167	263	KLIEAIWSS*FITGSSLRHNERLG ASTSSGEY
19193	49561	A	19302	258	396	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
19194	49562	C	19303	1	1641	
19195	49563	A	19304	1221	1327	ALHPRNRHLHKERLGCIPVAC* LYLFGQYDAHCTC
19196	49564	C	19305	1	1353	
19197	49565	B	19306	1	2047	
19198	49566	A	19307	80	429	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGILFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMNTNF

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19199	49567	A	19308	1	2597	MAMFMLLAAALLSTFLTNDVA LYTVVPLTITLKRCEIPYNRLII FEGAGSQRWVFATDANWQPAK YSYLGTFWFSVCRIYCPNGTAG WRNDADAPAPVVLAMQYHTGV QTPWKPRLVWSCLGLYIVFLT ALEFKQELWGLVIVAAGFALL ARRVLSVDWTLVLFVFMAMFI DVHLLTQLPALQGVLGNVISNV PSTILLNYPVPSLLLVWAVNV GGFGFLTTCRHARIAAPADLKDG LAVHEKRETRSLTEKTGKMLLP KLGVGSRECGNVKEVGIRAIE EFGPYKINGDKEIMRRMDLLQ GFDAQHRMKLPAQPTSLATKS ARRVRYPLFCPSIFNGFEEFIFH RFLAEQALEFFNLLHGGSKFRG RNNLFSGGDSRRKNQRSTRTHC HHPSPKIYSASAKEPWVLTATNL PVEIRTPKQLVNIYSKRMQIEET FRDLKSPAYGLGLRHSRTSSSE RFDIMLLIALMLQLTCWLAVG HAQKQGWDKHFQANTVNRN CKMATLKEKLIAPVAEEETVP NNKITVVGVGQVGMACAISILG KSRAHEHTTAGAPYTPRQQT QCNMMSLADELALVDVLEDKL KGEMMDLQHGSLFLQTPKIVA DKDYSVTANSKIVVVTAGVRQ QEGESRLNLVQRNVNVFKFIIP QIVKYSPCDIIVVSNPRDILTY GTWKLGLPKHRVIGSGCNLDS
19200	49568	A	19309	435	777	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNSTDCA*VIVTS TKSDSLYTVGMLALSVRAIRCP CRLVDWADIPEQKQLMVLIRAS VALHGRSVTLYEKAFFAFRAM FKRSS

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19201	49569	A	19310	69	1270	LCLLRHDCYRGLQSLLLILCKM ATLKEKLIAPVAENDEAIVPNN KITVVGVGVQVGMCAISIPGK VSWPDELIALVGCWFEDKLKG GNDGSFQHGEIIFQTP*NCGQ DKGLFL*PANS*RFVSW*LGS PVQPRRGIRLQSWVPEKWL VFQIPLFLKIVQVQSLICIIIGFN PQLDILTYVTWETKVGLPKHR VVGSGCNLDSARFRYLMAEK TWHFIPSSCHGWNFGGNGMDS SVIAVWNGVNVAGVSLQELIN PENGNI.TNDKLIWKEGA*IW WLKSAVEVILKLGYPQLGAI WI*VLAESYWNPMKKSYPR HPGCPTNG*RQGMVGHWRME SPSLEPSLCIPQCPRLNPAVIQ RSLKDDEVASASRKSARIPLWD NPEWTLKRPLT
19202	49570	A	19311	52	406	HVEAAGSR*CAAPAGALLRFLG TPSFEDVSIPEKPKLRFIERAPLV PKVRRPEKTLSDIRGPSTEATEF TEGNFAILALGGGYLHWGHFE MMRLTINRSMIDPKNMFAIWR VPAPFAH
19203	49571	A	19312	1	783	
19204	49572	A	19313	15	397	LLAEWTMGHTPVGGFRGAISL DAAP*EQGTMLVSWLCDLFLV LRILVGKTVSSKNIFIERVNGDG KHENIPMSSPPRSWFPSEKRFTH RRKTSSHLQNLVLGAVSLRQH WRGGVPRNLTRAPAGAAH
19205	49573	B	19314	127	181	
19206	49574	A	19315	242	1067	CAAPCGCPQIPGALLPASAGV KTLIPVPSFEDVSIPEKPKA*DL LERAPTCQAQ*RRP*KFKVTR GPISH*KPTIEFYRKAIFAILGIV VGYLHWGVHF*K*WRLTIQPAL WTPRTWFAIWRVPAPFKPITRK SVGASHGGEAKGAI*HYLTPV KAGRLVVMEMGRCEFARSAS VSLTQVALRSCPFASKRL*ACG TPREGCEQDQEERERQQRTPW TI*AE*PTAQHGWAYGVPEPH MTLTPQGEILGARFYMPTKCVV SVGDILYIGY
19207	49575	A	19316	1	520	

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19208	49576	A	19317	104	763	SAAADGPDRLRRPPANLRARP VLAPASATASARRACSPHPQT MSESKSCPEYASFFAVMGASA AUMVFSALGAAYGTAKSGTGI AAMSVMRPEQIMKSIIPVVM/A GIIAMLRPGWVAVLIANSLNDD ISLYKSFQLGAGLSVGLSGLA QPAFAIGFVGIDAGVRGTAMH AADIFRGA*FLILIFAIVLRVY GLIVALLILFHKVDLFRHQPT
19209	49577	A	19321	36	164	
19210	49578	A	19322	190	743	NDRGKEGSLSTVPSIRNTDSGH LAPRRKPQLKPSLNTSPFKAR KIHKGHEVASAGGNPPAIP KVPP*FNIHRRGPPWPDHVRFG SLFNTLFLNWCCLGVSLAFRL LP*KSRDRTGKMGLDVEPGAQ ALCLPPPKCLNTWALILGILMT IGFILLLVFGSVDSLTLWFQIIQ GKTGGY
19211	49579	A	19323	2	257	
19212	49580	A	19324	1	1227	MGRARKSGLGQRSRPTASRSEA AVQPQVRKARGAGNWRVGLQ TGEAAPSPHRDLRDTDPDRPW ARTHRMTTTLVSATIFDLSEVL CKGNKMLNYSAPSAGGCLDR KAVGTPAGGGFRRHSVTLPS KFHQNLSSLKGEAPALSSR DSRFRDRSFSEGGERLLPTQKQ PGGGQVNSSRYKTELCPFE NGACKYGDCKQFAHGIHELRR LTLTKD*TELCRTFHTIGFCPY GPRCHFIIHNAEERLAGARDL SADRPLQHSFSFAGFPAAAAAT AAATGLLDSPSTITPPILSADD LLGSPTLPDGTNNPFAFSSQELA SLFAPSMGLPGGGSPTTLFRP MSESPHMFDSPPSPQDLSLQ GYLSSSSSSHSGLSDPTLDSRR LPISRLSISDD
19213	49581	A	19325	204	456	
19214	49582	A	19326	1	323	IVEYHGPVDSISCTGMATICN MGAIEGATTSVFPYNHRMKKY LSKTGREDIANLADEFKVDHLVP DPGCHYDQIEINLSEMV**PDM LPAPRLAHGVTVVVVGGFLK
19215	49583	A	19327	2	131	
19216	49584	C	19328	2	283	
19217	49585	A	19329	1	206	
19218	49586	B	19330	217	435	

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19219	49587	A	19331	1	565	PWE*SPKGIIVSCGPLSGWS/SPKD/VILKVQ/GILRFKGGTVQIVESTGLG*TPFSCTGMRQFCNMGAEIGATTSVFPYNHRMKKYLSTGTGREDIANLADEFKDHLVPDPGCHYDQLIEINLSEKPHINGPFTPDLAHPVAEVGKVAEKEGWPLDIRVDALACQSLAFGAADVQCGCEEHGAWSQMAWA
19220	49588	A	19332	117	2603	GQHCLLPWGVFPFLKKALGVRRQ*HVAVSLCQRAR/VAMSHFEPNEYIHVLLLEKNINIVRKLNRPL/TLSEKIVYGHLDPAEQIE RGKSYLRLRP/DRVAMQDATAQ/MAMLQFISSGLSKVAVP/STIHCDHLK/EPQVGGEDL/RRAKDINQEVYNFLATAGAKYGVGFWKPGSGIIHQIILENYCVPWLSF*LGPDFHTFNGGGGLGG/ICIGSGW/PNAWEWNGLGIPWE/LKCPAQVIGVKLTGSLGWSSPKDVILKVA GILTVKGGTGAIVEYHGPVDSISCTGMATICNMGAIEGATTSVFPYNHRMKKYLSTGTGRE/DIANLA/DEFKVHLV/PDPG/CHYEPTELK/INSEL/KPHIQWGPFTPDRGSPCWQEVGKVGREGKGWPL/DIRGGS*L/VACTNFKLWKIWRSA/VAKQALAHGLKCKSQFTITPGFPRQIRATFERDGYAQILRDLGGIVLANACGPCIGQWD/RKDI/KMGEKNT/VTSYNRNFTGRNDPNPETHAFVTSPEIVTALAIAAGTLK/INPETD*PDGARMGKKFQAWRFPD/AD*VFPKG EF*PRGRDITYQHPPK/DSSG/QH VGT*APRSQRLQLLDPFDKWDGKDLEDLQILIKVKGKCTTDHISAA GPWLK/FRGHLDNIPN/NHLLIGAINIENGKANSVGNVAVTQEF GPAP*QLARIYYQETLASRLGW
19221	49589	B	19333	1	1311	

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19222	49590	A	19334	2	1390	PRVRPRVRARPTKMSALGSLSL PSVLWGQLFAVDSGNDVTDIA DD/GCPKPPEIAHGYV/EHSVRY QCKNYYKLRTEGDGVYTL/NTI EKQWIKLRLFGD/KLP*IVEADD GCPKPPEIAHGYV/EHSVRYQCK NYYKLRTEGDGVYTLNNEKQ WINKAVGDKLPECEAVCGVKPK NPANPVQRDPGVGHLDQCORS FFPWARKLDGFPFH*SSTHQGP RWIQLNQWLA*PRLKNLLSLN HSENCQQRKDICYF*HFMWG KKQLVGD*GRLFLQP*LTPRVD IGL/IKLQTEGCSC*LRRVMPICL PSKGLWQK*GRVGLCFLAGGR NAQF*NLTHLKVCPCCPVA*P KTQCHKAIYERPSNKSPRKRKN TRKKPL*GVQAPILK*NTFFLC AMS*RYPKERHPAYG/QNAGAS ALCPFHRPLEEDTPGMPTGIU/S FDKS/CAVA/EYGVYV/KVTSIQ/ DWVQKTIA
19223	49591	A	19335	65	665	GVRGFWAGTMASRAGPRAAG TDGSDFQHRERVAMHYQMSVT LKYEIKLIYVHLVIWAAAWLL R*AVGHPEALV/DMIRWPCPIQ WE/YPVFC*AFLPSLLGPSFPFPR NNIRLTWVL/YHESSMGIFFSIG SIHFIGQHGDVPWLHSSFYRHG KAYRFLFGFSVVSIMYLVVLVA VQVHAWSLYYSKLLDSWVH QHTGEEA
19224	49592	A	19336	65	665	GVRGFWAGTMASRAGPRAAG TDGSDFQHRERVAMHYQMSVT LKYEIKLIYVHLVIWAAAWLL R*AVGHPEALV/DMIRWPCPIQ WE/YPVFC*AFLPSLLGPSFPFPR NNIRLTWVL/YHESSMGIFFSIG SIHFIGQHGDVPWLHSSFYRHG KAYRFLFGFSVVSIMYLVVLVA VQVHAWSLYYSKLLDSWVH QHTGEEA

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19225	49593	A	19337	71	1265	RCSKSLRMSTFFSDTAWICLAV PTVLCRTVFCTYKKSSGQLWS WMVCLAGLCAVCLLILSPFWG LILFSESCFLMHTYLSGQELLPV DQKAVLPTGGDCGLDHALSKY LDELGFTVFAGVLNENGPAAEE LRRTCSRLSVLQMDITKPVQIK DAYSKVAAMLHDRGLWAAIN NAGVLGFPITDGEILLMTDYQR CMVVNFFGTVEVTKTFLPLLR* SKGRLVNVTSMGGGAPMERLA SYGSSKAAVTMFSSVMRLLSK WGKVASIQP/GEGFLTNIAGTS DKWIEKL/EKDILGPPPLRVQE DYGQDYILAQRNFLLINSLAS KDFSPVLR/DIQQAILAKSPFAY YTPGKGAYLWICLAHYLPIGIY DYFAKRHFQGDKPMPRALRMP NYKKKAT
19226	49594	A	19338	1	861	
19227	49595	A	19339	248	930	DVHQLGNMAVIHSHLWEGLQE KFLKGEPKVLGVVQILTALMSL SMGITMMCMASNTYGYK*PLFP CISGYTIWGSVMFIISGSLIAAG I*NTKGLVRGSLGMNITSSVLA ASGILINTFSLAFYYSITPYCNY YGOQPPN*LSMGTMSHLKGWV MGMLVLLSVLEFCIAVSLSAFG M*SALLVPPGGGCVNSAITFFT WAETASSTILNEGLRGTRQRFNR QMLPEIYA
19228	49596	A	19340	167	1164	RNRLPSSALAGVAPSHREPRV RTISQTDRRKDA/PDPARRDRVE LAPAYTSPPRCSANVGISTRRL RALCPARVRAPRLRPPASSPLG SEEQRRKVPAARMRPRAGAG RSTLPWLPA/WPGLPSLPLYL* ICGGNNSY*R*RKGEQFE*RNSS *DYRYLPSSPASPNVREERQFNE NGPDDKEKDRPERPSPLDTSPL LDPPAVSDIAGKMSDEFSLADA LPEHSPAKTSASYPDHMLVPTD PAAAGPLGPWGSMSGWPVPG MGGQYPTPNMPYPSGPYPVPP PPQASGAAPPVPGWTVPLGAW GPPAPYPAPTGSYPTTGLYPTPS NPF

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19229	49597	A	19341	2	716	SDPSLLDPTAVSDIAGKMSDE FSLADALPEHSPAKTSAVSNTK PGQPQGWPGSNPWNNPSAPSS VPSGLPPSATPSTVPFGPAPTGM YPSVPPTGPPGPPAPFPSPGSPC PPPGGPYPAPTVPGPGTGPYPT PNMPFPELPRPYGAPTDPAAG PLGPWGSMSGWPAPGMGGQ YPTPNMPYPSGPYPAPPPQAP GAST/ILFHGAPPPGAWGPPAP YPAPTGSYPTPGTSL*FPPGAW GPPAPYPAPTGSYPTPGTSL
19230	49598	B	19342	54	178	
19231	49599	A	19343	3	249	RHKGSPSPHQTEPSWLHPVDP ALGPQVELPASLVLCARTPOPL GGR*DWV/PGTPAGPQESRAAP VPASAPPSTPRGRGGRI
19232	49600	A	19344	2	504	WAPVRPEPFRRAPPPAPQRPVP STTQGLRSAGA/PAGLAGSYP CSPGYVNAIDSLYLATFMGIR VKRPPNR/PLCEQ*SFYHLGAGE *PGKSRVPIQFQSP/GDPTVRV VAPRR*SVPTSCATPRSWCCSD TPGHPLGSPEQLPQPGPAAELP GGVVPRSTPPCPAL
19233	49601	A	19345	3	335	
19234	49602	A	19346	2	447	CACTPQPLGGRWDWAPWSRG RRSSGRLRLHRNRRRGKAQA WRAAVPRPAPREGS*GGRPAA PSAGPPSRPPGTAPGQAPRAA PVPAVRLPHLPAS*GSLRPS AQKGAPTVQ/PVG*RAPQVPPK WEPQRRRRERARAVRTA
19235	49603	A	19347	108	729	QHAGSPQSPRLLSAPPLPGLPL WWHLRSPASPLHCGSPFLGW RLEPTPSACREVWREHKEWEP G/PACGACGPAGVPGGRG/PWW APHSEHPASPAGPG/PMGNLAP GPVAAEGLVSPAPVPAHRRCAR FLAGP*L/PFPRGRAWDLPAM PEPPTVPWAPV/PAEP*RAPPP APQRPVPSPPKGAQDWAAPP AAPVRDPLGEASWAPE

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19236	49604	A	19348	1	816	MWESLTLSRDFLNGFDQNADS GIDNKVQVEVASDEDEELVGN WNKERENPFSGEKLKPAEICIS YKEPNANHQDNGENVARACQ RPLQHPLPSQAQRPRRKQRFPG PGSGPTWDLVPCIPGAP/RLD*K GPRKPKSWYSEGQRYESPSFGIP LGSDLFPTNALLKPYKLPPSR PRDYCGRAAFPRGRVRDLQPA MPEPTTPPWAPVRPEPPR*APPP AP/PAPSPIDHPRAEECEHTAQD WQAAPPAAPVRDPLGEASWAP ESGGDVESLYV
19237	49605	B	19349	4	669	
19238	49606	B	19350	1	930	
19239	49607	A	19351	170	444	
19240	49608	B	19352	1	1122	
19241	49609	A	19353	1628	3591	KGLRLKLCFSVQLRFSIRNFRG ILTYWKKEFEIVGWPRLEPTPL ACREVWRERREREPGLRAALA GQLEFRVGVGLAGPSLGAAGQ PCWPRVIRDLAPGPVAAEGVLG PPAVPAHRRACAGLTP*LP SRG AGLGTCSPPCLSLPPTPWAPVRP KPPQRAAPPAP/PAPSPIDHPRAE ECERRAHDWQTAPPAALVPDP LGEASWAPESGISDEYITPMFSF YKSIGELKMTQEEYALLTAIVIL SPA WATERHPVFVKRERKKPSN CLEGVIAAAELAVGLPWNLG KFHTGDGTSAGLQGIAPNSVGP GQPAPEWMWGWERLLTDQDK TQGSASFCTATFQDAQQLLO ARFIHLSGLWEQQDGLWLSNW LSLKGQIGGPALTEPLRLSVNR GTWPPKLRDARRRSAGRADRR APTGRVLPGSPGAGPQTTPPPY DWSLRNRRRPAATDPEAQAAA AAAAGVQGRVGPQIEPSCRPA GRSDPPAPGPPEAEVCWVSRRLRE PVRSFAFWLRQSRALIGSWGK QGDVAFAFTCPNNAERGATGV RGGWGCWCGRAQLGRRDPAA TRPALNPERYQSPKSMQGLERP HVRNWGIELETLRDAFRPQPSV WRTARGEAGKRKGRLECLGS QRKVLEGVLLYAVTRGSPFNLF
19242	49610	B	19354	1	412	

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19243	49611	A	19355	951	1453	FQTQEPSSLHLVDPTGLQVEL PASPVPACAIQPLGGRWDVVP WSRGWCSSGRLGPHRSPWSGW EAQAWQAAGPEPCPMGRQVRP GEKSSAVPVGQPG/SGHSVHPP QPLARVLSPLPGASRAGRLLR VWGPPSPRPPGTPAGPQARHTA PVPARASPTTPCKLR
19244	49612	A	19356	111	658	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPQGAPPA/PAPSPID HPRAEECERTARDWQAAPPAA LVRDPLGEASWAPESGGIPTPS GPGVAGSGSTHTHALTHACTH AHTRAEPLRLPPPRPLPPPLSP /PPAPLLPSKPSLSTDRSSKSR QQKVPFGRDPEPRGVRA GSW NRTTH
19245	49613	B	19357	1	552	
19246	49614	A	19358	1299	1813	AHFPRAGTGAACSACWPAGVP GGRGLGGPRTRSSRPCWPRAK GDLAPGPA AEGV LGPAAVPA HRRCARFLAGP*LPYHGAGLGT CSPPCLSLPPT/SGSCAPEPPRR APPPAPRHPV PSTTQGPPWETC LLSIYGNAMNDERAWSLEGFW VLKPSDSWMTLSERTISFF
19247	49615	A	19359	380	905	WIPHWGCRWSCLPVLRRALAF LSPWVVDGTGRRGVGSGAGRG GSGRTGAHGVGGRLRHGGLQV PSPAPREGS*GPARNRAQPGGP ALLGDSVHPPQPLAQVLSPP/FP GPAGLAGCSECRGPPSPRPGTP AGPQAPHAAPVPARASPTTPPL VHLTNDVLRVKVKAFFFTLH
19248	49616	A	19360	1	1052	MGLAERCPLNHLTLTVSSVKCS FLLAHILSVAGACYGLRGAPH TFPGITCPGCSQENNPIKKWAE DLNRHLIQEDTQMANKHLKDA PHRYIIRQLQVKPTMRYPCHAPT GVAHIQSTNTPNAGEDVEHQEL TFIADGSPVTTTRGHMDLVQTS SRTLGVIRSTGSWSACAEFSHY CLAKRLQLLKHGNGNSNSGG NAECITRHQCKPLTGILSFILAL NKVKNTRPFDRCHSEGSEKEPS FCVTCPRRPEVNPQSPYMPQPG KSSTHLSVVQLRALEVGEPQAF PPVE/PEGFAGLRHPLWL*V*QG GSG/SSPCLSLPPTPWAPVWP EPPRRAPPPAPQRPVPRPKG

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19249	49617	A	19361	417	1092	KWCSKRTAFSFLQGGVEGEA RAGTRAACGACGPAGVAGRRG LGGPPHSGQPASGPG/PVRDL APGPVAAEGVLGPPAVP/APPA LCSIS/PPGCSCLPAG/PRLRTCSP PCLSLPPPPWAPVRPKPPR*ATP PAPRRPVPST/NPRAEECGRTAR DWQAAPPAAPVRDPLGEASWA PESGGDVENLYVQLRDCKYTN QHPVSSSGFVNAPISTLYLVNL VGTWIRIFMSS
19250	49618	B	19362	817	1596	
19251	49619	A	19363	350	644	
19252	49620	A	19364	60	1362	SRVEPRVRSASQDSRSRDNGPD GMEPEGVIESNWNEIADS\FDD MNLSESILRGIIYAYGFEKPSAI QQRAILPCIKGYDVIAVQPSGT\ GKTATFAISILQ/QIELDLK\ATQ GLGS*APT/RENLAQQ/QKVVM ALGDYMGVASICHACIRGAPTC VAEVQKL/QMEAPHIIVGYPLG RVFDMLYRRLYSKPYIKMFV LDEA\DEM\LSRGFGQIYGHQ KAQAAPPRVLLSATMPFD/VL EVTKKFMRGPH/IRILVRKEELT L\EGIRQ\FYINVEREEWRLDTL CDLYETPDPSQASHLPSTTRR\ KVDWPHPRRMHALRFPWESAQ HEDMAQKERR/DVIMKEFRLAS SRVLITTDLLA/RGIDV/QQVSL SHQLNY/SFPTTRENY\IHR\IGR GGRFG/RKGVPINMLTE/EKTKR NLEDIETFYNTS\EEMPLNVA
19253	49621	A	19365	911	1278	NCGIVISKHLVFTLA*MMCHFL ASLQRKGILKRSASV*AHSH/DP SFHMKIYNAGWGHRT*HPAGG FAGPPPWGSVWGLAARTRENA PRPALPLPRPAPSGLAHGADGD SNTEKIQSRDNRKG
19254	49622	A	19366	26	743	ETSADMAPSVPAAE/PEYPKGIR AVLLGPPGAGKGTQAPRLAEN FCVCHLATGDMRLAMVASGSE LGKLLKATMDAGKLVSDMV VELIEKNLETPLCNGFLLDGFP RTVRHAEMLDDLMEKRKEKL\ DSVDLNFSDLLIRITGRLIH PKSGRSYHEEFNPPKEPMKDDI TGEPLIRSDNEKALKIRLQA YHTQTTPLEIYYRKRGIHSAIDA SQTPDVVFASILAFAFSKATS

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19255	49623	A	19367	40	1002	VASGTRTELQDRFRDTS GDM FPSVP*EPEYTKGIRTVLLWPP GAGKGTQ/SGTEV*MACSLGY IASNLQSLHLNDSKAPALSAIY CPRHPNWAENFCVCHLATGDM WRAMVASG/SSELGKKLEGNL WDGWGNWVE*WKWVSWSSF GEGILENPLVAKNGFLLDGFPS GPVKARQK/SPMDLMGEGGKE KLDFC*FEFSIP/DSL/IRRNHKE GLIPPPKKWAGSYPRREFQPLP KEPP*KNMTGGNPLIRRSR**M KRPLKIRPASPTHQTITPLIEY YRKRGIHSTIDASQTPDVVFASI LAAFSKATCKDLVMEI
19256	49624	A	19368	793	1152	SGRRRRGCGGQSVKQAPALT PGPAPVFIPEAPAACAPHHPGQ GNRKRCNFPVCP/TPKTASSCP/ EPLPPPSLQR*PCPCHPWHHLE FSFLDEVTFNFNKTFRKLVSSK MLPLKVGH
19257	49625	A	19369	1	873	
19258	49626	B	19371	1	322	
19259	49627	B	19372	64	2250	
19260	49628	A	19373	20	368	CEARGSGHGGRAERAGVCGG PAELLPKGSKEEQRDYVFYLAV GNYRLKEYEKALKYVRGLLQT EPQNNQAKELERLIDKAMKKD GLVGM/AVGGM/ALGVAGLA GLIGLAVSKSKS
19261	49629	A	19374	3	492	
19262	49630	A	19375	62	570	GSRGQWPSEAVLNELVSVDL LKFEKKFQSEKAAGSVSKSTQF EYAWCL/VRSKYNDD/IRKGIVL L/EELL/PKGSKEE/QRGFTSFYL ARGGGTTRLQGITEKALKLRS GLLAAQEPQEQPRPKETGNGLI DKA/L*KKDGLRGAWPIVGGM ALGVLAGTRCSSDFAVFQ

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19263	49631	A	19376	1	944	MACHLQAGSPGNI.VVVFQSKP EGLRTREPMMSPVPVQVKGST RKLMMSEDLPLTGNWHELRS RTAKNGILQVDKQKIVEGMAE LQQVVGKNMDSGVGPVVHGG GLTRTGYLLNPESLQQAFAFRR QIQGCDEKLACVGGKQLGTWP LSESPSLTRLRYCRRQLTQGSIR MSLNAGVPGQTAPDQRSGEG VAAPAGPGEEVGREEGEGAAA GKRQCPCQQGSLCVDTSRPLP KSQAQIPSSSRSSPSSSEQRQG LPSVREHVEGGQGEERAPHCD GGGRVLLASGLAWLGTENIMD LASSPKDDWGVAVPSRGCERPS TFTLVLPSPIVRRRACSGQSPSP GGGQETHGADTSHLTNP*ICLL SKAFCCRDGSLSK*PVLVRPPPC \PQALPQSPSCYLLLAVALPFPP LSSAYPPVRFHSLLEIHEARAS
19264	49632	A	19377	1177	1603	WVSSFSSSFSSFPFPPPPPPPP PPSFLPPPPPP/PI*DRARRCQQ TSIPLNKLNNKLLLLLSRPD DREKFTPOQSARQREPIKGT SRRGEGPICPTLSLYFLHVFLCF SCLSSQIHIIYILRLSTVLVIKNS
19265	49633	A	19378	1	896	FPFSLPPPKMPKGGKAKGKKV APAPAFVRKQDAQE*WLNPLF KKRP*DFRIGQDIQPKRPPPL L*KWPR\YIRLQ\QRAILYK\RL KVPSAITPVSPRALDPANQLLS LLK\AHKYRPRDKAQRSKQ\LLA \RAEKAA\GKGRPNQRD PPVLARS*HPSPTLVEEQEKL WVVIA\HDVD\SELGLSFLA\AL CRKNGGSPYCIJGKGQDLGR\LV HRKDLAPLVAFTQ\VN\SED KRRFWLKLVGSYQGPNYNDRY RYDEIRRHGGNVLPKSVARI AKLEKAKAKELATKL
19266	49634	A	19379	3	491	AKAELDWEEGHQ*QDRL*SRN SQLGICGGLRGFRGDRASVFS R*AEKESVRQL*ARVPGALGVA ARANKHQRRWREGDSTQTATN TVDRRATRGRPMEWRAIRVAD EEDGDRRRGDNRPQARTFRPRT SVRRAAGTNNSEGRPTNAGT NGGRGVDIYTVN

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19267	49635	A	19380	1	1501	MRRSTPGVLPAAVGGARVRRRA VGLSGTGAEAGRAGAMVEKEE AGGGISEEEAAQYDRQIRLWGL EAQKRCHRMKEALSTAPFTDK ETHPKVSLAQVTRSSASVMVY GAFEVIGQRQSSAAKPRRSQSE SLGPEFQGLWEWLPASQHIMRS LKKQDGMGGQYRVSLWEVVG QLIFLEEKVTPEDPGAQFLIRT GSVGRNRAEASLERAQNFNP MV/DMLKVDTEDEIKKPESFFT QFDAVCLTCCSRDVIVKIDQIC HKNSIKFFTGDVFGYHYGTYFA NLGEHEFVEEKTVAKVVSQGV EDGPDTKRAKLDSEETTMVKN KVFFCPVKFVALDGWILDACDE MQMAALKRTTSDYILLQVLLK F/RVTDKGRDPSSDTYEEDSEL LLQIGNDVLDSLGISPDLLPEDF VRYCFSEMAPVCAVVGILAQ EIVKALSSAGTLP/PTTNFFFR WA*KGEWGLWECLGPQVNSG FGQPQRCLQHAHLYSLFPFFM
19268	49636	A	19381	2	411	PGTSQGVFSPHRLGGAVRSPCP PPQDSRQASAGGAESQLKQRG FPGE*GCRSPVSCA WPQNRMG* GPQHREAGAWSGE*KTIWLK QERCNRPLGLLVTAEAAPAPRP DGMAPGCGGIRCTPGRPRLLH SGPPSP
19269	49637	A	19382	165	309	
19270	49638	A	19383	1	825	LATQPEGAGRVPSPHPPQGPEA ALQDLRLTLMGSSRLHSGKESIG HNSSAGSSSQPHHPRRKTAIL EKGGKQPHRMLPSPGLGSSPE PANAGSPDTWLCP/AAARVL* NPVKPRKGRSEPRSGWASQLPG GDSRLPLRPGTSQGVFSP/APAG *AGKLVGLVLSLSLKQRGFPE *GCRSPVSCA WPQNRMGCRITSP GPSPTSPTAAGE*GSRPRRRKPG RVQGLQRDGP/TLTQEDALTA KRCPLPVTSPQTPETSTGAAA PGSQPVGAPPSR
19271	49639	A	19384	1	378	

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19272	49640	A	19385	381	1653	QRPRSGTFTMGRKSLYLLIVGIL IAYYIYTPLPDNVPEPWMMWI NAHLKTIQNLAFTVELLGLHHF MDSFKVVGSPDEVPPISDENV TVTETKFNNILVRVYVPKIRKS *STKEGGFLFYPCGGWRRGSYS LIVYDLPSSWTVEIRPGSSLVSN HLRLAT*FHFPLQLGELYDAL R*FLRKKVLAKYGCEP*GESGIS GDSAGRG*LSAVTQQLADDP \DVQDPNFKIQS*HYPALSAWWM *VLPSYQGGKFKFSYFYSKSLQC RFWSEYFTTDRSLEKAMLSRQ HVPVVESSHLFKFINWSSLLP*E GLLKGVYNNPNYGSSELAK KYPGLDVRAAPLLADDNKLRL GLPLTYVITCQYDLLRDDGLM YVTRLRNTGVSG*LNNHVEG GFHGAFLGLKISHRLNQYIE
19273	49641	A	19386	3	667	DAWADAWVPVSSEVAYLFGG CHTCGGLPVAHPMMPRGRSR TSRMAPPASRAPQMRAPRA QVGQPPAAAPPSAVGSSAAAP RQPLGLMAQMATTAAAGVAVGS AVGHITLGHATGAFSGRK*LPE PARP*HFFNQEASG/TPPAQH SKQQRHPLHQPCPYEIQTVFWE FCPGRTRDQAL/CEGFNEVLK Q/CRLANGFGPNEEVSTFGRD WKFSSHNLS
19274	49642	A	19387	81	1257	RHQSDQTVPRLSRPHVQSQKSS MAAAKPNNLSLVVHGPGLDL LENYPIPEPGPNEVLLRMHVS VIGCSDVHYWEYLS/RFGNFIVK KPMVLGHEASGTVIEKVSSSVK AP*NQGDRAVIEPGCSPEEN*W NSCKMGRYNLSPIFFCATPPD DGNLCRFYKHNAAFICYKLPDN VTFEEGALIEPLSVGIHACRRGG VTLG/HKVLVCGSWANRGWYT LLVAKAMGAAQVVVTDLSATR LSKAKEIGADVLVQISKESPOEI ARKVEGLLGCKPEVTIECTGAE ASIQAGIYATRS GGTLVLVGL GSEMTTVPLLHAAIREVDIKG VFRY/CNTWASGGFSLMCLVPKS VNVK/PLVTHRVSSWRKVLEA FETFKKGLGLKIMLKCDPSDQN
19275	49643	A	19388	2	431	

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19276	49644	A	19389	2	326	ARGSTRLMESRVQHL*CTRKEL TPEVLQEWLDELEEMMLVVH MPRFRIEDGFSLKEQLQDMGLV DLFSPEKSKLPGIVAEGRDDL VSDAFHKAFLEVNEEGSEAAAS
19277	49645	A	19390	2	368	
19278	49646	A	19391	1	2123	MAQFSIVGMCLGLFNQSPDTGDS GVQLFVIMNQVMAANLAETHA ALCPTLSSGTSARFRGNQFSG GLPQITLSPLAQPCGRLAAMYS NVIGTVTSGKSLPSTPLVPLLL SGFAPLFLKGLQNWQTQTQEG KSPSAAPASSQPQACPTDHYRE SALGACLSLPGEDGKIQKVYLL SLLLIGFWDCVTCGSPVDICT AKPRDIPMNPNCIYRSPEKKAT EDEGSEQKIPEATNRRVWELSK ANSRFATTFYQHLADSKNDND NIFLSPLSISTAFAMTKLGACND TLQQLMEVFKFDTISEKTSQDIH FFFAKLNCRLYRKANKSSKLVS ANRLFGDKSLTFNETYQDISEL VYGAKLQPLDFKENAEQSRRAI NKWVSNKTEGRITDVIPSEAIN LTVLVLVNTIYFKVLRMALERP QGLPLALQLTPFFKWRDRSPE RANGLPKATQGLWKSFPEN TRKELFYKADGESCSASMMYQ EGKFRYRRVAEGTQVLELPFKG DDITMVLILPKPEKSLAKVEKE LTPEVLQEWLDELEEMMLVVH MPRFRIEDGFSILKEQLQDMGL VDLFSPEKSKLPGIVAEGRDDL YVSDAFHKAFLEVNEEGSEAA ASTAVVIAGRS LNPNRVTFKAN RPFLVFIREVPLNTIIFMGRVAN PCVNLSEALAVLVNLTLMK RTHGESLDFMERKRRPAESILL

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19279	49647	A	19392	9	1630	PALCPTLSSGTSARFRGKNQFS GGLPQITLSPLAQPCGRLAAMY SNVIGTVTSGKRKVVYLLSLLLD SFGDCVCTCHG\SPVDICTAKPRD IPMNPMICIYRSPEKKATEDEGS EQKIPEATNNRRVWELSKANF PLLLTTLFSTWADSKD*H*LTF FCSPLSIFQGFLWTKVVGACND TLQQLMEVFKADTISEKTF*SR SHFFFAKLNICRLYRKANKSSK LVSANRLFQDKSLTFNETYQ\DI SELVYGAKLQAPGTSRENAEQ\ SRAAINKWVSNKTEGRIHRCS FPSGRPFNELTVLGGGFNTIYFQ GACWK\SKFSPENTRKELFYKA DGESCASASMDVTREGKFRYSG AWLEGT/QVLVVCPEFKGDDIT MVLILPKP*EGAWAKVEK\ELT PEVLAKSGWD*FWREMMLVV HMPRFRIEDGLQV*REQPAKN MGPLSDLFSRKSPTPPGIVA EG\RDDPPMSSDAIPIRHFLEVN EEGSEAAACKYPLL*LPGRS\LN NRRVTFQGQAFPVVFIREFVPL NTIYLHGAELANPCV
19280	49648	A	19393	3	737	
19281	49649	A	19394	1	705	
19282	49650	A	19395	2	757	
19283	49651	A	19396	1	1764	
19284	49652	A	19397	1	710	MAWALLLLTLLTQDTGSWAQS ALTQPASVSGSPGQITISCTGT NNDVGSYNLVSWYQQHPGKA PKIMIEVSKRPSGVSNRFSGSK SGNTASLTISGLQAEDADYYC CSYFTSSRPDI\VFSGGKT\TVL GQPKAAPS\VTLPSPSEELQAN KATLVCLISDFYPGAVTV\WK ADSSPVKAGVETTTPSKQSNK YAASSYLSLTPEQWKSHRSYSC QVTHEGSTVEKT\VAPECS
19285	49653	A	19398	1	679	
19286	49654	A	19399	1	743	
19287	49655	A	19400	2	736	
19288	49656	A	19401	2	718	

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19289	49657	A	19402	1	711	MAWALLFLTLTQTGTGSAQAS ALTQPASVSGSPGQSITISCTGSS SDVGGYNYVSWYQQHPGKAP KLIHYEGSKRPSRVYDRFSGSM SANTASLTISGLQADDEADYYC CSFAGSSALRIFGSGTRVIVIGQ PKANPTVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKAD GSPVKAGVETTKPSKQSNKY AASSYLSLTPEQWKSHKSYSCQ VTHEGSTVEKTVAPTECS
19290	49658	A	19403	3	720	
19291	49659	B	19404	1	711	
19292	49660	A	19405	105	858	RRQDSGQSPAWPAGALLTLT HCAVPGSWAQSVLTQPPSASG TPGQRVTISCSGSSNIGINDVT WYQQVPGTAPKLLMYSDNHRP SGVPDRFSGSKSGVTSASLGPSV GLQSEDEADYYCGTWGLAA*M VFMSSAGTTTLTVTSQPKAAPS VTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSPVKAG (WETTTSPKQSNKYAASSYLSL TPEQWKSHRSYSCQVTHEGST VEKTVAPTECS
19293	49661	B	19406	63	756	
19294	49662	A	19407	1	757	MAWTPLLLLFLSHCTGSLSQAV LTQPPSSLSASPGTSASLTCTLRS DINVGSPIYWYQKPGSPQF LLRYKSDSDNQGGVPSRFSG SKDASANAGILLISGLQAEDAE DYCYSSYVGTNNFGVLFGGIGT (KLTRP*GQPKACPPRVTL/FPHP PSEEASKPNKA/TLVCLISDFLP GKP*QLPWKAA*QPPSLAGVET PPHPTRSNKYAASSYLSLT EQWKSHRSYSCQVTHEGSTVE KTVAPTECS
19295	49663	A	19408	1	224	YISLPAGVLSLACCTLYGISWQF DPCKYQVEYDAYKL*RLPLH TLTCSRPTDRNVRFRSPHSVRQ QSLGRCLA

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19296	49664	A	19409	235	955	ESTVQVSFCHRVPARTSSQTA LPVLLGLLGFTVSGPLNLPESV IVNGELVGPQTCLHCGMEIYN GNAQDQF*VTELGAGP*EGP VTSYIVIEPTRIGDETARWITVG NCLHKTAVLAGTALLHPGLR CTLRFPFHISAPPLGVL\SLACC NL\YGIS\WQ\FEPPACK*QVEVR TPNKL SRLPLHTLLP PRVVLV RKDDLHRRKRLAHNPIGTGPPLV YCVK\KIYELYAVMIFK
19297	49665	A	19410	1	764	MRLGIGFACPWKGLADEFDLKI EKQRNQGRLLGFKLQHLVPFTE MEKMGGDRQKHRTAPRQAER RRSGRVSFQPLQPLDVTLLPG ATREGNCPRASRGRRPSPISHCQ ETQGPGRSDCTIRGVLSIPAA RPLRKSGGFPTVCEKRPEQGQQ PALGP/AGPAAVPAPAAASRTQW GSRPCGAGARRGYWRLLGL CNLISPLDPGSPGSGRWGSAGA LSRPADSCPPWPRAGA*RRG AAAEAGNSPSRCGASRPAAEQS GAFAGPLPSSPSQ*RAPGAEV
19298	49666	A	19411	209	536	TRSSCVTLVC*LAMVSLRVAR HGVPGTMFGKRKRVEISAPSN F/EHRVHTGFDDQHEQKFTGLPR QWQSLIEE/SARRPKPLVDPACI TSIQPGAPKEVCSPRASGTRSR
19299	49667	A	19412	124	1983	
19300	49668	A	19413	424	1582	PPWAAVHGDRPHRVPGTMFGK RK/KRVEISAPSNFEHRVH/TGF DQHEQKFTGLPRQW/QSLIEES ARRPKPLVDP/ACITSIQPGAPK WGETGSWPPF/RHLP EG*HGPP PGCQREPQRVSHEQ/FRAALQL VVDPGDPRS/YLDNFIKIGEGST GIVCTPPSGKLVAVKKM/DLRK QQRRELLFNERPWQCP*HP/RR* EAQVPLPVLQALSV/LHAQGV HRDIKSDSIL/LTHD/GQVSKEVP RRKSLVGTPT/WMAPELISRLP YGPVSPGWLGCPAVDSVRCH FQLQRWREMGPSLGS HCQNGA LDKEEGQRPSTGSLQWGS LG VERTLRVNMVECVHACNSFY LNKLFQKQDSTQEASVTMVPDP DKDGNRASQKRKAHSQGARR

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19301	49669	A	19414	488	707	TCGEGLSWTRPLPTASSLQVH* SLSAGERPYLCDYPDCGKAFVQ SGQLKTHQRLHTGEKPFVCSN GVNLVF
19302	49670	A	19415	16	454	GPAGRCPADCSEEEKGPSA/GD SGRPPSCT*PWKGLPVMAILPG EAPVPGPGWPEPDAGG/PLWR WGSPPSCAAALHRP/SGTTPPGR ALSGPGLERAKQRSRVSPAPR AAPHGHPHCLPIPA GPRPAKD HPAYGPPASCHHHLAAS
19303	49671	A	19416	166	1191	TAGSLVLAARGT*GPPPRARK* GPAGRCPADCSEEEKGPSAETP GTTTPGRALSGPGLERAKQRSP RVSPAPRAAPHGHPTHCLPIPA GPRPAKDHP/PTHQKPPPRTEGS TGGHCCGPP/IFLIPNTSMLTVYP SGPVMPAGFTLSPSDTRPSLLN GQEVLRKMNGAVQYLSLCDYII PTCQCLATTVLCVSMSLTVFA VSYMVELLLLQNAQVHQLVLQ NWMLKALPPALQDPHPVPPRV PRAARTRLPVAV

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19304	49672	A	19417	1	2481	MRSQDLKFGKSAAWPSGQKEK LVFRGKIEEGLEYLHKKKPSAN SQDNGKEASKAFHGPLQQPLLS QALGPDREEWFFGQAPWPHCC VHPQDTAGCIPVVPAPAMAQR CTGTAWVTASEVAPSLDCFHIV LSQQVYRIHRPTSSLHPQYGKA TRHTTTPAVSMRAAAGAEPCKA TGADWPKTLGAQPSHPCTMDV GQGFKKDDSGAALAPMAALM GWAGIECLWLFHTEGVNCWP WDLGEKNGLLGQPRGPAAVCS LRTLLPASQQQLLLRPWLKDA QVQLGSLLRVQAIGLGGFYIV LSQFIDPSKASYPPWVKNSRHS TAAQPMRAAAGAEHCKATGA ELPKALGAQSPSCVLDVGQGF KKNDFGAVGLNNWPAGFWNV MGTCKSRLCFVLLSGKSSFRV EVLTQCLDSHTLETYQFYNNREV AFEDVLESSQTGLVVQKPQTDNR LTKRGRGEATRNLRGLVPSMP RSLLPSTAQPTAWKCCQRGSPY THQDMALIPSPPTARCLSPAKEP KQEEVGEKSLPDPTLPLTDPR LTGSTEQAHAEGLAALMSALR VSHLQGRGGVTVLVDSQLGVI AVSSQTFNKGPSYRLLADVQN RLLPKYDSQKEAELRSWIKGFT GLSIRPDFQKGLKDGIIILCTLVN KLQPGSPVKINASV*NWH*LEN LSNFLKAMVSYGM/NPVDLFEA

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19305	49673	A	19418	1	1299	MHQEDLRAWYLDLGLPSHQNE TTDVSVVYERFSLTDATYPKQA KQWDFPFLRVSTAQPTAWKCO RAPSPYTHQDTALIPSPARWL SPEKEPKQGEVGEKSLLPDPTLP LTDPRLTGSTEQKKDLAAGPVG SALRRRPPAVSTQFNKGPSYR LLADVQNRLPKYDSQKEAEL RSWIKGFTGLSIRPDFQKGLKD GIILCTLVNKLQPGSVPKINASV *NWH*LENLSNFLKAMVSYGM /NPVDLFEANDLFESGNNMQVR VSLALAGAKTKGLRSGVDIR DKYSKKQNFDDTTMKASQCVI RLQITNKCAQSOGMTAYGTRR HLYDPKNRILPPMDNSTISLQM GTNKYASQVGMTAPGTQRHIY DTNLGIDKCENSSMSLKMGYT QVANHSQGVFGLGRQIYEPKY QPGGPVAHGAPSAAGNCPGGE
19306	49674	A	19419	135	290	HREEESKSSVFLNPRGVQGTGV GDHRMILGRGRAVLSE*AAAG PRGGRHES
19307	49675	A	19420	92	1058	KGQYLNPNRKGKGPPEPPPEPPV PPASRSDMAQNLKDLAAGRLPA GPRGMGTALKLLLAGAVAY GVRESVFVNEGHHRAFFNRI GGIVQDITLAEQFHFRIPIWF QYPH/IYDIRAKTSKKSPLQGS KDLQM/VNISPAKCWSRPAQE LS*ACTSRLGLGLTRER/CLPSI VNEVLK/AVVWAKFNCLTA*FT QRAFGYSLLDSAGSLTERAKGL SSLIL/DDVGSQSKLSFSPSYT AAVEAK/QVAQQAQRAQFL VEKAKQEQRKINLQGRG*GR GLPKMLGEA/LSKNP.GYIKTSQ RFEPAPETILQRRIAHIHRNP
19308	49676	A	19421	3	861	LDDSWEPVHPGGCGDFICQWSEE SGLWSTA EVWRERRRGREPLC EGARGTARVPGRGPPHSGSQ PVPPAPGS*GA*PGPAAVEGVP GPPAVPPASAALEFSRGFSCLPR CHLVVTKIGKQEDDVSIKRNK PDYWPAPPEPVAGCEGSDQEQV KPNATLEKHFLTEGTGPRSPSC LSWPPSGPHAAADPAMVPETPE PDRPQLTKKFCEARVMVGTST NVLGQTLKPSRTGGTSSWVVF YLLTANRLPFVDVKRKGPPSSI KPRPHYDHRLLQDFKEQVHHF

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19309	49677	A	19422	808	923	
19310	49678	A	19423	1	339	
19311	49679	A	19424	1	621	
19312	49680	A	19425	3	1836	MAAVEAAAEPTVVAAVGP AKDEEEEEEPPLPCEA/LRWAP VLRGPAWATAFLEEATAEEP GAAPGSPDPDRTLRRLRAER RRLDS/SLALSSDFAQVQFRLR QVVRGAPAEQQRLLRELEDF LKG/IPDILGYEGDPASDEGD GLPGDRPRLRGEDQSEKQER LETQREKQKELILQKKTQLDDL ETFAYQEGSYDSLQSVVLERQ RVIIDELIKKLDMLNEDISSLS TEELRQRVDAAVAQIVNPARV KEQLVEQLKTQIRDLEMFNFIQ DEVGSLQTGGGHCECKAGGK TGNGCSRTGSSRTPPGNSRTKA EDVTKVRKTGLHLMRRALAVL QIFA VTRLVVPQARSLOPCGRG SRLTETTLPC*R/ELEASVDRVK QLALTAEPHDHITSANLQDLS L*GKDELTMARVKELTVAVRD LLAHGLYASSPGMSLGMATIA* LLPAFSSVPEAMHPRELFVKYY HAKNGRAYVESPARKLSQTFA LPVTGGTVVTPKQSLTIAHVMV LTEHDPFKRSADSELKALVCM ALNEHRLVCWMNLICKSGSLIE PHYQPWSYMAHTGFESALNLL SRLSSLKFSLPVDLAVRQLKNIK
19313	49681	A	19426	366	477	
19314	49682	A	19427	3	432	WNSRDAGYEFDCITSVHLYAI RTLWTVLDAIDQMWPVVRT WRLNERHYGGLTGLNKAETAA KHGEAQVKIWRRSYDVPPPPM EPDHPFYSNISKDRRYADLTED QLPSCESLKDITARALPFWNEEI VPQIEGKIRVLIA

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19315	49683	A	19428	1	890	MTRRTTPRGEHLSAFSSCVDK ISRCKSFGLELENSIQT LWAR EQSICLVAAAGHLVSSSGMRNW CHARRHAAAYKQVLIRHGEVAW NLENRFGGWYDANLNPAGDEE AKRWEQALPDAGYEFDC/FRK TIRTLWTVPDAIDQMWPV\NV SKDRRYADLTEDQLPSCNSLKD TLARALPFWNEEIVPQIKEGW SDHCLGALVIPKDGCLNLDG VTTVSSLTPEERALEEPLNRP TN A/P*HQEG*CWESHQKPVFQT LGCLCEFSRGASRRKQARVVFR ERSNLCRSISGGEGF
19316	49684	A	19429	1	443	RALPFWNEEIIPIQIEGKRVLIA AHGNSSGAIVKHLEGLSEAIM VLNLPTGPIVYELDKNLKPIK MQFLGDEETVRKAMEAVAAAL VCVLESALPALFHGSEMPFGPVQ VYLSLISESCSCLTLPHGSSVH LSITVLNPFSSIV
19317	49685	A	19430	24	1039	AVLALLRGRGGLLRNLLIPV GAASPARROWPPYKLVLRHG ESAWNLENRFSGWYDADLSPA GHHEAKRGQALRDAGYEFDI CFTSVHLYAIRTLWTVLEMLA SEMWLVPVARTWRNLERHYWG S*PGLN*KQKLAAXHGLRPRLK IWRRSYD\VPPPPIMEPDHPPY SNISKDRRYADLTEDQLPSCIES LKDTIARALPFWNEEIVPQIKE GKRVLIAAHGNSLQGHCSRL EGLFVEAIGHSLNLPDLVFLPSI ELDKNFESLSSPMQFLGDEETV RKAMEAVACPGQGRSEGRRG RILSPGCTLPCPVFPSSPSHLA HVTLDHICKTS
19318	49686	A	19431	86	431	VYVSTMSLSCPAELAVRRQR WSSQFDHPGPGLPQRPV*EML LL*PTLDLQPVVPPAVAILSWKP SALTISSQIVTPGLKTRSFTRKT FMKIWNHRQKYQKTMVMFP RYPSL
19319	49687	A	19432	599	900	ATWLFISPTTTTCQLSKTLLVPL NFLEKQYLTLLFLEPTFSLFF RHTEDHLMRSGCLKVCSSISPLS/ PLPPSSSHVRHLTPSLPFAMIVS FLRAPQKLSR
19320	49688	A	19433	210	341	HFRKIFTVFQKLVEYNLLSGH STQSQHPGGTVLL*DLVCPPV

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19321	49689	A	19434	239	464	SPKGGPPNP SHGTFHTRPCEE TTKQALCEEHGCLFHLGAGGLS PKRESAKGDKGASVHVVCHI S*SPCS*LGP
19322	49690	B	19435	1	838	
19323	49691	C	19436	80	443	
19324	49692	A	19437	1	775	
19325	49693	A	19438	209	469	
19326	49694	A	19439	304	375	NVGE*SERHPCYD*TPREVCPPS P
19327	49695	A	19440	879	1188	
19328	49696	A	19441	615	917	ATWLFISPTTTTCQLSKTLLVPL NFLEKQYLTFLLFLEPTFSLFF RHTEHLMRSGCLKVCSISPLS/ PLPPSSSHVRHLTPSLPFAMIVS FLRAPQKLSR
19329	49697	A	19442	674	1554	GQMASSSVSLQGVPAADPG WVTAGASLTRA WAAGVQGDG PGTESSISASSRRVLRGMTRTL LWACVLLWVCILLGLCPAVG PVSISVGPVSYCGPVPCGPYP VGPCPA VGPVPCCGPYPS/VGP VPCCGVPVSCCGPVSCCGAVSCC GPVSVSGPVSC/VLGLCPAVGP VVSIS*CGP*PAVGLCPAVGPVPC CGPYPS/VGPVPCCGPVSCCGPV SCCWACVLLGLCPAVGPVVSIS VGPVPCCGPVPCCGPVSCCGPV SIVVGPVSCCGPVSCCGPVSCC DHSSSHLLLTFTML
19330	49698	A	19443	4688	4824	

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19331	49699	A	19444	1	2274	MLKPLMGGAHRRRAAGARK WDGTAIIASTSGLEVLWVTTSR SKTVESVGLAKPGQHNDARMN LAIALTAARYGAATANYMEVV SLLKKTDPQTGKVRVSGARCK DVLTGQEFDVRAKCVINATGPF TDSVRKMDKDAACQPSAG VHIVMPGYSPESMGLDPATS DGRVIFLPWQKMTIAGTTDTP TDVTHHIPSEEDINFILNEVRN YLSCDVEVRRGDVLAWSGIR PLVTDPKSADTQSIERNHVVDIS ESGLTIAGGKWTTYRSMAEDT INAAVKTHNLKAGPSRTVGLFL QGGKDWSPPLYIRLVQDYGLE SEVAQHAAATYGDKAFFVAKM ASVTGKRWPVIGVRLVSEFPYI EAEVKYGIKEYAC/DCCGYDFT SYSPGLS/EMSRQQRKPYPLGL N*/CGRELNWDDYKKQELET ARKFLYYEMGYKSRSEQLTDR SEISLLPSIDRYKRRCHKFDAD QRGFMTVVEVQRVLESINVMQ DENTLHEILNEVDLNKNGQVEL NEFLQLMSAIQGRVSGSRLAI LMKTAEENLDRRVPVDRSCG GLYFCVRNWWVGLTDFKNE AADPSGVKLQTTFTSVTARKGS VDPKNSGAQLASPSGSRGTAA GGAACQSRALRLHSSALGWSM GLGAVEHGAVLIGEARAAQEP MEGVGSGMAGCRSQVLPRG
19332	49700	B	19445	439	1542	
19333	49701	A	19446	2	418	CLSLPPTPWAPVRPEPPRR/CAT PCSTAPSIDHPRAEECERTVQD WRAAPPAAPVRDPLETGKIDQE IHKYNTPGFTGCLSRVQFNQIAP LKAALRQTNASAHVHIQGELV ESNCGASPLTSPMSSATDPWH LDHLD
19334	49702	A	19447	111	215	GTWLE*RGKPIFWGEIKAS CRNLHLQGAKE
19335	49703	A	19448	740	959	DLYPHILSWQSRNAARKRKS* RGQRPIPAIS*GRISQKQQQNVN TSTPSHCRLPYECRPLLHGAQS HRPPKG
19336	49704	B	19449	260	508	

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19337	49705	A	19450	11	490	RLSTSPDGAQLASRSGSHTG AAGGAACQSRMTMRSHSALGW SMGLGAPLQRH*INSSGGSWLV DKESFPVPSALNFSPLGRKSSPC SKVLYMPNPVSHSMIPSGSERS MDTNGSCWYLTCSLSAPGRRD TRIRKVFSGRLLVLTLMISPSV GHSTA
19338	49706	A	19451	42	263	SGVSPMSFNFTTSAPAFNRSWT TCLCPK*HARCRGVQPKLDLLL PLQLMSAITSFLAMVNSNCLTS ALPFLA
19339	49707	A	19452	662	1564	GSRICSFQTRSGHPECPQCHWT RQNHSSIQPHKAAAYTKKTTIH PPNRNSNCSIIWCKLQKLYMCG P*GRSFNFSANLHQPQKGHSGE RPFENKNGRAILLKSHRVHTQE MPFPCSKVKGGLVSSGLFQH QAIHNEKPCRSAMYGDMFHTQ QGHFKCIDYGEAFSPKDTGQGH QIIHTGEKPYVCTECEKTCRST NLIQHKPKGLLSLLVLSPTGN ALFSTLSQLTQLLLTFDVRSDA TFFRKSGSRHQLWLALPEDAR ARVTSVSGTRRRDHGGARGVV CLIHGCVPTDRSSPDVW
19340	49708	A	19453	1	1167	MIREQKVKEVYICAGKKKSHM HLWHNGEKNYRLGRKDRKMT HEGWLIKIPHPGRKYKASGLH WEQMKHMGGRGKVHLEFTEM YVAGRRGEVKDEVLEPMSLTE VYIPTENDREVWRERRLRAPGL CAALEGQLEFRVGVGLAGSAL EAAGQPCWPRAGRARDLQFAM PEPPPASVGSAAARSLRSAAP CSTAPSPIGHRAECERTAQD WQAAPPAAPVRDPLGEASWAP ESVMWPLDRSQSEEVSVSKRH MDATDKIKFPWLKEKRTIEFGE AAGYVCHRRYKDMEPHEKMG EAAKKVHVWQMRSRARDLQF AMPEPPTHSKGSAAARASPT/T HHPLLHDAQSHRPPKGLRSAAGT WRGTGRQLHLQPQCQGIHVVKP AGLLSL
19341	49709	B	19454	118	559	

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19342	49710	A	19455	26	813	LSHYLACSLRLPSGSRIRSAWLI PSIMLLNYTSPGLPRHRSKSEN LDDTARRSPGMAGPCPLPGG VPDVRAAAYGAPTSARQPRVW PPGGRWPRGARGARSFLKKPFR GTPTQVRGAWQCPLPLTVLEK *PWHPCGRFQGRHREKGGRE LGHSKSPPPRRSHYPAGEKGEE ERKEREESSCAGLRRGAHEHA QQQSLPGELPAPGDHPGRCVG GQGRSRMGPCS*SLAQHPVCT RGQREKQERRATNKPVRGAPK
19343	49711	A	19456	497	756	TWLKSGISFPALFTIAKTWR*P KCPMSIDWIKKMW/HIYTM YAAIEKDEFMYFAGTWMTLDT VILSKLSQEQTCKHRMFLSISGS
19344	49712	A	19457	100	819	EWSSVRRILVEKRALRRP LCFRMKTILSNQTVVDSQKNV DITLKGTPQ*SCKGPRGT LRLRD FNHIKCGTSALLGKEQQRGR VDIKWWGNRKGWATRSGLF GSHVQDHDPRGVTGASGYKD EGPVYASPSPHPTVVI PGRNGSS LLKSRNFLGAEKYPQGF RMKTR VLLCSVSQSPEKMKLILE GNDIA ELVFKFQRALIQVATT VKNGA IRKFFGWVWSMLEKGT VQPLI
19345	49713	C	19458	395	574	
19346	49714	A	19459	1	1476	
19347	49715	A	19460	2	323	
19348	49716	A	19461	539	711	HRFPQDRKAGECLLHE YEDLV PIRDTLRLFPGGRYL PRAKHVA PSEPDPGWLVLG*FYC* FCHSP ALLSGFCLAVNVYRERSV
19349	49717	A	19462	66	2873	SARTISYDYQNWGRDGG PRSS GGGYGGGAGGHGNGRGS R GGGGGGGGRG/WQGPAS RAPE RPRNRHVREKTGAEEQGS WR GKREL/LVHMDERREEQIV QVL DSGQAENG*RVRTTDFR FAPE DHGYGTEVSTKNTPCSEN KL/G HPGKEVDKSRKKNV/SESG TDH ILTRDSEYLLQENEPDGT LDQK LLEDLQKKNDLRYIEMQEL V NLIDNHQTVVISGETCGCK TTVQ VTQFILDNYIERGKGS

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19350	49718	A	19463	1	2112	FRKTTTRRLRKVKGRTAGCARF RKWLLRQHLRTLGLICNHTSR MTRCRWSAESDSGDEEEEGPIV LGRRQKALGKNRSADFNPDFV FTEKEGT YDGSWALADVMSPL MKKRAATTLHEKIEKARKRRK TEDKEAKSGKLEKEKEAKEGSE PKEQEDLQENDEEGSEDEASET DYSSADENILTKADTLKVKDRR EEEEERTGSRRI*RCIS/ATMKT SSFQDMNLSRPLLKAITAMGFK QPTPIQKACIPVGLLGKDICA/C AAPGTGKTPFPALPVLRLIYIP SPGSSL/TRVLVLPTRRELGMQ VHSVTRQLAQFCNITTC LAVGG LDVKSQEAALRAAPDILATPG RLIDHLHNCPSFHLSSIEVLILDE ADRM LDEYFEEQMKELIRMC SH HRQTMLFSATMTDEVKDLASV SLKNPVRIFVNSNTDVAFLRQ EVIRNRPNREGDREAI VAALLT RTFTDHWMLFTQTKKQAHRMH ILLGL/LGVQVQELHGNLSQQT RLEALRRFKDEQIDILVATDVA ARGLDIEGVKTVINFTMPNTIK HYVHRVGR TARAGRAGRSVSL VGEDERKMLKEIVKAAKAPVK ARILPQDVILKFRDKIEKME/KD VYAV/LQLEAEKEMQQSEAQI NTAKRLLEKGKEAVVQEPERS WFQTKERKKEKIAKALQEFDL ALRGKKRRKKFMKDAKKKGE
19351	49719	A	19464	354	446	RQHAH*ESSPLNLTYPGTQILR KAAGTSA
19352	49720	A	19465	42	388	
19353	49721	A	19466	177	497	
19354	49722	A	19467	271	773	TAMSSEEGKLFGGLNFNTDE QAL EDHFSSFGPISEVVVKDR ETQSRSGFGFITFTNP/EHASSC Q*RSQ*TGEVSWNG/RQIPLLDH AGKSCSGEPRGRWALGPMGVG SQLILEVVGDQGYGSGRYYDS RPGGYGYGGRSRDYNGRNQG YG YDRYSGGNYRDNYDN
19355	49723	A	19468	2	414	GRVGP PRRAGGPRASAAGDPA RGAAPKMSQTAMSETYDFLF KFLVIGNAGTGKSCLLHQFIEK K/WSVTRSYRGAAGALLVYDI TSRETYNALTNWLT DARM LAS QNIVILCGNKKDLADREVT LEASRFAQEN

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19356	49724	A	19469	397	445	GHRGAHRPRTLRSVVVRAHR CSYSGIWD/TAGPDRFRSVTRSY H*GRPGALLVYDITARETYNAL TNWLTDAARMLASQNVIIICGN KKDLADAREVTFLEASRFAQE NELMFLETSALTGENVEEAFVQ CARKILNKIESERMGSQYQGD AALRQLRSPRAQAPNAQECG
19357	49725	A	19470	2	559	
19358	49726	A	19471	1	483	
19359	49727	A	19472	95	352	RKATKMATIWASGTPKQPCPR ELLAQERRQTRTRYNQ* ^{DQ} *QE RRSRQRMGVGCLHMLRSEKA PQQRSAFCTPKSSRPSARLT
19360	49728	B	19473	247	1364	
19361	49729	A	19474	422	877	CHTQTQ*QHTP*QPTPIDMAPTS HARMPFHTHFLTQILTLVSRSP DPG/PHGGKVPTRIPIPPAQPWG PSTLPSSSFLGPPRPFPSPVPGP GGENRKPFSTPP* ^A * ^G FPGPPSG P* ^A GGE/PPVVGRTATPSPPTP SPACGLKCKWHLKLN
19362	49730	A	19475	168	522	LALHPTRLIPATDDEVTVTED KINAPH*KQPVNVNVEP/APGLF AKALANVNIGSLICNVGAGGP CCQPAAGGCTQPGGSCPLHCWL LPA* ^G RRKWEAKKEGFRGSFD* LTWGFSGF
19363	49731	A	19476	1	328	
19364	49732	A	19477	1	1204	MASRLLLNNGAKMPILGLGTW KGSILRVGFGSSREPPYRGQP LMGGPPVRILGPSGRPKRHINAR GRRGK WASQTGGPRAQTGTWS RRQQVTEA/VKVAIDVGYRHI DCAHVYQNEVEGVAIQEKL EQVVKREE/LFIVSKLWCTYHE ERGLV/KGACQEDTSSDLK/LAD LPGPLTLIHWPTGFKPGKEFFPL DESGNVGSPDTHISDTWA/AME KLVDGLVKAGISNFNHLQVE MILNKPGLKYKPAVNQIECHP YLTOEKLQYQCSKGIVVTAYS PLGLS* ^T GPPWPKP/EDPS/LLED RIQGGSQPKHNK/TTA/QVLIJRG SPCKRNLVVP/KSVTPER/VAEN FK/VDFELS/SQGYDPP* ^L SLPT RNWR/VWCPWCST/SHKDYD LPMKEVLKA
19365	49733	C	19478	300	489	

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19366	49734	A	19479	243	471	CDHLQVSRPRIPATVPVWEKRS EMDSKEEEKKEKKEKRRRR *RRRGKEEEEERRRRRRRRKK RGKKK*IKKRV
19367	49735	A	19480	1	365	MGLYKDLLDTRYLFYLVPGYG LTQIELEVIKDSAPVGTPTRV GLKLEMGYILSGHLDKFIFAMP FKIKDILSLKKEEEK/ERRRRRR RRKEEEDEEEEEEEEERRRR RKRRRRKKRKKKID*KKEEKE EEEGEGEKKKKMKKKRKKK KKKKGGGGGKGGERRRGRKK
19368	49736	A	19481	96	508	PAGSLVCPNQCSSARLFSSFFCS SAVMSASPAVGKRGWAELTGS FLPKPPLKTLGSGREDR*QVW WLTPVIPALWEAEVGGSEGOE FETSLGNMVKPLLYWLGSNGW LWKLGRRLWQLLWQDDWPT RGSHILVL
19369	49737	A	19482	3	1013	SRPSWGTHWNEYARRLTLAPS WPLP*GHPVPSLRVSC/LPHYY ESVLEKKGPCDRDYKKFWAGL QGLTIYFYNSNRDFQHVEKLN GAFKELTDEIPWGSRRDPGTHF SLILRNQEIKFVETLECREMW KGFILTVVELRVPTDLTL/LPGH LYMMSEVLAKEEARRALETPS CFLKVSRLAQLLERYPECGN LLLRPSGDGARQVRVGHHAADA QRDA/PWFRHYKVEAGRGPY VIRCGTAVLLHLPWTTVVNYF VSHTKKALVPFLLEDYKVL GYVEADKENGENVVWAPSAPG PGSPPLHKVPPSRCQPASSQDKL PPLPPLRNPGREIT

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19370	49738	A	19483	63	1496	LISAMACVLRPLVSVYSEKGESS GKNVTLPAVFKAPIRPDIVNFG SHPNLRKNNRQPVQWQGN*AG HQTSAEVSWGYPRAVGSKFP R\VRGGGTHRS\QGCFLETMC R\GGRNVLHPTKTLGRRWHRR SSTQPKKRIRPSGSAPGCPQLP ALGHGLKGHLY*GKFPETSFV* VER*KLKG*QEEPREAVFAPLR KLKRPGNDIQKGSMASSAK*RA GQKAKLRKPVARIPAAAGAPCI\N YNEDNGYSFKAF\RKHPWGLL MLNC*GKLEHF*KLAPLVGHV G\RFHLHGLLESALREV*DDLYG T\WR*SHFPLQGVNLPFSPWHK M\NNTDS*AESLKSPEIPREPLRA PR\KKIHSQSS*RRNPLEKL*EIM LKA*TPFAKAHAAGTPFFGQAR N\HKLRVDKAAAAA\ANLQA NSDEKAAVAGKKPVVGKKGK KAAVGVKKQKKPLVGKKA TKKPAPEKKPAEKKP\TTEKKP AA
19371	49739	A	19484	3	730	KRLPKMAEVQVLVL\DGRG\HL LG\RLA\VAIVAK\QVLLGRK\VV V\VARCEGINUSANFYRN\RLKY LGFSPPSGMNTNPSRRPLTTS APSRIFWRTVVRGMLPPQNPSG GQGRLLDRLQGV*RASPPPYGQ EKS\GMVVPAAALKVVRLKPTR KFCLIWGR\LAPEVGWKYQAV TAPPGGERGKRKAKIHYRKKK QLMRL\RKQAREETWRKKIDK YTEVLKTHGLPGLSPIKTVNSS KKKKKKRAAA
19372	49740	A	19485	1	660	PTRPRTGRRTRKSTPMKGLGA RYREYKVVGRCLPTQNA\nTRG PLL\nPAC\nE\nI\nF\nA\nP\nN\nH\nV\nV\nA\nK\nV\nP\nA\nF W*LCILS*KKMKKFFQGKIVYL WGKVF*EGSPLRVERTFGDLGL RLLT\nPRERAPH\nI\nV\nT\nG\nE\nY\nR\nG\nP* PTAGGCSTQLL\nTRDNG\nVARHR RPEAHFHFRFMEGWEGDRGP/C KIPPGGLVKASSNDSKIKVSRV PHRVLA\nAFRNKARFTTKRPNT

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19373	49741	A	19486	51	471	EAGRLPGNILLDSIMACGLVAS NLNLKPGCECLRVGEVAPDAK/ S*VLPARCVHGILSDRLVGQWG WSWPRWPHAHPLPPSFVLNLG KDSNNLCLHFNPRFNAHGDAN TIVCNSKDGGAWGTEQREAVF PFQPGSVAEVC
19374	49742	A	19487	59	527	ETQSWPCGLVAISNLFNFTLES CLRFKPSWLPDAIKSFRC*NLG QRPPTTWCLHFQPSASTAHGS ARHASLCNSQGTAGHEGGPTQ REAVFFPQ/PGKCCRGAFTFRT RANLNRSSLPDGITEFQVSPNGF NL/EAINYMAA/DGGLSRSKCV AFD
19375	49743	A	19488	2	440	KQQCRDTGDEVVCSCFVGYQL LSDGVSCEDVNECITGSHSRAF GESCINTVGSFRCQ/RISSCATG YELTEDNSCKDTLGSFRCRPKL QCKSGFIQDALGNCIDINECLSI SAP/CPIGVTCINTEGSYKCQKN VP/NCGPLVNHLEKE
19376	49744	A	19489	2	2061	
19377	49745	A	19490	2	2120	
19378	49746	B	19491	63	255	

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19379	49747	A	19492	2	1941	PPPMERAAAPSRVRVPLPLLLGG LALLAAGVDADVLLEACADG HRMATHQKDCSLPYATESKEC RMVQEQQCHSQLEELHCATGIS LANEQDRCATPHGDNASLJEAT FVKRCHCCLLGRAAQAQGS CEYSLMVGYYCCGVFQACCVK SQVETGDLDDVGGQETDKIIEVE EEQIEDPYLNDRCRGGGCKQS CRDTGDEVVCSFVGYQLSD GVSCEDVNECITGSHSCLRGES VCINTVGSFRQCRNSSCGTGYE LTEDNSCKDIDECESGIHNCLP DFICQNTLGSRFCRPKLQCKSGF ITRML*GNLLLDIQWSVLSIQLP RCMIGD*HGINTEGFYNVPEGT CPNCGPLGYHLQGRGRTRCVND VDECAAPCLSPVKG/HR/CVE LFPGSFPLAECKDGVTFDGI/SR DVLFDVQRSCQRLPRGACCI/GH K/CTENTLGSYL/CSCSVGF/RLS VDGRSCEDINECSSSPCKPGSVA NVVYGSYQCY/CR/IG*PASAIV GWEFTCERTFDGVAALPHRGH TFWFLTAGIQTWSGSFPVAACP SSGLTGWAPNGPATCQ/DIDEL C*LGHNCFHSTEDLVSNIPGAG FRCLGLSSCPENYRRAAT*S*G NSCMRAIGAGWEKEKGKLAGS
19380	49748	B	19493	123	237	
19381	49749	A	19494	285	456	VINKRLVCTRLRRKWSCLQPH RMM*VQAGSRGSQPKYHRHE MGWTGHTDTPPHRL
19382	49750	A	19495	383	693	NFLPAQPCLSAPPS*SRSLLDNS PLNCKAFHSSSHLLKLESCSE NSPGPLLQPGGTCLGACPGCFS FSPGISAGKPLSKAASPPVCTGS GAETSTTPPSPLR
19383	49751	B	19496	28	236	

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19384	49752	A	19497	1	927	PAAPQVAGRLGLGCPHLHLHVF AVVSAMLPRLRCVPRVLGSSV AGLRAAAPASPPRQLQAPAPRL CTRPFGLLSVRAGSERRPGLLRP RGPCACGSGGCSLHIDGDKAF VDFLSDEIKEERKIQKHKTLLK\
						MSGGWELELNGTEAKLVVRKVA GEKIPVPF\NINNSIPP\TFDGEEE TLARARRFEDREPELTSLPKF\V VE\VIKND*WQERPLVLD\VHYP EDEVGQEDEAESDIFS\REV SFQ STGESEWKDTNYTLNPD\FWT GPLYD\HLMGFP*PNRGVDNIF A\DELVELSTAPRSPGPVLPFP
19385	49753	A	19498	3	342	LDTNLPANRVPAGLEKRLCAA AASILGKPADRVNVTVRPGLA MALSGSTEPCQQLSISSIGVVG ARDNRRHGAPFFGFSPRELALG QDRILIRFFPLESWQNGKIRTGM TFL
19386	49754	A	19499	3	520	SSARAVSVPLPAMPFLELDTNL PANRSARGGWRKRLCAAAAS\I LGKPA\DRVNVDRYAGGFAIGA *AGST\EPCA\QLSISSIRRWGT AED\NRSHSAHFF*VSSPRELSP GARDRIILFRFFPLESWADWAR *GTVIDFFMIWGTGEGFQGHVNV LAASFQKRSSWAEVKGLG
19387	49755	A	19500	7	355	
19388	49756	B	19501	172	479	

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19389	49757	A	19502	1	1656	LEDPDSSSRPRRAGSGHSASFPP PPLEQLWRQVKTLNPKAEVAR AQAALAVNISAARGLDVLRIT NLGPKGTMKMLVSGAGDIKLT KVDGNVLALHRNCKFQHPTASLI AKVSNKPQE*YNLV DGTDFLIV LINWESLLKQADLYISEGLHPR ITTEGFEGAKEKALQFLEEVKV SREMDRETLIDVARTSLRTKV HAELADVLTEAVVDSILAIIKKQ DEPDLFMI/SVIMEMKHKSETD TSLIRGLVLDHGARHPDMKKR WRDAYILTCNVSEYEKTEVN SGFFYYKSAEEREKLVKAERKFI EDRVKIIIEELKRVCGSDSKGF VVINQKGIDPFSLDALSKEGIVA LRRAKRRNMERLTLACGWG/M PLNSFDDLSDDCLGHAGLVYE YTLGEVEKFTFIEKCN\NPRSVTL LIKGPNKHTSLRIQRWQ*GDG L*GAVIKNAIDDCVVPVGA VSGSQWAGSPGFKHKFSC*RA RAQLGSPKHLDDAFAHYFPKVL CFRNSGFLTQGNIKLKFKAEH SESGQLVGVD*TPGEPNWWP ARSKAVWG
19390	49758	A	19503	2	424	EGPVMAAPPNPGPATLGGPGDP DLGRLPLHEVFLHVRPARPRG APLHRRGLRGRHAVRAVRQRR REPEDGAAGAVDRAGGAGVLG RGDRESEGLTD*PREPADRAP LLQPERGRFSHPLPTLTCAPSPII FPVAERWG
19391	49759	A	19504	3	174	
19392	49760	A	19505	2	153	LPLHEVFLHVRPARPRGAPLH RRGLRGRHAVH*PSEPGDPARL LQPERG
19393	49761	A	19506	3	354	EDGRHGAPNPPATLGGPGDP DLGGLPLHEVFLHVRPARPRG APLHRRGLRGRHAVRAVRQRR REPKNGAAGAVDRAGGAGVL GPGDTEYEGPLTD*PSEPGDPA RLQPERGR

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19394	49762	A	19507	3	1246	GSTHASARMAMVMA ¹ PRTLPPAT LGGPGDPDDLGGPLHEGF ² LHI RVPARPRGAPLHRRGLRGRHA VR ³ AVRQRRREPEDGAAGARG* EARKGPE* ⁴ LGR ⁵ ANTESEGPTH ⁶ R LDPSEPGDPARLLQPE* ⁷ GRFFTP FQIMYGC ⁸ DVGS ⁹ DGAFSSAGYP QERLTNGKD ¹⁰ YIALNE ¹¹ DLRSWT AADMAAQIT ¹² KRK ¹³ WETPPMR ¹⁴ RR SLRAYLDGTC ¹⁵ VEW ¹⁶ LRRYLENG KETLQ ¹⁷ R ¹⁸ TDPP ¹⁹ KTHMTHHPIS* ²⁰ P *RPL* ²¹ RCWA ²² LAFYPCGDHT* ²³ P WQ ²⁴ RDG ²⁵ EDQTQGHGS ²⁶ LLETRPA GAG ²⁷ TFQKWAS ²⁸ WVPVSGQE ²⁹ R YT ³⁰ CHVQQ* ³¹ RVLPK ³² PLTLKM/W EPSSQAHPSPIRGAS ³³ FAGPW ³⁴ ESL GSL* ³⁵ ITGA ³⁶ VGR ³⁷ CW* ³⁸ C* ³⁹ RKEQLR WRRGER* ⁴⁰ KKEGAYSQ ⁴¹ GCKASD QCPGASDVSLHSFVKVLRQLAL
19395	49763	A	19508	1	392	
19396	49764	A	19509	1	220	
19397	49765	A	19510	3	500	
19398	49766	B	19511	28	134	
19399	49767	A	19512	1	1662	MAASVVCRAATAGAQVLLRA RRSPALLRTPALRSTATFAQAL QFVPETQVSLD ¹ NGLRVASEQ SSO ² PTCTVGVWIDVGS ³ RFET ⁴ EK NNGVAGYFLEHLAFKGT ⁵ KNR ⁶ P GSALEERRWRAWG ⁷ AHLNAYST REHTAYYIKALAKELPKA ⁸ VEL LGDIVQNC ⁹ SLE ¹⁰ FTD* ¹¹ GRNVDV ILREMQEN ¹² DAS ¹³ MRD ¹⁴ VVCN ¹⁵ YL HATAFQGTPLAQA ¹⁶ LEGPS ¹⁷ ENV RKLSRADL ¹⁸ TEY ¹⁹ LSTH* ²⁰ QG ²¹ PSKW CWAAGREWEHQ ²² QLFRTFAQE GTSVGIPW ²³ TYAEDAV ²⁴ PTLTPCR FTGSE ²⁵ NRH ²⁶ DDAL ²⁷ FAHVAIAV EGPGWASPD ²⁸ NVALQVANA ²⁹ ING HYDCTYGGGVH ³⁰ LS ³¹ SP ³² LASGA VANKLCQSF ³³ QTF ³⁴ SICYAETGLL GAHFVCD ³⁵ RMKID ³⁶ MMFV ³⁷ LQ QWMLCTS ³⁸ ATESD ³⁹ VDRGKNIL RNALVSHLD ⁴⁰ GTPVCEDIG ⁴¹ RS LTYGRRIP ⁴² LAEWES ⁴³ RIAEVDAS VVREICSKYIYDQCPA ⁴⁴ VAGYGR SLGLPFHLC ⁴⁵ SR ⁴⁶ TAAQLTEQ ⁴⁷ PK APSSPQSPGCQGVLAQK ⁴⁸ TC ⁴⁹ PSS SLTACQGA ⁵⁰ FINTLHPSG ⁵¹ PIEQ ⁵² LP DYNRJRSGMFWLRF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19400	49768	A	19513	2	1693	AQSTLARRNRADCSWKMAASV VCRAATAGA QVLLRARRISPAL LRTPALRSTATTAAQALQFVVPET QVSLLDNGLRVA\SEQSSQPTC TVG\WVIDVGSRFETEKND/SGA GYFLEHLAFKGTKNPALAVPW EKEVESMG AHL\NA\YSTREHT AYYRKALSKDLPKAVGALGDI VQNCSEDSQIEKERDVILREM QENDASMRDVVFNYLHATAFQ G\TPLAQAVEGSENVKRLSTA DFTRYL\STHYKAPESVLPQTEG VRTEQLLDL\ARNHRVHIP*TY AEGAL\PTITPCRTGTSEIRHP*D ALPFAH\VA\AVEGPG\WPAPD N\VALQVGN\IGHYDCTFGG\ GVHLS\SP LGS\GACGPTKLCQS FQTL\SCYAEDGLCWVHTLFC DRMKIDDMMFVLA/QGHWMR L\CTSA\TRSEV\ARGQKNIPQK MPLGISS*DGNYSLCVEDITPAA LLTLWARRNPPGLKWES\RIAG GGFQVVVR*DLAPRYIYGPSCP AVA\GYWPH*SMLPDYNRIP*P ACFWVAFFRAGKPMVKQKGR GGGLWSPPPPTQHFRLLLTCC
19401	49769	A	19514	46	422	
19402	49770	A	19515	568	1567	GPWAANGVVLAFPPCLGSPAP HLAPQKAVPPKWGISSLCSEHF HIYQVGGVAFCGRIRFLSSTDF KRRAGSGSLMSQEEKHELSG KIRSQIMDDHARPLYTMSNCP CWAGALGPQESKCSRGRLLHR AFPSLV\TLLLAGQATTGLLSCY QQQGAGWDKLDShRPRLAA WEEPCGMEAFPPKPSQSLVEAKI AQLATPGLLDCKAACPWGAPC PRGP\MQNATKVIGNM\TEDHV DAPGSRNAEPP*KVYPP/LKGSF P/EKNLRHLKNTMETIEWKAFE NWMHHWLLF\ELSKQSLWEQ/ QSPLDAPK/ENSELEDEPSSGL GVTKQDLGPVPM
19403	49771	B	19516	1	1428	

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19404	49772	A	19517	1	2293	MARSEAAAAGPGPGPPGLAAR ERRGGRGCVRGCEASVRVWS VALRRARRAPRPYVARCRRV RRPARVAIGCGGVSSPAGVSGC ARVSPERPPLRLCVWALSRAHG GAVCRAGPGPDSLKRGLTSHPP AFPLHHGSRTL.LLGPLSPPPAAL PFL.LLLWAGHLVAS/ACPGRCIC QNV/SPTLTMLCAKTGLLFVPP/ SIDRRVVLELRLTDNFRRHFAN MTSLV/QLTLsrNTIGQVAAGA F/VDLRALRALHLDSNRLAGC/ GGDQLRGLGNLRHL/VGNNQI RRVESAAFD/DLLSTVEDLDLS YNNLEA/LPWEAVGQMVNLT LT/LDHNLDHIAEGTFVQLQSW A/RAQAHHPLTVSFGGNPLHCN CE/LLWLRRLTREDDLETcASP N/NLTDRYFWSIPEEESCTRCQR FCG*ASLVAAELTSNSVLIRW/S TQRPVPGIRMYQVQYN/SSVDD SLVYRKYSLSYMNFTMR/MIPST SQTFLVNDLAAGRAYDLCVLA VYDDGATALPATRVVGCQVFT TAGDPAPCRPLRAHFLGGTMII AIGGVIVASVLVFIVLLMIRYKV YGDGDSRRVKGSRSR.LPRVSHV CSQTNGAGTGAA/AGPGPAGPG PLRGAARGGV/WLPPSPSRPR PWRPR/LASAEPEVVLGRSLG SATSLCLLPSEETSGEESRAAVG PRRSRSGALEPPTSAPTTALVP
19405	49773	B	19518	97	255	

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19406	49774	A	19519	1321	1728	EHAHDRDLHHAHYVQATLVR ASLREAVVGSPTDAWLQORTA RSSASLLARNRPATSVWLPRA GFIAGTGGRERRRGSEGWEG GAGGTGAGLSAHSQTSACEGS/ CGGSAGRGRCLLSAA TPPLQPP RPAPPTAGLVQPRQVPTAPPRA SAGNEHHQGWSGRL*KSLAAA RVGEAPGKLP RPDRFRKQSNGA LARASLRVSAQPGTSSSAAAF PPLGPAPLAAPARSCDESGPRQP DGRGGVPVPGQQQGA/ESEPCA AATRRPWVNNRR/TSRREARTS VACT*CAWCRSRSCACSHSPWS SASSSSAAICSSSPRA*STSS*RT GGRLRRWRRWSWGPTDPYAP AATAPTPAHFASP/ACAPHYQR LGEANLSESHLD/CRPFGKKRP VSPSPSESPHA WQSEESAQTLN SAESGKKRAIRAQNFGR/LLLT WNAGRPTVRRPFTRRWAKLW GQVERAGRGETQRH*SPCDRKS DLLKATQQTGHGVSQIRVRVRSP LFSLPPCPRKGGANKIPLNCKR ARFKKGFFVFCLEIQMFE
19407	49775	A	19520	192	447	
19408	49776	A	19521	1	591	
19409	49777	A	19522	281	421	
19410	49778	A	19523	174	512	
19411	49779	B	19524	67	1166	
19412	49780	A	19525	1	1620	MGAKDGRLLSESSQGLSSCGAS LVPFCVSKSRLLMKTVPRLDKE TVSTVDSGAPTDLAQLPTVLKQ PCCSVMASGQFVNKLQEEVICP ICLDILQKPVTIDCGHNFLCKCI TQIGETSCGFFK.CPLCKTSVRK NAIRFNLLRN.LVEKIQALQASE VQSKRKEATCPRHQEMFHYFC EDDGKFLCFVCRESKDHKSHN VSLIEEAAQNYQGQIQEQIVL QQKEKETVQVKAQGVHRVDV FTDQVEHEKQRILTEFELLHQV LEEEKNFLLSRIY.WLGHEGTEA GKHYVASTE/PTVERSQAHA*FP VCLLASDYDEISGGGASSQDTKT FDVALSEELHAALTSAPDLILS QDEIVTLNLASQGGSKQRGNPR RFYRRGFLEVEPLTGFVELHSS GSQCQALIESGREDLPVCPNK
19413	49781	A	19526	203	359	

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19414	49782	A	19527	135	466	DPAGSSAASMSSAAGLCALTPP /GLLSLGLLLLPLVVFASAEA\ EEDGDLQCLCKVKTLLPGSVPGH IHQLGG*FKGRDPHCPTCT**A TVEGMGRKILLGTWQAPLLQG
19415	49783	A	19528	46	468	TGPTHASAAAILVPRSLHKMPGE ATETVPATEQELPQPAETGSG TESDS/GKSPASDTYIVFGEAKIE DLSQQAQLAAAEKFKVQGEAV SNIQENTQTPTVQEESEEEVDE TGVEVKDIELVMSQANVSRAK AVRALKNNS
19416	49784	A	19529	337	509	ISQQLLVVLACINLRSWLPQKL CKYLKQDVLTAIDLSEVPEFC PFVDHLVVALEEEGPAL*GHPA SDTYIVFGEAKIEDLSQQAQLA AAEKFKVQGEAVSNIQENTQTP TVQEESEEEVDE/TGVEVKDIE LVMSQANVSRAKAVRALKNNS NDIVNAIMELTM
19417	49785	A	19530	91	1019	GELLALLGHRVPTRPWASGQK GVCGWCPGKSTLQGLRCGPTR ACRDGSSCSVEGGRGVRLVLG TASQDPEKEMPGEATEPVPAIT EQGVAASPRAETGSGTESDSD ESVPELLEEQDSHPGQPHNKAQ AGRQQSEIDEDPVS.KAKQSRN* KEGPGRAMSQTVGEQVTVGT KEFTNRKSKNILLCHPPKPDVY QGAPASRYFTIVFGGSPRSEDLS PSKHNLASCLRNKFKQGEAVSN IQENTQTPTVQEESEEEVDE TGVEVKDIELVMSQANVSRA KAVPSPEERTSNDIVNAIMVS
19418	49786	A	19531	1	261	MWGFHSHPGTGQARAYTDT GSPIPLIMHVNRGRHSEIPVLER NLLHFRMDAST*NLGMSSLM AILKNQFRHVS LAVSFAFSGEK
19419	49787	A	19532	277	349	
19420	49788	A	19533	792	1014	

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19421	49789	A	19534	849	1752	GESRGWERRKCVRLSSYATHL SVCDCHIGNVREGADPAGGAG *L*GARQQQTHTHKPAKATQR GEDREEKKRETKREERLQQQE NERDERGRREKEPRNRGTKRRE AEKGRRR/ESEKREEKGEEER QERQQKRAREKRRGRGARRRG REKKKTQRPRTQAQRPLKKIK DYTHHTTQTPTQQHHTHTTKH KQPHNTNTTVLFFFLAKEHR RAARKQHEPERGGGSKAGA KIKHTSIAAADRRHDPRTQD TRRKEGRRAQSGKHGRTAHKT EAGGGIPVHSTSRVQVILLQPP
19422	49790	A	19535	139	470	
19423	49791	A	19536	2	83	
19424	49792	A	19537	32	434	NRRKGA/GPVFQRA*KH/RV*R AGLRVDFAEHRYGKIVKDI IHNPRR/GAPLAKVVFRDPYRFK KRTELFIAAEGIHGTQGFVYCGK KAQLNIGNVLP/VGTMPEGTIV CCLEPRLCRKRRTSAEGLNKV CVYAT
19425	49793	A	19538	10	443	
19426	49794	A	19539	63	376	
19427	49795	A	19540	170	368	
19428	49796	A	19541	175	427	
19429	49797	A	19542	1727	2262	
19430	49798	A	19543	131	596	
19431	49799	A	19544	695	1337	GFGTQGERRRQCRLRVTPQLG ASSATQKITPALPETPVKAEQSC TLPLSPRTPGHLQPLRLDPSPW AVLIRG/QRKAGSVVRRATLR HGK/GAVRRLLRRWISPERHGY IKGVKDIHRPRSRAPPLRQR WFRDYSYRF*ER/TELFIAARG AFHTGPSFVYCRQERPSFNIGO WCSVPVGHHCLEGYNSCCLPWK EETLETCKGAGPAGFKGN
19432	49800	A	19545	1	813	
19433	49801	A	19546	227	381	
19434	49802	A	19547	135	740	PQPLPPTSMARHVLTGPPGV GKTLTIHKASEVLKSSGVVPDVG FYTEEVRRQGGRI/GFDVTVVVR HPGGLLSRVGLEPPP/RENVNAE LGSYVVDLTSFWSWALTRLE GM*ADCQQWAQGGQRVCVIDEE LGKMEALS VK/FSKAVRQTLS YPRDI*SL/VHKSQVPKGLPLAL VEEIRNRKDVKFVNVTQ/ENRN HLLARYS

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19435	49803	C	19548	251	574	
19436	49804	A	19549	2	450	
19437	49805	B	19550	721	3048	
19438	49806	A	19551	3	396	
19439	49807	A	19552	2	450	
19440	49808	A	19553	2	1152	GPPLHCTRAAGIRHEAPLGLAG LCRAADAGLCSAGWGFVKVV KNKAYFKR/YQVKF*KTPERV KRDYYARKRLVIQDKNKYNT KYRMIVRVTRDINLSRLLYA PV*RGDMSLAQR*LHTELAKI LVVEGLALTNLPAALFVPGPA CLAPQAFLQ*VLAMDKDLLEG PSWS*LGDEYNVIESIDGQPG FTCYLDADLARTTTGNKVFG APEGAVDGLSNPHSSKRFLG/ YVYPLHSTQTDSPGFMDEKQR NFNARSTSGKHIMGQNCIQDY IAL*WERKMKDAYKK/QFSQY IKNSVTDPMMMEEMKKAHA AIRENPVLWKRRPKERSLKRR GWNRSQNVPLLRKKDRVA/Q KASFLQSSRSGLLESLETPAIFP
19441	49809	A	19554	3	991	LTSRGVGSACVMLLVVRAGAR AWLRPTGSQGLS/LAEEAARA TENPEQVASEGLPEPVLRKVEL PVPTHR/RPVHAWIESLRGFEHE RVCLVDLHPDVFANAPRLDILH QDAMLQKNF*RSYAKTKTRA VR/GGGGKPLAARH/WAGPA WQHPLSALARRRCCPWPPGPT SYYYMLPMKVRLGLKVALTV KLAQDDLHIMDSL*LPTGDPQ LP*PELAHYRRWGDVLLVDL THEEMPQSIREATSRKTFNLH PAVGLNVHSMKKHTLVLTLP TVAFLEDKLLWQDSRLQTPLY PFSLPYSDFP/RPLPHATQGP ATPYHC
19442	49810	A	19555	31	305	
19443	49811	A	19556	213	541	DGGPAAHTPGAARGELSPVGD SGGYFRPSHLRCWILNLCISVPL SSAKDLLHPSSEEEVRRNPMKN RLVQSPNSYFMDVKCPGEETV CCIGESTGPQQLENVVLA VSY

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19444	49812	A	19557	164	591	DINSRDRSGPRATRIDGSGEGD KMAAQLRHRHQRRGASSPRFA KDILLHPSPEEEKRKHKKRL VQSPNSYFMGVKCPG/CFKFT TVF*AMAQTVVLVCVG/CAAPLF LCQPTGEKARLTEGCSFRRKHA LKATLSQDEWETILQ
19445	49813	A	19558	362	916	GGRCTMARTKADWPANRTGG KAPKEANWLTKSPLRKSAAFY LEGSKKPHRYR\PGTVAPP*NLD GYQKSTVELLIRKLPFQ/RLVRE IAQGLLKQDSRFQSAAGCFAG RQVRAYLVWPFLKDTNLCA/H AKRVTIYAKKTFQLSTPAYRG EPCFKDPLMDGETFHSQKKKK KISLLPVIGSSER
19446	49814	A	19559	849	1261	DGHIAGGPCS*GWPRDPAPKSQ PTMSSGSEPEKLPPAPRPQHYCS PAEVSGRPFAVGKALNQQAFT ERRLHTSLCPVPAALTVPSPEL PQQIFPGLAPATHLYSKAWA GATVSRPGAILGAGLYWGLVR ETAS
19447	49815	A	19560	3	1852	
19448	49816	A	19561	362	1298	QGGNRNVRHPSPLLAWGSDLIV KPHWLHWLLDLNHARLSALFA AAGARLPSHIPAPSAGSRRLLL LLGGCRACLLFPPEMANRGPST GLSREVQEKIEQKYDADLENK LVD\WILQCAEDIEHPPPGRAH FQKWLMDGRVLC\KLINRLYP PGTRSPYPRFSESKDGFGRWE QISQFLKAAETYGVRTTDFIS RRWFLWEGKDMAACAEGP*L ALGSVAVTKDDGCGYRGPSWF HRKAQQNRRGFSEEQLRQGQN VIGLQMGSNKGASPGGP*TGYS ECPRQIHVTRHPAPWLERTNV STPWSFTKKK

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19449	49817	A	19562	3	2518	AAGEWPQRPRAAVAAAGAAA RQRLPGSRQVAAGAPQAGGG DPSQRVPPGAELIKVQVYVSGE LVPLARASVDVFGNRTLLAAG TTDSEGVATLPLSYRLGTWVLV TAARPGFLTNSVPWRVDKLP YASVSLYLLPERPATLILYEDLV HILLGSPGARSQPLVQFQRRAA RLPVSTYSQLWASLTPTASTQQ EMRAFPCLPGH*GSSSGNGSW LELMPLTAVSVHLLTGNGTEVP LSGPIHLSPVPSETRALTVGTSI PAWRFDPKSGLWVRNGTGVR KEGRQLYWTFVSPQLGYWVA AMASPTAGLVTTTSGIQDIGTYH TIFLLTILAAALLVLILLCLLIY YCRRRCLKPRQHRKLQLSGPS DGNKRDQATSMSQLHLICGGP LEPAPSGDPEAPPPGLHSAFSS SRDLASSRDFFRTKPRASRPA AAEPSGARGGESAGLKGARSA EGPGGLEPGLLEHRRGPAGAAA FLHEPPSPPPFDHYLGHKGAA EGKTPDFLLSQSVDQLARPPSL GQAGQLIFCGSIDHLKDNVYRN VMPTLVIPAHYVRLGGEAGAA GVGDEPAPPEGTAPGPARAFPO PDPQRPMQPGHSGPGGEGGGG GGEGWGAGRAAPVSGSVTIPV LFNESTMAQLNGELQALTEKK LLELGVKPHPRAWFVSLDGRS NSQVRHSYIDLQAGGGARSTD
19450	49818	A	19563	206	1126	LESGSHIYAFSHESLLHVASAS V*TSFSDFATSVCHSPHCLH HALIPHGKGECSSVSGIVATGF GATGFLGRVCVNHGRVGSQIP QAIAQVSKEAEVGKFIHVAHLN VNIKSSSRYLRKKAVGEKAVR DTFPEAIIVKLLDIFGREDRFLN YFANMCWFGAIPLVSLGWKAV KQPVVYVDVSKGIVNAVKDPD ANGKTFAFVGPNRYLLDFLVK YIFAVAHSKGWVARDFEISPF SWTTRDKVERIHITDMTSLHLP SLEDLGIQATPLELKAIEVRLH HTYCWLSAEIEDVKLAKTVNI

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19451	49819	A	19564	196	553	KLSEFFLTHSINTAIRNGNLFV NRVTEVTRSGGNELGSFCLLAI KFTLLSFLGTGTTRRLPALRPRR LQQRGSHGLAGRLFTLWILHA GCHARGELEPDTC*LSLCRAR KPRLSTLK
19452	49820	A	19565	1	505	ATEDPGVAMGRRPARCYRYCK NKPYPKSRFCRGVPDAKIRIFDL GRKKAKEVDFPLCGHMSVDEY EQLSSEALEAARICANKYMKVS CGKDGFIHVRVLPFHVIRJNK MLSCAGAD/RHISKKGWFTKF NADEFEDMVAEKRLLPDGCGV KYIPSRGPLDKWRALHS
19453	49821	A	19567	6	904	AQLSSLA VPLLVTLPFRSVLVFR SDSLFFVAATEDPGVAMGRRP ARCYRYCKTKPIYPKSRFCRG CPLMPRIKIFDI.GRKKGKKN EFPLLC/HMSVDEYEQLSSESP GRLPRICPNKYMKVSCGKDG/ HISRVRLHPFHVIRIHKMLSCA GADKAPKQACRGAFWKSPPKGN LLARGSLAQVIMSIRITKLQN KEHVI*GPAARPSFKFPGRQKI HISKKWGFTKFQC*WNLKDM VAEKRVHPHMACGGQSTSPSR GPLDKWRALPLHEGLPNVAA HPLNTPIKFLLPWSKKKKKK
19454	49822	C	19568	346	471	
19455	49823	A	19569	1495	2780	EGLHLFCDLLDGLPGVQVAGG FDSFSSILASFTYWHDFNSTML LSTFRDINLGMNIKKSAVCFSR LGSETWEMPANLRPSEGART RTELSPQTSPRAHLAWRGRGG LGA VRPRRLSRRLS*KP*RSI* AEAPAGAPVRRCPAAPP/PPRP SRGSPSTPPPPSPGA/PRRRPP CSEHNKLSPPPPSSLCRLPAPSP RPAPRRSPSRRRRRRHPRPAD RREPLASATRVRLPPPPPP*PP SSSCPRRGRRFLAPWLARPA APRRAPCSRAARSRRAGASGAR VGDPAGAGRGWRRRAAGRP* APERPPPPPLPAVCEVSGGLRA SFADSVPGVRRRRPPGLGTLSS SGV*PRNERGVETTTWSGGGSE GAPGSGEGGNLFPAPQVIVARS GEGTVVPRFPVCQLRDSAVLLC LFD
19456	49824	A	19570	178	256	

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19457	49825	A	19571	622	1726	QSGSRTMMRMLVPASVGLLET GPPGDPSSLSHPLSGDVTVPED QSTVQKLA SDHKDIHSSVSRV GKAIDRNFDSEICGVVSDAVW DAREQQQILQMAIVEHLYQQ GMLSVAEELCQESTLNVLDLF KQPFLELNRIEALHEQDLGPA LEWAVSHRQRLELNSSEFKL HRLHFIRLLAGGPAKQLEALS ARHFQPFARLHQREIQVMMGS LVYLRGLGLEKSPYCHLLDSSH WAEICETFTRDACSLGLSVES LSVSFASGCVLPVLMNIKAVI EQRQCTGVWNH KDELPFIELS *SAWYHSVFACPIRQQTSDSN PPIKLCGHVISRDALNKLINGG KLKCRYCPMEQNPADGKTH
19458	49826	B	19573	271	392	
19459	49827	B	19574	58	296	
19460	49828	A	19575	215	861	QLPAESVTRTRGPAKAQARAGG PPGPWHCSYKWRAPSSLSGT GWPDMEGETTAAAPASRENSA DCSAIGEIRGPGKELWSPIQ VTATSS*MGRDFVLAT*EKVSH VDS*/EQPRSLQR\DP RPAGPAQ AKQGT PRAQASRESLSRPTAA VQLPSGQHPVITSGS*KGLAG KTSMGRKGLPWARGWAPWSL EAQNPRPTRLCDLFTGEDFDD DV
19461	49829	A	19576	65	782	SSSSAIQRKPRWVLYKYIQEL WRKKQSDVMRFLLRVRCWQY RQLSALHRA PRPTR/PDKVARRL GYKAKQGYVIYRIRVRRGGIRK RPSFLKGATYQQSPVHWSVFN QLKSFASE/VLSPFARGRRSLG RH/CGGLLEEF LNFFNWVVER FPHYQIFLKVIPHLPFP*KLFRR N/PDQTLHQNQVHKHR\EMRG LTSARPEKSRGLGKGHKFHHTI GG/SLRRATWRRRNTQLHRY R
19462	49830	A	19577	1	179	QEDYLRRELLTMDGR/FTDEEV DELYREAPIDQGG/MFN YIEFT RILKHGAKDKDLKEL

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19463	49831	A	19578	144	722	KKGLNHHHVEQNNTPRPRSG PQRATSNIVFAMFDIQSQIQEFK EAFNMIDPDQDGFHRPGKICND MLASLGAKNPT*WSILDAMMNE IAPGPPSNFTPWFPHHGFGEV* MATRS*KMVIRKCPCTCFE*KK PLGTIGEDYLRELLTTHGGIGF TDEEVDELYREAPI**KRGISITS EFTRILKHGAKDKDD
19464	49832	A	19579	3	429	VACLREHKQRCERATRSLLREL LQVRARVQLQGSELRLQEQEA RPAQAQPEKEAPEFSGLQNM QALDKRLVEVREALTRLRRRQ VQQAERRGAEQE/DRPQTGQA DRLAAAGGAGPGGGLRRPAEE PRGQQPEGGPGGGQN
19465	49833	A	19580	1	2454	RFPAGVAPRRAMANVSKKVSW SGRDRDDEEAAPLLRRRTARPGG GTPLLNGAGPGAARQSPRSALF RVGHMSSVKLDDELLEPDMDD PPHPFKIIPHNEKLLSLKYESL DYDENSEQLFLEEERINHTAF RTVEIKRWVICALIGILTGLVAC FIDIVVENLAGLKYRVIKGNIDK FTEKGGLSFSLLWATLNAAFV LVGSVIVAFIEPVAAGSGIPIQK CFLNGVKIPHVVRCLKTLVIKVS GVILSVVGGAVGKEGPMHSG SVIAAGISQGRSSSLKRDFFKIFE YLRRDTEKRDFVSAGAAAGVS AAGFAPVGGVLFSLLEEGASFW NQFLTWRIFASMISTFTLNFVL SIYHGNMWDLSPLGNFGRFD SEKMAYTIHEIPVFIAMGVVGG VLGAVFNALNYWLTMFIRIYI HRPCLQVIEAVLVAAVTATVAF VLJYSSRDCQLQGGMSYPLQ LFCADGEYNSMAAAFFNTPEKS VVSLFHDPPGSYNPLTLGLFTL VYFFLACWTYGLTVSAGVFIPS LLIGAAWGRLFGISLSYLTGAAI WADPGKALMGAAQGLGGIV RMTLSLTVIMMEATSNVTYGF IMLVLMATAKIVGDVFIGELYDM HIQLQSVPLHWEAPVTSHSLT AREVMSTPVTCLRRREKVGIV DVLSDTASNHNHGFVVEHADD TQPARLQGLILRSQILVLLKHK
19466	49834	B	19581	508	4413	

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19467	49835	A	19582	8	331	EVTACWQSSQPSLTLSASSAWA STLAALPEPFPPLHSESPLFGW PRPELGPSAAPCAPVPPEPPQRV PPAP*RPVPSTTQGLRSVGAW CRTGRQLHLIIPGVGSTG
19468	49836	A	19583	831	1121	
19469	49837	C	19584	1	1524	
19470	49838	A	19585	270	578	RFSKSPDPSGAQLAAPSGSRTG AAGGAACQSRVVRPHSSALGW SMGLGAMEQGAFLVGEAWAT QQPTVGGRLRHGGLQVPSAPAR GG*GPAKSHSSCWPRC
19471	49839	A	19586	2	298	
19472	49840	B	19587	113	515	
19473	49841	A	19588	1	569	MLPDLRSPVAHHRCSRASGNY HSGRHSAPAWRVLTGTWLDQ RSSRIHRSALFKDSYSKGEERT HIKMCSELLPSG/EARGLAGFR SEAADLRGECYSS*RQCGPKEL RSPAGFTQWIPHWGYRWSCLS VPRPAPALLSPWVVDGTGRGC AGGGAHRRGSGRSGAHGGGG RLRHGGLQVPSAPREGS
19474	49842	C	19589	1	1200	
19475	49843	A	19590	511	846	ARHRVLIGVFTPELIDKVLHVP TRLRSPASFTQWIPHWGCRWSC LPVPRRVPALLSPWVVDGTGG CGAGGGAHRRGGWGCTGAHGG GGRLRHGGLQVASAPREGS*G PARN
19476	49844	A	19591	9	481	QQPLREKSPASGDHPAKNANRR WPSPTRYPYVES*NWMPSLHLI KQSIQDGLKT*TLDLKP*KL*KK T*ALPFR*ARTSLKHQKQ WQKTKLTNGI*LN*ASA/PA KETKI/SSEQATYKMGFNHNL LF*QRANIQLQ*TRDLQEK KQPHQK
19477	49845	A	19592	1	3339	MSVRKDVKELEPSDIVCGNVQ CYSCMETNLTVSQVKHEVT GPREGATKPNRMKGKEGRSGS LLGEGDFFKDESMSSQSSKD GEKRRGKAQRWKWPMQGICR QLGVAKSMEGYQSRDQGG GVSDKWQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDISSSGGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPPRC
19478	49846	B	19593	1	631	

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19479	49847	A	19594	71	208	PCPKHCKSKFPMCPPELVGWSH* LQE*SHGSPSRFRLC*KQPQDLQ
19480	49848	A	19595	138	650	AWAQLPSALGSTRVSPPPSARS QPPWRRRRHKVCWRLNRCKE/L DEDAVASADFSMLSEEEKEEL KAELVQLEDEITTLRQVLSAER KAS/ELR*NKNSA*T*/CNELKPE LQKLA*HAD*HCLQEDT*YAE SRRAGKNCSPQQRWNGHQVEV RRHELLHSPFHKYACYETKVG
19481	49849	A	19596	1	1222	MRADGTA GKDPFATDKQLPEL LIQHCWDGLLA VCGGSTVGV LPFILHGSWVRPVAASFPPPLDN LHDSAEPAILLEPTQMRNRQK TNAGTMTKQISSTLPKNHHTSS PAMDPNKEIHDLLKEFSRLVI ELIREGPEKGAKCEEIQKDDT KVKGEIFKEVDLSKKQLNIQE NLETLLEVLNALESLSNRIQVE ERNSEREDKVFELTQSNKDKA QRIRKYEPSLQEVWDYVKLPKL RIISFPNEEENSLSLEIFRGRK EHFHSIARDLDIQIQEEQTTPGK LIVKRS�PRHIVIMRAPTPMDHP RAEECGRRARDWQAAPPAAPV RDPLGEASWAPDSEGRK/WNTS KHQRNKLRTRL*EL*HSSRGS VASFLKSVRPRTHQFTQSGYP KLRWRKES
19482	49850	A	19597	381	598	
19483	49851	A	19598	1	1906	
19484	49852	A	19599	493	589	
19485	49853	A	19600	60	261	
19486	49854	A	19601	1423	1831	PRRSANVNLPPQLATLSPGW EERKSVGSPTSPPPRPLRLSA APGSGGAWPEGAWSLD*TAS PAGAPVQRPAGNG/PSALDASH ARALYLQRIPRVTWTPASQPPA PLGPFPLIPPAASHRPQSSFFR RHR

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19487	49855	A	19602	1	1535	MEEKTNVQLPPGQTEQHVEIHI MNFCSKNHHRITPEKPKELTDP FKEAACCCCKLYEIDKKLYRMA EWIKIHKPSICCLQETHLTHKDS HKLKVSITFKDLAVRFSEEEWR LLEEGQREFYRDVMRENXYETL VSVPEGRAVGGGSHADEGQEP AGCG/VSPGPGAAAGGEDPRVLV WRSQGRYGGPRER\GRGASLD GERASPEAA/DGKRALPSRPA QLPSRRYPQAPPG\PTPTDSSCS SGPTGDGVQGSP\PIRISPGNSP L/PRPHQLSEGNPCAWAPAPRDI PKLLATSP*PGHVQANQSRPGA WEPALGRSDQACASGSALCLC ERW\PQQA/APPEEPPASPHPA APTG\PGFWESCGEPGAA\PGKG SAPKPSPLHCLASALRGIL\EGP CASPAWEAPAPAPAPAPARASA A/AEGEDPRPEPELWKPLPQER DRLPSCKPPVPLSPCPGGTPAGS SGGSPGE\APGEQSPGTAAASV Q/VSPAHWPCFS/SPVRYSSGSLP GFSAGEKAQG
19488	49856	C	19603	4	150	
19489	49857	A	19604	148	448	RTRDWSLFLMFQCVRSFFLLV GLWSCWLRSEAADLRGECYSS *GGAGSVVRSSWWVRGLTSFR SETGFTQWIPHWGCRWSCLPVP RCAPALLSPWVVNG
19490	49858	A	19605	136	439	LVHFTFC*LVRLQTLARHSTDW CIYKSLARQKSSPSPHSTQEVQL ASPLTGRQEDCSEPRSAPLHSSL GPTERDSICVAASSVRWTRPGA RFS
19491	49859	A	19606	2	399	SKLQKLKRSLSFKTKSLRSKSA DNFFQRTNSEDMLQAHMVAE ISPSSSPLPAPGSLTSTPARLVCI QVARLMPFRNTSSRSLFC/RCL QPHDSGFLFLRPARPRAHREER NNSRRVALRAVTLTTERLQLHS

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19492	49860	A	19607	1	1262	MPLSYAYKNAETLAGRHTSSW MSRGAYQRRNTRAAGRPEECT DRNWHAGRTRRIWLGQLEERC SDVFGVSFFWWVRGLAGSGAK LQFTTVSVTAHRGSKDQKSEQ KQDLLQKAKEQTIHNVKGDPS ELPLLAPAAACFSLICPRPPHIL LIGPFYRELIGPFYRELIGRLRP GEKSSTAA/VWPRC*AA/RLPGA G/WTAPSAGPAEPTPTWNSRWP ASATRRPGSRRLSLHTSPQAE GAGSGLSQPRKGLPQCSGRLKR SSSAARVGARQRRRRERASEG/ WPACCHSLVPLCPGFGFLEAHSS SPEQTDHEQNCPADIKVMRLA GQPTNARGAANRAQPLHSTSV SHLKAVIFIKIQRQQKNSHFPL FLEMTTSLATGRLRPSWVDYA RPALSVSVSRFSLTSLLELLV ETLGECGLL
19493	49861	C	19608	173	394	
19494	49862	A	19609	1	924	
19495	49863	A	19610	3	689	EVQEELEGVPRGAPHQLHQGP VEHLEAPHQHKFGKKVIYFNY LSELHEHLKYDQLVIPPEVLRIT MRSSRACTRAGRRLPPRHRR GPRCPHSSLASVCNTSKTKIKA NSSPLC*GSQ*RT*ERKACAPRA CSGDPPACRPSARSRGSTT/KGK PVNFDDYGDHHPAIVILKTFLRE LPQPLTFQAYEQILGITC/GGE QPACHSLPPDLTEPPRAQLRRPP LPHGLPACG
19496	49864	A	19611	1749	2411	APSCLVSEHSAGFPQRELQPLL TFQAYEQILGITC/GSCP/AQGW GAWSSDAVPQLLARRPPLPHGL PACGEWGRGELGVKPSGLPSH AGPAWGHQVRTVCAATAHPQD CISPEGAVEEIVGG*GC/TEGQ SQRVLQIWP/SQGVSSLSALVPL NMFTELLIEYYEKIFSTPEAPG EHGLAPWEQGSRAAPLQEAVP RTQATGLTKPTLPPSLMAARR

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19497	49865	A	19612	883	2164	EHRRPMRAQASHEGHRHPMRA QMSHEGYRRPMRVQASHENTG VP*GVQASHEGTGIP*EHRCMP RTQVSHEGTGVP*ECRRPMRTQ VGPMRGTVGP*EHRCMPRGTV P*EAQASHEGHRPMRGTVGP* GAQASHEGHRCPMRGTGVP*G HRRP/DENTGVP*GHRPMPRAQ ASH/REHRC/DEGHRRSP*GHR RPMRAQASHENTGVP*GAQAS HENTGVP*GHRPMPRGTVGP*E VQGV*GHRPMPRAQVSHGHR RPMRTQASHEGHRPMRTQAS HEGTGVP*EHRRPMRGTVGP*E FRRPMRGTVGP*GHRPMPRAQA SHENTGVP*GNR/PYHEGTGVP* ECRRPMRTQASHEGTGVP*EHR CPMRAQASHEGHRHPMSTQAS HEGHRPMPRTQASHEGHRHPM RTQASHEGTASHEGHRPMPRT QVSHEGTGVP*EFRPMP/PGH HPMRTQASHEGHRPMPRVQAS HENTGVP*GHRPMPRGTVGP*G HRCMPRGTVGP*GYRHPMRTQ ASHEGYR/PSHEGTGIP*EHRC MRTQVSHEGTGVP*ECRRPMP TQVSHEGTGVP*GHRPMPRTQ VSHERHRRPMPRTQASHEGTG VP*EHRCMP/MGHRPMPRTQASH EGTVGP*EHRRPMPRGTVGP*EH RRPMPRAQESHENTGVP*GAQA SHENTGVP*GHRPMPRAQASH
19498	49866	A	19613	1	552	VPQDSLQALAGQATPEIPLGL QLHTVLVQEIQELIEAQTRAPGP CAEVRLPAPAAEPAPAWEEAP PERALELEGAPAKDQTNELPEI TA/PYC/EPLALTLKAWLERE VGGRGIDQHSPSQQLPCCP*SW ARWQTCRQRAGHLA WPPVPRC REASLIH*NHSPAAAGPFILLILV YLCAGGA
19499	49867	A	19614	443	991	VDSRPMNLNRLMRTSGRRWTP RPQVDTRP*VNNKTQ*AIRPQ/C GYSPQVPQDSLQALAGQATP EIPLGLQLHTVLVQEIQELIEAQ TDTCSSWMCRSKSTASTSRWS Q/RPAWEEAPPER/GTAGGSSS QGPDRGAA*NHGGAGEH*KK AGRKSSERYACSRQPPPPGM DAGPQLGIQAVCP
19500	49868	A	19615	16	450	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
19501	49869	A	19616	2	477	PRVSRGHSMDMRVPAQLLGLL LLWLRGANDIQVTQSPDSL SVGDKVTITCRASQGISNGLSW YQQKPGQAPTLLIYAASSLQSG VPSRFGSGSGGTDFLTISLQPE DVATYYCLQDYTTPTFTVLQAIT KTPQR/IDV*VCTVLATPPGVIN WL
19502	49870	A	19617	2	675	LPLSSSALPTESGSHLPFSGIMA RPSDPLVKPQRSSKREPCKVHP GTQSDRIYVKIKR/NWAENPRG/ IDNMRVR/RRFKGQDLDAPTLG YGSNKKTKAHACPSGFREVPG VHNVQGSWEVACLMLQQLY CCRGSVHNVFLPRNRQSPSWG KELAQGLSGVHPTPLARAAQL KEN*VRQLMCNKSYCAEIAHN VSSKNRKAIVERAAQLAIRVTN PNAR/SEENE
19503	49871	A	19618	2	527	VWAANMPSRLRKT/RKLT/GHG AATGHGPHRPSTRKAPPGGPR* MPGGPAIHPPGSNFRQNTHPQA YFGK/VG**KHYPT*KRN/QSFL PPTVNL/DKLWTLVQ*NRHRVK CLPKNKTGAAPHHMLMLVRS GYLQSSGERGKLPKASLFFVEGPK FFSRRLREEGLRGVWGGPVSL
19504	49872	A	19619	45	233	
19505	49873	C	19620	95	154	
19506	49874	A	19621	2	241	
19507	49875	A	19622	63	320	RQWGNRLVTA/WSFFSWLSDC EGPGYGTIAEVGQLWGIMAKD LLRHSLASEELALNQLTCHDQ FAQSTRSSARACGSIFCSTTQGS
19508	49876	A	19623	2309	2560	RNREARFYMTTPNFETETKR/WF HERVICALEREREREVTKISRL E RDNRHLVGDISQLKKELDQYL QAISLDEDCNGKRLLQILEA

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19509	49877	A	19624	4994	7008	QWQQPKLTNDNLKFIWNQKR DRIAKTILSQKNKAGGITLPDFK L YYKATVTKTA WY WYQNRHI DQWNRTEPSETIPHIYNHLNFD KPDKNKKWKGDSL FNKWCWE NWLAI CRKLKLD PFLTPYTKIN SRWIKHLNVRPKTIKILEENLGN TIQDIGMGKDFMTKTPKAIATK PN*QMGSNILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEV LAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLS NFSKVS GYKIN VQKSQAFLYTN NRQTESQIMSELPFTIASKRKY LGIQLTRDV KDLFKENYKPLK EIKEDTNKWKNMPCSWVGRINI VKMAILPKVIYRFNAIPKLPMA FFTELEKTTLKF IWNQKRARIA KSILSQKNKAGGITLPNFELYY KATVTKTA WY WYQNR YIDQW NRTEPSETIPHIYNLIFDKPGK NKQWKGDSL FNKWCWENWLA ICRKLQLD PFLTPYTKINSRWIK DLNVRPKTIKLEEDLGITIQDI GMGKDFMSKTPKAMATKDKID KWDLIKLSFCTAKETTIRVNR OPTKWEKIFATYSFDKGLISRIY NELQQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKHKMKKYS SSLAIREMQIKTTMRYHLTPVR MATIKNSGNNRQ

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19510	49878	A	19625	1	764	GSSEKRRKFKTGNQKLSMEVEK NQQMRSLSLYQQRVEGSKCAV RRKGGSPKPKAFLAAAEKFLN VPVMRSASHEQLVLTGDPNKT LPGKSRLSGTDSPRACSTFPJW ATKJVTEMQVQLFAACRVQLIK HPRPSAARTAMEVLESGEQGV LQWDRKLSELSEPGDGEALMY HTACQGHEEQVWEEALQLGL RSGILLNHWKRQLVGGAGILRS AQLHSPYHHQMISLVSPSPAV MAVMENDDICMVLVCVKVMDE PNHILDAISEHQIPSLEDQWFSE CALWTSKAYENLVERHILGPHC RPTELETLGISEDDIDHNPYLDF PGVAGLGSRRNVKERGWLSEM KKEGDIFMKIQG*AICPTSGPAE GLPPPTPVPHVPDRPCGT*GP/PP SPGSDSSVPACGPTAARAPRSP APPWRCGPRWAEDVLLTGLCK QQIAEPAFRLQFWWPI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method in US 5,400,217	SEQ ID NO: 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
19511	49879	A	19626	1	1430	MNGTAEGQHPVWHSTFNGEPQ SLSSSVRVKNQGRDQAEIGFQ GNGSTVPAAQARTIARARGSGS GGGDALQGGGAGAGPGATKR TARLLARGLRRALRPDGRGV LGAGAGSSQRRGGRRRKMETH ISCLFPELLAMIFGYLDVRDKG RAAQVCTAWRDAAYHKSVMR GVEAKLHLRRANPSLFPSLQAR GIRRVQILSLRRSLSYVIQGMAN IESLNLSGCYNLTDNGLGHAFV QEIGSLRALNLNLCKQITDSSLG RIAQYLKGLVELELGGCSNITN TGLLLIAWGLQRLKSLNLRSCR HLSDVGIGHLAGMTRSAEGLP GPGAHAHATGLPEAHRSFSKAHL PRADGPEAPQPQLLWGNLGRW PPAPVAHQPAHAQPCAPCDNI SDTGIMHLAMGSLRLSGLDVSF CDKVGDDQLAYIAQGLDGLKS LSLCS/RRGLRRAALRPDGRGV LGAGAGSSQRRGGRRRKMETH ISCLFPELLAMIFGYLDVRDKG RAAQVCTAWRDAAYHKSVMR GVEAKLHLRRANPSLFPSLQAR GIRRVQILSLRRSLSYVIQGMAN IESLNLSGCYNLTDNGLGHAF/R AGDRLPARSQPEPLQADH*QQP GPHSPVPQGP/ARCWSWEVAAT SPTLAFCSPPGVCSASRALTSAA AATFRMWDRAPGRHDAQRGG GLPGPGAHAHATGLPEAHRSFS
19512	49880	A	19627	293	1520	TTMDGSHSAALKLQQLPPTSSS SAVSEASFSYKENLIGALLAIFG HLVVSIALNLQKYCHIRLAGSK DPRAYFKTKTWLGLFLMLLG ELGVFASVAFAPLSLIVPLSAVS VIASAIIGHIFIKEKWPKDFLRR YVLSFVGCGLAVRG/TYLLVTF APNSHEKMTGENVTRHLVSWP FLLYMLVEIILFCLLLYFYKEKN ANNIVVILLVALLGSMVTVTV KAVAGMLVLSIQGNLQLDYPF YVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYLSTTIAIT AGAIFYLDFIGEDVLHICMFAL GCCLIAFLGVFLITRNRKKPIPEP YISMDAMPGMQNMHDKGMTV QPELKASFSYGALENNDNISEIY APATLPVMQEEHGSRSASGV RVLEHTKKE

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19513	49881	A	19628	751	2034	VSSPTSLGCMRQKEYRIPKLL TNMPFLGSPSLLALRSCHPTG RTCSA/SQVALFCLAAHRVSQIG ALLAIFGHLVVSIALNLQVSFHI RLAGSKDPRAYFKTKTWLGL FLMLLGELGVFASYAFAPLSLI VPLSAVSVIGKTIIGHIFKEKWK PKDFLSKFVLSFVGCGLAVVGT YLLVTFAPNSHEKMTGENVTR HLVSWIILFCLLYFYKEKNAN NIVVILLVALLGKLTVVTVKA VAGMLVLSIQGNLQLDYPIFYV MFVCMVATAVYQAA*VSQAS QMYDSSLIASVGYILSTTIAITA GKGFYLDFIGEDVLHICMFALG *VLAFLGVFLITRNRRKKPIPFEP YISMDAMPKGVNMHDKGMTV QPELKASFSYGALENNNDISEIY APATLPVMQEEHGSRSASGVY
19514	49882	A	19629	19	933	QSARPSLKRARSQRGRPLPSRA LVFLFLFFFFNFPLPIHTQPSAH KDMTTNAGLPHYPWPQH/LRL DNFVPMNDRPTWAYTGLGLFSV TGLRSWTTWAVVQGRAPGLA PIGDFGRATVPCCWVLQWCGFI HLVIEGLVPFSNYERPFCGDQSL LYSQLWKEYGQGETARYILGV TNFTVICM/ETITSFA/WGEPFSL WVVIVFLLQHPLARFILQLVVS VGQIYGDVLYFL*RATPTDFQ HGKPGPTPLLLPGFSVFHEMP LWLVPAPGSPCLDA/V*KHPQ LMPQSNANNAKGPQPKSKK
19515	49883	C	19630	113	257	
19516	49884	A	19631	143	330	HHGPVFPFRGLIS*HSLHCPCPT PGGKNVFFFCFCEYFLKLAGIETT NCSADKRGKKVCCLIPR
19517	49885	A	19632	3	432	
19518	49886	C	19633	112	192	
19519	49887	A	19634	1	4410	MARPLALPLTGMSAPGSSLTITP HTPSHPRSPSTPDTVSHPRSPSTP DTVSHPRSRYPDTVPPTLPVY TRHRVPPTLPVYTRHRPHTHAPG IHQTMCTPHAPGLHQTPTCPHTA AGLHQTTPSHPRSPSTPDTVSHPR SRSTPDTVPPTLPVYTRHRVPPT LTVYTRHRVPPTLPVYTRHCPT HAPGLHQTMCPTPRSRSLPDTV PPTLPVYTRHRVPPTLPVYTRD RVPTLPVYTRHRPHTHAPRLHQ TPSHPRSR

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19520	49888	A	19635	1	444	
19521	49889	A	19636	3	1017	SSRPVPRPRAARLSAMSSTQFN KGPSYGL\SAQ\VKNRLL\SKYD PQKE\AELRTW\IEGLTGLSIGPD FOK\GALKDG\TILACTLMNKLQP G\SVPKINRSMQN\WHQLENLS NFIK\AMVSYGMNP\VDLFEAN DLFESGNMTQVQVSLALGG KRPKTKGAAEGGLDIGVKYSE KQERNFDDATMKAGQCIVIGL QMG\TNKCSAQSGMTAYGTRR HLYDPKNHILPPMDHSTISLQM GT\NKCASQV\MTA\PGTRRHI Y EYQAGNPTSCDNFSM\SLQ\M GYTQGAQTQSGQVF\GPRPDI *TPSTCPOGTIADGAPSGTG\DA CPDPGEVPEYPPYYQ\EEAGY
19522	49890	A	19637	1	479	MQGLRVSHSTFYTLIPEVTENP HRLDFHWFLSAQLERVASGTL KKKESPPRPKVLGSARWDLPV/ PPGW\CNSTALQ*SPRSDQV*SE RGMEAFFLPMPS\ESVASVCCRF SPWTSQKPOLSTSRDKLQGKR *WFSTGVWAS*DHS*ERRCSQC PKTTCW
19523	49891	A	19638	2	501	FVPEERSSETALQRCSLPPGRRRA APDPGLQGLRGS\LGSGSSELES RKAKLRAAEGLRRKTT\TEINQRD TADRCTRGHH*SPGESPPKPSAF SL*LSVPRSGKLRFLRSPRREPA AN*SHRLRRHREKKCFHPFTL NLIASGTSLEGGGVAPTWTSTGR SQRALPSTL
19524	49892	A	19639	1	1122	RFLILINHAVFEYQDIFVASFPPI FFNIHCRGEGEREKG\GAGKDRT PPSTLLCGSGHLLPPLASRRP PRCACCLPGGPLSSSALEAG*Y WRFPKLSG*KRSHTPWVPQPOQ PLPNPSPGKWWASSEALQ/GT RA*RGIAELTHLLRLPARRGTQ RPA\PGHRAGASPOFRREASSRG PGLRPRPGRTRELGFPKRRVWA TAASWPRGT\EPCAA*RRRRRR RRARGRELS\PRSTWSSDTESTF ALSCDPS*PRHQSVPKGRVGS KGKLANKGFFCPTWQRP\IRVAS VDMELLHFV\PKRALPGFTIAISF LSSAPPLCPWYSGSNPWLNRPL KPRLAALFQ\RSAA\PLHFSGAA SLQVGERRQ\IDFRVSAGA

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19525	49893	A	19640	14	618	GNENVKSGRKTSLSPFVLSDFT ASSALLASDSSRWMSLQSASEC \PGRAGSGPGYG*PVSEVTGG PLSAHTHSSL*TSQRCGCPGPE HHGAGPFP*GPGLKDVSGRGG NGCWGRRKPAHMGGLGPAT PLQFPFRPSPPPPLGPPQPPPP SPPLGPASSPP/CLPHRPPPPPP PSRCVTAPCVTAPGAPTAAAA RRH
19526	49894	B	19641	42	121	
19527	49895	A	19642	1	153	
19528	49896	A	19643	104	355	
19529	49897	A	19644	459	988	DPRTMNLAIISIA/LLTLVQVSR GQKVTS/LTA/CLVDQSLRLDCR HENTSS/SPSKYEFSLTRET/KKH /VLFGTVGVPEHTVYRSRTNF/TS KYNMEGPLTYSAFH*ARTRGTL QVLQHFHQFALSPPIFLSRNV/T VVQRTNWVK/EGI/SLLAQNTS WL/LRLLLS/LLQ/ATDFMSL
19530	49898	A	19645	1	950	
19531	49899	B	19646	55	1459	
19532	49900	A	19647	1	165	
19533	49901	A	19648	183	700	PNGNQPPRETQRI/SGIQR/LGT AVASSGGSRLSPRSASAEPAQG AAARRA/PGPAGRCRAARGAG AGSARRLP*APAHAPPEQGRR/ SRTARSR/AAQPPPPSQPSQOL GPRPSQGA/PQRRGPSSPGPRAG CRAQ*EALTPRLWRSSRTSSR GLGPHVRRGGSFKIPT
19534	49902	B	19649	71	264	
19535	49903	A	19650	3	810	GVSPCWPGWSRTPDFGSPKCP PIRASPAGELQALSSTVTTPYW GILVTA/VFPH*GLRPRQCRQDH PAGRQGP/PGPEVPEILGQSGCT DRTWSKAGGRTQAPGPRSRAG RRVSGQEIAPGLGCRHGG/V GAPWTP/EAASPLTATEPSPH/L QAPCGY/MLSVSPRRRYRGA GDQKV/KMLKFA/CLDYWQF LCLQPLHGAYKRDS/DMTWIW GLLPEVTGAAGT/SPNVHTSGR FFRACVFCPVHTLVKKEPHPGQ QEIHMEPSWSP

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19536	49904	A	19651	258	1378	REILSLDRLPGATPNQALSAEA ACPKGQTSLLCGAMGIQGLAK LIADVAPSAIRENDIKSYFGRK VAIDASMSIYHFLIAVRQGGDV LQNEEGETTSHLMGMFYRTIR MK\ENGKPI/YKSGELAKCSEL RAEAEKQLQQAQAAGAEQVV EKFTKWLVKVTQHNDKCKH LLSLMGIPYLDAPIEAEASCAAL VKAGKVPVATEDMDCFTFGS PVLMQHLTASSDYCKSIWSIGP KRAVDLIQKHKSIEEIVQRLDPN KYPLPENRLHKEAYQLFLEPEV LGPESVELKWSPENEELVKFV CGEKQFSEERIHSGVKRLRTEK GGGEPRGP/DWTQPGRASPTKR PDHQEDQHTRSRSSESGH*GWL
19537	49905	A	19652	1040	2322	LPACPPASTPASTMSIMVTQKS YKVST/SRWSSGPQAFGNCSYA RGPACISSLSFSRVGSSIFRGVL GGSYGGASGMGSITAVTVNQS LLSPLNLEVEPNIAVCTQEK/T LNNKFASSIDKVQFLEQQNKML ET/ESYNSLKQQLETLGLERLK LEAELGNMPGLVEDFKNKYED EINKRTEMENEFVLIRQYVDEA YMNKVELESCLEGLTEEINLLG QLYEEIEIKLQSQILDTSVVLC MNNSHSLDMSHAEVKAQYEE MANHSQAEAESMYQIKYEELQ TLAGKHGDDL RHAKTEI/S/EM NQNGAKQDMA/*QLHEYQELT NIRLALDIKITYRKLLGEESQL ESGMQNMNIHMKTTSGYAGGL SSAYEGLTSPSLSYGLGSSFGSG MGSISFSHTSFTRAIVVKKIEIHD GKLVSSESDVLPK

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19538	49906	A	19653	1040	2322	LPACPPASTPASTMSIMVTQKS YKYST/SRWSSGPQAFGNC SYA RGP GACISLSFSRVGSSIFRGVL GGSYGGASGMSGITAVTVNQS LLSPLNLEVEPNIAVCTQEKYT LNNKFASSIDKVQFLEQQNKML ET/ESYINSLKQLETLGLERLK LEAELGNMPGLVEDFKNKYED EINKRTEMENEFVLIRQYVDEA YMNKVELESCLEGLTEEINLLG QLYEEIQLKLSQILDTSVVLG MNNSHSLDMDIIAEVKAQYEE MANHSQAEAESMYQIKYEELQ TLAGKHGDDL RHAKTEI/S/EM NQNGAKQDMA/*QLHEYELT NIRLALDIKITYRKLLGEESQL ESGMQNMNIHMKTTSGYAGGL SSAYEGLTSPSLSYGLGSSFGSG MGSISFSHTSFTRAIVVKKIEIHD GKLVSESSDVLPK
19539	49907	A	19654	152	207	
19540	49908	B	19655	75	402	
19541	49909	B	19656	1	2319	
19542	49910	B	19657	1	1341	
19543	49911	A	19658	198	1118	LHAPNSLHHHLPRDLL*LLPLPL QHRVSDPGLHSALRPMEEHRA QS*QPSAPEDAVQA*WGHGGH SPGPDRA GCHHCRGDQERVST HHVLPVCHHPDDAYGGCGAG WNPDL/PQGMRSWMSPKIRPA NWTRTSWWALPQAPGLSPGAQ SWPSFVPRTPPTTPTGTCTPTPSW *SWRSTSRSTSSLNPFTESLKNS LRTSKPFGWSQSAMATPCLLP PASRVELWPETWPLGQGHATS SQWKCVPERKL*QGGEAGGEQ LGREPKSPSPSFLTGTQREQKSP EEYCSLLVPLQYFGSRGTHADL LHG

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19544	49912	A	19659	1	2707	MPGPHPASASCPPRLFTPRRRAF CPLRICAPLAAAAFCPPRFLPHT RRRAFLLLCRRGFLPPPCLGGG LAAAFPHPLPFLRPHRRGFLP HRRRGFLPRLGFLPAAAFYPP PPRVFARRGFVPPSPRLFARRA FCHTPPAAAFSPSAAAFACPTA DTAFCTLAALAFRRGFLPPRC RGFLPLRHRSLPHRRRGFLPT AAFCHRGFLATAFYPPRLFAP RCHGFLPPCRSDFFAAAAFPCR RRGFLPSPLFAPAAVAFCPRH RGFLPLRLFAPVTAAFCHRDfL PPPPRIFVPAATALRAGAADS ASSTGVLAARALRGPCGLHRV ALPVEAMGEKKEGGGGDAA ATEGGTGAASRALQCGQLQ KLIVIFIGSLCGLCTKCAVNDL TQQEIQTPPAKPAKPAQSTRQ PSQPSHPASQASQTSQPAKQPA SQASQPAKPAKPPSQPSQPSHR ASQASQATQPERPASQPASEPS QPSLPASQASQDRQPAKPAKPD SHPRQPSQP/YQPSQASQASQA SQPAKPSRQPSQPRQPSQLASQ ASQSTQPLKPAKSPVQQSQPSQ PASPDQSASQASQATQPAKPAK PPSQAAQPAKPAKPPSQACQP PSQRAKPAKPARQPSQPSQSSPP ASQPSQACQPSQPGSQASQASQ AAKPGMPAKPARQPSQPSQPAS QARHASQAIQPAKPAK*PSQTS

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19545	49913	A	19660	1223	2286	RQCFKATEQPPAIHHPSSQPSRQ PSSQPPIYSPICGRKSGIQPKFQ LNG*MVNG*MDEISRERHEWP CNYQVRPKAGEKQPGAEANRE TRPEGGTP/RGEGRGQGPATRR QKSTPEAGPSDLEKQIARQEAP AGTDEIERQQARPH*AP*KIPVE WVNGEWLNGRMPGDPHEWQC NYQPAIQPAIQPANQLSIHNLW TQFRHSTKIPVEWVNGEWLNG RMPGKHHEWQCNYQPAIQPAI QPANQLSIHNLWTQFRHSTKIP VEWVNGEWLNGRMPEDHHEW QCNYQPAIQPAIQPASQLSIH MWTQFRHSGQIPVEWVNGSRL HGRQQGIFMHGNATSSHSPSIQ PAIQPAIQPANQLSIHNLWTQFR HSTKIPVEWVNGEWLNGRMRQ NIMNGNATISHSPSIQPAIQPAIQ PVNHLSIHNLWTQFRHSTKIPV EWVNGEWLNGRMPGKNHEW QCNYQPAIQPAIQPANQLSIHNL WTQFRHSTKIPVEWVNGEWLN GRMPGDHHEWQCNYQIAPML QSNRTAAASHSPSIQPAIQAAIQS ATHLSIPNLWTQVRHSTKIPVE WVNGEWLNGRMPGRDMNGH ATIRYGPKEKNRAPRQTEKQ GQKGAHQRRREGKARAGNEETE KYRSRAIRPRKTDASRSSRGH RRNRKAASAATLGPIEDTNQNK LHVRDTGLEVKAIISIQPGTLM
19546	49914	A	19661	39	599	GASPNQGNRPHARQRAPPG/G /PPGEPERRAPLPSGHGEPCHRR PPPPFPQP/AGTQKPLLQPGGG *PAENAPTAALGSPAPPRGCQA APPPRSAGRPDLPTLAGPRPAP A\PPPSA\PPPPPSGAPSR/PAAG RQRLSGVSSGPSLGWW*VGRG RGLPFAQIAGHQVGP RRRTTP AGRKPRSPAGPR
19547	49915	A	19662	39	599	GASPNQGNRPHARQRAPPG/G /PPGEPERRAPLPSGHGEPCHRR PPPPFPQP/AGTQKPLLQPGGG *PAENAPTAALGSPAPPRGCQA APPPRSAGRPDLPTLAGPRPAP A\PPPSA\PPPPPSGAPSR/PAAG RQRLSGVSSGPSLGWW*VGRG RGLPFAQIAGHQVGP RRRTTP AGRKPRSPAGPR

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19548	49916	A	19663	1	379	YFPHTAIRYPPLHNRQDPLKDL VSLACDPASQQPGPLNGSGQLK MPSHCLSAQMLAPPPGLPRLA LPPATKAATTSEGGATSPSP/S PGIWDKGLLPSPLLHRRPNR GQHSRPPAHVFGGKLE
19549	49917	A	19664	3	285	
19550	49918	A	19665	2	1556	RLEFPGRRFRSAPAPAGPAPPA APGMYSSPLCLTQDFEHPFIEAL LPHVRAFAAYTWFNLQARKRKY FKKHEKRMSKDEERAVKDELL GEKPEVKQKWASRLAKLRKD IRPECREDFVLSITGKKAPGCVL SNPDQKGKMRIDCLRQADKV WRDLVMVILFKGIPLESTDGE RLVKAACQGHVLCVQPHHIG VAVKELDLVLAIFYRERDAEQ SGSPRTGMGSDQEDSKPITLVT TDFQESFVTSQVFSVTELIQVSR TPVVTGTGPNFSLGELQGHLAY DLNPASTGLRRTLPTSSSSGSKR HKSGSMEEDVDTSPGGDYYS PSSPTSSRNWTEDEGGISSPV KKTEMDKSPFNSPSPQDSPRLSS FTQHHRPVIAVHSGIARSPHPS ALHFPTTSILPQTASTYFPHTAIR YPPHLNPQDPLKDLVSLACDPA SQQPGPSWYLG*QRSSSLAPSPS SQESQGAAPAGPRFRWKIRV NKNTPADSQPGQKDKTHRRTH SGGKEKTKAE
19551	49919	A	19666	1	477	
19552	49920	A	19667	1	440	WTQDM/EGGISS/PVKKTEMAK SPFNSPSPQDSPRLSSFTQHHRP VIAVHSGIARSPHPSALHFPTT SILPQTASTYFPHTAIR/YPPHL NPQDPLKDLVSLACDP/SSQQP GP/SYSPPDTPANR/SFVGLGPR DPAGIYQAQSWYLG

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19553	49921	A	19668	2	1963	CPTGFEHGSPCARRTPTGRVSV TRCRRRAWGSLRVSVCGPRAQ LQAEVLQEEQGGVLCVIVMP LTPGRTPLRPRGRALCNGRGGV WGGGSGPRGLLPAQAPGDPEV CKFRFLDRCFPPYAGPSDL.SLR GRAVGPPSASLALL.TSRL.SGLQ DEFHPFIEALLPHVRAFAYTWF NLQARKRKYFKKHEKRMSKDE ERAVKDELLGEKPEVKQKWAS RL.LAKLRKDIRPECREDFV.LSIT GKKAPGCVLSNP.DQKGKMRRI D.CFRQADKVVRLDLVMVILF KGIPLESTDGERLVKAAQCGHP VL/CALKPQHIGVAVK/ENLDL YLAYFVRERDA*QSGSPRTGM GSDQEDSKPITLDTTDFQESFVT SGVFSVTIELIQVSRTPVVTGTGP NFS.LGELHAHLAYDLK.PASAGL TRTLSTSFSSGNKRYKAGSMEE YVDSTPWGDD*T*PSSPTSSSRN WTE.DMEGGISSPVKKTEMDKS PFNSPSPQDSPRLSSFTQHHRPVI AVHSGIARSPHPSSALHFPTVTSI LTPDGPSPPTFPHTAIRYPHLPN QDPLKDLVSLACDPA/SQQP.GP LNGSGQLKMPSHCLSAQMLAP PPPG.LPRLALPPATKPATTSE GATSP.TSPSYSPD.TSPANRSFV GLGPRDPAGIYQAQSWYLG
19554	49922	A	19669	332	551	ESWLGRGHQPPPGLFHSPKPS SGTAVLPAWRPPSPGPGAGDD ASPS*AGPGAGANPGA*QRS ASGEKGS
19555	49923	A	19670	1614	1673	
19556	49924	A	19671	72	227	EEFPMGHTA*WSCEKRATILQI QEW*IQQLAPCAWQSHRHST RAHESSHG
19557	49925	C	19672	1	604	
19558	49926	A	19673	653	889	VYPQT.NWKQNTGTRV.FIAALF TM.VKGENK*PSMGEW/KQM WSIHTMERHAAIKRIEAQVYAT M*MKLK.SMLLLERNQT

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19559	49927	A	19674	75	1619	EVSIQAQTMTWTADEIAQLCYEH YGIURLPKKGKPEPSHEWTLA AVVKIQSPA\DKACD\TPDKPVQ VTKEVVSMTGTGTCIGQSK/M* RKNGDIL\NDSHA\EVIA\RRSFQ RYLLHQLQLAATLKEDSIFVPG TQKGVWKLRRD\LINVFFSSHT PCGDASIIPMLEFEDQPCCPVFR NWNANSSVEASSNI.EAPGNER KCEDPDSPVTKKMRLEPGTAA REVNTGAAHHQSFGKQKSGPIS PGIHSCDLTVEGLATVTRIPGS AKVTDVYRTGAKCVPGEAGDS GKPGA\AFHQV\LLRVKPGRG DRTRSMSCSDKMAR\WTVLGC QGALLMHLLEPIYLSAVVIGK CPYSQEAMQ\RA\LIGRCQKVIS AL.PKGFVQVELKIL.QSDLLFEQ SRSAVQAKRADSPGRLVPCGVA AISWSA\PEQPLDVTANGFPQG TTKKTIGSLQARSQISKVELFRS FQKLLSRIARDK\WPHSLRVQKL DTYQEYKEAASSYQEA\WSTLR KQVFGSWIRNPPDYHQFK
19560	49928	C	19675	45	140	
19561	49929	A	19676	3	354	AKIKTG\YK\REHINLGCMDMDFDI VGPSIRGALVLGYEGWLAGYQ MNFETAKSRVTQSNFAVGYKT DEFQLHTN\VLLNLERTCFLTG PTPTPPPLSWLPGTTFSLTWAM TGRYTINSQ
19562	49930	A	19677	1	983	AARSAPLPGSAPCLRVAAPAVA ASEPAATSSSEQKMAVPPTYADL GKSARDVFTKG\YGFGLIKLDLK TKSENGLEFTSSGSANTETTKV TGSLETKYRWTEYGLTFTTEKW NTDNTLGT\ETV\EDQLARGT* SLTFDSSFPNT\GKKNAKIKT GYKREHINLGCMDMDFDIAGPSI RGALVLGYEGWLAGYQMNF* DCKIPE*PQSNFWQLANKT\DEF QASR*M*ND\GTEFGSIYQKV NKK\LETA\VNLPWTA\GNSNTR FEIAAKYQ\WDP\DACFSGKVNN SSLIGLGYTQTLPKPGIKL\TSLAL LDGKNVNA\GGHKL\GLGLEF QA

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19563	49931	A	19678	551	831	CHPSSHVLCAPASLSDHQWPP ALCPSSRPQ/PCALPWSGT.LSSR PQPCPTHFSGIEA*LCLPLVTLQ G*LPLPAPQHLVPPCPSTCTPTM LKL F
19564	49932	A	19679	47	980	VCQYCTARMADFGISAGQFVA VVWDKSSPVEALKGLVDKLLQA LTGNEGRVSVENIKQLLQCLVP GSTTLHSAEILAEIARILRPGG CLFLKEPVETAVDNNSKVKTAS KL/CSALTLS/SLVEEKELQREP LTPEEVQSVREHLGHESDNLLF VQITGKKPNFEVGSSMQLKLSI TKKSSPSVKPAVDPA AAKLWT LSANDMEDDSMDLIDSDELLDP EDLKKPDPA SLRA\ASCGEGKK RKACKNCTCGLAEEL/EKEKSR EQMSSQPKSA/CGNCYRGAMPS GCASCPYLGMPAFKPGKVLLS DSNLHDA
19565	49933	A	19680	29	1270	FPFWPAVFQVCYCTARMADF GISAGQFVA VVWDKSSPVEAL KGLVDKLLQAF/TPGNEGRVSV ENIKAAVAAILPTKNPSFGHYFV Q/CLVP GKAPLWHS A*DFWAG NPPGFLRPGWMFFFLKEPVETA VR*Q*AKWK TASKL/CSALTLS GLV/EKLKELQREPLTPEEVQSV REHLGHESDNLLFVQITGKKPN FEVGSSRQLKLSITKKSSPSVKP A VDPAAAKL/WTSLANDMEDD SMCFCGCSLTHRWPLEHVQV E/IMMDQPKRTRVDTVFTPT PKFPRSASPASHFSIKQKT/TRP VSLIALNTL/QDLIDSDELLDPE DLKKPDPSL LRA\ASCGEGKKR KACKNCTCGLAEEL/EKEKSR QMSSQPKSACGNCYLGD AFRC ASCPYLGMPAFKPGIEKVLSD
19566	49934	A	19681	3	405	QDFGTRALAAVQIKNGGSWWC PPVSLAAGVGRPQLGRPYVRV APHGQVIGLSFAMWKTLTFFR GASPGVGSQAMLKCV A*SPHH WRARRDPEFIAYPHLR/IRTKP FPWGDGNHTQYITPHVNPLS NLATED

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19567	49935	A	19682	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLKLHDERVLVAF GQRDGI RVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYP VSIRFGRPRLTSNEKLMASMF HSIKFVVLADP/RQAGIDSLLRK IYEIYSDFALKNPFYSLEMP
19568	49936	A	19683	1	2034	
19569	49937	A	19684	202	453	RRLWRGSCPRCGGKARDGMG VRGR/YSEG/REKV*FGGPPRGS TWPLCGRWRP/PA/PSAPLRWS AMCPTNSDAAGACAAAVRCG
19570	49938	A	19685	269	326	
19571	49939	B	19686	98	562	
19572	49940	A	19687	1	2223	
19573	49941	A	19688	374	1107	IPVSRQGS DWRFFSVYVVKNA GGLIYQLDSYAPTGLRLEKTFAS YPLDLAGSS*HDERVLVAFGQR GRHPEWGHAVLAINGMDVNG RYTADG/KEVLEYLG*PLLNYP VSIRFGRPRLTSNE/KLMGLP CFHSLFAIG/SQACLPGTREASR HLKILGRQDTFKLHVCYQTLTG IKFVVLADP/RQAGIDSLLRKI YEIYSDFALKNPFYSLEMP IRCELFDQNLKLALEVAEKAGTF
19574	49942	A	19689	119	288	ALHLNSSDVHQKLLPVQSLKKS *GRHRNNTCNQVRVHA/SSTSRE FFTCLNKNDILKP
19575	49943	A	19690	92	317	KSVGPNFPLPSGNMNE DN*M H*HPFSSVTQAFRLRVLQSIQR PL*TFNPSSSLFSSISGQSNFPL GVAVLRP
19576	49944	A	19691	27	389	NFKTLKNN*YK*MCSQEIKLS *KLIRFWYIEIHAFFPWAHGVVF CVAQEFC LPTVLLPVPRLLIM KDMVRRILQELRHTEQVQRAYA LNCGE GATVSYEIQIRVLR EFG LADAAEELLQN

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19577	49945	A	19692	313	2255	KTPQVQQPFPRQTGAAGAGAP SGRSGERAAGRAGPSGGSGGG QDSAHAGEAYVRGILLRKTQ CLKDYFLTYYTSSKVVPVKVPC RQVLTDKCSLPRSSHRNARTV SNDFPRKSCSRERCTHCMRPPE GRRPPNGNMNSWKWPSGDESK WRRGEPGAVPEPEPLTGEERAA AAAVGGGWPGVLAPVRTAVL VAAAAEATAAVPAAAAAAGG ASGHCHNPVMQGRNLSHRFLL PLHHSPLYQFGTSSYSQQGYGCE SKLYSLDHGHEKPDKKKRTS GLATLKKKFIKRRKSNRSADHA KQMRRELLSGWDVRDVNALVE EYEGTSALKELSLQASLARPEA RTLQKDMADLYEYKYCTDVDL IFQETCFPVHRAJLAARCPFFK/I TAFFLTRVWGRDNNGHQYSW Y*YAHVFCFVTLPLYRRVWEW EDSRFQNVLDLVQLSEGIWEHQI PLM*DMRGTLI/DMCYDYDVVL SFSSDSELVEAFGGNQNCDEE LKAHKAVISARSPFFRNLLQRI RTGEEITDRTLRTPTRIILDESIIP KKYATVILHMYTDVVDLSVL HCSPSVGSLSVQALVAGKPN MTRAEEAMELYHIALFLEFNM LAQGSCWECIPNDEANQEQR EGSRKWAPTREGSKGRSHASA
19578	49946	B	19693	4	3923	

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19579	49947	A	19694	1	2154	MEYYAAMKTKEIMSFALTWIE LEAIVLCELTHVLSSELMQKQKT KYHMLSLGSPVPTFALWNFDV AQDFHHFIENARSSQCRGRPRM TGAGAGAPSGRSGERAAGRAG PSGGSGGGQDSAHAGEAYRVR GILLRKTQCLKDYFLTYYTSS KVVVPVKPCRQVLTIDKCSLPR SSHRNARTVSNDFPRKSCSRER CTHCMRPPEGRPPNGNMNSW KWPSGDESKWRRGEPGAVPEP EPLTGEERAAAAAAGGGWPGV LAPVRTAVLVAAAAEATAAVP AAAAAAGGASGHCHNPVMQG RNLSHRFLPLHHSPYQFGTSS YSQQGYGCESKLYSLDHGHEK PQDKKKRTSLATLKKKFIKRR KSNRSADHAKQMRLLSGWD VRDVNALVEEYEGTSALKELSL QASLARPEARTLQKDMADLYE YKYCTDVLIFQETCFPVHRAI LAARCPFFK/ITAFFLTRVWGRD NNGHQYSWY*YAHVFCVTLPL LYRRVWAKEDSRFQNVLDIVQL SEFGTPNSLSDVDMRGLFDYM CYDDVVLFSFSDSELVEAFGGN QNCLDEELKAHKAVISARSPPF RNLLQRRIRTGEEIDRTLRTPT RIILDESIIPKKYATVILHMYTD VVDLSVLHCSPSVGLSEVQAL VAGKPNMTRAEEAMELYHIAL FLEFNMLAQGSCWECIPPNDIA
19580	49948	A	19695	1	163	
19581	49949	A	19696	1	207	
19582	49950	A	19697	1	579	PTRPGQAGSSSAMAQRLAKR VL/SKLQSPSRARG/PCAGSPGG LQK/RGHARVTVKYDRPSLQR RLDVEKWIDGPLEGLYRR/QEA D/MPMRSNIDELLE/LESEEEERS RKIQGV/LRDS*KSCGKPVEDFI QELLAKLQGLHRQ/PGLRQPSPS HDGSLSP/LDRARTASPLTLA LFPGPERRPALLCVLSCL
19583	49951	A	19698	2	151	PPSPPLPPPLPAPSLPLSLPSF DLQPPVLDLTGV/LF*LCKRKI SVS
19584	49952	A	19699	2	310	

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19585	49953	A	19700	1	688	LTWMTERVDFDTALLPLEPLPP GTLPPQSPPTPPDEAMASLLKK ELEQMEDFFLDAPLLPPSPPL PPPLPPAPSLPLSLPSFDLPQP VLDTLDLAIVCRNEAGQEV GMPLPPPPQAPSFLPPQPSR WGPLTHIPGQPTRGGPAKQKEE RPRNKSAALKVTPSGKRARG*S PWRAKSGLEGTEFASLKERA\ ESVEREIYVKDILLIEVYKARS QRTSC
19586	49954	A	19701	3	902	AAMATPARPGEAEDAERPLQ DEPAAAAAGPGKGRFLVRICFQ GDEGACPTRDFVVGALILRSIG MDPSDIYAVIQIPGSREFDVSR SAEKLALFLRVYEEKREQEDC WETFGGAGGEASPA*RRSSSSS GTRRWTRWTL*LGSSATATCW PCGESDRQVLDLD/LGSTNARS SCARGRAGSGTCQGPSSWGPR G/CYSWYKGPCTCFKCGSRTH MSGSCQDRCFCGEEGHLSPY CRKGIVCNLCGRGHAFACQP KAVHNSVAAQLTGVAGHLNTR LPARVNTQASLLKCPKLF
19587	49955	A	19702	1359	1981	QSPFNDTLPGVPVSA*LHSLPPE HHPKSG*GVAKSPVPYPAGILL VCNNCAAYRKLLAQTPSVRK WALRRQNEPLEVRLQRLERER TA/KKSRRDNETPEEREETDEQ RARRLQRDREAMRLKRANETP EKRQARLIREREAKRLKRLLEK MD/MMLRAQFGQDPSAMAAL AAEMNFFQLPVINGVELDSQLL GKMAFEVQNSSSLH
19588	49956	A	19703	1	1875	

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19589	49957	A	19704	1	673	MSAKDGTCTLQDCMYKDVQK DWPGYSEGQQLLKRVLVRAH NTQRQRQNERSDTRPCQRAAP RRFSHGTRRGTLPLASPDRAARA PRTGHCRTRQRLDRTGGGFPL TGAWAMLADWIHEGTPSRGRS DNDEPSAGSVGGLRQHGPGR APKLTTTKVKALASPLGQKIA ALCLGLTAQGLNIMDNPGSLAI HVHPDSVLTTRKTNPCTHIWGFT QREPLVANMSAKDGTCTLQD CMYKDVQKDWPGYSEGQQLL LKRVLVRAHNTQRQRQNERSD TRPCQRAAPRRFSHGTRRGTLPL LASPDRAAPRTGHCRTRQRLD RTGGGFPLTGAWAMLADWIIH EGTPSRGRSDNDEPSAGSVGGL R/HAWPRTKSPKANNH*SESTG QPGAGPKNCSPVLGAYSPGPQH HGQPLPGHTCP/SRTQC*PGRP TPAPTSVSLRGNPLWWPT
19590	49958	A	19705	1088	2273	SPCLLTGGHLPADTSYRRAPAG IWQVPLWDEASQRKE*YQHQQ KKMSTQKPHPKDHNSSPAREQ/ SSMENKFHELTEVGFRKITSLE KNINDLMELKNTARELREAYTS IKSRIDQAKESIEIEDQLNEIKC EDKVREKRMKSNKQNFQEIWD YVKRPNLRLTGVPESDRENGTK LENTLQEIHQENFPNLRQANIQ IQEIQRATAQRQSSSRATPIHIVR FAKFEIKEKMLRAAREKDISM QKINKDIQDFNTVLQVDLIHV YRTVHPKSSEYTFFSAPHHTYC KTGHIIGSKTLLSKCKRMEIITN TLDYSIAIKLELRICKLTQNHHT TWKVNLTLLVNEY

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19591	49959	A	19706	318	873	AYELTPEPSPLPVFPVSADGTT HPLADKRKASPVPEQHEEHLPA RPVTQRCLTYPPNITTASEFGP ATGFRARRSGRGSTVCCNPGCY PRARPEPEPRGTPPSVSAPRAAQ EAPARQRAVGPVLADTV/SPAP RGKRDISPLFGNAHSAPKPSLD LWAPP* AAGRRGPQQA* DVTE DTQQQQWSAMAVGGTAKWM AALGRFLVTYVEVEGVKLQTF TVTTLTQSFKYSLSKYLQQQPL LSRRTIYPTFYLLSLRLNRAFK LNAAEAKPMSSPQNLVLFCLF SLQMAAPPRLQTKGKQAQCQS STKSTFQGRSLRGVSPTLSPTS QQPRNLDQQLASEQGEVGEAP LCAVIQGVIPVLGRSRSREEHPP VSALPGLHRKRQRDKEAGPVL ADTVPFPRPHAGKGTFLRCLLET TRRAPNPRWTFGLPLRKLQGA VAHSRPEIRTHSVPNRT
19592	49960	A	19707	1	690	DQDMTSSDIPVRLEGLWLP*IF IGTFKAFDKHMLILCDCDEF KIK*GVDCGGRRLLEDGNLSG WAKQ*SLVSMTVEGPPPKDVS QSRKP/CWRRGGPTVSQALC*IL YPSWGSHPGSCRTCWASPWG WRAIPTGEELGKGYHLLVAKIK DKGEGP*FSNPVPTWPWGSSPT YGPRSTPSR*GAHKETSAN**K MPSWINDEI*PPMGMPPPGMRP PPPGMRGKCLQW

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19593	49961	A	19708	1	1348	MVFWARPTLLCAALGLGAL YTATPAPTVAKRGGQTAQALS SEGASPKPWVLRHGIEPCKQSY WEVRETEQSPGVSEKAAAPVR GLEIKLPSPWDKAPEGGGGCGH SFSRLKCSFMPVLKRAVDLPAQ RSSPANGQTACSSGLAPVLPD WEIPPSKGRQTPYATGELRLAS DGCPSGTKLPEEGTDSNLCCSA SSAESNNININININKDAHGKT PSKGPOHQRSKLDKSMKTRKN HHKNAENSKNLNASSPPKDHN SSTAKEQNWTENEFDELTEVGF RRRVIANSSKLKEHVL7TQCKEA ENFEKILEELLTRITSLEKNINDL MELKNIAQEHREAYTSINSQID QAEERISEIEDKLNEIKREDKIR GKRIKRNKKSLQEIWDYVKRA NL*LIIVVPLNKITSPTSETLST STNMSRSTLSCLLSSFCSPASCT ATSAALF
19594	49962	A	19709	718	1138	GGRAAEGSQPPVAEPRCSRGAR ALPLDPTSWRQPS/APQAAP*D VELPASPSAPFAVLLSKPRLSQN KPKSPFSVASP*HGDKRQPPSRH LI*IPHLSSRAPVHS/PLGWPSNR K/HKHLRPDTAHAPAEGPLNY VRKQKQOS
19595	49963	A	19710	5	760	RAAACGGAAAPGRKRCAPGRKR CGPRRKRLGPPTLGQRPRQPS QQLRKPRRRRGSPGLPKSSPLP SSTGKTGWSTRGRSVRPPVITS RCCPPGHPCSRRAPSCSTARAPLP PT*PPTTAPCRASPPAPRPPRRPR PPPGTRSPTRSGRCRWTRSGAG TSRCSWRAGPGTAPAAAGARS RPGAPGVSAAVPCAACSWMT SAPEVRAASSPGTPSRGSGGRS HPPCSRGLPTTGATTAPAEAPG CWSCRRRS
19596	49964	B	19711	180	300	
19597	49965	A	19712	249	700	RQDPVSGGQSCPASCPSLWAA ARVWLGGQIPAPRAR*CPVCSSC PGPGAPEDTPEAGGCGCSCRC CLRTQEPAPLQPPHPPMAQTP REEVGRRGWTPGCGTDPCLW GLRLLCPLWDPHRSGRTPWAQ VQRDTTETKAQRGLVRCQRGC
19598	49966	C	19713	273	485	

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19599	49967	A	19714	35	779	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFSLPLPL LLGFLLLSAPHGGSGLHTKGAL PLDVTIFY/KDYGDKLNMELSE KYKLDKESYPVFYLF RDGDFEN PVPYTGAVKVGAQRWLKGGQ VYLGMPGCLPVYDALAGEFIR ASGV EARQALLKQGQDNLSV KETQKKWAEQYLIKIMGKILDQ GEDFPASEMTRIARLIEKNKRSC KKAVCDFPGFGGGRVGRVNL AVSPLWNIRG
19600	49968	A	19715	2	253	
19601	49969	A	19716	494	1443	LAVPRPAYGPRSPGSLRIPVPG LHLLNLNVWSRGSAALHTKG ALPLDVTIFYKVIPIKSKFVLVK FDQYYPYGEKQDEFKRAENSA SS\DDLLVAEVGISDYGDKNLM NELS\EKYKLDKESYPVFYLF DGDFFIEPSSHYTGGSR\LGAIQ RWLKGKGVYLG DGLVCT V*LTLAGEFIR\ASGV EARQAP LEAGQDNLSKCERRLRKKW AEQYLIKIMGKILDQGEDFPAS EMTTESLGLIEKN\KMSDGKKE EL\QKSLN\ILTALPRRKGAER GAVNKA VCD FPRVWWEYGRG ELTLAVSPLWNIRG
19602	49970	A	19717	286	332	HHHHHHPHYHHHHHPHYHHHH HPQYHH\HHPHYDHHHRHQGD HHGQLQYDDDHQPQCHQHDH LRCEHQHYIQ*WLINNLRASRY KPLN\NIMLVFAAEMIVLVALGL MVVVVLELTVVVALTMTVVVI VRMMGGDIGDDGGGGSGDDG GGGSGDDGGGVWQFFDSMS KNDSHPTTTTITPTTTTITIRA EQFTILT WKPVVSSQKNTSSFR
19603	49971	C	19718	1	546	
19604	49972	A	19719	1	90	
19605	49973	B	19720	217	951	
19606	49974	B	19721	67	1708	
19607	49975	B	19722	218	3267	

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19608	49976	A	19723	1	634	LGRLSFPRPEQPDGPHRAHPSPSP PRPRRPHARGRRGPRRRHH/YHD TGANRAPEVRPPCPES/SPVGVA AFEPNGLRGQQFSPRSPGAPKG L*PTPPSASSPKPREPSALGRPC CRCEESRFLHRNSNPRVKDSR QARGRHAEFHGRTGVFERRRS RDHLPTHFPA SVRWKELSWCA RKNGLSGLRLCHGSQHFSGYSN RKVGTESLNQVWE
19609	49977	A	19724	3	1090	
19610	49978	A	19725	1	609	
19611	49979	A	19726	23	636	FSYLPGPSHGTWGLWELQFK MRFGVCRHLMEDSMDMDVSP LR/PQNYLFSCELKADKDDHFK VDNDENEHQLSLRTPVSLGVF EITPPVLLWLKCGSGPVHISGQ HLVAVEEDAEEDEEEDVKLL RISGKTKTFMATNGKEYKHVKI SSEKSLDNKYKTRTPGFQAFGF EDLHPWPLGSAFYLSLRTVTP VFLVLRLLDFD
19612	49980	A	19727	1	830	MEDSMDMDMSPLRPQNYLFGC ELKADKDYHFKVDNDENEHQL SLRTVSLGAGAKDELHIVEAEA MNYEGSPIKVTLATLKMSVQPT VSLGGFEITPPVVLRLKCGSGPV HISGQHLVAVEEDAEEDEE DVNRVLFMKP/KRQGPQAYVR GFGVQLEIGH*DEPQQF*RD QPSLATPSTPHLQALLCLSGQV LRLPLWGQRL*GLQGLLPQHP EEHGVHVSPGQELHHQQGDPE PLPVLPTAEVL*SGHVQGVCEK RPKQEEEGGAQARVL
19613	49981	A	19728	1	684	
19614	49982	A	19729	3	535	DSVLRGCSLEQRSFISVRLLSYL SACRHPMEDSMDMDMSPLRPQ NYLFGCELKADKDYHFKVDND ENEHQLSLRTVSLGAGAKDEL HIVEAEAMNYEGSPIKVTLATL KMSVQPTVSLGGFEITPPVVLRL LKCAGSGPVHISGQHLVYRRK HQELQAMQMDCRALSTS*ASS APRPS
19615	49983	B	19730	1	2268	
19616	49984	A	19731	198	472	AHDIGCEVSPPLVLEVARDEGP AHRPRFHS*SSHCSHWGTSQRA APPCHPCIQTTW/PGAVTGLG G*PKTRSGPGKDRSSGAASSFP GGRV

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19617	49985	A	19732	92	2049	LTALPPAVSPGGHSSSSSRRTIS GIT*ELQR/LLQAVVPGPWQED VADAEECAGRCGPLMDCRAFH YNVSSHGCOLLPWTQHSPTTR LRHSGRCDLFQEKGEWGYMPT LRNGLEENFCRNPDPGDPGGPW CHTTDPAVRFQSCGKISCRVAA CVWCNGEEYRGAVDRTESGRE CQRWDLQHPHQHPFEPGKFLD QGLDDNYCRNPDGSERPWCYT TDPQIEREFCDLPRCGSEAPRQ EATSVSCFRGKGEGYRGTAANTT TAGVPCQRWDAQIPHQHRFTPE KYACKDLRENFCRNPDGSEAP WCFTLRPGMRVGFQYQIRRCT DDVRPQDCYHGAQEYRGTVS KTRKGVQCQR/WSLE/TG*DYP ATTSPLPFRFTTSEPHAQLEE NFC/RDPDGDSDHGPWCYTMDP RTPFDYCALRRCDQVQFEKCG KRVDRLDQRCCKLRVAGGHPG NSPWTVSLRNWQQQHFCGGSL VKEQWILTARQCFSSCHMPLTG YEVLGTLFQNPQHGEPLQR VPVAKMLCGPSGSQLVLLKLE RYVDNLGGWTKCEIAGRGETK GTGNDTVLNVALLNVISNQEC NIKHRGHVRESEMCTEGLLAPV GACEGDYGGPLACFTHNCVVL KGIRIPNRVCARSRWPAVFTRV

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19618	49986	A	19733	2	2296	HSAGQSRSPSNDFFQVLRGTQLQH LLHAVVPGPWQEDVADAECA GRGCPDLLSRAFHYNVSSHGCGQ LLPWTQHSPHSRLWHSGRCDLF QEKGEWGYMPTLRNGLEENFC RNPDPGDPGPPWCHTTDPAVRF QSCGIKSCRVAACVWCNGEEY RGAVDRTESGRECQRWDLQHP HQHPFEPGKFLDQGLDDNYCR NPDGSERPWCYTTPQIEREFC DLPRCGSEAQPRQEATSVSCFR GKGEYRGTTANTTTAGVPCQR WDAQIPHQRHFTPEKYAC/KVR WAGGRALGRAAAGETGGG*SR A*GWRLAG*G*VERLLRDLREN FCWNLDGSEAPWCFTLRPGTR VGFCYQIRRCTDDVVRPQDCYH GAGEQYRGTV/SKTRKGVCQ RWSAETPHKLQ*VPGAPGPAR ALTLGRHALMSGTRAWKWL LSLPRFRSRRLGSRLTSEPHAQ LEENFC/RDPDGDSHGPPWCYTM DPRTPFDYCALRRCADDPSPIL DPPPDQVQFEKCGKRVDRLDQ RRSKLRVAGGHPGNSPWTVSL RNR*GTTACLPQRGAEEVSSVV MPLGAGNLSLPPEVLARRWQV *HLSQESVPCPNPPLL*QQQHF CGGSLVKEQWILTARQCFSS/CE PPLCLGTQSHPTFPFPQAS*QVS LGATD*ESQMT*QSFSPSHMLPL TGYEVVLGTLFQNPQHGEPL

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19619	49987	A	19734	727	3012	PAPTHAHSAGQRSPLNDFQVLR GTELQHLLHAVVPGPWQEDVA DAEECAGRCGLMDCRAFHYN VSSHGCQLLPWTQHSPIHLRR SGRCDLFQKKDYVRTCIMNNG VGYRGTMATTVGGLPCQAWS HKFPNDHKYTPTRLNGLLEENFC RNPDPGDPGGPWCYTTPDAVRF QSCGIKSCREAAACVWCNGEY RGAVDRITESGRECORWDLQHP HQHPFEPGKFLDQGLDDNYCR NPDGSERPWCYTTPDQIEREFC DLPRCGSEAPRQEATTVSCFR GKGEGYRGTTAGVPCQR WDAQIPHQHRFTPEKYACKDL RENFCRNPDGSEAPWCFTLRPG MRAAFICYQIRRCTDDVRPQDC YHGAGEQYRGTVSKTRKGVQC QRWSAETPHKPQFTTSEPHAQ LEENFCRNPDGSHGPWCYT DPRTPFDYCALRRCADDPSSIL DPPADQVQFEKCGKRVDRLDQR CSKLRVAGGHPGNSPWTVSLR NWQGGHFCGGS LVKEQWILT AR/QCFSS/CHMPL/TGY*GMVG ATFFQNPQHGEPSL/QRVQ*AK MLCGPSGSQVLVLLKLEERSVTL N/HRVWALHILP/PEWYVVPPT KCEIAGWGET/KGTG/NDTV/LN VALLNVISN/QECNIKHRGRVRE SEM/CTEGALLAPVGACESDYG GPLACFT/HNCW/VLEGIIPN/R
19620	49988	A	19735	66	234	WCSAWHSWLPSPSGPAASYP PAACRSAPQWPDPR*RCPRTHR RRSPWRAPWHCP
19621	49989	A	19736	3	500	GRGGGGVRRCARPAPGRPPAA ARRRGDQRGGRIGR/HVPGKTF CCGICGRGFRRET/LKRHERIH TGEKPHQCPVCGKRFRESFHLS KHHVVHTRERPYKCELCGKVF GYPSLTRHRQVHRLQLPCAL AGAAGLPSTQGTGACGPGAS GTSAGPTDGLSYACSD

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19622	49990	A	19737	899	2348	GRRRGGGRCWRGCGSQSGPERF SCATCGQSFKHSW/DLVTHKYV HLMMLPPSCEAVAPRGWRRSC SCPECCRVCELSSAA/RSATAR CFRRRSPIIAQAPAGPQVPQDW RSPRARIRLPVGPVGMFAFPTSA SGKAWPSLRVSPHAFWKYHT SPPAMQPSGLWASVPACAP*K NIPSPTIWQRLAFSGGLPICWV ENHGPAATSSQWLVSGPRSPHLL S/RAEHPFSRPLPRWVATAERQ RRPSGKRTNFPFASPAPPGA/G PEVSVPPAGALPGEALGPARDL WPCSSWT*AGLPALG/DTGGGE APAP/AAAAPSEDITLYQCDCG/ TTFASAAALASHLEAHSGPATY GCGHCGALYAALAEHRRV SHGEGGEEAATAAREREPAS GEPSPSGRGGKIFGCSECEKLF RSPRDLERHVLVHTGEKPFPC ECGKFFRHECYLKRHLLHGTE RPFCHICGKGFTLNLNRHLK LHRGMD
19623	49991	A	19738	2	358	
19624	49992	A	19739	635	2441	LKAIKRHPFFVTIDWNVSCMPQ SPPPFKPAVGRPEDTFHDFEPT ARTPTGVCHSGSLYNAHHLFR GFSVASSLIQEPSQDLHKVPV HPIVQVTVFACSGFTDGYEIKE DIGVGSYSVCKRCVHKATDTE YAVKVRQAC*VSSLVFPAGTG APGIGEYSGKLVSILCAQDSP HNLLPQRKVEKPSLSILVGESRS HVDKGQEVLDILEMGEFFFFIE FLVSPLATG*CFPMARSPCMGC SLSVCTAL*GQPLQGNTPTFKY QQVTWPQAKPPTPTAVLSPETA NVTSPQEQTRCLLKDRWLYPV VRNSSTRGPEEIEILLRYGQHP NIITLKDVSGPRATASVMELM RGGELLDRILRQRYFSEREASD VLCTITTKTMDYLHSQGVGAMP GAAFNILYRDESGSPESIRVCD GFAKQLRAGNGLMTPCYTAN FVAPEVSIPRLQTQACDIWSLGI LLYTMLAG*AVTSNRCHDTPPE ILARIGSGKYLSSGNWDSISD AAKVSTCPSVALDPHQRLTAM QVLKHPVWVNREYLSPNQLSR QDVHLVKVPAGAVRTEWWE WDLNRTQPAPRLEPVLSNLAQ

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19625	49993	A	19740	144	1143	REAGRCSAGVGGRRRRRRK GAASRARLPFSLSIMDPSSLRER ELFKKRALSTPVVEKRSASSE/S SSSSISKKKTKVEHGGSSGSK QNSDHSNGSFNLKALSGSSG/Y KFGVLAK/VNYMKDTGIQRGD THPLTLDENLDETQHLDIGLQQ KQWLMTEALVNNPKIEVDGK YAFKPKYNVRDKALLMLLD QHDQRLGGILLIEDIEALPNS QKAVKALGDQIPIC*SGPVRR KILFFNDKSCQFSVG*RIFRKL WEECQLVDSHGTEEK/VEEYLE ADRVFSSHARESG/PK/KVGPYS RRKGKSPAFTRRKPTFLRTSLT NHLAWNC
19626	49994	A	19741	677	1590	AHPHSPRRTLERQARISGAGR SSPNAANRGSA PPSRRLASFT AGSA/GRPA*SSPCSGPWTAVSA PRSPGPRGGRRPPSGRRRPPCCS VFSGGASPPSARVSSPSGSCSAS PPAAPAAWSLRGCGCWPG/VW EVHVNTGSDSVAAAPAAWGRS AACGPNLGGSHPRAGRRAH RCGHPWSPRAPRPSCCGRSPR PGPPGASGCRPAPRPPTPASRS GRPCSWRRARAAGWPRGWG SSAGGCRRGSGRREWCPCGTA RGSPAAGVSRWTAPRCRHRS DASASGTPARFPGAGRGRTL WQ

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19627	49995	A	19742	754	2179	SKMSRLAACKPSLCKSEPLTTE RVRTLSVLKRIVTSCYGPSGR LKQLHNGFGGYVCTTSQSSALL SHLLVTHPLKILTASIQNHVSSF SDCGLFTAILCCNLIENVQRLGL TPTTVIRLNKHLLSLCISYLKSE TCGCRIPVDFSSTQILLCLVRSIL TSKPACMLTRKETEHVSALILR AFLLTIPENAEGHILGKSLIVPL KGQRVIDSTVLPGLIEMSEVQL MRLLPIKKSTALKVALFCTTSL GDTs*IPGEGTVVVSYGVSLEN AVLDQLLNLGRQLISDHVDLVL CQKVIHPSLKQFLNMHPHAIIDR IGSDSD/VEPLDLKWTGTQPIGS LGSICPNYSYGSVKDVCTAKFGS KHFFHLIPNEATICSLLCNRRND TAWDELKLTCTALHVLQLTL KEPWALLGGCTETHLAAYIR HKTHNDPESILKDDECTQTELQ LIAEAFCSALESVVGSLEHDGG
19628	49996	A	19743	1	652	LMPKPGDRDTTKKNFRPISLMN INAKILNKILANQIQQHKKLLN HDQVGFIPGMQGWFNHKSINV IHIIKRTNDKNHMIISIDAGKAF NKIQCFMLKTLNKLNIHGYYL KIIRAIYD/KPPANIILNGEKLEA FPLKTGIRQG/CPLLRNIV/LEVL ARAIHQEKEIKGIQSGNEEVKLS LFADDMIVYLENPVSAQNLLK LISNFSKVSQYKISVQ
19629	49997	A	19744	1	834	MGDFNTPLSTLDRSTRQKVNK DIQELNSALYQVDLIDYRTLHP KSTYTFFSAPHHTYSKIDHIVG SKALLSKCKRTEHITNCLSDHSA IKLELTIKKLTQNRSTTWKLN LLNDYWKYKQPSENKHLVYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPIRSEIEAITNSLPT/ KKSPGPDGFTAIFYQM LEVLA RAIRQEKIKGQLVKEEVKLSL FADDMIVYLENPVSAQNLLKLI GNFSKVSQYKI/NVQKSQAFLY TNNRQTESQIM
19630	49998	B	19745	1	1521	
19631	49999	B	19746	1	1461	

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19632	50000	A	19747	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNMNLP TKSPGPDGFTAIFYQRYKEELVP FLKLQFQIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKLLIH HDQVGFIGMQGWFNIRKSINV IQHINRTKDKNHMIIISIDAEKAF DKIQQHFMKLTKNLKLVLEVLA RAIRQEKEIKIGLKGEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSQYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRJ NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNLIFDKPE KNKQWGKDSLNFNKCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKHKMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQL*RRI/W KRLQRTLSPVLDAV*PPMF*AS
19633	50001	A	19748	1	1818	

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19634	50002	A	19749	1	1725	MELKTKARELREECRSLRSRCD QLEERPNIIRLIGVPESDGENGT KLENTLQDIHQENFPNLAQVFN VQIQEIQRTPQRYSLRRATPRHII VRFTKVEMKEKMLRAAREKGR VTLKGKPIRLTADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKSFTDKQMLRDFV TTRPALQELKKEALNMERNNRS WFFEKINKIDRPLARVIKKKRE KNQIDAINKDKEDITTNPTEIQTII IREYYKHLYPNKLENLEEMDTF LDITYTFPRLNQEEVESLNTSITG SEIVAIIS/NSIPTKKSPGPDGSTA EFYQMLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRKICLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPKLPMTFFTDLEKTTL NFIWNQKRARITKSILSQKNKA GGITLPDFKLYYTATVTKTAW YWYQNRWYQNRDIDQWN RTEPSEITPHVYNYLIF

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19635	50003	A	19750	1	1719	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRRNREHGKKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTLTSQKLELEKQEQ THSKAGRRQETKIRAELEKET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTETIQTIREYYKHLA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPTGSEIVAINSLP TKKSPGPDGFTAIFYQRYKEEL HINRAKDKNHMHSIDA EKA F D KIQQPFMLKTLNKLVLVFLARA IRQEKEIKGIGLKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWNIPCSWVGRJNI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP

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19636	50004	A	19751	2	2133	WRRYQANGK*KNK/QKKAGV VILVSDKTDKPTKIKRDKEGH YIMVKGSIQEEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTIITDCLSD HSAIKLELRKLTQNSSTTWK LNNLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDCTCA VCREKFIALNAHKRKQERSKID TLTSQLE/LEKQEQTHSKASRR KSRNRG*IPGHIHPKTKPGRI* VPE*TNRRV*N*GNN**LTNQK KFRTRRHSQILPEHSAGSSGQG NQAGERNKGY SIKRKGSIQVVP CR*HDCIFRKP HHLSPKSP*AVK QLQQSRLIQNRAKITSSPIHQ* QTNREP NHE*TFIHNC FKENKIP RNPTYKGCEGPIQGELOTTAQQ NKRGHKQMEHSMMLMDRKNQ YHENGHSAQGNL*IQCHPHQAT NDFLHRIGKNYFKVHMEPKKSP HCQVNP KPKEQSWRHHA* LQ TILQGYSNQNSMVLVPKQTYRP MEKNRGLRNNTTHLRPSSL*QT *QKQEMGKGFPI**MVLGKLAS HM*KAETGSLPYTLYKN*FKM D*RLKC*T*NHKNLRRKPRQYH SGHRHEQGLYV*NTKSNGNKS QN*QMGSN*TKELLHSKRNYH
19637	50005	A	19752	1	1314	

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19638	50006	A	19753	1	1998	MVKGSIQEEELTLHIYAPNTG APRFKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQAALIDIYRTFH PKSTEYTFFSAPHHTYSKIDHIV GSKALLNCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKA/PL ARLIKKKREKNQID/TIKNDKGD ITTDPTIEQTTIREYYKHYANK LENLEEMDITLDTYTLPRLNQE EVESLNRPTGSEIVAIINSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFSIEKEGILPNSFYEAII LIPKPGRDITTKENFRPISLMNI DAKILNKILANRIQQHIKKLIHH DQVGFIPIGMQGWFNIRKSINVI QHINRAKDKNHHMISIDAEKAF DKIQPFMLKTLNKLVLVLEVLAR AIRQEKDIKQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS KFSKVSQYKIHVLKSQAFLYTN NRQTESQIMRELPTTIASKRIKY LGIQLTRDVKDLFKENYKPLLN EIKEDTNKWKNIPCS WIGRINIM RRSSAPSGCHLCPSSLYLHSPN VELKQASFSVAGFQWKLGITAP TQPRGVGDDFVTSTSPSLDMF PRLKGAENSPHRSGRD
19639	50007	A	19754	1	3288	
19640	50008	A	19755	1	1293	
19641	50009	A	19756	264	490	VYLLIVLAVLYTNNRQTESQIM SELPTTIASKRIKYLGIQLTRDV KDLFKDNYIPL/LKEI*EDTSKW KSIPCSWI
19642	50010	A	19757	1	1845	
19643	50011	A	19758	1	3144	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHV GSKALLSKCKRTEIITNCLSDHS AIKPELRICKLTQNRSTTWKLN NLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKA/VS RGKFIALNAHKRQKRCCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAEKLEIETQKTLQKINES RSWFLERINKIDRLARLIKKR EKNQIDVIKNDK
19644	50012	B	19759	1	1743	

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19645	50013	A	19760	1	1500	MGKKQSRKTENSKNQASPPPE ECSSSPAMEQSWMENDFHEL EEGFRSNFSELKEDVRTHSKEA KNLEKRLDEWLTGITSVEKSLN DLMELKTMARELCDKCTSFSS KFHQLLEERVSVTEQDMNEMKS WFFEKINKIDRLLARLIKKKRE KNQIEAIKNDKGDITTDPTETQT TIREYYKHLTYNKLLENLEEMDT FTGTYTLPRLNQEEIESLNKPI GSEIEAIHNSLPTKKSPGPDGFTA EFYQRYKEELLFNIRKLNLIQL INRTQDP*PPL/VLSRIGRRVHQ YLENPVSAQNLLKLSNFSKV SGYKINVQKSQAFLYIKKRQTE SQIMSELPFTIASKRIKYLGIQLI RDVKDLFKENYKPLLENEIKEGT NKWKNIPCS WIGRINIVKMAILP KVIYRFNAIPIKLPMTFFTELEKI TLKFIWNQERACIAKTILSKKN KAGGIMLPDFKLYYKA\TVIKT AWDWYQNRYLQQWNRTEPSEI TPHIYNHLIF
19646	50014	A	19761	1	3192	
19647	50015	B	19762	180	190	
19648	50016	A	19763	1	3212	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRKKNLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRQKERSKIDLTSQL KELEKQEQTHSKASRRQETKIR AELKEIETQ

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19649	50017	A	19764	1	2607	MTNHCFKRQFQKHEMLLKEDC EPGDSSFILGEQHWENMLCEPK QHPPQQGEGRAAGQAQNP.LNT DVSPGAGAKESEEKIQHLNYT YFKQKCMSCSGFTFSSYAMHW VHQAPGKGLEWVSAIGAGGGT YYADSVKGRFTISRDNAKNSLY LQMNSLRAEDMAVYYCARDTI DAYGDEKPSTIVTRIRVLRKLR DTCHMGADRTFLSPIAQHPPV CHVETHLGMQVANSSEEDLV WSKWDVDVKFILCCAKYHREQ LQESALDLKSLHCPASPALFL ATPSQPVLTTGPGSASSQGGAE MGAHFLVQLVQSGAETRESFD PALPEMETQRTDEQCRAVHPGP QKERHGNMSP.LLMKGSSSPVP SGPGEEPSHREPVSFICGRCLLT LLLGDC.LWGE.GAWTQGDVLQ PSDRASFLAMGVNTTVQQVGD LSGYFPNSVGKACKCREFHLLT PLAHTSSTTHETFPGAQCEVQL VESGGGLVQPGGSLR.LSCPDG FTFSNHYMSWVRQAPGKGLEW ISYISGDSGYTNYADSVKGRFTI SRDNANNSPYLQMNSLRAEDT AVYYCVKHTARGKLEKQEQT SKASRRQEITKIRAELEKETETQK TLQKINESRSWFFEKIYKIDRPL ARLKKKREKNQIDA.KNGKGD ITTDPEITQTLREYYKHLYAN KLENLEGMDFK.LDAYTLPRLN
19650	50018	A	19765	1	1251	
19651	50019	A	19766	1099	4113	
19652	50020	A	19767	1	2628	
19653	50021	B	19768	1	2970	
19654	50022	B	19769	1	4142	
19655	50023	A	19770	1	4091	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKEL.MELKTKAR ELREECRLSRCDQLEERVSV MEDEMNMKQEGKFREKRIKR NEQSLQEIWDYVVKRPNRLIGV PESDGENGTKLNTLQDIHQENF PNLARQAKVQIQEIQRMPQRY LTRATPRHIIVRFTKVE

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19656	50024	A	19771	156	450	LQVEIYKTVKMHCIWHKQMVSYFFFYQKKNELSNFEVFLKTAGSMFFSTVVGCHPTRCGEFEKNNPDLYLKELLNLAENNGKVVVFIGECGLDFDRLQ
19657	50025	A	19772	173	1009	LHGGNLQDSKDALHLAQTNGMFFSTVGIHPTRCG*/YFEKNNDLYLKGVAKIFA/EKTLKGKILWQLGECGLDFDRLQFCPKDTQLKYFEKQFELSEQTKLPMFLHCRNSHGWNFLDIMKRNDRDCVGGVVHSDFGTKEAASLIDLDLYIGFNG/CASPENLEANLGRFWKSTPSEKLMIEA/DAPWCGVKSTHA/GSKYIRTAFFPSKKKWSGHCCLKDRNEPCHIIQLEIMSAVRDEDPLELANTLVNNTIKVFFSWNIGICLPLSIMYVKFHSKTS
19658	50026	A	19773	16	1558	QEIHLQRASPRLLQLLPPLPPPPPPAAGGSLSSLSGRMSRQV/VRSKFRHVFGQPAKADQICYEDVRVSQTTWDSGFWC/SVN*VLWALICEASGGGAFLVPLGKIWTLWDKNAPTGGGSH/APVLDIACWPHNDNVIA/SGSEDCVTVMVWEIPDGGMLMLPLREPVVATLEGHTKRVGIVVAWHTTAQNVLLSAGCDNVIMVWDVGP/GAAMLDTGPRGA/HPDANYRGDWEP/DGGLICTSCRDKRVRIIEPRKGTVVAEKDRPHEGTRPVRAVVFSEGIKLTTFGRMSERQVALWDTKHL EESPV/SLRKLHTRNGVPVAFFGP/DTNIVYLRKG/SGPIRVFEITSEVAPFLHYLSMFS/SKESQRMGYM/PKRGRKVNK/CEIAGFYKLHDGR/CVSPMPKVPVRKSDLFQEDLGPTPPRGPDPA/LTAIEEWLGGRDVG/PLFISLKDGYV/PPKSRELARVNRGLDP/GRRR/AAP EASGTPSSDAVSRLEEEMRKLQATVQELQKRLDRLEETVQAKL
19659	50027	A	19774	229	475	

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19660	50028	A	19775	225	965	EWAWRSQRLRSEHSRADPTRSSC RSCGAKMSGEENPASKPTPVQ DVQGDGRWMSLHHRFVADSK DKSGSKKKNPPEVVFVIGDSL VQLMHQCEIWRELFSPHLAUN FGIGDGTQHVLWRLNGELE HIRPKIVVVVWG/TPNNHGHTA EQGLLPRGQHPNPLREKNRQV NELGTGGTWLGHPRAHFLDAD PGFVHSDGTISHHDMYDYLHLS RLGYTPVCRALHSLLLRLLAQD QQGAGLLEPAP
19661	50029	B	19776	691	1077	PSVAFL*PSLHRYGHTGTAGPG WPCAAGS*AA/SSSRGLPSVLQ ASSNSSHRCNSTPSGAGQRR VRRAP*MASTTPGGTESGPCKA RNAFRMRSTSAFCRGQ*QRPVP SSSSSRSSSRACAVAGETASGDP RAQRQLRS*DESSSPSLDFRQA /PWPTAPCVKVSYSRRMFSGM SPWRSSDNKRNSFLRKTGGSN FSADLDTPPMPEVCLLPSLGYP LVPPVAEVHMPVPAPILPSAGIR RKIQKAASAKQLPLFQMDDFS QHRVQGDTKK
19662	50030	A	19777	481	1308	
19663	50031	C	19778	41	318	INNHIRDSCWTCHCSC/QPPPPPP LLPQPPP*LSAPRVIERKE*DRL/ CPGEQTSSPTSPRTQSAATA QLSLPPP
19664	50032	A	19779	970	1193	
19665	50033	A	19780	1	494	MDGRVMAAGGRQAPGQKKAG TSEAPPSSQEWPEAWYGCLQQ KLRAVYLVQSQPCTGPVLAPG AACPAAAASTPGCAQW/CGPR ACSPQTSSQLCAWFAFSSRCPD FCPNPPRPL*DPSPWPTDADRC SPELTIRDSCTWCHCSCRRRHR RPFCCSRRPDSPRHG
19666	50034	C	19781	120	392	
19667	50035	A	19782	174	375	

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19668	50036	A	19783	33	1154	QFALCAGWWLCGRGGGRTPAT MSGFSTEERAVPFSLEYRVFLK NEKGQYISPFHDIPYADKDVFH MIVVEVPRWSNAKMEIATKDP LNPIKQDVKKGLRYVVALNLFPA YKGYIWNYGAFPPQTWLEDPG HNDKTLGCGCLTMDPMDVC* NWEKGVCARGEIIGVKVLGIL AMNDGGGTDWKVIAINVDDP GCQPINNDINDVKRLKIPGYL* KLPIVDWFR/YKVPDGGKPENEF AFNAEFKDKIDFAIDIIKSTPWT LGKALVT*ENRMGKGISCMNT NFVLRAPFKVLCILDAQSPPLWD ALPHTPCGICPCSTQQTVDKG VPITQKNLMRFPLEYQADIAVIR VPSWMVLEVKVVAFSKAFKVV EPHPNLK
19669	50037	A	19784	1	612	VTQEDDIIEEHKPRTPRSPPLL APSPACQAFGEGHSPGHPAIST GAGPRPSASFSPHLSGLHREPP LNWSVCPGLVWSPKPALEDTH PFVQQPFHQATLEWGVFHRDV GRRWGRRLLGNLQIGSEVARRR RVGGGGLQCRRLGVGASPGAD W**SG*EEACGGRWAA/GADG WGLGRPRELIGCRWRRSLAA APGPQRPGFVSSTPRCPRPSG METQTPALRVQQDDLFS
19670	50038	A	19785	1	951	MEEGISSQIGRENECQQKKCQ TLIKPSDLVRTHSYHENSMTGETI LVIQLPPPGTAFDMWELQFKLI TQTFSHHNQLAQKTRREKRAR QEAERREKAERAARLAKAKS ETSGPQIKELTDEEAERLQLEID QKKDAENHEAQLKNGSLDSP GKQDTEEDDEEDKDKGLKP NLNGEDLPNYRWTQTLSLD LAVPFCVNFRLKKGKDMVVDIQ RRHLRVGLKGQPAINDGELYNE VKVEESSWLIEDGKVVTVHLE KRGPADAHSRALSVLQASRL GVHCVPGTVPNAEIQVVDVFIY FWQSVIPQASPISE

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19671	50039	A	19786	87	1191	SAELRDVDRSAARLGGEQEEER FDGMLLAMAQIQHEGGVQELV NTFFSFLRRKIDFFIGGEEGTAE KLITQTFSHHNQLAQKTRREK ESPRRAEVRREKAERARLAK EAKSETSGPQIKELTDEKAVERL QLEIDQKKDAENHEAQLKNGS LDSPGKQDTEDEEEDEKDKG KLKPNLGNRADLAQ*RLNPDPC RELDLAVPFVFNRLKKGDMV VDIQRGTPRVGLKGQPSDSL GELYNEVKVEES\SWLIEDGKV VTVHLEK\NKMEWWSRLVS/S DPEINHPRKINPENSKA\SDLDS *DFASMV EKDDGMTQRTESPM GLPNFTQNRKKQEI LK\KFM\DQ HP\EMGFPPKAKFPTNPCCFPP
19672	50040	A	19787	3	403	
19673	50041	A	19788	281	1952	DPVPGCRRLVAMAPTITQTAQ REDGHRPNSHRTLPERSGVVC VKYCNSLPDIPDPKFITYPFDQ NRFVQYKATSLKQHKHDLT EPDLGVITIDLINPDYRIDPNVL LDPADKLEEEIQAPTSSKRSQ QHA\KVVPVWMRKTEYISTEFN RYCIFHEK\PEVKKWGSVKQQF TEEEIYKDRDSQITAEKTFEDA QKSVIEGLGWGEARISQHYSKP RVTPVEVMPVPDFKMWINPC AQVIFDSDPAPKDTSGAAALEM MSQA\MIRGMMDEEGN\QFVA YFLPVEETLKRRKRDQEEEMD YAPDDVYDYKIAREYNWNVK NKASKGYEENYFFIFREGDGVY YNELETRVRLSKRRKA\GVQ SGTNALLVVKHRDMNEKELEA QETRKAQLENHEPEEEEEEME TEEKEAGGSDEEQEKGSSEKE GSEDEHSGSESEREEDRHEAS DKSGSGQDDSSDY*ARAARDK EEIFGSDADSEDDADSDDEDRG QAQGGSDNDSDSGRN\GGGQR TRSHRSASFPSPSGSEHSAQENG SEAAASDSSEADSDSD
19674	50042	A	19789	1	885	
19675	50043	C	19790	164	361	
19676	50044	C	19791	22	156	

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19677	50045	A	19792	1	1344	PGRTTRSMADVFLSAPIPRGC ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEEEE EEEEDAVLVAEEA VAAAGWM LNFLCLSLCRAFREGRSEDFRRT RNSAEAIHGLCLSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKEHDKLHE EIQNLIKIAIACVMENGNFKG AEEVFERIFGDPNSHMPFKSKL LMIISQKDTFHFFQHFYSYNHM MEKISYVINYVLSEKSSSTFLM KAAAKVVESKRTRTITTSQDKPS GNDVEMETEANLGKKKC*LT NSLR*LNPRVQYPPY*GSHKNL FYLKLQHGTTQQDLNKKERRV GTPQSTKKKKESRRATESRIPVS KSQPVTPKHKRARKRQAWLWE EDKNLRSGVRKYEGGNWSKIL LHYKFNNRTSVMLKDRWRMTM KKKLKLISSDSED
19678	50046	A	19793	1	1444	IPGSTISCLKGQYPSEFPNMAED VSSAAPSPRRCADGRDPDTEE QMAETERNDEEQFECQELLECC QVQVGAPEEEEEEEEDAGLV AEAEAVAAAGWMLDFCLCLSLCR AFRDGRSEDFRTRNSAKAIHY GLSMLTACPLRTIYICQFLTRIA AGKTP*MHRFENDERITPLGISP *MIWGSIEKEHDKLHEEIQNLIK IQIAIACVMENGNFKEAEVFER IFGDPNSHMPFKSKLLMIISQKD TFHFFQHFYSYNHMMGKIKSY VNYVLSEKSSSTFLM/KAAAKVV ESKRTRTITTSQDKPSGNDVEME TEANLDRKRSHKNLFLSKLQH GTQQQDLNKKERRVGTQSTK/ RRKKEGRRATESRIPVSKSQPV TPENDRARKRQAWLWGRKDK ILRS/GVREFGEGN\WS*ILLHY KFNNRTSVMLKARWRTMEG NLKLDLQDSEDWIVFVKSFDG KGQFKYFDHCLFETCVIDVI
19679	50047	A	19794	1	1020	
19680	50048	A	19795	411	769	SHLGFPGTWTRLWPSRMSPCPP QQSRNRVIQLSTSEL/APALGN WARLPQVTEQ*FRGLRKGSRT MPGSSPATWTKGCLLA*Q*CL CPQLGWSRVAP*CRLGALFLAC SLLLAAPLRFC

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19681	50049	A	19796	171	325	ETVAVSSAGARASSIMRMVSS RPSETSLSEVFPDSAP/PGL*PPP CLSFL
19682	50050	A	19797	335	1536	GCSPPCPQ\QSI\NRVQLSTSEL GEMELTW\QI\MSITEACRVLN APSEPSFEAKPQLPYL/GPPPT TY/CP/CSIHDPDGGFPV/PPPYEL PASTSHVPDPPYSYGNMAIPV SK/PLSLGLLSEPLQDPLALLD IGLPAGPPKQEDPESDGLSLN YSDAESLEEGTEAGRRRSELC RRCPV\VEYPYSLMPNSLAHSN YT\PAAEPLALEPSSGPAVRA KPTARGE/AQGSRDERRAL\AM KISF/PTDKIVNFPVDDFNELLA RYPLTESQLALVRDIRRGKNK VAAQNCRRKKLETIVHLERKL ERLTNE\RERL/LRA\RGESRT LKVMRQQLQEL\YREHFP\SHLR E*NPQQTAYS*KK*RAKQAC PNGDPSFPCGPRGT/KMEAHRL
19683	50051	A	19798	1	408	LNLMRWEAVQARGGAFRIPRV DPGPTPIPHNSSRFDNSVSTA PRVLVSGICAAGSFVLVAFSHS VGTSLC/GYFLLLTSPEAQDPGG EEEEESAARQPLIRTEAPESKPG SSSLSLRERWTVFKGLLWYIV PLV
19684	50052	A	19799	1	759	
19685	50053	A	19800	1	1815	
19686	50054	A	19801	1	942	MGGCAGSRRRFSDEGEETVPE PRLPLLDHQGAHWKNAVGFV LLGLCNNFSYVVM\LSAAHDILS HKRTSGNQSHVDPGPTPIPHNS SSRFDNSVSTAPRVLVSGICA AGSFVLVAFSHSVGTSLC/GYFL LLTSPEAQDPGGEAAESAARQ PLIRTEAPESKPGSSSLSLRER WTVFKGLLWYIVPLVVVYFAE YFINQGLVSEGCLFRPFPSALN VCEVNLVKV\SQHGGWVAVV TQKKKHPISCRRLLNVDGMNIIS NDGSNKLNRSRKARVSYKVQR TINASLNAATSTRAVSSNPNFV

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19687	50055	A	19802	82	1620	SLSPVADPHPSRGSPLWLTLYDP GPSGDLNLMRWIGCAGSRRRFS DSEGEEETVPEPRLPLLDHEGAH WKNAEGFWLLGLCNNFSYVV MLSAAHDLCHKRTSG\NQSHV\ DPGPNGDSPTTAYSRFDCNSVF TGAVLLADILPTLVIKLLAPLG LHLLPYRSGPRVLVSGICAGG KFRPGFAFHSVSGVTSLCGCWSF ASISSGLG\EVTFLLSLTAFYPRA VISWSSSGTGGAGLLGALSYL GLTQAGLSPPQTLTSLMLGIPAL LLASYFLLLTSPQAQDPERGEE AKVQAGQPFIRTEGPE\GKPGSS SSL\SLRERWTVVKGLLWVPLF PWFEVTFPKYFITQGLFELP/LFF WTTSLSHAQYRWYQMLYQA GVFASRSSLS\CSIGFTWALAL LQCL\NLVFLADVWFGFLPSI YLVFLI\LYEGAPWGSASLREK PF\HNIRPWRPSDEHREVCCKWR PPCHL*HTGGFILSGASLALPLH DFLLPSSPDTRDPQDAGHIHLW ARGTGYQ
19688	50056	C	19803	270	542	
19689	50057	A	19804	271	449	CLELRNLFYGACSWEVSISSDS EKPGIFNASPASAVHC**GFARP SSWRVLGAICTFHHSVYAKTA KRKAST*RHFFH
19690	50058	A	19805	21	79	
19691	50059	A	19806	1242	1560	WATRSCSSMMEMPPWCPCGC AGRWRGGASRGPREAAAGH* KPRTSNQGEQPTRRSPYAACA RRAFAGPWASLPSPSPLSAGGL AWGAPCVAHPTRSPYLLV
19692	50060	B	19807	148	2949	
19693	50061	A	19808	1335	2173	KQAHRPREEKRREEKRKEG\PS VPETLKKKQRNFTELKIKRLRK KFAQQMLRKAR\RKLIYEKAK HYPKE\YRKMYRT*ISNGRGWA RK\AGQLYLVLKNPKFAV\VIRN QKVS\MGVSPKLRKVVSFLRP SSKSSNETFVKALKQRPSD*TM P*GLVRGP*LPWGYPQPS*SPV NEP*SYKRGYAKIQ*EAEPLT DNALIASISWVNSAFICM\DDLI HEIYTV\GKRKF\EANNFLWPLQ IVLLPRGG\MKKKTTHFVEGGD AGTQRSDQINRLIRRMN
19694	50062	A	19809	3	186	
19695	50063	A	19810	272	428	

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19696	50064	A	19811	50	2237	RSLKAFICSLSDMDKQSRDPPVK MQGSITTPGSIALAQAQAQAV PAKAPLAGQVSTMVTTSTTTTV AKTVTVTRPTGVSFKKDVPPSI NTTNTIDLLVATDQTERIVEPPE NIQEIAIFNNLSQSNMTQKEE LVNNTLVQSYRQQIGNVVNQ ANLQLFWNMYNSRRDLINRP GTVFNAKTLRCPVMLVVGDNA PAEDGVVECNKSLDPTTTTFLK MADSGGLPQVTQPGKLTFAFK YFLQGMGYMPSASMTLRASR TASLTASSVDGSRPQACTHSE SSEGLGQLNLKFEIEVLCKNLA LDINELKPGNLLKDKDRKLNLD EQLSAPKKDVKQPEELPPIITTT TSTTPATNSTCTATVPPQPQYS YHDINVYSLAGLVPHITLNPTA HPQLKQCVRAIERAVQELVHP VVDRSIKIAMTTCQIVRKDFA LDSEESRMRIAHHMMRNLT GMAMITC/RE/PLLMISSTNLKN SFASALRTASPLQREMMDQAA AQI*AQDNCFL/CKVGGVDPK QLAVYEEFARNVPGFLPTNDLS QPTGFLAQPMKQAWATDDVA QIYDKCITEQLHAIPPTLAM NPQAQALRSLLEVVLVSRNSRD AIAALGGLQKSMENGLNYMAV AFAMQLVKILLVDESRVAHV EADLFHTIETLMRINAHSRGNA PEGMDITTRQKVNKKREGFND
19697	50065	A	19812	1	3777	KNPEFNKMLVNETYRNKVLTT SDKAAANFSRSLKLNGLHWL GMITLAKNKPILHTDLVKSLL LEAYVKGQQLLYVVPFAKV LESSIRS VVFRPPNPWTMAIMN VLAELHQEHLKLNLFKFEIEVL CKNLALDINELKPGNLLKDKDR LKNLDEQLSAPKKDVKQPEELP PITTTTTSTPATNTTCTATVPP QPQYSYHDINVYSLAGLPHIT LNPTPLFQAHPQLKQCVRAIE RAVQELVHPVDR

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19698	50066	A	19813	160	1002	KRLGSSAISM SKYKLI MLRHGE GAWNKENR FCSWVDQKLNSE GMEEARNCGQ LKALNFEFDL VFTSVLNR AIPTARLILAEELGQ EWVPV ESSWRLNERHYGAL GLNREQMALNHGE EQVRLW RRSYNVTPPIEE SHPYQEIY NRPGGIKVC DVPALDQLPRSE LKDVLERFLPYWNERIAPEVL RGKTLISAHGK*AVGALLKHL GRYPSGLKTSINIYSFLLGVPIIL VELDENLRAVGP HQFLGDQEA QAAIKKVEDQGKVKQAKK
19699	50067	A	19814	200	1155	NHYISLFQYSQDTCKLLFRNQ MTSQFLCIFSGLMVFFLIITTSQ VSFTNFFTGLKIFFLVIKFWVSE FLHHQTGTYIHIYLLFISMKSFF LYASPLTFMILSHFAQSLSSIFGF CSSLFRQSSFFSNILFF*VYTQSY REFRTYYETIPCFDITFVIFKM CCILILCFD LNNRRNGSI IQKFG IYGLVKIFIF*IFTNIHLLQ*FFQV VFLOFFNIVKKSFLQAPGSKR* KFFSKVRFFSFL*F*KWEARSSA SKLFLLIY**VYR/IFSFLVFPV V/CPVGWYLLFFFLYLFLFLN LSKNSFYSQWYWFKR
19700	50068	A	19815	1	168	RPWLHLHGRPGWPAPETPPQD PEQAPPPGRAGPAGEGLSCV /P*APSRPRPTM
19701	50069	A	19816	1	531	PVGQGARQDDSSSSASPSVRAT SQGGHLSDFLNKLVMRRKGI SGKGP GAGEGPGGAFVRVSDSI PPLPPQPPQAEEDDDWES*G AP*HLPPPDPLGRCSMDMTAR TSCSDLLPWEGVTEPAVCGDQL QGAEGWLEATQLGRGLVCLYF MGGRLHPACATVFLRGFORRR HTNQ
19702	50070	B	19817	61	969	
19703	50071	A	19818	60	436	RGSREYLHTGCPRSRGGCRSQCP GPPTQSPKVRPPQRGAPRLRGG DFPPSRLLDTVSFPSPA*AAFPP CPVPHLPAPVQGAPEVVDPSG GWATLLESIRRAGGIGKAKLRS MKERKLEKKKQEQ
19704	50072	B	19819	575	1666	

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19705	50073	A	19820	515	1110	MFHPTCLTCPAFANRPHVHCRP GAPAFAPSAGPTPELPTFHTEV SPSHSRQTLQDQVT*TA PPPPPP PPPPPPAPEVLGQLQPPLPTLQP RPLLGGGAREGRTAAAA/PSPS/ GPGSSQSGRPLRWLGHSARV HPPSWGHRQGLAAQHERRNV EKKKQKEQEQVRATSQGGHLM SDLFNKLVMRKGGHLWEKDPG AW
19706	50074	A	19821	1	191	MQK*ITAWAPAPMKIKIIPASPER KYSVWIGGSIW/PQLST/FQQMW ISKQEYDESGPSIVHRKCF
19707	50075	C	19822	791	970	
19708	50076	A	19823	13	1260	INPPLSRRQCLSHSVLPPLRRR VSLPVAMEEIIAALVIDNGSGM CKAGFAGDDAPRAVFPISVGRP RHQGVVMVGMGQK\DSYVGDE AQSKRGILTLKYPIEHGIVTNW DDMEKIWHHTFYNELRVAPEE HPVLLTEAPLNPKANREKMTQ\ IMFETFNTPAMY\VA\IQA VLSL* \ASGRTTGIVMDSG\DGVTHTV\ PILRGLPHCSTPFLRLGPGLARD LTDYLMKILTERGYSFTTHGPS GKTFRNIKGEACATSPLDFEQE MGTVAASSSSLEKSYELPDGQVI TIGNERFRCPEALFPQSFGLMES CGIHETTFNSIMKCDVDIRKDL YANTALSGGTTMDPGIADRM QK\ENTALAAPAP*KIRIIPAPER K\YSVWIGGSILASLSTFQQMWI SKQEYDESGPSIVHRKCF
19709	50077	A	19824	93	534	

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19710	50078	A	19825	1	1462	WEVSAQSPSPAVPRRAPRLGLSA TRSAAGTMREIVHIQAGQCGN QIGAKFWEVISEDEHIGIDPTGSY HGSDDLQLERINYYNEAAGN KYVPRAILVDLEPGSMDSVRS GPFQGIIRPDNFVFGQSGAGNN WAKGHYTEGAELVDSVL/DVV RKESESCDCLQG/FQLTHSLGG RHGVPGWGTLLHQQSGGEEYP DRIHETPFSVH/VSPKPVFKTRL LEPLQRHTSRFHHLVENT/VKP YSIDNEALVYVICLPTAES*PTPT YGALNPPGCSATMSGVTT/CLR FP/GGQLNADLRKLA/VNMVPF PRLHFFMPGFAPLTSRGSQQR ALTVE/LTQQMFDSKKMIA/AP CDPPPTGR/YLTVAAIFGRGMFH GRRWDEADGSNVAGTRNRQVI SWEWVP/NNVKTAVCDIPPPG AWKMSATFIGNQPRPSRRLFK RIYE/QFTAMFPAQGPSLHWH GRRAMDGDGSSPEAREQHERP WCPEYQQYVGTPTPT
19711	50079	A	19826	2	180	
19712	50080	A	19827	28	185	
19713	50081	A	19828	179	307	
19714	50082	A	19829	438	663	
19715	50083	C	19830	99	335	
19716	50084	A	19831	1	320	AYADQL*LRRHKSSSSSSSSSS SSSSSSSPLAP*LGSGDLP*EIN PPSSCSLLREKDPPTTSGP/PTS PRNISP/SPNDPTGNRTVQLTWQ PLPQPLELWPKAL
19717	50085	A	19832	578	753	LCTPTPPLFWKTVRKYSNNQ KGE*NTVLMVEVCPRSPRTN*KD SQ*PFELLTKMTSQGSDISGDLF WEINPLSSCSLLHEKDPPTTSGP QTDQPKKHLTNFKSETKETHFI RGPKTPVLVTDWEGRLPLVFN HSRDASLIHPRFRGVPRRDAC LGPSPLAASPAFLEEGQVPQPLL SMSLTPSLFWRRGKKPSTPSSP LAASPAFLEEGQVPQPHISVPRS LISTPQPLITLHPDPFAFLEDSK EVLKQPKGRIKHCADGGMSK EPKNQLKGLPVTKAGNIHGIND
19718	50086	A	19833	95	259	SHRPSQ*VLQLIKVAHPELFVPP SGFVVSLSGMLQLTTLTREW MRILLIFWNG
19719	50087	A	19834	1	939	
19720	50088	A	19835	391	792	

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19721	50089	A	19836	1	1317	
19722	50090	B	19837	1	1665	
19723	50091	A	19838	573	902	YSCLLILIRKITQNSVEVLGRRK FLGGGMEREWMFL/EGCFKR D*GQRGNQFQIRVTAPNFMVCV CVKRPNNRLCVSNKAVYFTWV QVGFQIFKEPEPIEICKVCWRP
19724	50092	A	19839	1802	2229	GGGAEEELGPSSAWRGAAC PCPRKAGLVAKAEGPRQASLR GLTPLKRECHIREASLQ*LNTK/V KAAFPVRDRRWSFGFTDKTCLF CLGSEIGEVLGLVGLRT*GRR WIFLMEQRAGGQIDLPREVPR SKSGHQISLVS
19725	50093	A	19840	19	4153	PPDPLPGLPCPPGGPPLPAFGGG WGGARGSWHWSRACSRRRR LVHAPRALPLPRAAAEKAKRP AGARQMGLKARRAAGAAGGG GDGGGGGGGAANPAGGDAAA AGDEERKVG LAPGDVEQVTLA LGAGADKDGTLLEGGGRDEG QRRTPQGIGLLAKTPLSRPVKR NNAKYRRIQTLYDALERRPGW ALLYHIALVFLVGLCLILAVLA TTFKYEYTVSGDWLWLLLETFALF IFGAEFALRIWAAGCCCR
19726	50094	A	19841	355	640	ILDYVFSSSHLFQSKLLGRRGR ASHGTKL*AGPGGGGEVIKGL* GGGAEEELGPSSAWQGAAC SFPRKAGLAAGGEGPRQASLH GLTPLKCG
19727	50095	C	19842	55	189	
19728	50096	B	19843	96	401	
19729	50097	C	19844	558	725	
19730	50098	C	19845	448	540	
19731	50099	C	19846	140	334	
19732	50100	A	19847	362	710	ILGGRKLRLEKSLGCAAQGGG AL/YEWELELRNGCLCCSVKD NGL*/RAIENLMQKKGKFYDYL LETTGFADPGAVASMFWDAAE LGSDIYLDGIITIVDSKYGLKHL AEEKPDGLIQ
19733	50101	A	19848	181	543	
19734	50102	A	19849	1	594	
19735	50103	B	19850	29	746	
19736	50104	A	19851	45	362	EEQHSMLGSGFAERLRVNL LVINRLKLE/KKDERARIRVEH IREDYLV EAMEILELYCDLLA RFGLIQSMKELDSGLAESYSTLI WAAPRLQSEVAELKIVA

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19737	50105	A	19852	344	951	EEQHSMILGSGFKA EHLRVNLR LVINRLELL/EGKKKKKTELAQ KAGKEIADYLAAGKDERARIR VEHIIR E D Y F V E A M E I L E Y C D L LLARFGLIQSMKELDSGLAESV STLILAASRLQSEVEGFPNIYSS* IPSN SPII.NL.*MAIKGCKNY/RL LHQIVVPGPSQKPLQNFLDLR LPWTTLLWPIFGLEGKIPLWERIK
19738	50106	A	19853	1	1077	
19739	50107	A	19854	1	1140	
19740	50108	A	19855	1	3426	
19741	50109	A	19856	1	942	
19742	50110	A	19857	342	1499	EEQHSMILGSGFKAERLRVNLR LVINRLKLEKKKTELAQKARK EIADYLAAGKDERARIRVEHIIR EDYLV E A M E I L E Y C D L / L C L A RLG/LYSSY*KELDSGLA/ESVST LIWAAAPRLQSEVA\ELKIVADQ LCAKYKEYGKLCRTNQIGTV NDRMLMHKL/SVGTPPPQILVERY LIEIAKNYNVPYEPDSV\MAE APPGVETDLIDGGFPDDVKR\ GPWKKEGSGGFTAPVGGPDGT VPMMPMPMPMPMPANTPFSYP LPKGPSDFNGLPMGTYPQAFPNI HPPQIPATSPIRIESVRWTFNCLI KEYS/IFLAQICLGPGBKARRPF AKFP/SRPADNF*QLLFLPELPSV PDTLPTASAGASTFRILKDIDF DDLRRFEGAGKRKT
19743	50111	A	19858	2	255	GCISTSRGSMPTTTLRLQLKIS *RSYSSAPASCLISIVKSASD*RA RAPTRGSYGGPLRLSSSSSLAS GRCVTSRASLRPRS
19744	50112	A	19859	1	276	
19745	50113	A	19860	3	151	GAVPAVRLGGPLHVHLPHAR*P SNLSALQFYQDGLRWWQTVS *RAASRSPPTRPVTIKSVCTPILP GWLSSLVANCIVKSASD
19746	50114	A	19861	1	386	DCVIATDAEVLGAPVKGKRRG RGPKGDKASDPEAGVARGIDF HHVSAVLNFDLPPTPEAYIHRA GR**CDGPGICMVGLRDLGCA GQSLRVGDASCTVFPCTARAN NPGIIVLTFVLPTEQFHLCKI
19747	50115	B	19862	26	186	

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19748	50116	A	19863	2	1839	ARGQVRRAALLSSAMEDSEAL GFEHMGDLPRLLQAVTDLGWS RPTLIQEKAIPLALEGKDLAR ARTGSGKTAAYAIQMLQLLLHR KQRQVRW*NRQ*EGLVLVPTKE LVARQAQSLIQLATYCCSGMS ELANVSAC*KTQSLRELCLMEK PDV VVGTPSRILSHFAARQPET FVTPWSFLVVERSLTFFFPFGFE EELKKSSSGKAESLAPDFNKAF LMSATFNEDVQALKELILHNP VTLKLQESQLPGARPVTA VSGG L*DLREDKFLLLYALLKLFIDSG ASLWLFCSL*EREFTGLRLFL WEQFQ/LSPTCVLNGELPLRSR VPHHL/QQFNQGFYGLCHRO/L NAEVLGAPVQGGASGPRAQRG Q/VPLDPEAGVARGIDFHHCVC/ VLNF*SFPTPEA\YIHRAGR**C DGPICMDSTR*QPRAS*PFVL PTEQFH/CRQD*GASQWREQGA P/SLLPYKFGMEEIEGFRYR*GV HPQDAMRSVTKQAIREARLUSLI KEELLHSEKLVYTFGRQPLGD LQALRHGPLYLCTPQLVEAPTW GHVPDLPGSSCFSVLGAAPFTK KREEACLPSCKRAQESKVPRT LRSFKHKGKKFRPDSQALREVV
19749	50117	A	19864	3	378	TTTKFAGRRPKVTVLGQP/KAA PSVTLFPSPSEELQANKATLVCL ISDFYPGAVTVAWKRGSPPVKA GVETTTPSKQSNKYAASSYLS LTPEQWKSHKYSYSCQVTHEGST VEKTVAPTEYLLRVY
19750	50118	A	19865	1	546	MAWTPLLLLLSHCTGSLSQPV LTQPPSSASPGESARLTCTLP DINVGSYNIYWYQQKPGSPRY LLYYYYSDSKGQSGVPSRFSG SKDASANTGILLISGLQSEDEAD YY/CGCFTVFWSF*VLVPEHQ QSWLPLWTPGVVSLV/CLVPS FVPPPLTKVPSSLSPVKESAILA VDIH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
19751	50119	A	19866	2	838	RVRVSTMAWTPLLLLLLSHCT GSLSQPVLTPPPSSASPGESAR LTCTLPDINVGIYNFYWYQK SGSPPRYLLYYSDSYKGLGSG VPSRFRSGSKDASANTGILLISGL QSDDEGADYYCATWDSSLTGQ VFGGGD/TKLTRP*GQPKACPP GVTLVPNPFS/SRSFQAQQGPQL VMSS*SDFLTPGSPLNSCPWK\A DSQPPFKAGIVETHTIPPKQSN QVRGPAGYLSLTA\EQWEVPTE SYSCQVTH*RGAPWEKTVGPY RMFHRFLNPSPPHHGMT
19752	50120	A	19867	1338	1854	NSETREHNHRYVPQRETSGGTD GWKSKQPE*L*RRQLVQSWAK S*NQPKLPSSPH*ELPWVTPSA RNFRSGPYSPPPPPQPLPSSHL SSLHFYSPFVSYTSFDLYSSSYH SYLMDEDTVPEKLRSSQKVIG HSFTGFQPTLSANPYDRGDGKII ELLPRKAQTFPVVRT
19753	50121	A	19868	1	500	GSTYSELLSGTACVVITALHLAQ QRRHHLLGGLASRHDAPEQLA VGAPVQPRPLPAPAGAQLVG HAHVVEGGP/PGSGGPGEGAI ARGPGAAAAAGAGPGAPRRRR LQASAGPCSRSEPGRRSAPRA APPAPSAGPHVAFPSRRPAAGS PPRSRPPPPGIPGTGGR
19754	50122	A	19869	20	507	TRQVYSGGVRTPPCQSHPHRPR SSCRPPPPRRPRSSRRRRGLSP RRAPAHWSSRSTRPAWWAPSR RHAPRPPWSPGASG*CSVYFPI LPLALFPLPVHHGGVHVCGREG VGLVQEGDSSHSGEWS*RSAWG STSLRAAPRSGGRPPAGGGWR YTRPPSRR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19755	50123	A	19870	236	1191	GSGRIPGRAGLEGPGPAFQKSR LSPASGSAGPRGASPSAVPPGR/ RPGVPAFPASNPPPVAAVPGPW VTCWKGKLGQEGKAPRAPH GTPQR/SPGSARPTGLSPFA*PSR *RARRRSPETP/PGHGRAGPPPP DGA VQRQGPGRAPASASRPPGS ARARRRRWPAARPPGCPARPG PRGGRPRRRPSPPAAGRARRRA PRTPAARSR*VCPGRRRSAAPP RGHGTA PCAA AAPP PPRGLGRP ADAEQ/PRCRCARPAPLPAPA GAQALVGH AHLLK AALGHDF TFLWATIH EVIPKMRWGQSQS QRGGPSSTPDLSA
19756	50124	A	19871	24	286	LRGQKVLLLGDRARLSQKKKE RKREEREREGHGRNGR/RRNG QGRGPEGQR*NERTGQERTGH GREGRKEGRKEGRKEGRNERE
19757	50125	A	19872	43	373	PRFTDENLEMCTVIQSVQCYHR SWH/HSSPPEPAPIHQSPAHSP VLCWFRRLLGGGEDWAPSSGGR AVWRSHCSFCSSSSCCSCSQ SGKRTAAAPWPTTSPAPSRSCC A
19758	50126	A	19873	3387	4083	AGRSALPVDVAVQVQAEGLWPP AVLLHHHHHPHHHHYHHYHHH HHHHHHHP*HHHPHHHHHHHHRN HHHHHHHHLLHHHHHHHHHHHL YHSHVHHHH/HHHHH DHHYHH FHDHYHHHHH/HYSHH/HHHP/ HHHH*RHDHY/AHHHHHQ/HH CHHCHHPHRGHYHYHHHGT VAFGALEDSAVARTGLPLPEGV LCGAPTAASAAVPPPAVPAPN QGRGPQLHPGQQLRPLLAHA ALQWPTTHL
19759	50127	A	19874	3	411	
19760	50128	A	19875	1	1095	
19761	50129	A	19876	1	471	
19762	50130	A	19877	1	554	FRGRLASPRFPVPMELGKLGQ FDA YPKTLED FRVKTCCGATV TIVSGLLM LLLFLSELQYYLTIE /VKGRGLMRGRGLAF*E*DL*G WEWGRRGLGLSLTEVALPQVH PELYVDKSRGDKLKINIDVLF HMPCA YLSIDAMDVAGEQQLD VEHNLFKQRLDKDGIPVSSEAE RHVLSFVVSAD
19763	50131	B	19878	1116	1274	
19764	50132	A	19879	28	389	

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19765	50133	A	19880	75	448	
19766	50134	A	19881	276	830	QEDSCPLHPLSGIPFRRFQPTPE EAGAVVPGEPTHDQGPSSALT RR*ACQGPLHLARTTAEPGHAH PWH*RWQRYMGKLRDLEKV CPVWSSVACSSPGLSWAGKTE AKTSLEGGNSASASASSWA WG RSSLAPVRDILGSREFSGLLEGT FVLSVTLSADFGIGTWVDLGKV TGSSSKEGRL
19767	50135	A	19882	223	1269	APVTKRKEVFAKDSKGSALDA GRDPKRPALEPETLCESGWASNT APTAPPQPGWCLCGKDFKSSCQ TPGREKERRLATMHGSCSFLML LLPLLLLLVATTGPVGALTDDE KRLMVELHNLRYAQVSPASD MLHMRWDEELAFAKAYARQ CVWGHNKERRRGENLFAITD EGMDVPLAMEEWHHEA*/DTT TSAP/HSCSPGQMCGRYTQVVW AKTERIGCGSH/SCEKLQGVET NIELLVCCNYEPPGNVKGKRPYQ EGTPGSQCPSGYHCKNSLCEPI GSPEDAQDLPLYLVTEAPSFRA EASDSMKMGAEKPSVVS LNSGPGHVWGPLLGLLLPLV LAGIF
19768	50136	A	19883	2	281	FVPALGSSAVMLSRRCVSRF SRSLSAFQ/KGVSLCQGPYPNS RKVVINNSVFSVRFRRTTAVCK DDLVTVKTPAFASVTEGDVR WEKGKI

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19769	50137	A	19884	1	1320	MPAVTILKPNLKQILGLKAAE VSSLPPSIVLDAKEITTTQITRQIL KGNCPLGRHSLPGVSLCQGPY PNSRKVVINNSVFSVRFFRTTV CKYDLVTVKTPAFAEPVTEGD VRWEKAVGDTVAEDVVECEIE TDKTLVQVPSPANGMIEALFVP DGGKVEGGTPLFLRKTGAAP AKAKPAEAPAAAAPKAEP AIVPPRAAPIPT/QMPVPSPSQPP SSKPVSAEAQNTCA\MLTIFNEI DVSNIQKMRARHKEAFLKKN LKLGFMSASVKASAFALQEOP VVNAVIDDITKEVVYRDYIDIS VAVATPQGLVVPVIRNVEAMN YADIEQTITELGEKARKNEFAIE DMDGGTFTISNGGVFGSLF/GTIP IINPPSAILGMHGIFDKPVAIGG KVEVQPMMYVALTYDHRLLIDG REAVTFLRKIKAAVEDPRVLLF
19770	50138	A	19885	1	1559	MESEALVVCINHCMAVNYGMI YQRGSSNMNLSLSLKHPEKTGI SPTANHGISDLQEGEAACGSLR TPLVGRRVLRPAFLPVVVRPYI RCPPALGSSAVMLSRRCVSRA FSRSLSAFQKGNCPGRRSLPED DLVTVKTPAFAESVTEGDVRW EKAAGDTVAEDVVECEIETDKT SVQVPSPANGVIEALLVPDGGK VEGGTPLFLRKTGAAPAKAKP AEAPAAAAPKAEPAAAAVPPPA APIPTQMPVPVPSQPPSGKPV AVKPTVAPPLAEPGAGKGLRSE HREKMNRMRQRIAQRLKEAQ NTCAMLTTFNEIDMSNIQEMRA RHKEAFLRKLKLRMLMSAIV EGSA\FALQEKPLLMGIDDDTT KEVVYRDYIDISVAVAIHPRGLV VPVIRNVEAMNFADIERITITELG EKARKNELAIEDMDGGTFTISN GGVFGSLFGTPIINPPQSAILGM HGIFDRPVAIGGKVEVRPMY VALTYDHRLLIDGREAVTFLRKI KAAVEDPRVLLDL
19771	50139	B	19886	239	3045	

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19772	50140	A	19887	3	809	RGRFLPPCHPAALPPCRPAALLP VVAARGAPSPPPHVLPCVGS LGYNMLGMINKSLFGSVETWP WKVLSKGDKEEVAEERACEG GKFAFTEVTDKPVDEALTGK QLPKVAKYAGGTNDKGIGMG MTVPISFAIVFPN*RWLSCRKCL KVWFDPDFQTNFQSDPPAPS/DKS VKIEEREGLHCLIPQFGGYAK/ EADYVVAQATRLRAALGG/PAT YRGDIYFCTGYDPPMK/PYGR NEI/WLFEDMSDPTERTYWEV CLCVSFLRG
19773	50141	C	19888	164	208	
19774	50142	A	19889	1542	1929	NLVPSLGSGLPWEINP/LSSCS LLHEKDPPPTSGPQTDQPKKHL TNFKAARPTVSWGRGKYPSTPS PSPLAASPAFLGKNPIAYFHT PYSYLCAPIPYFCAPTSLFLWR ARTTTPTPSLCLKSFL
19775	50143	A	19890	1	208	MPEPQRPVGPPEPPPGACYAC RKSGHWA/RNARSPLGFLSRVP SPPGPSRTPSFG*LSQWKPTCTQ VK
19776	50144	A	19891	1	1662	
19777	50145	B	19892	1	915	
19778	50146	A	19893	183	569	
19779	50147	C	19894	71	344	
19780	50148	A	19895	147	446	
19781	50149	A	19896	167	373	
19782	50150	A	19897	142	363	
19783	50151	C	19898	52	174	
19784	50152	C	19899	228	260	
19785	50153	A	19900	1	753	
19786	50154	A	19901	1	1077	
19787	50155	A	19902	500	912	LGSGDFPWEINPLSSCSL/LREK DPKTTSGPQTDQPSKHLTNLKS ASTPPPPNPFITSPPHTRSGLQFR STSSPPAPAQQFTLKKVAEAKG IVKVNAPFSLSDLSQISVRLGFI KYEKSSPVHGSFGSNPETLYSP
19788	50156	A	19903	1	861	
19789	50157	B	19904	174	222	
19790	50158	A	19905	1	756	

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19791	50159	A	19906	1035	1852	NLVPSLGSGLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARPTSWGRGKYPSTPS PSPLAASPAFLGQRQVPLSWGR GRCPSTPSPSAASPAFLGQQGQ RQVPLSWGRGRCPTSPSPSA ASPAFLGQQGRQVPLSWGRGR CPSTPSPSAASPAFLGQQGRQ VPLSWGRGRYPSTPSPSAASP AFLGQQGRQVPLSWGRGRCP TPSPSPSAASPAFLGQRQVPLSW GRYPSTPSPSAASPTFLGQDL PLSWG
19792	50160	A	19907	1644	1981	LGSGLPWEINPSSSSCLLREKD PPTTSGPQTDQPKKHLTNFKSA *KRTNTASYK/WHQSQRVPAPR DGLVAAPTESEVAFLVPVPHQG PPLGNLGPSTVTTSFRCWLLDP RS
19793	50161	A	19908	1011	1154	
19794	50162	A	19909	1043	1168	
19795	50163	A	19910	1328	1470	
19796	50164	B	19911	406	1191	
19797	50165	A	19912	2848	3140	SFYHLSSSHLVRLTVSFRD*PSP TCPAIYS*KGGWSQRHSQGACY TCRKSGHWA/RNARSPGFLLSH VPSVWDPTENRTVQLTWQPIPE PLELWPKAL
19798	50166	B	19913	1	941	
19799	50167	A	19914	656	1983	NLVPSLGSGLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSEAKEICFIREKTPAPVT DWEGSLPLVFNHCRDASLIHS RFKGVPRPRDACLGPSPAAASP FLGKGQRLKTDARLPRKPPRP SRMPSFGVKHVNVTIDCLPEGA ATRGTARTSKPTTKSQKTLPT SPGHWTQSTPWASALRSSPWTE TAAPSETEETLNTGRPPPELARA TATWFSASHTLPALATRRVART QWLTAQRQTWASISSVPWAQT ISEKKPGGSLWETRSPPTTAGT EEAMNTTSLAPAAEIMATPGS PSQASPTSGAFTHGQTSPSTKA TAPRYPQTGNSILTFGRPFLPFA GDLFAEWPFTAGEEPVLVPRPH QVSKTRSPPSFHLTLKTVTVLAL LGNGEFCYVYLSVSELREIRTR LYSPDAGLNEEKMLTKLLLI
19800	50168	A	19915	117	432	
19801	50169	C	19916	122	289	

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19802	50170	A	19917	1	516	
19803	50171	B	19918	212	3302	
19804	50172	C	19919	181	444	
19805	50173	A	19920	151	485	SPRGHYQLLLSGRALADRYRKRI YTAALNDRDQGGGAGHPAS/ RSENLENTV/IIPDIKLHNSPSAFN IYCNVRHC/VLEWQKKEISLAAA SKNSVQSGESDSDEEESKEPPI
19806	50174	A	19921	1	3465	
19807	50175	A	19922	1	176	
19808	50176	A	19923	114	14211	AAPVAAPGALFMPVPDGSVAA AGLGLGLPAADSPGHYQLLLSG RALADRYRRIYTAALNDRDQG GGGAGHPASRNKKILNKKKLK RKQKSKSVKTRKSENLENTV IIPDIKLHNSPSAFNIYCNVRHC VLEWQKKEISLAAAASKNVSQVS GESDSDEEESKEPPIKLPKIIIV GLCEVFELIKETRFSPSLCLRS LQALLNVLQGGQPEVLQSEPPE VLESFLQLLEITVRSTGMNDST GQSLTALSCACL
19809	50177	A	19924	375	1191	SQGIPELHYTPGPRGRWCGW/W PIVEPRMGASQGCCVLGHQAQ QGGGASQAVRGANGVHAGCR GDPHPRSDHYPGGRFWLPGAS QDPAVAPGGHGHPSYLARLPC AAEPGTP/PAEPPRSSLPGAAT APAGT*/PALADAPPRRVGGAG QPGRGHV*PKLVPGWQSQDSI* PSL/PSSPARHTLAASATP*APGS GARPAW*C*WAPALAPVIPVD AHSPP/GGAGHGGPH*GPRGSV LGLRLPAGCPGPRQPHRPQSG PQPSSPPGGALRSASR
19810	50178	A	19925	3	543	SDDQPEKPHFDSRSVIFELDSN SGSKVCLVYKSGKPALAEDTEI WFLDRALYWHLTDITFTAYYR LLITHLGLPQWQYAFVSYGISP QAKGITKATCEWGEHIPLGSM AINSISKLTQLTQSSMYSLPNAP TLADLEDDTHEGRKGTEGSQL KCEHQLPPPMHSHVGGGQRESL ARKEK
19811	50179	A	19926	1	392	FLDRALYWHLTDITFTAYYRL LITHLGLPQWQYAFVSYGISPQ AKITYNIKMNRRKCVHWKLAIV EPLQWELRSCVSGMGTGPKQ KVSSMKPRSCVCSRRQNSMG TTVSQSFLSYGKNVLFPPVRCC

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19812	50180	A	19927	1	1081	RAMEEEASSPGLGCSKPHLEKL TLGITRILESSPGVTEVTIEKPP AERHMISSWEQKNNCVMPEDEV KNFYLMTNGFHMWTSVKLDE HIIPLGEALAINKHLKTDFSFTQ SSMLFTFLIAPTLLGQTWEDDTH GSQWMIQPEKPIIFGLFAVLIF* GWVSI CNGSGKVCVLYKSGVK PALAEGHWRFLEPGTELLYWH FLTDFTTAYYRLLITHLGLPQ WAILPFTSYGISPAQKWFSM Y*TYSPYNTNLV/TQKETDSFCG IKLDPSKVF*GGKNKIVIPKKKG PVQAGGQKGPFRDPPVPSISSI FKSSSGLWGNPTREVSTPPNSL PAPEWWFPCTDGRGDLQFCV WTVGLFLVE
19813	50181	A	19928	1	2835	MDALMLALGALMLALGLGDP KSAQVSDPDGAEPGPRATGT DPLVQIHWKLGISEALSIPGGRL YRDLWSLTPVCLHIPGIAHHGP FTLGRMDVVEVAGSWWAQER EDIIMKYEKGHRAGLPEDKGPK SFGSYNNNVDDLGVHETELPP LTAREVKQIRREISRKSWVKM LGEWDTYKNSRKLIDRAYQGIP MNIRGPMWVLLNIEIKLKNP GRYQVRSARAQPTGQAVSGAQ VSSWRERQDHPGELGVKI
19814	50182	A	19929	3	142	TISSIIIRKARKPQDLLNNYTPRS SPLRSSGRTRMYKGNVRPGNS S
19815	50183	A	19930	904	1295	WALMNGSESFFVSSSQGRSEL VPNS/NYAVDY*PLTAHAVSSG GTSPVLARLLREKLESLLPLHL GQVAKYAGQLRGRVKQGFAT MGERRRFWEKLFVNDR/AGAV AGKQRSSEHY*NDRTVNQRTA RPSR
19816	50184	B	19932	1	1050	
19817	50185	A	19933	303	384	

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19818	50186	A	19934	375	1161	EALESAPEG/RR*GSGTKTSLSPS P/PAGSWVCRIPMGRGCRHGAE R/P/PGSQESSPSNGHGKLAGPSP YLGGRFKSSS*T*QSPQTPAQGV AS*GLGAAPVLRLLQGPVPPSHC GKSRPDPC*PSPGSPDPGERES QQESQ*WPPVGELCTDPTGNPE RGGRHLQSHAPSGGGLSGFPS DSFPCSCYYGSTPVARKKRFAK CRGYIYDFVYELLSLKPPSQGV AEMPPFAVGQQG/QAEPGRIPQ SPAGGRVFFQDFYSLCLNTS
19819	50187	B	19935	62	346	
19820	50188	B	19936	1	1629	
19821	50189	A	19937	1	1218	
19822	50190	C	19938	718	1053	
19823	50191	A	19939	54	212	
19824	50192	A	19940	122	451	
19825	50193	A	19941	329	398	FFSYFRPSGCILPL*ELPEARCP
19826	50194	A	19942	92	346	VGSSPSRL*SLRGQVLNKN*/S/ QLGCLHIVGNPI*NS*DVPWAG WSED*GRRWISSRSSSKDRGPV S*RSPPVPGQLQHQMASHAM
19827	50195	A	19943	284	374	LKNHNRSEYALPHLN**PSTTK EV*/M/DRS/SALSDITL*KSFSW LILAQKSPPLSTLQPLLPAEQ TLFDCNSPLPTQL*NGPTLISLR *LSQDEPGKGLSQGNVIT
19828	50196	A	19944	1	1674	MAPPSPFADSLFGLSPAPRDK GDTFYPTWQNSGARHGLGRQP SLGVSSLQGRSLDHSPTFQRCQ TTQGRPLPWSFTLSGKSCFSEEG AIPTPSVAESFQSSFTDPSDLSP PPQPAHRQAEPSNSSASTPPP YNPPTTSPPHTRSGLFSSATSS SPPAQFPLREVAGAEIGVNAH VPFSLSDLQSISQHLGSFSSDPT KYIQEFYLTLSYNLTWSDLNV ILTSLSPDERERVFPVSQSHAD NRRLHEP

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19829	50197	A	19945	1746	3501	ESDPSNSTTSMDRITLL/MSSIVP RLPSACRILPTGFTIPE*SCVHRT ASLIPPLPPGSRKYSPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTSPLDISHQQAALLRTY LKNLSPIYNSTPPIFGPLTTQTIT PVAAPLCISWQRPTGIPLGNLSP SRCFTLHLRSPTTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCLSLHPWLSPPCSDSP PRPSSCLLIPSPENNERRLLVDT RRFLIHENRTFPSTQLPHQSPL QPLTAAALAGSLGVVWQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPILPLMVLGLSASTVA LGTGIAGISTSVMTFRSLNDFS ASITDISQTLVLQAQVDSLAA VVQLNRRGLDLLTAEGGGLCIF LNEECFYLNQSGLYVDNIKKL KDRAQKLANQASNYAEPWAL SNWMSWVLPVSPILIPFLLLF GPCIFRLVSQIFQNRQAITNHSI RQMFLLTSPQYHPLPQDLPSA
19830	50198	A	19946	1392	1676	GFCILHIVLEPWFSAPSAPLSTSL YWL*LYILLNFFQSFQLLCLW FECPPVAQSNLIV*SLLSARQS HSPSFFPLLVRCNCPLEERCS
19831	50199	B	19947	1	1500	
19832	50200	A	19948	107	691	ITMLLIQSLFGGLFTWTRMKFG AVARIGGHPGLGQSPSSCSLLP EKDPPTTSGPQIDQPKKHLTDF KSGTPL*LYTHVSRVSDHAGTP ALVLHPYVGKSRFSGEGATQRQ YPIPQALKGLMPAITRLLQHG LLKPINSPYHSPILPVLKPKPY KLVDQLPLSTKLFCSTPWQCQT HILFYQYVLPQLPIILF
19833	50201	B	19949	1	2628	
19834	50202	B	19950	1	585	
19835	50203	B	19951	178	462	
19836	50204	C	19952	1	825	

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19837	50205	A	19953	644	1795	RPSKSQTMNLNSLSTALIIISKIYFL PHT*HIYFLLPGSFCYTHSLLSLP QLPLFL/CLDLNAAASHIIDTTPD PHDCISLIHLTFTFPQISFFPVSHIP DHTWFDIGSSTRPNATTHQQRQ AML*YLPHLSLRLPLCLPPLPLS KPN*LP*LPKPSNYPNSPILPVQK PDKSYRLVQDLRLINQIVLPIHP VVPNPYTLSSIPSTTHYSMLD LKDAFFTIPLHPSSQPLFAFTWT DPDTHQSQQLTWAVLPQGFED SPHYFSQALSHDLLSFHPSASHL IQYIDDLLCSPSFESSQDDTL LLQCLFSKGYRVSPSKAQISSPS VTYLGIIHLKHNTHALPADRWPS CLRAAAAAALILVEALKITNYA QLTLYSSHNFNQLFSSSHLTHIL SAPRLLLLYSLFVESPTITIVPGL DLNAAASHIIDTTPDPHDCISLIH LTFTFPQISFFPVSHPDHTWFD GSSTRPNHHSPAKAGYAIVSST SHIETALPPSTTSQQAELVTLT QALTAKGLRINIYTDISKYAFHI LQHHAVIWAERGFLTQTQSSIN ASLIKTLTKTLLPKKAGVIHCK GHQKASDPALGNAYADKVAR QAASSPTSVPHSQFFSFASVTPT YSPTESTYQSLPTQKGWFLDQ GKYLLPASQAHSILSSFHNLFH VGYKPLDRLLLEISFSPWSKIL KEITSQCSICYSTTPQGLFRPPPF PTHQARGFAPAQDWQIDFTHM
19838	50206	A	19954	52	641	RPSKSQTMNLNSLSTALIIISKIYFL PHT*HIYFLLPGSFCYTHSLLSLP QLPLFL/CLDLNAAASHIIDTTPD PHDCISLIHLTFTFPQISFFPVSHIP DHTWFDIGSSTRPNATTHQQRQ AML*YLPHLSLRLPLCLPPLPLS KPN*LP*LPKPSLLQKDYASISILI LNMPFIFCTMQSYGLKEVSSL HKGPSSL MPL
19839	50207	A	19955	3	380	ITPDPHDCISLIHLTFTFPFHISFF RVPHPYHIWFDIGSSTRPNATH QQRQAML*YLPHLSLRLCLCPP PLPLSKPN*LP*LPKPSLLQKDYA SIFILTLNMPFISCTTMQEVSSLIH KGPLSLIPL

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19840	50208	A	19956	154	485	TFIRTHFLTQFPQPCPRHQPSR*L SSSPAG*TG/IFARLLIFSCLLQI LNHM/QHTLAGQSVLVKNLTP QTLQPRWTGPYLVYSTPT/VRP PAGSSPLGSPFQSKAVSISQPA
19841	50209	A	19957	158	416	ISGTCSNLLGEEVLEERLAAAV QAFGSSRVLEMWLGFSVQWRQ VIVTQKCIWVLLPLYYCTP*R QG*LIPVVGFEQILIFEVFS
19842	50210	C	19958	1	1755	
19843	50211	A	19959	2	394	
19844	50212	A	19960	710	1093	KEPTQHSFSYTHSLSLPOLPLF L/CPDFNPASHIIPDTPDPHDCI SLIHLTFTPPHISFFPVSHPDHT WFTDGSSTRPNATHQQRQDM Q*YLPHELLTLPCLPPPLPSKP NQLP*LRPSLLQKG
19845	50213	C	19961	1	1287	
19846	50214	A	19962	1	1293	MEEPLGFKQLTVVAQQNPLWT SGGGGHSPPSGGHRGVCIITLP VPEGSSQKETHPVSEKLKEKNE SLPGNPENSSSRERPPRRHSKA RDSDENDPDEDAVNVAVGC LGKNSGFLAPELQKYQKQIKDG TAGTPAISTTTVEIRKSSVMTT GDHLLSGKKAQRPA PGHSSCPS TETEEKGKRLLYVWVWQVA VNSASQLEAHNSENVPVLSERI RERPGLVHGYRPSRSLPHSL GSYSLWALRTDTVCD
19847	50215	C	19963	1	846	
19848	50216	B	19964	377	1172	
19849	50217	A	19965	564	1163	FKPSIFFLPPDAYTFLFPWLLQL YSLFVESPTTHCSWPRLQSGLP HYSGYHT*PS*LYLSDPPDIHPIS AYFLLSCSSP*SRLIY*WQFHQA *SPHTSKGRCLCYSTSH*PAS*NL SFPFHRGNVSSRK*LLSVPSAIL LLLRDYSGLPSLHIKLRDLPPP RTGKSAVYTCPESGN*NTSWSR *TLICQS
19850	50218	A	19966	1382	1778	PIGTNTECVVLFQPMETGHSSR VNMSGYK*PC/PPLFGVLSWQN CWRVYFPCLLFGGPLSVMDPE GSPSGC/SNSLGLGADSVTLSTG GVFQPNVRGLNCGKIVMGRC PLEFVPIPATSPISRKPERSTAF

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19851	50219	A	19967	239	737	RPSFKTPENSPTLVPTWTTLFYA LFFSYPHLPISLRPKYFNQICF PDYSWSTATSHCCPSSQSK/CLL CV/SLTSPQYQPLPQDLPSA*SLP L*VPTPLPLEAALRNIAHLSI PPPKNFRRSNTSTLFCFICLINIR RQECQASEPRPGHRIPCDLHVYI QMA
19852	50220	B	19968	1	1321	
19853	50221	A	19969	1	1069	
19854	50222	B	19970	758	6451	
19855	50223	A	19971	53	319	CSGSMPSSSVSRRPTSPFGSPLLS SPATSSSPKTPPTSATSGSSCPTT GL*MTWTWSGFTGPVKAATWR WTSATYPRWSWRPRAPLCP
19856	50224	A	19972	1427	2103	RPVHGHLHAPVVRDVSVRGLA PSSSPRVPGRDLIKQTPRLRARV VLSPFKTADAASHPGLTQPGR GRMKADISAATPGPFMCRTPL ALGVSTEPSARLVLFVLFCE VLRRLSALSPRLEVLDLGLSL QPPPPGFKQFCLSLPSSWIDYR CMPPWAG/QFLEF*VEDGV*HI GQADLELLTSGDPPASASQSAG ITGVSNRAQPQVSECCHGVAL RRQ
19857	50225	A	19973	3	320	VRMVIKKSENRCWRCKGEIG MLLNCW*ECKLVQPVWKT/VD PAIPLLGYPKDYISFYGKDTCT HMFIVALTIAKTGNQPKCPMI DWIKKMWHIYTMEYYAAI
19858	50226	A	19974	2	79	
19859	50227	A	19975	308	630	GREKAREQVDLTFTIAKTWN QPKCPSVIDWIKKIWHIYTMGY YAAIKKDEFVSFAGTWMKL*T VSVEADPHIEGRFFRKNYASK TPSLKLQRQSRPFQETSHPTGIE KRSPPNLQKATQPHIMSKEYA FSRKMVGKTRKKGEVKVRER KGKGAGRSDDTYNSKDLEPTQ MPISDRLDKENMDIYTMGYA AIKKDEFVSFAGTMDAENVQ YSSRARTRHWSMKILLQLAR CLPKWPLSFVLESQGLGGVGS

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19860	50228	A	19976	2	508	KTTMRYYLTPVRMAIIKKSENN RCWRGCGETRMLLHCWFECKL VQLLWKTW*FLKDVELKIPFD PAIPLLGVPYKDYKSCYYKDT TRMFIAALFTIAKTWNQPKCPS VIDWIKKMWHIYTMYYAAIK KDEFVSFAGTWMKLETILSKL SQGQKTKHRMFSLSIGS
19861	50229	A	19977	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIIKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DLDPAIPLLGVPYKDYKSCCYK DCTRMFIAALFTIAKTWNQP
19862	50230	B	19978	1	1899	MIILDAEKAFDKIQQPFMLKTL NKLIGDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTQRQCP LSPLLFNIVLEVLAQAIRQEKEI KGIGLQKEEVKLSLFADDMILY LENPIVSAQKLLKLSINVSXVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWQEGEHHTLGPV VGWGKRGIALVDIPNVNDKL MVLVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSINFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPKDNKKWGNDSL FNKW CWENWLAICRKLKLDPLTPYT KIHRSWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVVKLSFCTA KETTIRVSRQPTWEWKIFA1YPS DKGLISRIYKELQIYRKVTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSLVIREMQIKTTM
19863	50231	A	19979	1	2142	
19864	50232	A	19980	1	5127	

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19865	50233	A	19981	209	3816	QGRPTFRFRKYREHHKDTPREELQLQDT*SSDSPKLLK*KKK*GQPERKVKLPTKGSPD*KRISRQ/KTLQARRQSWFFEKINKIDRPQARLKKKKREKNQIDTIKNDKGDITTDPTETIQTIREYYKHLIYANKLENLEEMDKFLDTYTLRLNQEEVESVNRNPTGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVPLLLKLFQPIEKELIPNSFYEASII LIPKPGRDITTKGNFRPISLMNIDAKIL
19866	50234	A	19982	1	1698	MELKAKAQELREECRLSRRCNQLEESVSVMEDMNMKREGKFKREKRIKNEQSLQEIWDYVKRPNLRLTGVEHSDGNGTKLEN TLQDIIQENFPNLRQANIQIEIQRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKGWVTHK GKPIRLTVDLSAETLQARREWGPINILKEKNFPRISSYPAKLSFI SEGEIKSFTDKQMLTDFVTTRPALQELLKEALNMERKNRDTHRLKIKGWRKIYQANGKQKKAGVAILVSDKTDFKPTKILDKKEGHYIIVKGLIQEELTILNTYAPSTGAPRFIKQVRSDLQRDLDSHTLIIGDFNTPLSTLDRSTRQKVNKDTQELNSALHQADLIDYRTLHPKSTEYTFFSAPHHTYSKIDHIVGSKALLSKCKRTEIITNYLSDHSAILKELRIKKLTQNHSTTWKLNLLNDYVYHNEMKAEIKMFFETNENKDDTYQNLWDTFKVVCTGKFIALNAHKRKQERSKIDTLTSQLKELEKQEQTHSKASRRQEITKIRAELEKEIETQKTL/QKINESRSWFFERINKIDRPL
19867	50235	A	19983	1	3450	
19868	50236	B	19984	1	2265	

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19869	50237	A	19985	1	2526	MFFETNENEDTSYQNLRDFTKVV VFRWKIILNAHKRQKQERSKID TLTSKLKELEKQQQINSKASRR HEITNIRAELKEIETQKTLQKIN ESVNWFFEKIIRLLARLIKK KREKNQIDSINKDIEDITDPVE TQTTVREYFKHLYANKLENLEE MDKFLDITYLPSLSQEEVEPLN RPITGSEIEAIINSLPTKKSPPGD RFTAKFYQRIINTEKCLKELME/ PESQSSRTT*RMQKQPESMRST GRKGFSDGR*NE*NE*RGWVN QVGKHSAGYYPGELPQTSKAG QHSDSGNTENATKILLEKSNSK TYNCQIHQS*NEGKNVKGQRE RNTNYHQRIQLQTPLRK*TRKS/K EMDKFLDYTLPLNNEEEVESL NTPITGSEIVAIINSLPTKKSPPGD DGFTAELYQQRQTESQIMSELPF TIASKRIKYVGIRLIRDVKDLFK ENYKPLLSEIKEDTNKWNIP SWVGRINIVKMAILPKVIYFRN AIPKLPMPPFTTELEKTTLNFIW NQKRAHIANILSQKNKAGGIT LPDFKLYYKATVTKTAWYVY QNRIDEWNTTEPSEIMPHIYN YLIFDKPEKNQWEKDSLFNK WCWENWLAICRKLKLDPLFTP YTKINSRWIKDLNVRPKTIKTL ENLGTIQDIGIGDDFMSTPK AMATKAKIDRWDLIKLSFCT AKETTIRVNRQPTKWEKIFATY
19870	50238	A	19986	1	3723	
19871	50239	A	19987	1	1023	
19872	50240	B	19988	91	1596	
19873	50241	B	19989	1	3171	
19874	50242	A	19990	1	2952	MLLNQGRKLPRVFAEETLKFK GTSNKPQTLEQISTSIQAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLEFEQTLNLYQEFLLTP QWHLECCQERTVHSPGKAAEA REPSVIDRHLEQESSNWHLVGA ALGQSFQRKEQAAIFAVLPQLL VIPRQTGSGVDLQKTPPTDLQQR GLIVRRKTNKQKGIHVNSTTRE QNWTENEFDKLTGGFKRWVI TNSSELKEHVLQCKEDKNLEK SAIKLELRKLNLIQN
19875	50243	A	19991	1	1797	

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19876	50244	A	19992	1	2367	MVKGSIQQEELTNLNMYPAPNT GAPRFIKQVLSDLQRDLDSHTLI MGDFNTQLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYISDHS AIKLELRRIKNTQNCSTTWKLN NLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKVVC RGKFIALNAHKRQKERSKTDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKEITQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAINKDKGDIITDPTEIQS TIREYYKHLYTNKLENLEEMD KFLDTYTLPRLNQEEVESLNRP TGAEIVAI/NNLPTKKSPGPDGF TAEFYQRKEGILPNSFYEASILI PKPDRDITTKENFRPISLMNID AKILNKILANRIQQHITKLIHHD QVGFIPGMQGFNFIRKSIRVIQ HINRTKDKNYMISIDAEEKAFD KIKQCFMLKLTNKLKIDGTYYF IIRAIYDKPTANILNGQKLEAFP LKTGTREGCPLSPLFNIVLEVL ARAIHQEKEIKGILGKEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSQYKINQKSAQFL YTNNRQTESQIMSELPFTIASKR IKYLGILQLTRDRKDLFKENYKP LLEKEIKEDTNKWNIPCSWVEK INIVKMAILPKVIYRFNAIPKLP
19877	50245	A	19993	2	2910	WRKIYQANGK/QKKAQVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIHQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTIIMGDFN TPLSTLDRSMRQKVNKDTQEF NSALHQADLIDIYRTLHPKSTE YTFFSAPYHTYSKIDHIVQSKAL LSKCKRSEIITNCLSDHSAIKLD LRIKKLTQNHSTTWKLNLLLN NYWVHNEMKAEIKMFFETNEN KDTTYQNLWDTFKAVCRGFIA LNAHKRQETS
19878	50246	A	19994	1	4729	
19879	50247	A	19995	1	1566	
19880	50248	B	19996	1	2796	
19881	50249	B	19997	127	2479	
19882	50250	B	19998	1	2907	

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19883	50251	A	19999	1	3210	MVKGSIQEEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYVVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQ LELEKEQEQTHSKASRRQEITKIR AELKEIETQ
19884	50252	A	20000	1	2052	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNCLSDHS AIKLELRINKLTQNRSTTWKLN NLLNDYVVHNEMKAEIKMFF ETNENKDKTYQNLWDAFNAV CRGKFVALNAHKRKQEGSKID TLTSQLELEKEQEQTHSKASRR QEITKVRAELKEIETQKTLQKIN ESRSVARLIKKKREKNQI/DAIKN DKRDITDPTEIQTITREYYKHL YANKLENLEEMDKFLDTYTLF RLNQEEVESLNRPTGSEIVAIIN SLPTKKSPGPEGFTAIFYQRYK EELVPFLLKLFQSTEKEGILPNS FYEASIIIPKPGRDTTKKENFRP ISLMNIDAKILNKILAKRIQQHI QKLIIHHDQVGFIPGMQGVFNIC KSINVIQHINRTKDKNHMISID AEKVFQKIQQRFMLKTLNKL LEVLAARVQEKKIKIGIQLGKE ELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSEYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLEKEIKEDVNKWKNNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTSFTELEKTTFKFIWNH KGARIAKSILSQKNKAGGITLPD FKLYYKATVTKTAWY

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19885	50253	A	20001	1	2314	MDKFLDITYTLPRLNQEEVESLN RSITGSEIVAILNSLPTKKSPPGD GFTAIFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEAIIIPKPG RDTSKKENFRPIPLMNIDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVQHTNRA KDKNHMIIISIDAFAFDKIQLF MLKTLNKLGDGMYLKIRRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLFNIVLEVLARAIR QEKEIKGIGLKEEVKLSLFAD DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTLASKRIKYLG IQLTRDVKDLFKENYKPLLNEI KEDTNKWKNI PCSWVGRINIVK MAILPKVIYRLNAIPIKLPMPFF TELEKTTLKFIWNQKARVAKS ILSQKNKAGGITLPDFKLYYKAI VTKTAWYWYQNRDIDQWNRT EPSEITPHINNYLIFDKPDKNKQ WGKDSL FNKWCWENGLAICRK LKLDPF LTPYTKINSRWIKDLN VRPKTRKTEENLGITIQDIGMG KDFMSKTPKAMATKDKIDKW DLIKLSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYA AKKHMKCCSSLA IREMQIKTTMRYHLTPVRMAII KKSGNNRLFTVAKTWIPKCA

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19886	50254	A	20002	1	2685	MGDFNTPLSTLDRSTQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRINKLNTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLEKEKQEQTHSKASRRQ EITKIRAELEKETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHLVANKLENLEEM DKFLDITYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAIFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD

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19887	50255	A	20003	1	2502	MTELTGIQQPQIVLFEHKGHKL VQSSSDAGKVNRIYQHYEAS DKFNYTTGLAWKTAPEQTGKT VRKQIQKLNKVMESRSKMQE HSSPPMEQSWRENDDELREE AFRRSNYSLEQEEIQTKGQEVK NFEKTLDEYITRITNTEKCLKEL MELKAKARELREECRLSRSCD QLEERVSVMEDEMNMKREG KFREKRIKRNEQSLQEKWDYV KTPNRLIGVPESDGENGTKE NTLQDIQENLPNLVRQANIQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTTR EYKHLKYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPTGS EIVAIHNSLPTKSP/GPVGFAT FCQRK/EGILSISFCEASILIPKL GRDTTKKENFRPISLMTIDTKIF NKILANQIQHHIKLIHHDQVG FIPGMQGWFNICKSINVIQHNR TKDKNHMIISIDA EKA FDKIQQL FMLKTLNLKLGIDGTYFKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLGAIR QEKEIKGVQLGKEEVKLSLFAD DMIVYLENHIVSAQNLLKLISNF SKVSGYKINVQKSLAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLNEIK EDTNKWKNIPCS WVGRI NVK MAILSKVIYRFNAIPNLPI TVFT
19888	50256	B	20004	1	2115	
19889	50257	A	20005	1	2382	
19890	50258	A	20006	1	2742	
19891	50259	A	20007	1	2250	
19892	50260	A	20008	1	2982	
19893	50261	A	20009	1	4791	
19894	50262	A	20010	1	2499	
19895	50263	A	20011	1	3259	
19896	50264	A	20012	1	3654	
19897	50265	A	20013	1	2391	

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19898	50266	A	20014	326	1158	LWICEVMVKQRSRLKICLQKQ WQKTLAMWLKPCMGTFLQL C*LDIAWV/RAIAVHTASSNLVP SLLGLCMIDVVEGTAMDALNS MQNFLRGRPKTFKSLENAIEWS VKSQGQIRNLESARVSMVGQVK QCEGITSPEGSKSIVEGIIIEEEE DEEGSESISKRKKEDDMETKKD HPYTWRIELAKTEKYWDGWFR GLSNLFLSCPIPKLLLAGVDRL DKDLTIGQMGGKQFQMVLPQC GHAVHEDAPDKVAEAVATFLI RHRFAEPIGGFQCVFPGC
19899	50267	A	20015	1	2860	
19900	50268	A	20016	1	2956	
19901	50269	A	20017	1	3359	MNNSIKEVKVLSLTKWEMQTK PNNNTV/DLKDAQEVNLTSTDY RKQHVM/LPTEINSDSLKIGVI RLANWIKSQDPSVCCNQETHLT CRDTHRLKIKGWRKIYQANGK QKKAGVAILVSDKTDKPTKIK RDKEGHYIMVKGSIQGEELTIL NTYAPNTGAPRFIKQVLSLQRL DLDSYTLIMGDFNTPLSTLDRS TRQKVNKDTQELNSALHQVDL IDIYRTLHPKSTEYTFPSAPHHT YSKIDHILGSKALLS
19902	50270	A	20018	3	3130	
19903	50271	B	20019	8	2398	
19904	50272	A	20020	3	3398	SNSHITLTLNVNGLNAPIKRHR LANWIKSQDP/SVSCIQETHLTC RDTHRLKIKGWRKIYQANGKQ KKSTVAILVSDKTDKPTKIKR DKEGHYIMVG*IQ*EELTLNI YAPNTGAPRFIKQVLRDLQRL DSHPIMGDFNTPLSTLDMSMR QKVNKDIQDLNSALHQADLTDI YRTLHPKSTEYTFSPPHHTYSK TDHIVGSKALVSKCKRTEITNC LSDHSAIKLELRKIKLTQNRSTT WKLNNL
19905	50273	B	20021	483	2210	

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19906	50274	A	20022	1	5316	MVKGSIHQEELTILNIYAPNTG APRFIKQVLSDLQRDLDFHTLI MGDFNTPLSTMDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFYSAPHHTYSKIDHILG SKALPSKCKRDTIITNYSLDHSA IKLELRINKLTQNHSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYENLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQE TKIRAEQINKIDR
19907	50275	A	20023	2	2712	WRKIYQANGKQKKAGVAILVS DKTDFKPTKJKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPTFI QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYSLDHSAIKLELM IKNLTQNHSTIWKLNLLNDY VWHKEMKAEIKMFFETNENKD TTYQNLWDTFFKAVCRGKFIAL NAHKRKQERSKIDTLTSQLKEL EKQEQTLSKASRRQEITKIRAE KEIETQKTLQKINESRSRFFERIN KIDR* ¹ TLARVIKKKGEKNQIDTI KNDKGDIITDPTEIQTITRESYK HLYANKLENLEMDKFLDTYT LPRLNQEEVESLNRPIITGSEIVAI VNSLPTKKSPGPDGFTAIFYQR YKEELVPFLKLLQSIEKEGILP HSFYEAHILPKPGRDITTKK ¹ EN FRPISLMNIDAKILNKILANQIQ QHIIKKLIHHDQVGFIPGMQGW NTCKSINVIQHINRTKDKNHMII SIDAEKAFDKIQPPFMLKTLNK LVLEVLARAIHQEKEIKGIQLGK EEVKLSLFADDMIVDLENPIVS AQNLKLLISNFSKVS ¹ GYKINVQ KSQAFLYNNRQTESQIMSELA FTIASKRIKYLGIQLTRDVKDLF NENYKPLLNEIQEDTNKWKNNP CSWVGRINIVKMAILPKVIYRF

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19908	50276	A	20024	1	4461	MVASRSSRVGVFYGGQNSVDG VSRSDGSLNELCLYRPPTGAY LAYDTLDVLPQGQFTVNTPPID VNGKSLALLWEHTSLTSMG GGRWAMQPLGQLGQLEHLGD RRDQVLD RSGRSRLDAAQHL RHRPDRRPQGMVGVLTNQKEP RTRWIHSRILPEVQGGTGVPS TIPIDRKEGILPNLFDEASILIPK RGRDTTKKENFRPISLMNIDAKI LNKILANRNQQHIKKLIHHDQV GFIPGMQGWENICK
19909	50277	B	20025	1183	4247	
19910	50278	A	20026	1	2671	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSLDQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNLYSDHS AIKLELRJKNLTQSRSTPWKLN NLLNDYVWHNEMKAEIKMFF ETNKNKDTITYQNLWDFAKAV CRGKFIALNAYKRKQERSKIDT LTSOLKELEKEQTHSKASRRQ EITKIRAELEIETOKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDTIKNDKGIDITDPTIEI TTIREYYKHLNANKLENLEEM DTFLDYTLPRLNQEEVESLNR PITGSEIVAHNSLPTKKSPGPDG FTAEFY/PESYL*QTHSQYHTEW AKTGSIPFENWHKTGMPSLTAP IQHSVGSSQGQNAQEGNKGY SIRKRGSQIVPVCVCR*HDCLSRKP HRLSPKSP*ADKQLQQLRIQN QCTKITSILHQKQTNREPHE* TPIHNCFKENKIPRNPTYKGCEG PLQGLQTTAQRNKRGHKQME EHSMLMGRKNQYRENGHTAQ GNLQIQCHPLQATNDFLHRIGK NYFKVHMEPKKSPHRQVNP KEQSWRHHTT*LQTLQGYNSQ NSMVLVVPKQRYRSMQNRAL RNNAAYLHYSDL*QT*EKQA WGKGIPYKMLALGKLAS/PM*

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
19911	50279	A	20027	1	3159	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLNDYVWHNKMKAIEIKMFF ETNENKDDTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTSHKASRRQ EITKIRAEKIEITQKTLQKISES WSWFFEKINKIDRPQARLIKKK REKNQIDTIKND
19912	50280	A	20028	2	3767	HIRLANWIKSQDPSVCCIQEAYL TCRDTHRLKIKGWRKIYQANG KQKAGVAILVSDKTDFTPTKI KRDKEGLYIMVKGSIPEELTIL NIYAPNPEAPRFTKQVLSDLQR DVDSHTIILGDFNTPLSALDRSM RQKVNKDTQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHHTY SKIDHRVGSKALLSKCKRSEIIT NCLSDHSAIKLELRIKKLTQNC TTWKLNNLLNDYVWHNEMK AEIKMFFETNEN
19913	50281	A	20029	3311	9648	KLYVCITRITNAEYLKELMEL KAKAQELCEECSRLSRHDQLE ERVSVMEDQMNMKQEEKFRE KRRKRNEQSLQEIWDYVKRPN LRLIGVPESDGENGTLENTLQ DIIQKNFPNLRQANIYIQEIQEI QRTPQRYSPRATPRHIIVRFTK VDMKEKMLRAVREKGFKPTKI RRDKEGHYIMVKGSIQEEELTI LNIIYAPNTGGPRFIKQVLSDLQ RDLDSHTIIMGDFNTPLSTLDRS MRQKINKDIQEL
19914	50282	A	20030	2031	6332	QDSNSHITLTNINGLNAPI*R HIDRNCNWKSQDPSVCCIQET HLTCRDTHRLKIKGWRKIYQA NGKQKKKAGVAILVSDKTDN PTKIKRDKEGHYIMVKGSIQEE ELTILNIYAPNTGAPRFIKQVLS DLQRDLDSHTIIMGDFNTPLS TLDRSSRQKVNKDTQELNSAL HQADLIDYRTLHPKSTEYTF SAPHHTYSKIDHIVGSKALLSK CKRTGHTNYLSDHSAIKLELRI KNLTQSR
19915	50283	A	20031	2	178	
19916	50284	C	20032	88	228	

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19917	50285	A	20033	3	382	VDRTIMSDSLVVCVDPELTK LRKFRFRKETDNAAIIIMKVDKD RQMVVLEEEFQFVVYSKYV HDDGRVSYPLCFIFSSPVGCKPE QOMMYAGSKTRLVQTAEITK VQTGMWLQSVRERWCGSWV
19918	50286	A	20034	89	633	KTAE LRKEACGQNNHALPGS LRQSDSLVVCVDPELTKLRK FRFRKETDNAAIIIMKVDKD/RG QMVVLEEEFQNISQRELKMG FPRRDKPRFVVVYSKYVHD/D GARVSYPLCFIFPRPVGCKPEI QOMMYAGSKNRLVQTAEITK GVPKSRIT*LTSLRPWLQEKLS FLSLISGAGD
19919	50287	A	20035	78	638	WLDLTWKESSADSQFLFKMD HSHHMGMSYMSDSNTMQPSH HHPTTSASHGGGDSMM MPMTFYFGFKNVELLFSGLVIN TAGEMAGAFVAVFLVAMFYE GLKIARESLLRKQVSIRYNSMP VP/GQNG/TILYGRTHKTVG/QQ MLSFPHLLQTVLHHQVVISYFL MLIFMTYNGYLCIAVA
19920	50288	A	20036	1	849	MSQKMENLIGNAHISAYEIIKEF QKEQHQAAGLP GTTVPCSCQVY KCSKRP ERVAREGPSEDEPLP QTVRKCGQGCTLHGAGGSGQG VGARPF GIGVEALWFLASPSY WAPLIPQCQLGKLLVVRVLQV QARRELAPMLAPGAACPMVAT ACLTVQWPDPM LTHPTLPIPHL TCSLLGGNVELLFSSLVINTAGE MAGAFVAVIILA VFYEGLIAQE SLL*PNGTILM*THKTVGQQML SFPHLLQTVLHHQVVISYLLMLI FMTYNGSSELLFRGERPR
19921	50289	B	20037	308	568	
19922	50290	A	20038	394	528	
19923	50291	A	20039	186	856	TWKGKDILRRPRRKMSY/SHF FVQTCRGGHKKKHPRLQVN/ FSEFSEKVLQGRWPMSC LKR KGKILKIWAKAGQGPFLERELK TLYPLPKGEDQKKKFKDPNCTP RGPPSAFFPLLALEYPPQKSKG EHPWPVPLVDVAEENWETMW ELTLQMDKQPYEKKA'AKLK EKYEKDIACISLLKGPDAKK RELSRPEKSKKKKEEEDDEDE EDEEEDEDE*DEDEEEDEDE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19924	50292	A	20040	1	413	GAMRGDRGRGRGGRFGRSGGP GGGFRFPVPHIPDFYLCEMAF RVKPAPEDETSFSEALLKRNQDL APNSAEQASILSLVTKINNGNE KLAVGSGTLKAHIEKFTRGIPY KRGTVSRGHNVADLGGLKILA PPLEAV
19925	50293	A	20041	70	1451	GAMRGDRGRGRGGRFGRSGGP GGGFKPFVPHIPDFYLCEMAF PRVKPAPEDETSFS*GLA*RRNQ DLAPNSAEQASILSLVTKINNN VIDNLTGSGQHFEVAKLEEV RQVGDPKRGMTTGHNV*/L WVVIQEFWQRLAEVACPGGN KVVESLR/SHQDPSESFKPCLTN EVTGFEISSDATVKILITTVPPN LRKLDPELHLDIKVLQSALAAI RHARWFEENASQSTVKVLIRLL KDLRIRFPGIPELTPWILDLGL HYAVMNNPTROPLGLKRWHN RALAWQISGLAGTVSCQGSVG YSIDPCESWQL*ELHTVMTLEQ QDMVICYTAQTFVRILPHGGF RKILGQEVDSYLASEISTWD GVIVTPFRKRLYEKPEKKEG EEEEENTEEPTSRGRGRKHGN SGVTIPLPLFPNPRGKTGALSC PAYWALHGDRHFPWDREDSRK
19926	50294	A	20042	253	379	
19927	50295	A	20043	284	1062	APRNYLPQRATASVRRQISFS NEHTPHQSLHEIPNVRQRHSL MKLNTMGAMTTSTTSAVANH* PSNKRTPLVSV/MQASPEQRQ AVRERMQTNPKIQRRREARE RIQSASPEQRQAVREKMQTNPQ NQQRDAARERIQSASPEQRQV FKEKVQQRPLNQQRDNARQR VQSASPEQRQVREKVQESRPQ RLNDSNHTVRLNNEQRSVACE RLSERGARRLESYGRHMQAN PEPPKKNNDKSKKISKPLAAK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
19928	50296	A	20044	1	2269	MSPDIPQVSPEVGLYPVANHSSI VVP TCHLSSEEDTEAQRNHELD TVKALREDAQVLKIPNQSPKDT LVTALQLAQKGTKAAAIRLGA KVGQKQSRQAKSSPALVVPGL LSFPRARFFFEWQSPGLPNTAAM ENG TGPYGEERPREVQETT VTE GAAKIAFPSANEVFNVPVQEFN RDLTCAVITEFARIQLGAKGIQI KVPG EKDTQKVVDLSEQEEE KVELKESENLAGDQPRTA AV GEICEEGLHVLGLELAASGLRSIR FALEVPGLRSVVANDASTRAV DLIRRNVLNDVAHLVQPSQA DARMLMYQHQRVSERFDVIDL DPYGPATFLDAAVQAVSEGG LLCVCTDMAVLAGNSGETCY SKYGAMALKSRACHEMALRIV LHSLDLRANCYQRFVPLLSIS ADFYVRVVRVFTGQAKVKAS ASKQALVFQCVGCGAFHLQRL GKASGVPSGRAKFS AACGPPVT PECEHCGQRHQLGGPMWAEPI HDLDFVGRVLEAVSANPGRFH TSERIRGVL SVITEELPDVPLY TLDQLSSTIHCNTPSLLQLRSAL LHADFRVSLSHACKNAVKTDA PASALWDMRCWEKECPVKRE RLSETSPA FRILSVPEPRLQANFT IREDIANPSSRQGLKRFQANP EAINWGP RP RSRPGGKA ADEA MEERRLQLNKRKEPPEDVA
19929	50297	A	20045	1578	2356	PLRRWACNHKL RQNAHQLSSTI HCNTPSLLQLRSALLHADFRV LSHACKNAVKTDA PASALW DIMRCWEKECPVKRERLSETSP AFRILSVPEPRLQANFTIREDANP SSRQ RGLKRFQANPEANWGPR PRARP/GVSGGKVGVL SQGKK G* RADGVPTTPSPSHRGKA ADE AMEERRRLQLNKRKEPPEDVA QRAARLKTFPCKRFKEGT CQRG DQCCYSHSPTTPRVSADAAPDC PETSNTQTPPGPAAAGPGID

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19930	50298	A	20046	1	791	MGPSIIHSSQHATAPQILPKVR AGPRSSGCRISECRREEKPPKGR RGLKDATRPGVNWGPDGGVQS GAGAPW/SLTPLPGSVSPAGR AQRSMRAAAQERSPPGRRRL GKEPLIRESWTRAPWRCLSQD AGRAGSQVCGSSPQTRGAAAE KVAVTGAKSCSGRGKKAAR AKSRGGGGGRKTQKAAAKSRG C/AGQSPKSRGSRG*IPRGRGQ KAAVAGAESNGGGGKSRRRR HKAAKTRSSGGKNPWRQKAAS AGAK
19931	50299	C	20047	76	327	
19932	50300	A	20048	336	814	ANFSLEDPSCSPPRLLAGSFVD SPQSLSCMRSKNPLIGSGSPLS PTYIL*ATTPHFLPQPLITTSPPS PSPPSPPLPPPPFSFSSSYSSSFF E/NRVPLCCPCFGSAIRKPSPSVS TKARPQGETGRSLALLFLPQRP SSSLHRSDTLYRDCVHRI
19933	50301	A	20049	1	310	
19934	50302	A	20050	1	1482	
19935	50303	A	20051	3	2455	
19936	50304	A	20052	3	1441	

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19937	50305	A	20053	1	2322	MAEKGKEAGTFFTGQDDRLLF VFFIITIVVGLFRCSVFSSSSSSSS LSSSSSSSSSSSSSFLHLFFIFIF VFFVFIFVFIFVFVFAFFIFFVF VVFFVFFVLLVEILMRPTISIR GQKLKISDEMSKDCLSLYNTC VCTEGVTKRLAEKNDFVILFT LMTSKKTF\QTATLIEDILGVK KEMIRLDEVNLSLVSNFDQQ QLANFCRILAVTISEMDTGND KHTLLAKNAQKKSLSLGPSA AEINQAALLSIPGFVERLCKLAT RKVSESTGTASFLQELEEYWT WLDNALVLDALMRVANESEH NQASIVFPFPGASEENG\LAHTS ARTQLPQSMKIMHEIMYKLEV LYVLCVLLMGRQNRQVHRMIA EFKLIPGLNNLFDKLIWRKHS ASALVLGHGHHY\CDSPDITL\ KIQFLRLQSFSDHHENKYLL NNQELNELSAISLKANIPVEAV LNTDRSLVCDGKRGLLTRLLQ VMKKEPAESSFRF\WQARAVEE FPSRGTTSYADQMFLKRGLL EHILYCVDS\ECKSRDVLQSYF DL\LGEL\MKFNVD\AFKRFNKYI NTDAKFQVFLKIQ\NSSLVDSN MLVRCVTLSLDRFENQVDMKV AEVLSECRLLAYISQVPTQMSF LFRLNIHIVQTLTQENV\SLNT\ SLVILML\ARRKERLP\YLRLL\ QR\MEHSKKYPGLL\NNFHNL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19938	50306	A	20054	237	2033	TSPTPLPLPATMPKTSIVRVTTM DAELIEFAIQPNTTGKQLFDQV VKTIWLEGGKFGFFGLQNQDTN GFSTWCLKLNKKVD*PRNVKKE \SPLLFK\FRAKFYPIEDVSEELIQ DITQRL\FFLQVKEGILNDDIYCP \PETA VLLASYAVQSKYGDFNK EVHKSGYLAGDKLLPQRVLEQ HKLNRDQWEERIQVWHEEHR GML/RGEDAVLEISERLLQDLE MYGVNYFSI\KNKKGSELWLG VDALGLNIYEQNDRLLTPKIGFP WSEIRNISFNDKKFV\IKPIDKK APDFVFIAPRLRINKRILALCM GNHELYMRRRKPDITIEVQQMK AQAREEKHQKQMERAMLENE RKKREMAEKEKEKIEREKEEL MERLKQIEEQTKKAQQELIEEQ TPRAPGTL\SQERKRAQSEAEKL AKERQEAEEAKEALLQASRDQ KKTQEQLALEMAELTARISQLE MARQKKESEAVEWQQAQMV QEDLEKTRAE\KTAMSTPHVA EPAENEQDEQDENGAEAS\ADL RA*SMAKDRSEERTTE\AEKN ERVQKHLKALTSELANARDES KKTANDMIHAENMRLGRDKY KTLRQIRQGNTKQRIDEFESM

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19939	50307	A	20055	2	2230	PRVRLGAHGCPGPPGRRCGCCW ANGLRSSERCVLESRLPCVQSA TRGLRCGCDSAANLDTMAKPP QGAGDRGSIHDFPGFDPNQDAE ALYTAMKGFSGDKEAILDIISR SNRQRQEGCHSYK\SLYGK\DLI ADLK\YELTGKFERLIVRLMRP PAYCDAKEIK\DAISG\IGTDEK\ CLIEILASRTNEQMHQLVKRITK MPTERDLEADIIIGDTSGHFQKM LVVLLQGTREEDDVVSEDLVQ QDVQDLYEAGELKWGTDEAQF IYILGNRSKQHLRLVFDEYLT TGKPIEASIRGELSGDFEKLMLA VVKCIRSTPEYFAERLFFKAMKG LGVTRDNTLRIMVSRSELDMLD IREIFRTKY*\EKSLYSMD\IKND TSG/QSYKKTLLKLSGGDDAA DQFFPKAAQVAYQMWELSAV ARVELKGTVIRPANDFNPNAD AKALRKAMKGLGTDEDTIIDII THRSNVQRQIRQTFKSHFGRD LMTDLKSEISGLARLILGLMM PPAHYDAKQLKKAMEGAGTDE KALIEILATRTNAEIRAINAEAYK VEDYHKSLEDA\SSDTSGHFRRI LISLATGHREEGGENLDQARED AQVAAEILEIADTPSGDKTSLET RFMTILCTR/SYPHVRVVIQEFIR LTNYDVEHTIKK\EM\SGDIRDA FVAIVQ\SAKTKPLFFPDK\LYK SMKGA\AGTDEKTLTRIMVSR\G
19940	50308	A	20056	3	368	
19941	50309	A	20057	1	936	MMKCEEQKEEEEETVRMFSA SQPLDPDGTFLRLRFTAMVWW AITFPVFGFFFCIIWSLVHFHEY VATDCGVSSAPAPGSGPGVNP YLPSVSSAIGGEVPQRYVWRFC IGLHSAPRFLVA\FAYWNHYLS CTSPSCYRPLCRLNFGNLNVVE NLALLVLTYSSESDFTHENAF IVFIASSLGHMLLTCLWRLTKK HTVSQEVRSIPSGGSKAAQKKI KDICPDQSGNGEDRKSYSWKQ RLFIINFISFFSALAVYFRHNMY CEAGVYTI\AILEYTVVLTNMA FHMTAWWDFGNKELLITSQPE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
19942	50310	A	20058	119	930	ESLFPSLAFLSPSKPLFSHPSPSFH LSNKQDTPSCSCVLSSPFLSLRTE ASIGVPGIKMDGGNAQEHGHFL RLPQVPNYLPSVSSAIAREVPRQ YVWRFCIGLHISAPRFLVAFAY WNHYLSCTSPSCYRPLCRLNF GLNVVENLALLVLTYSVSSDEF /TWVPG*GRSGEVFPEGTGLPLP HSDLPTSWCGHSLQCGSQSSFP PAIHENAFIVFIASSLGHMLLTCL LWRLTKKHTVSQEVRSIPSGGS KAAQKKIKDICPQDSGNGEVGT EF
19943	50311	A	20059	3	206	
19944	50312	B	20060	80	304	
19945	50313	A	20061	1	2111	MAATGTAAAAATGRLLLLLV GLTAPALALAGYIEALANAGT GFVAEPQIAMFCGKLNMHVN IQTGKWEPTDPTGKSCFETKEE VLQYCEMYPQLQITNVMEAN QRVSIDNWCRDDKKQCKSRFV TPFKCLVGEFVSDVLLVPEKCC FFHKERMVCENHQHWHTVV KEACLTQGMITYSYGMILLPCG VDQFHGTEYVCCPQTKIIGSVS KEEEEEEEEEEEEEDEEDYDV YKSEFTEADLEDFTEAAVDED DEDEEEGEEVVEDRDYYYDTF KGDDYNEENPTEPGSDGTMSD KEITHDVKVPPTPLPTNDVDVY FETSADDNEHARFQKAKEQLEI RHRNRMDRVKKEWEEAELQA KNLPKAERQTLIQHFQAMVKA LEKEAASEKQLVETHLARVE AMLNDRRRMALENYLAALQS DPPRPHRLQALRRYVRAENKD RLHTIRHYQHVLAVDPEKAA/Q MK'SQVMTHLHVIEERRNQSL LLYKVPYVAI/QEIQEIDDVLQ EQRADMDQFTASISE/TPVDVR VSSDESEIIPPFHPFPAPT* ERRILGVGRAGWGGLIGAEKE VINSKINKVDEINMVH*TRLLD VKEMIFNAERVGGLEEEERESV GPLREDFSLUSSALIGLLVIAVA IATVIVISLVMLRKRQYGTISH GIVE/VVDPMLTPEERHLNKMQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
19946	50314	A	20062	61	2634	SQPAEGK\WSTGNAATATAGVL LLPAACGA* TAPALAL\AGYIEA LAANAGT\GFAVAEPSNSPMFC GKLNMPCE\TFQTK\WEPADPN QAPKSCF* NQKEEVSSSYF\QEM YPRAYRSQNVMEAKPAGL\RID N\WC\RRDKKQ\CKSRFCYTFSS CLVG*IL* SDVPAKFPEKVPSPFF HKERMVEVCENHQ\HW\HTVSQ KKAMS* PPGK* PLIIANGMPASP CGGRTSFHGTE\YVC* PSAQRLL GSCV\TKEEEEEE\EKEEEEDE KGD\YAVYKGNFLL* ADLEDST EA\A\VEDDEDE\REGEDV\VEDR EYY\YDTFKGDDYNEENPN\DPG SAATMSD\KEITHD\VKAVCSQE A\MTGPCRAVMPLWYFYLSKG KCVRFIYGGCGGNRNNF* SEDY CMAVCKAMIPPTPLSTNDDV\F F* TSKDDNEHARFHKAKEHVVI RPRNRMDRLK* EW* YAQL\QLK N\LPKAEQ\TLIQH\FQA\MVKA I\EKAA\SEKQVL\ET\HTLARV EAMLND\RC\LMALENY\LAALQ SD\PRP\HR\VLQALRRYVRAEN KDRLHTIRHYQHVLAVDPEKA AQMKSQVM\THL\HVIEERRNQ SLSLLYKVPYVAQEIQEIDELL QEQRADM\Q\FTASISE\TPV\DV R\VS\SEGRGEIPFHPFHPFALP ENEDTQPVLYHPMKKSGSVGE QDGLIVAEK\VINSK\NKVDE
19947	50315	A	20063	734	1049	CCPPGGTGRCLGTCGYHN\CGC SI* SSDLPQR\CCVSGRR* TFWM VWSACVCASGCLPGGNRCCCP VLS\PERIAVLGGLLPRKPPCRV VGERRSVLTLQATSQCPR
19948	50316	A	20064	6	1174	
19949	50317	A	20065	285	567	RRRRSSSYERSGSYSGRSPSPYG RRRRSSPFLSKRSLRSPLSPRK SKSRSRSPAYSRRHSSSHSKKKR SSSRSRHSSISPVRLPLNSSLGAE LSRKKKERAAAAAAAKMDGK ESSYERSGSYSGRSPSPYGRRRS SSPFLSKRSLRSPLSPRKSMKS RRSRSPAYSRRHSSSHSKKKRSSR SRHSSISPVRLPLNSSLGAELSR KKKERAAAAAAAKMDGKESK GSPVFLPRKENSSVEAKDSGLE SKKLPRSV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
19950	50318	A	20066	214	805	LGLQAANDLHLEYAMGKRYFC DYCDRSFQDNLHNRKKHLNGL QHLKAKKVWYDMFRDAAAIL LDEQNKRPCKFLLTGQRDFG SNCRFSHMSERDLKELSIQVE EGRGEPREWLLDAPELP ¹ EGHL GGLGLEERRAKRLELQPQVSQ G*NPFR ¹ TT/VSFQ*PRRVGQPSS GSLPPNSCGHPPPGGLALLQPR V\QWG
19951	50319	A	20067	2	418	
19952	50320	A	20068	1	1134	ATTARRRGAPGT ¹ PSLAAEGNGL SARVDEGV ¹ EEFFSKRLIQDRL WAPEEDPATEGGATVPVRTL ¹ RK KLGTLFAFKKPRSTRGPRTDLE TSPGAAPRTRKTTFGDLIRPPT RPSRGEELGGAEGDTSSSDPAG RSRPPTQEIA ¹ RPTR*YCCLPRRR QRWVPDPTSGGPWSGEKQNW ¹ L HPLNSGYK* ¹ CRCG*ASAEAAGV PKARGSKAKMARSRLAQMV TLWTVPRRPLPSRSSPAPT/PVS ADPSCRPGPGSQGPESATWKTL GQQLNAELRSRGWGQDGP ¹ GP PSPGQSPSPCRTSPSPDSLGLPED PCLGPRNEERPLRLQRS ¹ PLKR RPKLEAPPSPSLGSLGT ¹ EPLPP QPTEPSSPERSPPSPATDQRGGG
19953	50321	A	20069	3	206	
19954	50322	A	20070	3	349	
19955	50323	A	20071	226	610	
19956	50324	B	20072	18	1306	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
19957	50325	A	20073	3	1665	LRPQGREGGDWEGRSPFSLPY GSLRGRVSTAQFRVPMPSASA SRKSQEKPREIMDAAEDYAKER YGISSMIQSQEKPDRLVLRVRD LTIQKADEVVWVRARVHTSRA KKGKQCFILRQQQFNVAQVA VGDHASKQMVKFAANINKESI VDVEGVVRKVNQKIGSCTQQD VELHVQ(KIYVISL)AEPRLPLQL DDAVRPEAEGEGRATV/NQD TRLNDRVIDLRTSTSQA/VRL/Q SGICHPLRET/LINKGFVEIQT/KI ISAASEGGANVFTVS/YFKNNA/ YLAQSPQLYKQMCICADFEKVF SIGPVFRAEDSNTHRHLETFVG LDIEMAFNYHYHEVMEEIADT M/VQIFKGLQER/FQTEFQTVNK QFPCEAISNFWPTLRLEYCEAL AMLRGKLESEMG/DEDDLSTPN EKLLGHLVKEYDT/DFYILD KYPIGL*RPF/HLYPGP**PPRNPQ QVPTLTNMFHEREKKYLSGAQ/ RIHNDPQL/TERALHHG/DLEK IKAYIDSFRFGSPSP/HAGGGIGI/ ENRVTMLFLGLHNVRQTSHPV
19958	50326	A	20074	3	424	
19959	50327	A	20075	178	859	
19960	50328	C	20076	304	592	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
19961	50329	A	20077	1381	2936	PTNPRPSPGLARWAESYEAKECE RRQEIRSRRCRPNVTTTCRQVG KTLRIQQREQLQRARLQQFFRR RNLELEEKGKAQHPQAREQGP SRRPGQVTVLKEPLSCARRISSP REQVGRVKGHATAVCSGTLSSGQ GGWV/R/PPSLHRAKRES*DNC PSSLALTLSPHSSSLERTQ*/SH ALTFWNSMIYPRSSRLILPQASD SSW/KGGKGMKFFLNKA WASMC SHLIFLSTGKHSEGYFHLRNLEL NEKNVFEPKAKESLQKVLEEK MNAEQQLQSTQVWGCHIDMG LGTGSLGNKGSQQLQRTLTGTH RELESQHLVQLQSKLQVPGTGGG EGROGMGRDGDERSCSAKIE CLQGDRDLCSLDTQDLQGTLL GGLECMAMAK*AKKKETEAF QILKVHRVFLGSWPTKGTQVW SPKSFNPEVEPEGTGKEKDWDL RDQLQKKTLQLQAKEKEVRG* PEIVRAHLRNSRETWEAVKNCR EELNQSQQLPPRVGRSLLPIKP WMMGRFLL*PSFAHKDNLMI
19962	50330	B	20078	1	1173	
19963	50331	A	20079	16	1584	SSRFLFSLGWLWEAPEVGTSG WLQRRPGLGAGLGGVQEKQFL PALLSFFIYNPRFWPREGEEENK ILFYHPNEVEKNEKIRNVGLCE AIVQFTRTFSPSKPAKSLHTQKN RQFFNEPEENFWMVMVVRCP IEKQSKDGKPVIEYQEEELDK VYSSVLQRCYSMYKLFNGTFPE SHGRRR/VKLLKERLEKFFHRY LQTLHLQSCDLLDFGGISFFPL DKMTYLKIQSFNRMEESSLNIV KYTAFLYNDQLIWSGLEQDDM RILYKYLTTSLFPRHIEPELAGR DSPIRAEMPNGLQHYGRFLTGP LNLNDPDAKCRFPKIFVNTDDT YEELHLIVYKAMSAVCFMID ASIHPTLDFCRRRTGTASLGPQL HSGWASGHLVEQFNINKGDVP GLRKAEPQKFIFYFNHMLNVEK STVHIEENAPACPLTSVHPDLAM KIPR*PSNSDLYPRVDEDEGDH C*RALSDYWWVVGK/KSDPAGS LYVIFEIQKNAKP*LKVK*KRSK KPLCNASSNNILPSLD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
19964	50332	A	20080	85	420	LSNLFHATNDGALTSTTIPHP MRQPTS/S/GDGSEIFLHTELKLL EPHAWPQSCPPRL* MTRQQLL PMTFLLKAHSAKAGIESPGLNPR PGSLHPVLPAASSAAFLPSFR
19965	50333	A	20081	220	563	
19966	50334	B	20082	1	576	
19967	50335	A	20083	111	3586	TMFGLKPPLYFLPGSSLSSESSP VSSPATNHSSPASTPKRVPMPGI IVPPGGHSPSTPPVVTIAPT KT VNGVWRSESRQDAGPRSSSGG RERLIVEPPLPQEKAGGPAIPSH LLSTPYPFGLSPSSVVQDSRFPP LNLQRPVHHVPPSTVTEDYLR SFRPYHTTDDL RMSSLPLGLD PATAAAYYHPSYLAPHFPHPA FRMDDSYCLALRSPFYPIPTPG SLPPLHPSAMHLHLSGVRYPPE LSHSSSLAA
19968	50336	A	20084	576	1261	GDDLCSVGAPCRSTWACSTPLR CVRRSREFPGLPHAAAGARGFR LPAGRPVPARPGAAAAAARAAA GEAHRPLPCGRRPGPVRRAAVP PRPRPPRRGLRGRREGPAAPAG PGGSPLLCASAGRHGPPGLRAG QGLRDSAGEAGGEPAP/AGPRP EASP*RSSLCENTCTEAGLGPRR AAGDLGSPWLTSGLLWGSFFLF FLFFFVILRQSLLSPKTEVAVA QLMSHCSL
19969	50337	A	20085	248	356	EGEEEGDEENDPDIMTQRRIKT QQSASSSEAGCMWP
19970	50338	A	20086	1043	1191	NFYFSCKNKNKANKQKITWKV KGLSNGCKFILSGGRQKGRITLP QRERMA

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19971	50339	A	20087	287	1401	CQNPQIPCSPFKKRLDG/LWVET PTGYIESLP/RVVKRR/VNALKN LQVKCAQIEAKFFE/EKVHGFEE RKYAVLYQPLFD/KRF/EIINA1 YEPTE/EKECEWETR*RKDEDF GGNWKEKGQIEDEKKDEEKE DPKG/IFPEFWLTVFK/INVDLLS DMVQEH/DEPIKHN/KDIKVKF SDA/GQPMFVLEFHF/EPNEVF TNEVL/RTYRMRSEP/DTRLIL DPFSFDGPEIMGCTGCQIDWKK GKNVTLKTY*GGGRKHKGRGT VRTVTKTIVS/NDSESNFFPP/PE IPE/DVGDLDLDDAGSLFLAGRLS EIWFTFYRERIIPRSSVNILPGEA/ IEDDDDDYDEEGEEADEEGEEE GDEENDPRLLTQR/RIKTQQSAS
19972	50340	A	20088	1	350	DNLEAEA VAPCTAAARAVAPD LFVFAA*PESVSAGGPQQPCRSP IVKPLGPSFRSSCTQPWLTHSW AEDVDLRVNFAMNVGKARGFF KKGDVVIVLTGWRPGSGFTNT MRVVPVP
19973	50341	A	20089	1	399	
19974	50342	A	20090	1	394	
19975	50343	B	20091	82	351	
19976	50344	A	20092	3	789	CGTSRMCHTTEELA/SDPIL/YRP LAVALDTKEPEI/RNGLIKSGGT SEVELKKGATLKFRNNAY/ME KCDENILWLDYKNICKVVEVG SKIYVDDGLISLQVKQKGADFL VTEVENGSLGSKKGVNLPGA AVDLP/VSEKDIQDLKFGVEQD VDMVFASFIRKASDVHEVRKV LGEKGNIKNIISKIENHEGVRRF DEILEALGHWAVVPLKPTLALA LTCFSSSLGLSSLHLSPPSTQLSC SKHSTLHLPFSPTTAAAPGLLL
19977	50345	A	20093	3	424	
19978	50346	A	20094	2	173	IYHLQLFEELR/RLAPITSDPTEA TAVGAVEASFCKCSGAIIVLTK SGRSAHQQLGP
19979	50347	B	20095	1	1362	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
19980	50348	A	20096	1	1982	QRDNLEAEAVAPCTAAARAVA PDLRLCSVRPSRAPEDRQQP CLFSHSEAGTAFIQQLHAAI MADTF/LWEHMCRL/DIDSPIT ARNTG/IIC/TIGPLPDQVETLK EDD*SLGMKCGSVLNFSSWEL HGVTRMRETIQGMWRTANGKA FAFLTPFLPGPLAVGFRTLKGP EIPNWGSSKNGTVAEVGA*RK GATLKFTLADNAYMEKC/DENI L/WLDYKNICKVVEVGISKIYV DDGLISLQGGKQ/GADFLVTEV ENGGSLGRMKGVNLP/GAAVD FACLCRRKDIQDLKFGVE/QDV DMVFASFIPQSILMFHEVRKVL GAEKGKDHQGLSSKIRESMRGF RRFD/EIL/EASDGI/LWVARG*F *ALRIPAEK/VFLAQKMIDLDRF NRA/GKPVICATQMLESMIKKP RPTRA/EGSD/VANAVLDWKPT CIMLSWEKQPKGDYPL/EA/VIR MQHL/AIAREARWLPSYHLQLFL EELRPPGAQLTSDPTEATAVGA VEASFKCC/SGAII/VLTSGKVC SPRLARYRPRPIIAVTRNSPGK LVRAHL/YRGIFGVCQGPDSR RAWA*DIGLRVKLCHGMFGK ARGFFQERGDVVHCA*PEWRP WLPAPPNMRVVPCCRDGPRG PSSSRPCSHFFPKPIPFPSNGL VELHSGAVNVATG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19981	50349	A	20097	215	1893	TVTFSQCRFGKMLPLEKAFASP QELPSPAGSAHAGVSSRSSRK NPRPSLRGPLLTLEFSRLRFREF VYQEAAGPHQTLARLHELCRQ WLMPEARSKEQML/ESLLVLEQ FLGILPDKVRPWVVAQYPESCR SSLLVEGLADVLEEPGPSTVDR DAAGLPCGLILNS*RWSVREAH GPSAATRRAREPQGPWSWGD PGTF*DTLAFSGPPVSGTEEGQ/ MKQRPKRTALP/HTEQVGGHE QVGGRSQ/RTTNVSEAEVLSRG PSAPGGVGGPPGCEENLKSRYK LLLWEGRRQESAGCACEEAA PAG/GCLSLRRRPLGTPLPIPRR AH*GGGRAAWEGPGPAGPPGR GVRLCHRIAEAVRHPAACP/ET GARRNWEPGRTPRMGTGRAS RA/CSSGDSAGLEAGQGPAD EPGLSRGKPYACGECGEAFW LSHLMHHSSHGGRKRYACQG CWKTFHFSLALAEHQKTHGKE KSYALGGARGQPSTREAQAG ARAGGPPEVVEGRGSPRTPRGA EVSRCAPFRGRGFAGRESQTR HWAFFRPWVAASCGVCGRPLP
19982	50350	A	20098	5	372	
19983	50351	A	20099	1	129	
19984	50352	A	20100	1	627	
19985	50353	A	20101	1	441	
19986	50354	B	20102	1	477	
19987	50355	A	20103	2007	2156	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19988	50356	A	20104	1	717	MKLRRLAVSVTALKVARLGSA PSDVQMCLEFLPSDSGAQLASP SGSRGTGAAGGAACQSGAVRSY SSALGWSMGLGAVEQGVVLV GDARAAQEPMEWMGGSGMAG CRSRALHRGKAAKARREIEHSA GRKGLFGSARLIPATAMAPRSR LLSLGRRGNFRSRVLRKRSRPL EEAARRWRDCPTGFGALVAGA GSGRAPGVPPKRLPARTKAQVS RETRGSGEVTAAQGGKGPRLW ILLWGFYNLLPTTSHAESYPERL IQKVVSSEKIARALARYLHLPFG LLGGNKTIIVYSWEALRFHHQLT PSVITNTVIK VYEEPKLSQQKSR TLDVSTDEEDKIHHSSESKDDQ GLSSDSSSSLGKELSSSTVKIPD AAFIQAARRKRELAQAQDDYIS LDVQHTSSISGMKRESEDDPEIS RNEETSEESQEDEKQDTWEQQ QMRKAVKIIIEERDIDLSCGNGS SKVKKFDTSISFPVNLKIKKQL NTRLTLLEQETHRSHLREYKVV QDVKSSKSTIQNLESSSNQALN CKFYKSMKIYVENLIDCLNEKII NIQEIESSMHALLLKQAMTFMK RRQDELKHESITYLQQLSRKDET STSGNFSVDEKTQWILEEIESRR TKRRQARVLSGNCHQEGTSS DDELPSAEMIDFQKSQGDILQK QKKVFEEVQDDFCNIQNILLKF QQWREKFPDSYYEAFISLC*RQ
19989	50357	A	20105	154	744	SQRNLCGRVWYILFFLFAFLQ TLELVSHERRGTGITNA*VSNS PRRELGFHVL*R*QFLLFLFHS RLRSPAGFT*WIPHRGCRWSCL PVLRLHALAFLSPWVVDGTGRR GAGGGARRGGSGHTGAHGVG GRLRHGRLQVPSPLRARSFLLS CTLSCQLDSPCLTCSQGHQYKY QHSKDGKRLTIVTKSFDIFPS
19990	50358	B	20106	1	531	
19991	50359	C	20107	99	323	
19992	50360	A	20108	305	658	
19993	50361	B	20109	79	936	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
19994	50362	A	20110	381	1169	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPQGAPPAPRRPVFST TQGLRSASARHGTGRQLHLQP WCGIHWVKLAGLLSLVGSQHL RGQGSRAAAALTHMHS/PHAC THAHTRAEPLRLPPPRPLPPPL SPPPRLRLCCLRLFPCLTESAA KAGSKKFHSVQEIIPSAVCELG VGTVLHIDPEKWRAGRENVET GGKRTSGSKDSTGRGWGQTD YGLGKKERTEEASRSCICLVCV SMRRDALCGQSVGSHFCQWSL
19995	50363	A	20111	3	4804	KRLNIQKTLEAVFSAEAVWMQ PSVVLDDLDLIAGLPAVPEHE HSPDAVQSQRALAHALNDMIKE FISMGSLVALIATSQSQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVINKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSTREKLV TTLDFOKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
19996	50364	A	20112	2	1844	
19997	50365	A	20113	746	1215	PNINRFLKHYREPVPKKRERNY STLWPLCPSTLNKIYTIMSYLSP ATKEYPFFLLLLLEQEC*AE*LLA LAVSQPLLSSTTNCLKN*MVTW NGSLIPWSPCKINLTP*/PAVVL QNRRAIDLTLAESGGTFLFLEE KCCCVYNQSGIITEKVKIEQGRI
19998	50366	A	20114	1	1338	
19999	50367	B	20115	1	4935	
20000	50368	A	20116	3	421	
20001	50369	C	20117	33	571	
20002	50370	A	20118	3	323	
20003	50371	A	20119	146	809	EKCRHNCCSRVWQSLVQSQSVW ATEGQYGRKTNARPVQVKIDS ASFPYQRRYPLRLAQGLQKI VKDLKAQGLVKPFNSPCNTPII GVQKPNQGWKLVQDLRIINEAI VPLYPVNPYTLSSQIPEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSLTWTVLPQG FRNSPHILFGQALAQDLSQFSYL NTLVRLYDLDDLAAHLETLCH
20004	50372	A	20120	3	1147	
20005	50373	A	20121	2	1658	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
20006	50374	A	20122	2	211	MGYDFSYFFPGGCLKSRKSS RGSQE*LALSPGFSGFSQIDL TQV*CIQDSTPATL.TAVGVDKM
20007	50375	B	20123	86	586	
20008	50376	A	20124	66	433	SSSRTEGARGKRQMPSP/STEP RVCLTIEGQEVNCLLDTGAAPS VLLSCPGQLSSRSVTI*GVLGQP VTRYFPQPLSCDWGTLTFSNAF LIMPESPTLLGRGILAKAGAIH HAVLVTAAL
20009	50377	A	20125	1	459	MAVRYTDENVLRKGTREAGT MMRLRGTTCCADFAAWDVT HDALRATGGELPGAQVMLTTT ECGRHVDFCDRAVWLPWMWG YPLALPGEMRKLYTVRMAGRD ILAKAGAIHNLNIGEGTPVRCPL L/EGINPEVWKTEGQYRQAKNA RPVQVKL
20010	50378	A	20126	260	392	VEVVILMPVPNLPSPARITKG RMGTLLRLGLTT*LYKSCSV
20011	50379	A	20127	1	1740	
20012	50380	A	20128	1	858	MEWEDNLPLELGRVTAKLSD HSQTPLGIQMFLLFSLSLRKSP VCLSYLFNFRFTLESEVQHLG AITLTAWPKIPFLGIREAKSPRS ENTRLATILEAGHRHLGTSVSK DHPVTVWRPRDLQSDLKQIKI DLGKFSNDPDGYIDVLQELGQS FDLTWRDIMLLNQTLTPNERS ATITAREFGDLWYISQVVA AGLVSEAVKIIQGLTVWT/SHD VNGILTAKGDLWSDNHLLKY QALLLEGPVLRRTCATLNPAT FLPDNEEKIEHNCQQVIAQTYA
20013	50381	A	20129	1	6530	MWGSDDLGAAGGGGAAVTVA FTNARDCLFHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGQELHVASLEQHLLDQI RIVFPKAIFPVVWDQQTIFYQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAIEYKLLHS YGRDQKGMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSQSEKKQETSWG LTEINAFKNMQSKVPL
20014	50382	B	20130	1231	2065	
20015	50383	A	20131	68	372	
20016	50384	A	20132	1	1461	

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20017	50385	A	20133	1	806	AVVWCTHCCAPTSPGVLPHSAA MSFLKSFPPGPAEGLLRQPD TEAVLNGKGLGTGLYIAESRL SWLDGSGLGFSLEYPTISLHALS RDRSDCLGEHLYVMVNAKFEE ESKEPVADEEEEDSDDDVEPITE FRFVPSDKSAF*FPCSVAMFTA MCECQALHPDPEDSDDYDG EEYDVEAHEQQGDIPTFYTYE EGLSHLTAEQATLERLEGML SQSVSSQYNMAGVRTEDSIR DYVEDGDGRDLTPVTVCLGQFA EDADV
20018	50386	A	20134	225	420	RLLDGVCGRRLRPRGHEEQRP GPGRSHSRSGPRMGRDCAGA VPRVTPK*SACAAGRGGPAT
20019	50387	A	20135	1	687	
20020	50388	A	20136	1	2979	MLRRKKQEDWAAKGSSHACG QIPEEREKGFAVGNVAVNLGLD LGSLARSRRFVVGASRRFFEV NRETGEMFVNDRLDREELCGT LPSCVTVLVLVVENPLELFSVEV VIQDINDNNPAFTQEMKLEISE AVAPGTRFPLESAHDPDVGSNS LQTYELSRNEYPALRVQTRDS TKYAEVLRLALDREREPSLQL VLTALDGGTPALSASLPIHIKVL DANDNAPVFNQSLYRARVLED APSGTRVVQVLATD
20021	50389	A	20137	2	296	
20022	50390	A	20138	1187	1292	
20023	50391	A	20139	2	3250	LTSRWRPWPRPPTSSAGWFC ASTGPWTAAPAKAPPSWASWT SRALSSRPQTSRLWRR*PRSR AATPSSSGRGTCGIRPTSVFSTT RARSTTRPTSG**KTWTL*MTT SQ/RLHQSITDRLTAIWKDVE GIVGLEQVSSIRATAHQVAAPV GVCSSQWSS/IIKESLSRLMAT LSNTNPSFVR/CIVPNHEKRAGK LEPRLVLDQLRCNGVLEGRICR QGFPNRLFQEFRQRYEILTPNA IPKGFMDGKQA
20024	50392	B	20140	1	1816	
20025	50393	A	20141	500	866	QVCLYPGWQHSRGRQRVSG*A HLHTAPLWICQ*SGDCDWHES* GGGM*CVRFEPPTSSPPSAT GSLJK*KEKTGLSNSPCSTSTSS GGRTPTSDRMGKTRRQYPSGA GNSDEKVGFPQVF
20026	50394	A	20142	130	226	

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20027	50395	A	20143	846	1555	GRKTPSQGRRWSSPRVFLLPGG PKPCYTYPLVGEKLLFRVLPLFP HKPSASNLEKVSHCPCEGKTF RSSYLVRHQRIHTGEKPSQVPV ECGKGFF**ALPT/CTAH/HYGTH TGERPYCQCQCGKSFNQSSSLI VHQRTHTGEKPYQCI/CGKRF NASSQFSAHRRHTGESPYKCA VCGKIFNNSSHFAHRKTHTGE KPYRCSHCERGFTKNSALTRHQ TVHMKAVLSSQEGRDAL
20028	50396	A	20144	93	764	AQERKALKSTPSHSSFSR/WLSR IILKNGSSSSSSSSSSSSSLRE RERKSCENVNITRNR/LTAETI ADTIDTSNGSVFLIWTER*EWN WLPKPWHQYQLQARASLSEIIL NNRWEQDPEAFQDPEDQARS/ QWLPRGGSAPV/KQRLLHHDS VPDHAFLRTAAAGQDLPWETV RRPPDNPDAPDFSLFPCLGK LLAERRCFSLQRRVPWPPENQP PHRQ
20029	50397	A	20145	1	433	
20030	50398	C	20146	312	443	
20031	50399	A	20147	1	94	
20032	50400	A	20148	2	122	DLLCPQMG*GWKLTALSLQCS LQDGIERSRAKASQCCLSI
20033	50401	C	20149	25	328	
20034	50402	C	20150	157	309	
20035	50403	B	20151	33	2996	
20036	50404	C	20152	167	274	
20037	50405	A	20153	3	130	AGAVQFQALGVPNKDTKSLEL HQPCKPR*GQDDNHRMSPVYV
20038	50406	A	20154	2	453	
20039	50407	A	20155	1	1317	
20040	50408	A	20156	1	1350	

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20041	50409	A	20157	970	2559	FPLAYSLLFP/CSRLSRELLEVV EPEVLQDSLDRCYSTPSSCLEQP DSCQPYGSSFYALEEKHVGFSL DVGEIEKKKGKRRRRGRSTK KRRRRGRKEGEDQNPPCPRLS RELLAEKEPEVLQDSLDRWYST PSVYLGLTDPQCPCRSFVYLE QQRVGLAVDMDEIEKYQVEVE DQDPSCPR*L*AITDA*FCVDT WRCQVQKGQECVQFHVFNEG* ITPTDIAVGFHCSRCLGFHFFLP LSFTHLL*VDHTSKAVWQLHGI LSKFMENY*AHSFHDHCSLCVP RALTQSVL*PLHQCVTRPIR*AH FLLSLSLPLPVFLFHSFLPGPGLS QHKGNNSLPH*WICPFSF*TVPY VSHEI*LGLCGF*FPLAYSLLFFT /CSRLSRELLEDEKEPEVLQDSL RCYSTPSSGYLELPDLGQPYSSA VYSLEEQYLGALDVEDRIKKD QEEEEQGP/PCPRLSRELLEVV EPEVLQDSLDRCYSTPSSCLEQP DSCQPYGSSFYALEEKHVGFSL DVGEIEKKKGKRRRRGR
20042	50410	A	20158	2790	5320	LHLFCHKRQHGGISRALGSSKK PEMNILEISETLRPLAEKKQOF RSLKECKFLTQLAGFLANRQKK YKYEECKDLIKFMLRNERQFKE EKLAELKQAEELRQYKVVVH SQERELNQLREKLREGDASRS LYEHLQALLTPDEPDKSQGGDL QEQLAEGCRLAQHLVQKLSPE NDEDEDEDVQVEEAKEVLESS APREVQKAEESKVPEDSLECA ITCSNSHGPCDSNQPHKNITF EEDEVNSTLVVDRE
20043	50411	A	20159	394	3251	GRRVCLFSEDEECKDLIKFMLR NERQFKEEKLAELKQAEELR QYKVLVHAQERELTQREKL EGRDASR/SLNEHLQALLTPDE DKSQGGDLQEQLAEGCRLTQH LVQKLSPENDNDDEGV/SQVE VAEKVQKSSAPREMQAAEKE VPEDSLECAITCSNSHGPDNS QPHIKTKITFEEDKVDSTLIGSS SHVWEEDAVHIIPENESDDEEE EEKGPVSPRNLQESSEEEV/PQT PWHE*LSHLSIL

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20044	50412	A	20160	245	641	ILSVLIAVLCVVGKIPLEPLCP AAGSAAEACVGGQMPVIVQ/PC SQQRPSMCMWPRNACQSSRAL GGDESYVPKNRKSFTKHPVSSC /PSPSLGWGRG*/R/PGGPGRSPG LALGFPSFSGPAGFGQGTSSPRF
20045	50413	A	20161	7	194	RPLVESRGIPRSPAASFSTACPR NTASIPSAPSWWETAWTQTSS* APPVA*RPS*PSPESPL
20046	50414	A	20162	232	509	MGVLMHRRCTKAPAWAVATY EAPLHCQQLLVGVVGLAGDPS LLDLGGIHHQQPGLPITVLHQ EEADLVLLRAVTDAAALPVEQ HRP*GAPGLLPDPGGQ*SGDP AAAGGYLQGRGLGPQGHPP HPGAAGSAGEPRKWLPRRGL WCSACA*GPSTGPGEQRPGD SG*FISASTSASRATSACRSFAT SQTEPPTWPSLARQSSGLARPP APGRTAAGRD**TLPPGK
20047	50415	A	20163	3	859	SLGGNKSRRPTRCCSGSRRCR DKSAAYSGALWRGCRSPRAP PPAPQTIPRAWPSPTAVLTHPLL AGPSRWGSSCTGAAPKPPPPGRG PLRGSPALPAAPCGCGGCPGWGP KPLGPWRYPPAAAGSPDHCPPS GGGSRPGAPQGGNRCRSARRT APPSGCGSEVGSGL*WSPRSGPRP PGWFGWAGACGGSGGSAASA ALAWEGPEQSQEALQPQSPQRP APAAAAAGAGPRLSSPRRAW SSPG*/HGIPWPTHASAAALPAAG HRGSFGILP*RAGKRSAMLST
20048	50416	B	20164	179	438	
20049	50417	A	20165	1	930	MESPWQRWLRKVARSGGGR LSNKRKLHLKKKKKGERGGGG AEREKAAAAPGCKAGAGN AKKFVQNGPGTKESSAQVPTG PSAAGLLEFARGPLQTLFAWVS AAVSAEPRIFMIRECCCLIVPLE VLSQRSTWPCFELISDCCASNQ QDSMGVGPSEPGAGYNLLVRH FLSPSEKCSIRVGVARFSRVLPP PLLGISAAAAAGGAARQAAQL REGSRCRLTDIPHAPSTPPEQG HSAEGAAKEPKRRSARLSAKP APAKVEAK/PKAAAKDKSSD KQVQTKGRGAKGKQAEVAN QETKEHLPAV
20050	50418	A	20166	199	419	

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20051	50419	B	20167	969	1313	
20052	50420	C	20168	481	738	
20053	50421	B	20169	56	3476	
20054	50422	A	20170	1	2679	
20055	50423	A	20171	1	1467	
20056	50424	A	20172	208	379	NPCKKGVLFQF*LKIHKRQFIC ADLEFVISE*CTRYPIVAFNWCK PSLLRRSTPVK
20057	50425	A	20173	1	921	
20058	50426	A	20174	197	355	
20059	50427	A	20175	1	3180	
20060	50428	A	20176	1	1309	
20061	50429	A	20177	1	2295	MFYNDVKKQQQMAALTKEKD QLSQSIVMYKSLFEASQQLLNE MKCQVEEARLKEAQLRNELKI HNIDIPITQQVPHIEALLKRKLS EQEELKKKPRRSCTLPNYTKGS GDVLGKIAHLAQIEDDRAAMVI SWHLASDMDCCVVTLTDAARR IYDETQGRQVPLPLDSIYKKT PDWKRSLPHFRNGKLYFKPIGD PVFARDLLTFPDNVHEHCETVFG MLLGDTIILDNLDAANHRYKEV VKITHCPTLLTRDGD
20062	50430	A	20178	3	2550	
20063	50431	A	20179	256	3680	NRGLFCFLHLHLKEHERHL ATVYVFPILSCTIYRSVLLTSSQ THIYTHVGDREAQAALKLGRWS HPRTPNAVGA GPPEGAGGGD AVTSQSALLTFSRTRFASGAHA GAHPVLLRNEEEKGAPALVAPI FSAEGPTCSLWWTLPASTAGL KLPAASTRPSQRGLTADGGGP GGASVGTEDGGGVGHRTVYL FDRREKESELGDRPLQVGERSD YAGFRAYETVKDGVTLYLQGS VNQLLTATKERIDF
20064	50432	A	20180	8	267	RGEMPGERLKA EVFLPPSPLSPT QVVGPLHRVWS*IGNASSQRGE AQVRS*VSFSLRLDSTPWIPGT RALRG CWLWRDFQTLQSG

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20065	50433	A	20181	1	3692	MNPIREMQVSGIALKGTMKGW TELKSPVWYTGNGKGRNYFTN LALSLLFEDDTKLNPYAGGDAI RVRI SVGPFGKGERFTVPGLASEC GKNSFLRFPNSRRKQLCGRVH GSFLWFSMMSQSMGGDNLSL DTNEAEIEPENMREKFFRSLAR LLENKSNNTKIFSKAKYCQLIK EVKEAKAKAKKESVDYRRLAR FDVILVQGNEKLIEAVNGETDK IRYYLHSEDLFDILHNTHLSIGH GGRTRMEKELQAKYK
20066	50434	A	20182	24	131	PVHKRWS*NDECYRHCTV***Q PGSEENNPALENR
20067	50435	C	20183	99	281	
20068	50436	A	20184	1	4200	MVILKDFMKFEMNSEEGDFLR TCDFFFLRHLVAVKQLAHVKV DRFFPRRQSLAESRTAGIRLQTN VQKMVSSFTTSDRKQTSPPSYS VSFIPEFHFLGPPTHCPQTAVSQ CDLLFQLHSPAELFPARTLPG GPRSPHLRVPAAPLQHDPRH TGPPLPPTANRGATPPLPLGPGA LERSGRLGELNSASSFLRRDN PQSPAARPRGSHLAGIEGERT LINYYCQERYFHHVLLVASEGI KRYGSDPVFRFY
20069	50437	A	20185	1	1464	
20070	50438	A	20186	335	855	RIASMPRLPPRTQGRGSARLPSR ARPLHWHHRHTMLPPKPRRW R/RALGPAEAGMLEKLEFEDEG ECAPPAAGPALPRGPRPTGTR GDPAPHLRRCPATSCVLKPRG RGNGRGGDAGELGLRGPCD LPSQNFCLFVLDVLKNGLLALQ LFSSNPTASCAESLPMRLTPVI

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20071	50439	A	20187	2	1160	SARPAASPAGERASQLMLIAV LLLPLRRRWRRALGPAAEAGML EKLEFEDEAVDESSEGVYMRP MRSHKCYDIVPTSSKLVVFDTT LQVKKAFFALVANGVRAAPLW IESKKQSFVGMILTITDFINILHR YYKSPMVQI/YMELEDHKNLET WRELYLQ/ETFKPLVNI/SPD/AS LFGWLYTSLIKNIHRLPVIDPIS GNALYILTHKRILKFLQLFMSD MPKPAFMKQNLDELGIQTYHN IAFIHPDTPHIALNIFV/EKDRIS ALP/VLWDESGKSW*IFNSPNLN VN*ILACLEENIPNNLR*STVT/Q A/LQHRSQYFEGVVKCQLSWKF LETHRWTIRVRAEGPSGLVVV NEADSVGIISLDIL/QALIL/TP AGAKQKETETE
20072	50440	A	20188	58	205	
20073	50441	A	20189	347	1581	NPSPC/WAVFFQKDAITSKIQT LSMLHLYN**SSPSKENTRTVE KLYKCSVDIRKIRRFKKGVL RR*KPYVERNCRIFYQELGAR* D/VASINLERCEAIV*SPATAVN TQRKLVQLVCKNEEELIKLIEQ FPESFTIKDQENQKLNVOFFQ DVGTKKCGHICRLTAAPNCF NPVEKNKQMV/EFQESYLDL GGSEANMKSGFLKLFKPKPFY FV*ISPTAIKETLEFLQEPFP LKFQLPIPNKGFQKCPKYY TE*YFLL*KCLLNAQIFMDP/V N*VLKWPFCFILFVPLEERM QGLLREGISIAQIR/ETPMVLELT PQIVQYRIRKLNSSGYRIKDGHL ANLNGSKKEFEANFGKIQA ALQNLRLSLNYYDELTVGEC GNRKGRGTNVNITL
20074	50442	A	20190	3	455	
20075	50443	C	20191	72	218	
20076	50444	A	20192	3	452	LGILLVDDFVNVLSLAVYAED SEPSDGEAGIEAVGSAAEK GLVSDAYGEDDFSRLLGGDE YEEEEEDENSQSEDDDSSETE EADDPKE\NSAQ*QRHPGLSKL MAQLVGLRGQKNHILNMIRDV TQQPQLSLAAHTPHTPHILQ
20077	50445	A	20193	1	334	
20078	50446	A	20194	1	687	

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20079	50447	A	20195	1	1280	RPGCGNKMAGKKNVLSLAAY A*ISEPESDGEAGIEAVGSAAD EKGGLVSDAYGEDDFSRLLGGD EDGYEEEEEDNSRQSEDDSET EKPEADDPKDNTEAEKRDPQEL VASFSERVRNMSPPDEIKIPPEPP G/RCSNHLQDKIQKLYERKIKE GMDMNYIIQRKKIEFRNPSIYRE /RLIQFCAIDELGTNYPKDMFD PHGWSEDSYEEALAKAQKIEM GQIGKRPKKERNQKFEFCGAP KKGT/TRTNATSTTTTTCQAQL FADCFRRGKRQVGIRAIPTSATKP KRTPPPKPPNTLTATLPS/V VVTVTHPSASGSKDPPVSCCG APIVKERPQVTLRGPPLGLER DRAAPVTHCPVGGAHFVYFRT GTYSRCHLRGASVWHSRWKD RQHGSQALWTGSVHAPPGVCR LLKVPYSYLLASQKK
20080	50448	A	20196	1	542	MAYSAPKSCTEGHESPH/HHT AGHSGWHGG*ALRQRGHSCPK EGTRGHQPQLAP/HHQCPQHAA GLPR/HNQLLHD/WFRHHHHHRH WHHHHHHHQ*FPECQPSSTSHQ ANPHHRPDLHQRAPDSGYEG VSPKRVAEAFSLGSAPQAAQ GRSHGQSPGVHGFSSHGSPAAS SDIMKRLPPPLF
20081	50449	A	20197	45	171	RKTRERIGHDVICNLL*C**SS/C GCGLS/CICS*IRHSKSSRKA
20082	50450	A	20198	277	467	GLGPHDYLYSILSIERSCCC*CC CCCCRRRRCCCC/CV*GCSRFL CSIAESTPSGALRRLRGGR
20083	50451	A	20199	1	1080	
20084	50452	A	20200	34	119	
20085	50453	A	20201	1798	1894	
20086	50454	A	20202	363	778	GLGPHDYLYSILSIERSCCC*CC CCCCRRRRCCCC/CV*GCSRFL CSIAESTPSGALRRLRGGRSGGS GGCCSPGGCREGGRGNTKPAT RCEVICGGSGGGGARPAAPP GPDA SRVCWFLNTSIVFSCPF
20087	50455	A	20203	1	360	
20088	50456	B	20204	1	3681	
20089	50457	A	20205	1	293	
20090	50458	B	20206	38	282	

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20091	50459	A	20207	1	1124	VDTVKRL.LJKKL.PPVLA.IQLKRF DYDWEREC.AIKFNDY.FEFPREL DMEPYTVAGVAKLEGDNVNPE SQLIQSQSESESETAGSTKYRLV GVLVHSGQASGGHYYSYIIQRN GGDGERNRWYKFDDGDVTEC KMDDDEEMKNQCFGGEYMG VFDDHMMKRMYSRRQKRWWN AYILFYERMDTIDQDDELIRYIS ELAITTRPHQIIMP.SAIERSVRKQ NVQFMHNRMQYSMEYFQFMK KLLTCNGVYLNPPPGVAEKTOL LKLSPATFMLVSLDEGPGPIK YQYAE.LGKLYSVVSQ.LIRCCNV SSRMQSSINDAETA.FNKIQHRF MLKILNKQGEETYIKITRAIYD KPTANIILNGQMI.EALPLNRRT
20092	50460	A	20208	1	1053	
20093	50461	A	20209	1	7785	MTATTTRGSPVGGNDNQGPAPD GQSQPPLQQNQTSPPDSSNENS PATPPDEQGGDAPPQLEDEEP AFPH.TDLAKLDDMINRPRWVV PVL.PKGELEV.LLEAAIDLSKKG LDVKSEACQRF.RDGLTISFTKI LTDEAVSGWKFEI.HVSLAFDFK GSDLHSDACEWEERCINNTHR LVEL.WCGPSCPDW.FPLLELL AMALNPHCKFHIYNGTRPCESV SSSVQLPEDEL.FARSPDPRSPKG WLV.DLLNKFGTLN
20094	50462	A	20210	1201	9141	ADKIAKICPVSSMTATTTRGSPV GGNDNQGPAPDGGQSQPPLQQN QTSSPDSSNENS.PATPPDEQGG GDAPPQLEDEEP.AFPH.TDLAKL DDMINRPRWVV.PVL.PKGELEV KLEANIDLSKKGL.DVKSEACQR FFRDGLTISFTKI.LTDEAVSGWK FEIHRCLVEL.CVAKLSQDW.FPL LELLAMALNPHCKFHIYNGTRP CESVSSSVQLPEDEL.FARSPDPR SPKGWLV.DLLNKFGTLNGFQIL HDRFINGSALNVQ
20095	50463	A	20211	2	710	

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20096	50464	A	20212	1	1703	RPLDVGGAAGTPGVLSRPCPS TAALAPKPFCAAPRPQPDAPAC AGATGGSCADFDGVDVFRRR SSGLWGQPPLFPVKNYTEDPV AFKDVAVNFTQEEWALLDISQ KNLYREVMLETFWNLTSIGKK WKDQNIIEYEQNPRRFRSVT EEKVNEIKEDSHCGETFTVPD DRLNFQKKKASPEVKSCDSFVC EVGLGNSSNMNIRGDTGHKA CECQEYGPKPWKSQPKKAFR YHPSLRTQERDHTGKKPYACK ECGKNIYHSSIQRHMVVHSGD GPYKCKFCGKAFFCLSLYLIHE RTHTGKPYECKQCGKSFSYSA THRIHERTHIGKPYFCQECGK AFHSPRSCHRHRSHEMGEKAY QCKECKAFMCPRYVRRHERT HSRKKLYECKQCGKALSSLSF QTHIRIMHSGERPYECKTCGKG FYSAKSFQRHEKTHSGEKPYKC KQCGKAFTRSFSFYHERHTHG EKPYECKQCGKAFRSAPNLQL HGRTHTGKPYCKECKGAFR SASQLRJHRRHTGKPYECKK CGKAFRYVQNFRFHERTQTHK
20097	50465	A	20213	3	2413	

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20098	50466	A	20214	1	2124	MGKNTPMIQLSPGPFHNSEYR FPVLSVSAFLLYTCMFQDPVA FEDVAVIFTQEEWALLDISQRK LYREVMLETFRNLTSLGKRWK DQNIIEYEHQNP RRNFRSLIEEK VNEIKDDSHCGETFTVPDDRL NFQEKKASPEVKSCSEFVCGEV GLGNSSFNMRGDIHGKAYEY QEYGPCKPCQPKKAFRYRPS FR TQERDHTGEKPNACKVCGK TFISHSSVRRHVMVMHSGDGPY KCKFCGKAHFCLRLYLIERIH TGEKPCECKQCGKSFSYSATHR IHKRTHTEGKPYEQECGKAFH SPRSYRRHERIHMGEKAYQCKE CGKAFTCPRYVRIHERTHSRKN LYECKQCGKALSSLTFSQTHVR LHSGERPYECKICGKDFCSVNS FQRHEKIHSGEKPYCKQCGK ALPHSSSLRYHVRTHTEGKPYE CKQCGKATHNGEKPYACKECG KPFQSAQNLRIHERTQTHIMHS VERPYCKKICGRGFYSKSFQI HEKSYTGEKPYECKQCGKAFV SFTSFRYHERTHTGENPYECKQ FGKAFRSVKNLRFHKRTHTEGE K/PL*IEKHTHTGRKHYECKQC GKAFTSSSSFYHERTH/S/GEK PYQCKQCAKAFISSTSFQYHER THMGEKPYECMPSGKAFISS/SS LQYHERTHTEGKPYEYKQCGK AFRSASHLQMHGRTHTEGKPY
20099	50467	A	20215	23	265	
20100	50468	A	20216	40	470	
20101	50469	A	20217	235	392	

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20102	50470	A	20218	7	1439	EGADKMATSVGHRCGLGLHGV APWRSSSLHPCEMTALSQSLOPL RKLPPFRAFRTDARKIHITAPART MFLRLRPLPILLVTGGGYAGYRQ YEKYRERERELEKLGLEIPKLA W SLGSVALYKSVPTRLLSRAWG RLNQVGAAHTGLRRPRFTSLYI WTFGVNMKEARVEDLHHYRN LSEFFRRKLKQARPVCGLHS/V GEA*PFPAGNRTFSCLPSTAPL VSSVSGRGRMTRGGGCGCLGG GDPALPGSKPLLPQISPSDGRIL NFGQVKNCVEQVKGVITYSLE SFLGPRMCTEDLPFPAASCDSE KNQLVTREGNELYHCVIYLA PG DYHCFHSPTDWTVSHRRHFPGS LMSVNPGMARWIKELFCHNER VVLTGDWKGFFSLTAVGAT NWGSTRIYFDRDNTNNPRHSK GSYNDFSVTHTNREGVPMRK GEHLGEFNLGSTIVLIFEAPKDF NFQKLTGQKIRFGEALGSL
20103	50471	A	20219	170	1144	ARTRLAPSPGCRGPAVKKM RHEELTKTFQGPVVCGTPTS HVYMFKNKSGDSGDSSEESH RVVLRPRVKERHKSGVHQPPQ AGAGDVVLLQRELAQEDSLNK LALQYGCCKHSE*LTMA/NVADI KKVNNFIREQDLIALKSVKIPV RNHGILMETHKELKPLSPSET TVTVELPEADRAGAGTGAQAG QLMGFFKGIDQDIERAVQSEIFL HESYCMDTSHQPLLPAPKTPM DGADCGIQWNAVFIMLLIGIV LPVFYLVYFKIQASGETPNSLNT TVIPNGSMAMGTVPQAPRLA VAVPAVTSADSQFSQTTQAGS
20104	50472	A	20220	1	626	RYSSLTLTRPWQTPTPTASPHS PVAGALTARPPSPRPTKPSRAG VHASRRPPQDLGPIGKGSATK GPRHQKHHESITPPSRSPTEKA PPGLNDDAQIFASQESVAPLWIP VTAP*AHRLVSSCEFGAAFESA GEEEGEGEVSASQAQVAGTQ TRR*GATSAPCGVPEGASVPA L*AAGAAGRAEAERPVCVPAQ AVGLSGQPLS

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20105	50473	A	20221	2492	4619	WHSWRQQGWGAHLGSSATGP GC*QGRPTCVMRPAGT/TRPGE APIGSGTGAVEMPAREPGDEKP PAPFP*QRHFVPRAHLLFGTAL RSLPELMRRVARNPRHILSAEE SLLFSLPGSPWKGWSSWNGQA PPLAPPAQGPLLPVPLSAGPGV AGERTVPSSPRWWRPHLFLAPT APSPPPCPTVSAPGHLLGVAQK PDCHPPASQRRRHLPLPGEA FAE/SAANS*ISSISASFTFS*SSS WSLD/STKSSLPLHLPTLTSRV PGKFSALLSQFSASFSSHGLPSE SVAIGTCST/PERAHSRQTCCGP GSSAQ*GQEEGQCPQCRDSAG TCGRPRCSRHPAGHAGSEPRPL QRRSLHCSHTG*GAGIGHKART CGRKAPPRCPSETGHHSGVGY* PWRQSQQPAARGRARCGRPCP GACPAMAPQTQSEEGRRAPR/T NPAVPSEPARP/STAGPRAGASV PPSGPRGPAGPGAPSAAGRRRR APGATACSGGAVESG*PSL/GSA LSAQVAPEAARAPA*GPGQAA GAREEGPAWPCRSPP/GPGPSQC AALPQK/GSALRSGGRRTLGPL LSHPSFKILLAGSGGVLDNSTSS ERSRATRSSICRPVSVESWTNN NGGDTGG/SSCDFYSPGADGL SQGHSSDHTNLLLVLSSQKRHF PA*ALVQPHAPSPSTGTEPWPP AGPRTVPRPPSASSVAPSCWVV
20106	50474	A	20222	103	538	PQLSLPLLJIRDRRRPSKCANLT LTLTVAAARHGLQSLGKVGISRR MPPANLPSLKAENKGNPDNV NIVPKDGTGWASKQEHEEEK TPEVPPAQPKPGVAAPPEVAPA PKSWASNKQGGQGDGIQVK*Q FQQEFPSLQAAGDQK
20107	50475	C	20223	1	569	
20108	50476	A	20224	1	1095	

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20109	50477	A	20225	1	1970	MWKGFTILDSFKNISDSWEDVR ISTLTGVWKKLIVTLMDDLEEF KTSVEEITLTQRKLFFVMESPV GPISPPQPPSVSAWNKPLTSFGS APSEGAKNQESGLEIGTDITQ FGAPASNGNENEVVPVLSEKSA DKIPEPKEQRQKQPRAGPIKAQ KLPLDSPVDNKLEHKPGPIGKER SLKNRKVKDAQQVEPEGQEK SPATVRSTDPTTKETKAVSEM STEIGTMISVSSAEYGTNAKESV TDYTTTSSSLPNTVATNNTKME DTLVNMMESARKAWENSPNVR EKGSPVSTAPPIATGVSSASG PSTANYNSFSSASMPQIPVASVT FTASLSGAGTYTSSLSKSTTT SDPPNICKVKPQQLQTSSLPAS HFSQLSCMPSLIAQQQNPOVY VSQSAATLTACLS*WSTAQI PAFYMDTSHLNTQHARLAPPS LAQQQGFQPLSRSQPAFMQS SLSQSPVVLSGTAIHNFPTVQH QELAKAQSGLAQQTSNTQPIPI LYEHQLGQASGLGGSQIDHTL LQVTVPPLPASQLSLPNFGSTGQ PLIALPQLQPPPLQHTTPQAQA QSLSRPAQVSQPFRLIPAGTQ HSMIATTKGMSEMLKAFGSGI DIKPGTPPIAGRSTTPTSSPSGL LLQVRTASPAK
20110	50478	A	20226	260	8485	VSTEMSEKSGQSTKAKDGKKY ATLSLNFNTSKGKSLTQKTTVA ARHGLQSLGKVGISR/RMPPPC* PPKFLKPE*QRANDPNVNIVPK DGTGWASKQEHEEEK/TPEVP PA/QPKPGVAAPPEVAPAPKSW ASNKQGGQGDGIQVNSQFQQE FPSLQAAVDQEKKEKETNDDN YGP*PSLRPPNVACWRDGGKA AGSPSSSDQDEKLPGQDESTAG TSEQNDILKVVEKRIACGPPQA KLNGQQAALASQYR
20111	50479	A	20227	330	485	RQGDVSLCCLGRS*TPGLK*F SHLDLLNCWDYRCETVHLAEI AQVSEKQI
20112	50480	C	20228	1189	1413	

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20113	50481	A	20229	1	407	MPFSLADCDSDQHCLLFAVVDLGTAKATSCMSDFTDFYSSSGNSANLKEGGKSPGPGKGRGAKQRKYSQSPWNRKESCKKHEGVKGAEGRGGTVASVRES/REPRFKMAAFSMHPC*RLSRHRGHLAGRCFCFCR
20114	50482	A	20230	1	408	HMDLAQSPQPVDELESLVLERQPEENTPLNGADEVPFSLDEEVPVPAEANKESPWSSCNKNVVGRCCKLWMIITIFLGVITVIIIGLCLAAVTYVDEDENEILELSSNKTFFIMLKIPPEECVAAEELPHLLTERL**SL**HLGKWR**SST/GLHLPTTFLLQELQGLSLASAGGTSSSKEGKTSSAPLRGVFSSGCRSSTESSSTSGCEGWARMS
20115	50483	C	20231	144	383	
20116	50484	A	20232	1	530	AKDSESRRLRGYNPQOMSEGHRQKSEFYNRTASESNVYLSNFHYPDHSYKQDAFDTLSDSSDSMETSISACSPDNISASTSNIARI EEMERLLKQAHAETRLLESREMEAKKRALEEEKRRREILEKRLQEETSQRQKLEKEVKIRERQRAQARPLTRYLPVRKEDFDL
20117	50485	B	20233	10	543	
20118	50486	A	20234	370	556	
20119	50487	A	20235	3	3160	TELQQLGQKTADGSPGLKRALIFALNFHSSPPGKDMAAVQRTL MALGSAVAVTKDDGCRYGEPSEWHRKAQQNRRGFSEEQLRQGQNVIGLQMGSGNKASQAGMTGLSDTPWTAHLGMYVQGNAKFVSPVRRIVVHEYYNSQTDFDYDIALLQLSIAWPETLKLQIQPICIPPTGQVRVRSGEKCVWTGWGRRHEADNKGSLVLQQAELIDQTL CVSTYGIITSRLCAGIMSGKR DACKRRKLGTERTPGTQAAAP
20120	50488	A	20236	231	873	KKFRALGSGVPGFRASGVQVADEVICRIFYDMKVR/KCS/TPEE DQDKERSAVIFCLSDAKKCIIV EAGKEILVGDVGWNP*TDPFIR HFVGMLP*KKIVRYAFVMDGK LLETGFGQKRKSLMFFVF/WAP EL/APLKK*K*SYCKLQGMFAFKNFQGIKHECQA/NGPEDLNRA/CIAEKLGGSLIVAFEGCPCVDHHSVPQIEKLPMFNCYPLAI

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20121	50489	A	20237	915	1255	GHGQKPAGKKKILAVRSGSEP AGGFQGY/RGGHGTAS/GSPGD DDSPGALWEQSPGPL*AWPGA VSEPMVCAEPVQEQSGPQLPP PRHSRSPSGDSGQPGVPAERRRI MGMAA
20122	50490	A	20238	3	227	LLMDTF/FQIVIVL/GETIAQWR KAGYQDMPEYENFKHLLQAPL DDAQEILQARFMPVKLRIQPG NATVSDCVQNV
20123	50491	A	20239	1	642	RRDTIARNWANVQSQRHIEQ AFDQEAALVLMARLG/VFEPK SKEGPDVLRWLDRLQLCQKF GQYTKEDPTSFRLSDSFSLYPQS MFHLRRSPFLQVFNNSPDESSY YRHHFARQDLTQSLIMIQPILYS YSFHGPPPEPVLDDSSRFMPRYI NTEHGGSQARFLLSKVNPSQTH NNLYAWGQETGAPILTDDVSL QVFMDDLKKLAVSSAC
20124	50492	B	20240	20	277	
20125	50493	A	20241	1	3030	

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20126	50494	A	20242	1	2677	MAEVKVKVQPPDADPVEIENRI IELCHQFPFHGITDQVIQNEPMHI EAQQRAVAINRLLSMGQLDLL RSNTGLLYRIKDSQNAKMKMG SDNQEKL VYQIIEDAGNKGIWS RDIRYKSNLPLTEINKILKNLES KKLIKAVKSVALGIPAGCSVCP KCGASNHL SARFCGSCGICVKS LVKLSLDRSLAAAEPRPFSES LNPLPRSDVGTGRDIGTQTVGL FYPSGKLLAKKEQELASQKQR QEKMSDHKPLLT AISPGRENIG ENLQVIGLVKNFLSNIPQAPAT QAKMGKWDPRQGAQSPLIFL YVVDTCLEEDDLQALKESLQM SLSLPPDALVGLITFGRMVQV HELSCGISKSYVFRGTDLTA KQIQDMLGLTKPAMPMPQARP AQPEHPFASSRFLQPVHKID MNLTDLLGELQRDPWPVTQGG RPLRSTGVALSIAVGLLEGTFP NTGARIMLFTGGPPTQGGPMV VGDELKIPRSWHIDIEKDNRNF IMKKATKHYEMLANRTAANGH CIDIYACALDQTGLEMKCCAN LTGGYVMVGDSFNTSLFKQTF QRIFTKDFNGDFRMAFGATLDV KRQVQGERGREAKNLWTVH AHSSWRALNTGLRSFDFIPGTV REPVKILGRRLTSDLQIRNSPLE AAVQGGVSKTVSTVSLAHAMR AHPHLLMEDLRILVIDLDPQSS
20127	50495	B	20243	453	3318	
20128	50496	A	20244	2	1367	

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20129	50497	A	20245	1	1459	MLEGKYGPPGSFQTRRTALAR SHTNTSPSTSPAANRLNALGIGE RDASPSWLGQDQVVKRQPG SGSRKIPRCAMTYGSLGQQA QAAGVHAPNVFVASLLCQFLQ FVYRNSMGWTGGADFSYSCQE GETKELWSSGHHLKACRAVAF SEDGQSEYWGROPAMWWKGA VSSTMTLGTFSPELITVSKDKAI HVLVDVEGQLERRVSKAHGAP INSLLLVDENVLATGDDTGIGC LWDORKEGPLMDMRQHEEYIA DMALDPAKKLLLTATYCSSTLY SGDGCLGIFNIKRRRFELLSE SGDLTSVTLMKVQLVMWGKK VACGSSEGTIYLFNWNGFGATS DRFALRAESIDCMVPVTESLLC TGSTDGVIRAVNLPNRVVGVS GQHIGEPVEELALSHCGRFLAS SGHDQRLKFWDMAQLASCGG G*LPSAQKKGRRTTAGSEQQDLE HR*LLRRTAARGRLHGSQKKR RRLGMTVTEGMN
20130	50498	A	20246	221	847	RHIFSFSGHVLAVSI.GKFIFEST LFPSEARAARRRRPVQWPRFK ARDLRGKKKEELLKQLD/DLKV EAV/SQLRVAKVTGR/AASKLS KIR/VVRKSIARVLTVIN/QTQKE NLRKFYKGKKYKPL/DLR/P*GR HRAMRPPASNQARRENLEGPK EAGSGKGAFTRCGK*RGSR LRGLRQ*KHKENLTKKQQR KERLYPLRKYAVKA
20131	50499	A	20247	1	415	FFFFFECG*SFTNSFSVTIHRRIH NGEKSYECSDCGKSFNVLSSVK KHMRTHTGKKPYECNYCGKSF TSNSYLSVHTRMHN/TANVNSI TVGKAFIDLSCLR*HEQTLTRC MNHLLLCNKLPPKILWLQTKTL VISKFL

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20132	50500	A	20248	196	1768	RRSVLLPGCPVAVGVTGWRLSS CPQLPLCLPCSQPLSEKDTQRA ESWLMSS*KAG/YKGLVTFEDV AVEFTQEEWALLDPAQRITLYR DVMLENCRNALSLGNQVDKPR LISQLEQEDKVMTEERGILSGTC PDVENPFKAKGLTPKLHVFRKE QSRNMKMERNHLGATLNECN QCFKVFSTKSSLTRHRKYSILGE RPYGCSECGKSYSSRYLAVHK RIHNGVVPYECNCGKTFSSRS YLTVHKRIHNGEKPYDCSYCG KTFSSNS*YLRPHLRHTGEKPYK CNQCFREFRNSIFTRIHRVHT GEGHYVCNQCGKAFGTRSSLSS HYSIHTGEYPYECHDCGRTFRR RSNLTQHIRTHTGEKPYTCNEC GKSFTNSFCLTIHRRIHNGEKSY ECSDCGKSFNVLSSVKKHMRT HTGKKPYECNYCGKSFTIGQGD GFEIVLPPPQLQQLIAFFLGNT HCLSDRLSVQCIHYSIRYLHLNI HYLHYSIHYLHYSICYLHYSIM DPPQQSPHPLQHPLQNPLQ
20133	50501	A	20249	2	408	
20134	50502	A	20250	1	280	
20135	50503	A	20251	2	469	RGIREGEEFDVDLAGMEVAVG GWGRGLWLRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFSSNTTCQQFRDPGFR GRYPASPHLTLPPETAHL*LLL CLPAAGVLPHTWPLLDQGWHR RGHAR

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20136	50504	A	20252	1	1762	FRMAAPLVLVVAVTVRAAL FRSSLAEFISERVEVVSPLSSWK RVVEGLSL.LDLGVSPYSGAVFH ETPLIHYLFHFLIDY AELVFMITD ALTAIALYFAIQDFNKVVFKKQ KLLLELDQYAPDVAELIRTPME MRYIPLKAALFYLLNPYTLSCV AKSTCAINNTLIAFFILTTIKGKA LKGEYKGS AFLSAIFLALATYQ SLYPLTLFVPGLLYLLQRQYIPV KMKSKAFWIFSWAYAMMYVG SLVVIICLSFLLSSWDFIPAVYG FILSVPDLTPNIGLFWYFAEM FEHFSLFFVCVFQINVFYTIPLA IKLKEHPFFMFQIAVIAIFKSYP TVGDVALYMAFFPVWNHLYRF LRNIFVLTCIIVCSLLFPVLWHL WIYAGSANSNFF*GITLTFNVG QLPHEL FIMVPEGGGPGALMA AIERNVDRAVPGGSAERDPIER STLHILLISDYFAFLRREYYLT HGLYLT PQGIAP EAMLVLQSRP GWHIRASWTLRGLVGPEAGPKL SSPELPAGECLGRRGSSPRVTSS LVPKRD PWLTD SKAYGEELGA PQLGPPPCGSAHQGAPSQTGRR
20137	50505	B	20253	102	406	
20138	50506	B	20254	200	408	
20139	50507	B	20255	347	458	
20140	50508	A	20256	2	430	
20141	50509	A	20257	3	567	
20142	50510	B	20258	1	1317	
20143	50511	A	20259	928	2067	
20144	50512	A	20260	2	4498	VHELQSLSEMLKPEVLSPTVKG KLLTGIKSPRSYTPKPNPVTHVI STGIQKIWIGATVGVSTEVSAV TPDGYADAVRGDRFMMPAERR LPLSFVLDVLEGRQHHPGVLYV QKQCSNLPSELPQLLPDLESHV PWASEALVHKHHYENLYCVVS GEKHFLFHPSPDRFPYELYTP ATYQLTEGTFFKVVDEEAMEK VSVLFLGSRREGQKPGSEEQ QKIWGVAAVQRLGML EAGIL PQEGRFQALAEIADI

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20145	50513	A	20261	3	3137	DTPAWHGDANRTKAALEAARS DYLEFPPAAARELCVPLAVPYLD KPPTPLFHYRDWVCPNRPICIRN ALQHWPALQKWSLPYFRATVG STKVSVAAVTPDGYADAVERGI RF/M*LPVERRPLPSFVLDVLEG RAQHPGVLYVQKQCSNLPSEL QLLPDLESHVPWASEALGKMP DAVNFWLGEAV*VTFCHKDHY ENLYCVSGEKGHFLFHPPSDRP FIPYELYTPATYQLTEEGTFKVV DEEAMEKAEVSRCT
20146	50514	A	20262	164	1236	AQSRRSRDRGQAFSNHHAAEHI TCTPGSGSGSRVSSGQAARRRL SGRAGLWAAVTNPPPHPTWLE VSRSAATAARAALCRRSACL RTPHLSAMISASRAAAARL/VG AAASRGLRAARHQIRSNQGT VGIDLTGTTNSCVAVMKKNVPF KIVRASNGDAW/VEAHGKLYSP SQIGAFV/LMKMKETAD**LFLS SEPPQPGQAGFLQPSCCGAYY LYPWLREQRSSILWGGAAAPQ RKSGPLGRSDQPPSPHVVGGF QKRCRHRSSRLPSERLFAASYS SFIRHDKCQPSCSPSRGAAASR GLRAARHQIRSNQGTVVGIDLG TTNSCVAVMKKNVPFIVRAS NGDAWVRLMGNCLRVRLLEHL CDEDERDCRLIVALPEGMEEP FDYQNDMGNSQDLERRRGCA EPWEEGVGQSLALPLVSLCLKC RWYRSPCTQGQHPATFSGPAEG VISERSMLEHWHEEINQCKAYN EDVFSTMRNTPARISSEAMAPA DIIDHSSQRPDFTSGKMLADEF GTASNIKSRVNAFQSWEPHLHY NKDSNL
20147	50515	A	20263	216	728	

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20148	50516	A	20264	1	2519	MAPSSRSGAGNTSTPGGCARAR APPGNAGVHSGTQTGA VRDTA FISPPSPGLFLSSEPPQPQRAGF LQPSCCGAYYLYPWLRERQSSI LWSGGAAAPQRKSGPLGRSDQ PPSPHVVGGFQKRCRIIRIAQL FAVGALVCLVLLHLSAMISAS RAAAARLVGAAASRGPTAAR HQDSWNGLSHEAFRLVSRDY IASVEAIKGA VVGMDLGTNSCV AVMEGNQAKIVLENAEGAKTT PSVVAFTADGERLGGMPAKRQ AVTNPNNTFYATKRLIGRRYDD PEVQKDIKNVPKIVRASNGDA WVEAHGKLYSPSQIGAFVLMK MKETAENYLGHATAKNAVITVP AYFNDSQRQATKDAGQISGLN VLRVINEPTAAALAYGLDKSED KVIAVYDLGGGTFDISILEIQKG VFEVKSTNGDTFLGGEDFDQAL LRHIVKEFKRETGVDLTKDNM ALQVRVREAAEKACELSSSVQT DINLPYLTMDSSGPKHLNMKLT RAQFEGIVTDLIRRTIAPCQKA MQDAEVSKSDIGEVILVGGMT RMPKVQQTVDLFGRAPSKAV NPDEAVAIGAAIQGGVLGADV TDVLLLDVTPLSLGIETHGAVF SKLINRKTNIPTKKSQVFSTAAD GQTQVEIKVCQGEREMAGDNK LLGQFTLIGIPPAPRGVPQIEVTF DIDANGIVHVS AKDKGTGREQ
20149	50517	A	20265	1	168	LERERKRSRKELNLFYAWQH RESKMEHLR/QLRKKFEEDKQR IELLRARQKFRPY

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20150	50518	A	20266	3	1085	ARAGAEPQLPATPALPGGKMY ARSLAGLSSG*PGHPSPPISFPAI PIKFSEKQQAASHYLYVRAHGIQ QGTKWREALGW/SRMLTLGF P/PPCS/EESLSCLQSTCGLVQSV ELKFPDLPHPCTSCLAFSVPC*S SRTVSAGHLQGLPRLPSCFTE GAPSPGLGAGSPGALLFRDLVP DVGRSPQPLTSLSLQGFQVAYV VFQKPSGVSAALAVGPKCQA* GSPVSLAPFSSEWISDYADSVDP PGWRLREVPGAHRTMGSPSLQ EEAKAKEEEGVPEDEGWVKVT RRGRRPVLPRTAAASRLVLERE RRKRSRK\ELLNFYA\WQHSRE/ SKMEHS*GKCARSFEEDKQRIR ACCGPKRKIPDRN
20151	50519	A	20267	2	334	SLQVQPFASLISKAPLSTPRLIN KEKAGQSDPFLGMIMGLGGGM DFDSKKA/YAELLGWKKELEDL VRREHASIDAQSGAGVNPST ASPKKSPPAKDEARTTEREKP Q
20152	50520	A	20268	124	407	QSDPFLGMIMGLGGGMDFDSK KAY/RVRRPRLGQPGMDRVR WERGHEGR*EEQAGASPPGNS DLLLHRRDVAWLGECDQGCLA LAELLGWKVR
20153	50521	A	20269	193	458	
20154	50522	A	20270	55	1165	RDRAVGDSLKGFSAPMAEPD PSHPLETQAGKVQEAQSDSDS EGGAAGGEADMDFLRNLSQT LSLG/SQKERLLDELTLEGA/R YMQSERCSQSSCLVGAGISTS AGIPRLFASPSTGLLLNLEK*P SFPNPEAIF*DSAIFKKH/PEPFFA LAK\ELYPGAVSRPTICSIISGL LERDKGGLLLR/CVKRREH*VT WERIAGLEQEDLVEAHGTFYT SHCVSASCRHEYPL.SWMKEKIF SEVTPKCEDC/QSLVKPD/VVFFG ESLGARFFSCYCSDFLKVDLL L/VMGTS/LRDVAWLGECDQGC LALAELLGWKKELEDLVRREH ASIDAQSGAGVNPSTASPKK SPPPAKDEARTTEREKPQ

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20155	50523	A	20271	3	357	FGFNGCSKRIIKLQELSDLEERE NEDSMVPLPKQSLKFFCALEVV LPSCDCRSPGIGLVEEPMKVE EGPLSFLMKRRTAQKLAIQKAL SDAFQKLLIVVLG/QDCLDHP* TSVSVSK
20156	50524	A	20272	696	1123	IPLKMMNLFQSLKSPQLSHQLR L*LPQVEPSLTQQNFPAQTP/V PPMEAEPSPNQEATVQASEPP KNIELSSQQMVPENIFPPTMENS NQLPEPPTEVVAQLPPRYEVTIP TQGGDQAQLSTLASVTLPQLDL GFIITPESTTEIELSPTMQETPTQ PPKEFVPPPPV/LSRESSEETGPL PVQQETS AESPEPTKD ENFPIQ *EAAFSSEISSQGSWHQT
20157	50525	A	20273	1	727	GIPAADREASLELIKLDISRTFP NLCIFQQGGPYHDMHLSILGAY TCYRPDVGYYVQMSFIAAVLIL NLDTADAFIASNLLNKPQMA FFRVDHGLMLTYFAAFVVFEE NLPKLF AHFKNNLTPDIYLD WIFTLYSKSLPLDLACRIWDVF CRDGEFLFR TALGILKLFEDIL TKMDFIHMAQFLTRL PEDLPAE ELFASIA TIQMQRNKKWAQVL TALQKDSREMEKGSPLRH
20158	50526	A	20274	3	435	CGGIPKMEESA EYEAARHKRE KRMENINLAGSKRGKEDGKDS EFAAIENLPGFELLSDEKVLCS SLNLSPARYVTVKTHIKDHLQK RQGIP/CQKPPS*LPQSPKEKD FEFPHRKRLDLQGRVLKLRFFE SQGDAQTVCPQK
20159	50527	A	20275	46	513	

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20160	50528	A	20276	3	1084	NQEWKRSPPITVAKATQGA YL NILKDTLRAQKEQKEGKEEVIH KGAKLHPNGYRMAQGS ETLVA RGGPCRSVEPSAASPQELRGW WEAQALKRWGLMGGVVWVME VDPSSLGAI SAIVSSASRL LKS VWHIPCPHFLLRPQLKEAQRR KKQLFEERCVEESIGNAVLTW NNEILPNWETMWCSRKVRDLW WQGIPPSVRGK VWSLAIGNELN ITHELFDICLARA KERWRLSTG GSEVENEGLCVAVCAQQGHVG VMGFGSDEPSAVSPCEKGKSLA AWVLIFVDFRVGLQKSFQKRK ERESTKLQQLWSWCLMLTYFA AFEVFFEENLPKLF AHFKNNL TPDIYLD/W*FRLLVGC
20161	50529	A	20277	60	556	EDSEMAPPAGPASGGFGEVYE LFDVKNAFYIGSYQQCINEAQR VKLSSPERDVERDVFLYRAYLA RRDSIVAELDREMSRSDVTNT TFLMAASIY LHDQNPDAALRA LHQGDSLECTAMTVQILLK LDR LDLARKELKRMQDLDEDATLT QLATAWVSLATGG
20162	50530	A	20278	1	628	FFYKSVLAQKEVRCVLDE/ISPL GPPELKPVRMFADL/LPHESRR DSSVPELA EKMSRSDVPTPPS LLMAASIY LHDQNPDAALRAL LHQGDSLECTAMTMQDAYYIFQ EMADKCSPTLLLLNGQAACHM AQGRWEAAEGLLQEALDKDSG YPETLVNLI VLSQHLGKPP EVT NRYLSQLKDAHRSHPFKEYQA KENDFDRVLQYAPSA
20163	50531	A	20279	1	884	RKFGVVLDEIKPSSAPELQAVR\ MFADYLAHESRRDSIVAE LDR MSRSDVTNTTFLMAASIY LH DQNPDAALRALHQGDSLECTA MTVQILLKLDRLDLARKELKR MQDLDEDATLTQLATAWVSL VATGGEKLQDAYYIFQEMADKC SPTLLLLNGQAACHMAQGRWE AAEGLLQEALDKPPHGCSCERK LVSPFMVETEAKQSPVCKKVPC HGPPWAGRALGASSLDSGYPE TLVNLIVLSQHLGKPP EVTNRY LSQLKDAHRSHPFKEYQAKEN DFDRLVLQYAPSA
20164	50532	B	20280	512	903	
20165	50533	A	20281	18	413	

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20166	50534	A	20282	1	1195	MKHPNINSALQAPHPFPVGRPH LVAGVAPPALSNHPQARATAA AGKPHPRCAEAAIGLACTAPG SHWLKMGELPLDINIQEPWWD QSTFLGRAPHFHFTVTDPRNLLL SGAQLEASRNIVQNYRAGVVTP GITEDQLWRKYYVDSAFHPD TGEKVVILGRMSAQVPMNMTI TGCMLTFYRQGSKDEGHCRRG RSECLCSLRKTPVVFQWVN QSFNAIVNYSNRW*HFPSLVR QLGTAYVSATVTGAVATALGL KSLTKHLPPLVGRFVPFAAVAA ANCINPLMRQELQVGIPVAD EAGQRLGYSVTAAKQIGFQVVI SRICMAIPAMAIPLIMDTLEKK DFLKRRPWLGAFLQVGLVGFC SIHISNLEPELRAQIHEQNPSVE VVYYNKGL
20167	50535	B	20283	24	51	
20168	50536	C	20284	1	1182	
20169	50537	B	20285	1	372	
20170	50538	A	20286	1	4610	ELAQNHRSRPAPASAPGGGGGG DPNMTARTFGPEREAEPAKE ARVVGSELVDITYTVYIQVTDG SHEWTVKHRYSDFDHLHEKLV AERKIDKNLLPPKKIIGKNSRSL VEKREKDLVLYLQKLLAFAFG VTPRVLAHFLHFHFYET*VIHA A\LAELFEKGEQLLGAGEVFAI GPLQLYAVTEQLQGGKPTCAS GDAKTDLGHILDFTCRLLKYLK VSGTEGPFGTNSIQEQLLPFDLS IFKSLHQVEISHCD
20171	50539	A	20287	1	4670	MAAQRAAGATGGGGRGASAP GGGGGGDPNMTARTFGPERE AEPAKEARVVGSELVDITYTVYI IQVTDGSHEWTVKHRYSDFDH LHEKLV AERKIDKNLLPPKKIIG KNSRSLVEKREKDLVLYLQKLL AFAFGVTPRVLAHFLHFHFYEI NGITAAELFEKGEQLLGAG EVFAIGPLQLYAVTEQLQGGKP TCASGDAKTDLGHILDFTCRLL YLVSGTEGPFGTNSIQEQLLP DLSIFKSLHQVEISH
20172	50540	A	20288	2	227	ERFRPPIARVIDVSNKGVHVAE/ SCLEETGGLGVDIVLDAGLDPP DSHCLFLKGATLAFLNDEVWN LSNVQQGRYL
20173	50541	A	20289	3	487	

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20174	50542	A	20290	2	222	
20175	50543	A	20291	1	296	HLSPGKSVLIMDGASA\FGTIAI QLAHHRGAKVISTACSLQEDKQC LERFRPPIARVIDVSNKG\HVHA ESCLEETGGLGVDIVLDAGGYI FQHSSYIFT
20176	50544	A	20292	353	512	
20177	50545	A	20293	2	396	VRLYSKDDPEAVKLQLLPHKH DIITLLGVGGHWVTTEENLQLD PPDSHCLFLKGATLAFNLNDEVW NLSNVQQGK\YLS*QSFQLRIK DVMEKLSTGVFRPQSDHEHIPVF EARI\SLIVEKNQGR*NLKLF
20178	50546	B	20294	1	1182	
20179	50547	A	20295	1	1189	PTRPDQWEQGAGSLTKDWKV AVVKVQAVGAQRQVTMTKGL YFQQSSTDEEITFVFQEKEDLPV TEDNFVKLQVKACALSQINTKL LAEMKMKKDLFPVGREIA\GIV LDVGSKVSPFPDDEVVGILP LDS*KTPGL\CESLLRVHEPLL FINPEKVTW\TEAAGSISGMGV RAYYSFLHLS\YLHLLSWGKSV LIMGGS/ASAFGTIAIQLAHHRG AKVISTACSLQEDKQCLERFRPPI ARVIDVSNKG\HVHAESCLEETG GLGVDIVLDAGVRLYSKDDPE AVKLQLLPHKHDIITLLGVGGH WVTTEENLQDPPDSHCLFLK GATLAFNLNDEVWNLNVQQGK YLCILKDVMEKLSTGVFRPQLD EPIPLYEAKVSM\EA\QKNQGR
20180	50548	A	20296	3	115	FFKFSFFNGC*SIKRQSQGQALD RDIICFVDICTKDC

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20181	50549	A	20297	1	1401	MKEEELTRQIVLVQEAGKGVV RTKDGACAEVWQALELEKGL CAGIVRVEGMAAAPSYCFVAF PPRAKDGLVVF GKNSARPRDE VQEVVYFSAADHEPESKVECT YISIDQVPRTYAIMISRPALW GAEMGANEHGVCIANEAINTR EPAAEIEALLGMDLVRLGLER GETAKEALDIVVLSLEE HQGG NYFEDANSCHSFQSAYLIVDRD EAWVLETIGKYWAAEKVTEGV RCICSQLSLTTKMDAEHPELRS YAQSQGWWTGEGEFNFSEVFS PVEDHLDCGAGKDSLEKQEEI TVQTMNTLRDKASGVCIDSE FFLTASGVSVLPQNRSSPCIHY FTGTPDPSRSIFKPFIFVDDVKL VPKTQSPCFGDDPAKKEPRFQ EKPDRRHELYKAHEWARAIIES DQEQRKRLRSTMLELEKQGL* AMEEILTSSEPLDPAEVDLFY
20182	50550	A	20298	1	356	QTPKIVADKDYSVTANS/KIVV VTAGVRQQEGESRLNLVQRNV NVFKFIIPQIVKYS PDCIIIVSNP VDILTYVTWK/ARFRYLMAEKL GIHPSSCHGWILGAHGDSSVAV WSGVNLAG
20183	50551	A	20299	1	322	
20184	50552	A	20300	25	1086	
20185	50553	A	20301	1	864	
20186	50554	A	20302	13	190	

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20187	50555	A	20303	1	1350	MEKPKRLRLWGPAPSSLLAE PAPEETHAADVFVSARLLQRSP EPSLSWGGRALAEEQKAEGSSC GSAERLVAFAAKTRPYLSLCK MATLKEKLIAPVAEEATVPNN KITVVGVGQVGMACAIISLGKS RAMEHTTAGAPYTPRQQTCC NMMSLADELALVDVLEDKLGK EMMDLQHGSLFLQTPKIVADK DYSVTANSKIVVVTAGVRQQE GESRLNLVQRNVNVFKFIIPQIV KSPDCIMVVSNNPRDMLTYGT WKLGLPKHRVIGSGCNLDSAR FRYLMAEKLGIHPSCHGWILG EHGDSSVAVVSGVNVAGVSLQ ELNPEMGTDNDSENWKEVHK MVVESA\YEV\IQA*KGYTH\WA IGLSVA/EILNESMLKNLSR\HP VSTMVKGMYGIENEVFLSLP\CI \LNAGGLTSVINP\KVKDDEVAQ LKKSAADTLWD\QKDLKDL
20188	50556	B	20304	1337	1706	
20189	50557	A	20305	178	344	
20190	50558	A	20306	2	297	TKMTVNNLHPRVTEED\I/GQP MKCNLHMNGNVITSDQPIILRL SDSPSMKKESELP RRVSASSS NPPAEVDPDTILKALFKSSGAS VTTQPTFEKIKL
20191	50559	B	20307	8	478	
20192	50560	C	20308	146	391	
20193	50561	A	20309	3	735	HRQKDARFRIKGVQDAREML NSRKQQTTPQKPRQVADARE KISLKRSSPAAFINPPIGTVPAL KLTKTIQVPQKAMAPLHPHPA GMRINVVNNHQAQNL\YDLD EDDDGIASVPTKQMKFAASGG FLVHHM\AGLSSSKLSMSKALPL TKVVQNDAYTAPALSSIRTKA LTNMSRTL VNKEEPPKELPAAE PVLSPLEGTMTVNNLHPRVTE EDIVELFCVCGALKRARLVHPG VAEVG

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20194	50562	A	20310	1	1763	MEIASFVGPVNVTVGNI.RPAQS AAGDGDDEVQSVHSQRQDCQAT GSLNNGENNEKNAFTTYQQET KNTTTPQSVYFLGVNKMSSQH REGSRGTPPLPVLACFELAVA RVGPRTPPEVVRSLAAEGAGSR GLDCFRLLARRIKMADISLDELIR KRGAAAKGRLNARPGVGGVR SRVGIQQGLLSQSTRTATFQQR FDARQKIGLSDARLKLGVKDA REKLLQKQDARFRIKGVQDAR RDV*TRKQQTTPVQKPRQVVA DAERERQLGRGRSPAFLNPPI GTGTPALKLTTTIQRMHVDVPG WILTTECFQVPQQKAMAPLHP HPAGMRINVVNNHQAKQNLV DLDEDDDDGIAVPTKQMKFAA SGGFLHHMAGLSSSKLSMSKA LPLTKVVQNDAYTAPALPSSIR TKALTNSMRTLNVNKEEPPKELP AAEPVLSPLEGNKMTVNNLHP RVTEEDIVIEVFCVCGGLRRRA RLVPSGG*PKVVFCERDDAIT AYKKYNNRCLDGQPMKCNLH MNGNVITSQDPILLRLSDSPASM KKESELPRRVNSASSNPPAEV DPDTILKALFKSSGASVTTPTE
20195	50563	A	20311	1	915	
20196	50564	A	20312	3	3238	LDTDDDLNSDDYEYEDAKLVI FPDHYEIALPNIEELPALVSECA RLLARCAWLCVSLKSLTLLTDD TGLLTVRNKEEVLARS AKVTIA CDAVLSSKSPYRKQDPDTWEN ELPVSKYANNLTQLDNGVRIPP SGWKARCDLRENWLNLTDG SVLCGKWWFFDSSGGNGHALEH YRDMG\YPLAVKLGTTITPDGAD VVSFQEEEPVLDPHLAKHLAH F\GID\MLMHMGTE\NGLQ\NDI KL RVSEWEVIQES

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20197	50565	A	20313	2	2716	AEFRGIPRRRRQTPRSGSGSAR SAPVRAEAMQRRGALFGMPGG SGGRKMAAGDIGELLVPHMPTI RVPRSGDRVYKNECAFSDSPN SEGGLYVCMNTFLAFGREHVE RHFRTGQSVYMHLLKRHAREK VRGASGGALPKRRNSKIFLDLD TDDDLNDDYEDYED*AFLVIFP DHVEIALPNIEELPALVTIACDA VLSSKSPYRKQDPHTWENELPV SKYANNLTQDNGVRIPPSGW KSARCDLRENWLWN
20198	50566	A	20314	2	322	
20199	50567	A	20315	1285	3331	GAGAPRDWLRRRRGGAALCLK VLFDVRSFPREAAALTPIRLLQ FPRSSSPGDQMAAARLLPVP AGPQPLSFQAKLTFEDVAVLLS QDEWDRLLCPAQRGLYRNVMM ETYGNVVSGLPGCKPDIIHFLE LRGISLGPVPEWG*EEGPVE*L L/ENVETKGESQNTDLSKPLIS EQTIVLKGTPLRIDQENNETK* SFCLSPNSVDHREVQVLSQSM LTPHQAVPSGERPYMCVECGK CFGRSSHLQHQRIHTGEKPYV CSVCGKAFSQSSVLSKHRIHT GEKPYERNRACISLYSEPHLAH LSLIHTGEKPH*CLECPKFTQL SHLIQHQRHTGERPYVCPCLG KAFNHSTVLRSHQVRHTGEKP HRCNECGKTSVSKRTLLQHQR VHTREKPYTCSECGKAFNDRSV LIQHNNVHTREKPYECSECGKT FSHRSTLMNHERIHTEEKPYAC YECGKAFVQSHLIQHQRVHT GEKPYVCGECGHAFSARRSLIQ HERIHTGEKPFQCTECGKAFL KATLIVHLRTHTEKPYECNSC GKAFSVRTQLLIQHQRHTGEKP YECGECGGAFFNQHGHLIQHQ SAQKSCDPWLTQE/CPFSQKLH VEPTSSLPKRSCL*LYRKLFPG DSVSQNSRKKHLACSCGKTS ETTCFIFLNHLEV/HVGE*SYNC
20200	50568	A	20316	1	319	
20201	50569	A	20317	1	2433	
20202	50570	A	20318	2	293	GELAGTQCTRGACPHSP*PLHR Q/HTTVTHITAFDPDSTGQQVW QDLLQDQGQLDSPTGDDGSDWE MVGREVVPVLGPGVGGLVISRP CFHVRDPYPWG

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20203	50571	A	20319	1	537	GGGTITRGWRGQFCRWQLNPG MYQHRTVIADQMRTLRSREV** HAQGHKFTVCLRRREGQTVYQQ VLSLERPSVLRSWNWGLCGYF AFYHALYPRAWTVYQLPGQNV TLTCRQITPILPHDYQVRPPHLY LPLPSLPQDLPLETAWPARRG SHACNPNTLGGKAGGSRDQEIE TILANT
20204	50572	C	20320	3	170	RVGVSRREPEVRNWA TRDCRAQ ERMTHCLLHGMGRAGAASLTP KPMSLISAYCGGLWLA AVAVM VQMAALCEGTGQSRI SFLSSA GAKKPMRDCCGMVSSGSLSSL KAAERTPGALFFSSSTPGRYYN YDSSSRPQSRVMSDQVCWTV GVPEGLWP*EKGDT EVREEEEQ PERKMGFPWRWEVFPTQHVVVR ALQTIFELNVQAFAGGAMGAV NGMQPHGVDPKSSVQSDEVW VGVVYGLAATMIQE
20205	50573	A	20321	278	1018	
20206	50574	A	20322	3	627	

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20207	50575	A	20323	270	2945	NTSSFKLSPTTGPGRYLTTTGA RIWNRLARYLVSESGSLGAIEV MGTDQDPGNMGTGVPASEQISC AKEDPQVYCPETGGTKDVQV TDCKSPEDSRPPKETDCCNPED SGQLMVSYYEGKAMGYQVPPFG WRICLAHEFTEKRKPFQANNVS LSYMIKHIGMGLRYLQWRDRK THVEKKTFFIDMNKSPVPIQSYF VPLGGLRGGTSTRGWRGQFCR WQLNPGMYQHRTVIADQFTVC LRREGQTVYQQVLSLÆRPSVL RSWNWGLCGYFAFYHALYPRA WTVYQLPGQNVTLTCRQITPIL PHDYQDSSLPGVFVWDVENE GDEALDVSIMFSMRN/GTGWW RRCPRGFVGMSPSVWSVGVT VRGLLLHSSNPSPKPLHDGLWLA RSSRAATTNPH/CTAFDPGR TGA/VWQDLLQDGLDPTGQ RTPTQKGVGIAGAVCVSSKLRP RGQCRLEFSLAWDMPRMFGA KGQVHYRRYTRVFGAGIDAP PALSHYALCRYAEWEERISAW QSPVLLDDRSLPAWYKSALFNE LYFLADGGTVWLEVLDSLP EERAEVTSAPTLDYRRFG*LE GQEVRYMYNTYDVHFIYASFALI MLWPKLESLQYDMALATLRE DLTRRRYLMGVMGTCEKEGT FIPHDIGGPRWMEPWASAFNAY LHIDTADWKLNLKFAACRFI
20208	50576	C	20324	123	359	
20209	50577	A	20325	1	259	KPVGEKDTWSGMRTTGQLRPA HGVRKANKDSLYKPILRQKK HFNSLHIPKALQKALPFKNKPK TQAKAGKVPKDRRR*TVSNITV
20210	50578	A	20326	297	585	
20211	50579	A	20327	182	374	PDFRIAAT*VVLDLKSIKIVKK LKLTFGPKYKFNKTSFIKACISY SHIYKSPYCLRKGMKYL

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20212	50580	A	20328	1	1267	MAANRKDFIHRRCGPELSQSEA VPQGLCRAERSSALAMLSGSVP RRTQLRPCKGTQRRRCRRGGEA DSGGEAVGGGAERSSAAARR RGGRRRGGGEAVGGGAERSS AAARRRRGGRRRGGEAGGG GAAEARRAAARRAAARRA AAARRAAARRAAARRIAES GGEAHSRGEAHSGGEAHSGGA GAERRRPRLHSPALKTHPGQSS EGHVEYKLNHFEDQDDDEAR VQYEGFRPGMYVRVEINVPCE FVQNFDPYPIILGLGNSEGNV GHVQMRLLKHLWYKKILKSQ DPIIFSVGWRRFQTILLYIEDH NGRQRLKLYTPQIHCGAAFW DIVFMRTWYLVSIAPFYNPVT LLKPVGEKDTWSGMWTTGQL RLAHGVRLKTTKDSLYKNIHMI VETDTYSDHEEINTS
20213	50581	A	20329	66	1414	KEELYGDFEDLETGDVHKGS GPDTQNEDEVKEEIDPDEEES AKKKHLDDKKRLKEMFDVEY DEGESTYFDDLKGEMQKQAQV N/RHTRFPAPRHVQLNHAEF EDQDDDEARVQYEGFRPGMYVC VEINVPCEFV*NLDPYPIILG GLGNSEGNVGVYVQVGFPAAYL VPEALWISPPSILPSHPPQMRK KHRWYKILKSRDPIIFSVGWR RFQTIPLCYIEDHNGRQRLKY TPQHVHRGAAFRSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSR IAATGVVLDLDSIKVVKLLKL TGFPYKIFKNTSFIKGMFNSALE VAKFEDAVIRTVSIGRQIKRA L*APEGAFQDSLEDKLRMSDIV FMRTWYVPSIPAFYNPVTSLK PVGEKDTWSGMWTTGQLRLA HGVRLKTNKDSLYKVLVVCVL VEMKPVLYRQ

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20214	50582	A	20330	4210	5099	AKDQKKHRKKNSGPKAAKKK KRLQLDLQLGDVEEDAWKRN KAFVAFQSAVWMARSFHRTQD LKTCKHHIPVVDARTPLEPPV VVVMGPPKVGKSTLI*CLARNF TRQKLTEARGPVTIVSGKKLRI THDCGCDINMMIDLGVEADLV LMLIDASFGFEMETFEFLNICQV HGFPMKIMGVLTHLDSFKHNKQL KKTCKRLKHRFWTEVYPGAKL FYLSGMVHGEYQNQEIHNGLH FITVMKFRPLTW
20215	50583	A	20331	56	467	
20216	50584	A	20332	282	452	
20217	50585	A	20333	1	1356	
20218	50586	A	20334	80	1096	GLGVVRVLRCPGVYRGPTRAA YLGWLWTTLSPYCCLRSADMN PIVLVHGGGAGPISKDRKERVH HGMVRATTVGYGILREGGSV DAVQGA VVALEDDPEFNAGCG SVLNTNGEVEMDASIMDGKDL SAGAVSAVQCIANPIKLARLVM ENFPFCFLTQGA AHFAGAMG VPEIPGKKLVTERNKKRLEKEK HEKGAHKTDCQKNLGTVGAV ALDCKGNVAYATSTGGIVNKM VGRVGDSPSLGAGGYADHDF* AVSTTGHGEISFLKVNLRLLTF HIEQGKLTLEEAADPIG/CG*MKS RVKGLGGLIVVSKTGDWVAK WTSTMPWAAAKDGKPLRN
20219	50587	A	20335	1	1416	
20220	50588	A	20336	3	277	

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20221	50589	A	20337	235	2811	VKMEAPLRPAADILRRNPQQD YELVQRVGSQGYGVYKARNV HTGELAAVKIILEPGDDFSLIQ QEIFMVKECKHCNIVAYFGSYL SREKLWICMEYCGGSLQDIYH VTGPLSELQIAYVCRETQLGLA YLHTKGKMRDIDKANILLTD HGDVKLADFGVAAKITATIAKR KSFJGTPYWMAPVAAVEKNG GYNQLCDIWAAGTAEIELGELQ PPMFDLHPMRALFLMSKSNFQP PKLKDKTKWSSTFHNFKIALT KNPKKRPTCLKDF*HHTFVAQ PGLSRALAVELLDKVNPNPDNH AHYTEADDDDFEPHAIIRHTIRS TNRNARAERTASEINFDKLQFE PPLRKETEAREDEGLSSDPNFM LQWNPFV*WQITGKSTSKRA IPPLPPKPRISSYPEDNFPDEEK ASTIKHCPDESRAQILRRQSS PSCGPVAETSSIGNGDGSKLMS ENTEGSAQAPQLPRKNDKRDFF KPAINGLPPTPKVLMGACFSKV FDGCPKLKNCATSWIHPDTKDQ YIIFGTEDGIYTLNLNELHEATM EQLFPRKCTWLYVINNTLMSLS EGKTFQLYSHNLJALFEHAKKP GLGCPIFQTHRFPPDRILPRKFAL TTKIPDTKGCHKCCIVRNPTG HKYLCGALQSGIVLLQWYEPM QKFMLIKHFDPLPSPLNVFEM LVIVEQEYPMVCVAISKGTESN
20222	50590	C	20338	365	389	
20223	50591	A	20339	1	350	FDVTELGGQWLSRGGEIEGFRL SAHCSDSRDNTLQVDINGFTT GRRGDLATHGMNRPFLLLMA TPLERAQHLQSS/RAPCCVPQAL EPLPIVYVYGRKPKVEQLSNMI VRSCCKCS
20224	50592	A	20340	1	708	
20225	50593	B	20341	229	1249	
20226	50594	B	20342	49	375	
20227	50595	A	20343	42	305	GARAHAPVLVQEEDLHGPHPL RPERL/PSVPSGRSSPPASRPVG PGG/DQLRPSDRQQQVSGME WC/PWSGRSPGLSPTVGRGGC HPTST
20228	50596	B	20344	8	1990	
20229	50597	A	20345	1	1512	

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20230	50598	A	20346	1	1663	SGRDRRGRAWKRNRREPPTRG RSPDPQGPSARPLPSLGARISAA DRLSGLAARLIGNSRPVAGANA GVGPDLSHAGLVPTCARLRRLR KNGLGRRRRRPPSPRPSLESS SRLTTLGTSPQLKFNFFPCDLRI FQTFNC\WGNPVL*AKHR\ADR MRRFGRPF*TQESFDLALLEEV WSEHDFQYLRLQKLSPTYPAAH HFRSGIISGLCVFSKHPIQELT QHIYTLNGYPYMIHHGDWFSG KAVGLLVHLNMGELNAYVTH LHAEYNRQKDIYLTHLVGIQA WELAQFIHHTSKKADVLLCG DLNMHPEDI.GCCLLKEWTGLH DAYLETRDFKGSEEGNTMVPK NCYVSQQLKPFPGVRIQVYL YKAVSGFYISCKSFETTTGDFPH SGTPLSDHEALMATLFRVHSP QQNPSTHGPAERSPL/MCVCL KEALDGSGLGMA\QARWWA\ TFA\SYVIGLGL\LLALLCLVA AGGGAGEAAILLWTPSVGLVL WAGAFYLFHVQEVNGLYRAQ AELQHVLRAREAQDLGPEPQ LYALL\GQQEGDRTKEQ
20231	50599	A	20347	175	544	RLRCQKGIPPSLRGRAWQYLSG GKVKLQQNPGKFDQLDMSPG DPTWLDVIERDLHRQFF\FHEM FVS/RGGH/GQQDLFRVLDAYT LYRPEGSYCKTQAPIAAVLLMH MPAEQAFWCLVQICEKYL
20232	50600	A	20348	1	434	CAAGIRHELRRRLGWRTAT ERMGRACPRPGKACREPGRA* ARALTPQPPTNSALSGLTRRPT ASPS\PHRQVRLDRGLAGRQGR AGGSTPGGAEEAGVQVAGHAQ AMVVAARDACPPQHVPKDS APKDSAPQDLAPQVSAH
20233	50601	A	20349	3	510	

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20234	50602	A	20350	1	1669	MAKSNGENGPAPAAAGESLSG TRESLAQGPDAATTDELSSLGS DSEANGFAERRIDKFGFIVGSQ GAEGASILGQTVPSPHGRVGE PPIRSYTASSTGTGNRLVEEVP VLRQRESKWLDMLNNWDKW MAKKHKIRLRCQKGIPPSLRG RAWQYLSGGKVKLQONPGKF DELDMSPGDPKWLDVIERDLH RQFPFHMFVSRGGHGGQDLF RVLKAYTLVRPEEGYCQAQAPI AAVLLMHMPAEQAFWCLVQI
20235	50603	A	20351	1	243	
20236	50604	A	20352	70	382	
20237	50605	A	20353	2	322	
20238	50606	A	20354	86	215	
20239	50607	B	20355	1	735	
20240	50608	A	20356	92	1104	MSSPQAPEDGGQCGDRGA/PPG DLRSVLVTTVLNLEPLDEDLFR GRHYWVPAKRLFGGQIVGQA MVAATSV/SEDVHVHSLHC YF/VFRAGDP/KSLPVLYQVERT RTGVEA/FRLRSVKGP*NMKGPI FNCQIASFQQA/QPSPMQHQFS MP/TLPTTEELV*IVRTLFDQY LRDPNLQKRYPLALNRI/AAQE VPIEIKPVNPSP/LRPAEEWEPEK QMFVWVRARGYIGKSTPWKM/ HC/CVAAAYIS/DYAFGLTALAA LTQWPSTRCHFHPPLD/HNPM WFHAPFRAD/HWMLYECESPW AGG/SRGL/VHGRLWRQDGVLA VTCAQEGVIRVKPQVSESKL
20241	50609	A	20357	3	1106	LRRQLQPLLPLKSPPRSGAHL GSLFRSPQSPYVPRPPGSAGTPP PACLPPAQPCQGSAMNLFRL GDLSHLLAIIILLKIKWSRSCA GISGKSQVLFVAVFTARYLDLF TNYISLYNTCMNVVVIACSF TVLIYTKFKATYDGNHDTFR SGSSRVV/VPQAILGVSWSNHD FTPLAELWTFISIYLVGSPSLPQ LFHG*GKTGRGRETHSPATYLF CAKAFNPHALSLSNW/IR/YHF VEGFDLIAIVAGPGPRQSSYCD FFVLYYSPKFLKGERKFEFCRI RPRFLSISSPRAAAGRAGGKAG RKMKSFSHPRGDFFKNPTSLCS PIPPSCPLKGNSARIPGLWGAQ RLGAVCSFLAF

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20242	50610	A	20358	356	1356	TPITSGRTRKMWPRPGT*PP/A NCSANINLTHQPWFQVLEPQFR QFLFYRHCYFPMLLNHPEKCR GDVYLLVVVKSVITQHDRREAI RQTWARAAVRGWGPSAVRTL LLGTASKQEERTHYQQLLAYE DALYGDILQWGFLDTFFNLTK EIHFLKWLDIYCPHVPFIFKGDD DVFVNPNTNLEFLADRPQENL FVGDLVQHARPIRRKDNKYIIP GALYGKASYPPYAGGGGFLMA GSLARLRHHACDTLELYPIDDV FLGMCLEVLGVQPTAHEGFKTF GISRNRRSRMNKEPCFFRAMLV VHKLLPPELLAMWGLVHSNLT CSRKQLQVL
20243	50611	A	20359	221	1579	CCVDEGLEPTCFERTEDIGGVW RFKVS EIFLGLQVVLFFQGESQ LMSCFSDFMPEDFPNFLHNSK LLEYFRIFAKKFDLLKYIQFQVL YFWGNGFLCISSAHI*IENTQSN GKEQSAVFDAVMVCSGHILP HIPLKSFPGETRWDSQLGVGF QVLYM*FEGKRILVIGMGNSGS DIAVELSKNAAQV*CSLLTMYL EGRKWGCHTGDWDSVFHTRFR SMLRNVLPRTAVKWMIEQQM NRWFNHENYGLEPQNK*SYFA FLMVYSLVSKVV*RCLKVKST VKELTETSAIFEDGTVEENIDVII FATGYSFSFFLEDLSVKVENN MVSLYKYIFPAHLDKSTLACIG LIQPLGSIFPTAELQARWVTRVF KGLCSLPSERTMMMDIIRNEK RIDLFGESQSQTLTQNTYVDYLD ELALEIGAKPDFCSLLFKDPKLA VRLYFGPCNSY
20244	50612	A	20360	3	200	
20245	50613	A	20361	292	570	
20246	50614	A	20362	2	511	RLRSGPLRLPGADSGSGPKAVC SPPFIVAPTGRGYCGDHESFGA MEEPGVTPQPYLGLLLEELRRV SPGAMSVTWPEGSREPPGEGSS RPALGSKPPWSEVPKPVLVCCP APARFEAVVRLVGRLSGFCVM EEDLGLWEGREKKLALMLSGLI EEKSKLLEKFSLVQKE

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20247	50615	A	20363	2	3262	FLSDLEENFENNIFSFQVCDVVL NHAPDFRRVYLPYVTNQTQYE RTFQSLMNSNSNFREVLEKLES DPVCQRLSLKSLILPFQIRTRL KLLQLNILKRTQPGSSEAEAT KAHHALEQLIRDCNNNVQSMR RTEELIYLSQKIEFECKIFPLISQS RWLVKSGELTALEFSA SPGLRR KLNTRPVHLHLFNDCLLSRPR ESVTGVAGQGTRGEGDEERG SEREREGSEKLRLWISALAMPRE ELDLLECYTAE
20248	50616	A	20364	2	2339	TGRGYCGDHESSFGAMEEPGA TPQPYLGLLEELRRVVAALPE GMRPDSNLYGFPWELVICAAY VGFFAVLFFLWRSFRSVRSRLY VGREKKLALMLSGLIEEKSLL EKFSLVQKEYEGYEVESSLKDA SFEKEATEAQSLATECKLNRS NSELEDEILCEKELKEEKS KHS EQDELMA DISKRIQSLEDESKSL KSQVAEAKMTFQIFQMNEERL KIAIKDALNENSQLESQKQLL QEAEVWKEQVSELNKQKVTFE DSKVHAEQVLNDKESHIKTLTE RLKMKDWAAMLGEDITDDD NLEEMNSESENGAYLDNPPK GALKKLIHAAKLNASLKTLEGE RNQIYQLSEVDKTEELTEHIK NLQTQQASLQSENTHFENENQ KLQQLKVMTELYQENEMKL HRKLTVEENYRLEKEEKLKSV DEKISHATEELETYRKRAKDLE EELERTIHSYGGQIISHEKKAHD NWLAAARNAERNLNDLRKENA HNRQKLTETELKFELLE KDPYA LDVPNTAFGRGSRGPGNPLDH QITNERGESSCDRLTDPHRAP DTGSLSPWDQDRMMFPPPG QSYPDALPPQRQDRFCNSGR LSGPAELRSFNMPSLDKMDGS MPSEMESSRNDTKDDLGNLNV PDSSFP/AKKEATGPGFVPPPLA PVRGPLFPVDARGPFLRRGPFPF

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20249	50617	A	20365	160	2810	GLRVPLSPSPRSRLRSGPLRLP GADSGSGPKAVCSPPFIIVAPTG RGYCGDHESFSGAMEEPGA TP QPYLGLLLEELRRVVAALPEG MRPDSNLYGFPWELVICA A V V GFFAVLFFLWRSFRSRSRLYV GREKKLALMLSLIEEKSLLLE KFSLVQKEYEGYEVESLKDAS FEKEATEAQSLEATCEKLNRSN SELEDEILCLELKEEKSKHSE QDELMA DISKRIQSLEDESKSL KSQVAEAKMTFQIFPMNEERLK IAIKDALNENSQLQESQKQLLQ EAEVWKEQVSELNKKQVTFED SKVHAEQVLNDKESHIKTLTER LLKMKDWAAMLGEDITDDDN LELEMNSENGAYLDNPPKG ALKKLIHAAKLNASLKTLEGER NQIYIQLSEVDKTEELTEHIKN LQTEQASLQSENTHFENENQKL QQKLKVMTELYQENEMKLHR KLTVENYRLEKEEKLKSVDEK ISHATEELETYRKRAKDLEEL ERTIHSYQQIISHEKKAHDNW LAARNAERNLNDLRKENAHNR QKLTETELKFEL/LEEDPYALDV PNTAFGREHSPYGPSPLGWPPS ETRAFLSPPTLLEGPLTSLPLLP GGGGRGSRGPGNPLDHQITNER GESSCDRLTDPHRA LSDTGFLS PPWDQDRRM MFPPGQSY PDS ALPPQRQDRFCNSN SGR LSGPAE
20250	50618	A	20366	131	461	

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20251	50619	A	20367	1	1761	MARGYGATVSLVLLGLGLALA VIVLAVVLSRHQAPCGPQAFAH AAVAADSKVCSDIGRAILQQQ GSPVDASIAALVCTSVVNQSM GLGGGVIFTIYNVTTGKVEVIN ARETVPAHAPSLLDQCAQALP LGTGAQWIGVPGELRGYAEAH RRHGRLPWAQLFQPTIALLRGG HVEAPVLSRFLHNSILRPSLQAS TLRQLFFNGTEPLRPQDPLPWP ALATITLETVATEGVEVFYTGRL GQMLVEDIAKEGSQLTLQDLA KFQPEVVDALEVPLGDYTLYSP PPPAGGAILSFILNVLRGFNFT ESMARPEGRVNVYHHLVETLK FARGQRWRLGDPRSHPKLQNA SRDLLGETLAQLIRQQIDGRGD HQLSHYSLAEAWGHGTGTSHV SVLGEDGSAVAATSTNTPFGA MVYSPRTGIILNELLDCERC PRGSGTTPSTVSGDRVGGAPGR CWPPVPGEPSSSMEPSILINKA QGSNLVIGCAGGELIISAVAQAI MSKLWLGFDLRAAIAAPILHVN NKGCV EYEPNFSQEVQRGLQD RGQNQTQRPFPLNVVQAVSQE GACVYAVSDLRKSGEAGY

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20252	50620	A	20368	341	2239	LCASSCPFCFPIRPSVCPPAAPL LLGCRAMARGYGATVSLVLLG LGLALAVIVLAVVLSRHQAPCG PQAFAHAAVAADSKVCSDIGR AILQQGGSPVDATIAALVCTSV VNPQSMGLGGGVIFTIYNVTTG AQWIGVPGELRGYAEAHRRHG RLPWAQLFQPTIALLRGGHVVA PVLRLHNSILRPSLQASTLRQ LFFNGTEPLRPQDPLPWPALAT TLETVATEGVEVFYTGRLGQM LVEDIAKEGSQLTLQDLAKFQP EVVDALEVPLGDYTLSPPPPA GGAILSFILNVLRGFNSTESMA RPEGRVNVYHHLVETLKFAKG QRWRLGDPDRSHPKLQNASRDL LGETLAQLIRQQIDGRGDHQLS HYSLAEWGHTGTSHVSVLG EDGSAAVATSTIYTPFGAMVYS PRTGIILNNELDLCCRCPRGSG TTPSPV/SGDRVGGAPGRCWPP VPGERSPPSSMVPSILINKAQSGK LVIGGAGGELISAVAAQIMSKL WLGFDLRAAIAAPILHVNSKGC VEYEPNFS/QETVSCFVALAVL KLLASSDPATLAPKWLRL*EVQ RGLQDVRGQNPDEGPFFLDV PACV/SQEGACV*RPST*RKSG EAAGLLKTLCCPELEVLAPP
20253	50621	A	20369	203	1518	RCYLQFLALLLTSTSAARAAAI AAAEEPPAGSPVMTRAGDHNH QRGCCGLADYLSAKFHL*LG HSLSTWGDWRMWHFAVSVFLVE LYGNSLLLTAVYGLVVAGSVL VLGAHGDWVDKNARLKVQAT SLVVQNVSVILCGIILMMVFLH KHELLTMYHGWVLTSCYILITI ANIANLASTATAITIQRDWVIV VAGEDRSKLANMNATIRRIDQL TNILAPMAVGQIMTFGSPVIGC GFISGWNLVSMCV EYVLLWKV YQKTPALAVKAGLKEEETELK QLNLHKDTEPKPLEGTHLMGV KDSNIHELEHEQEPTCASQMAE PFRTRDGVVSYYNQPVF/LGW HGSCFPLYDCPGL*LHHHRVRL HSGTEWFHPQYFDGSISYNWN NGNCSFYLATSKMWFSGDRSD LRIGTAFDLVCDLCIHAWKP
20254	50622	A	20370	1	497	
20255	50623	A	20371	1	1575	

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20256	50624	A	20372	251	1351	SLKSTDGVKCLGINIFHKRRN ILFGMGNPLLDISAVVDKDFLD KYSCLKPNDQILAEDKHKELFDE LVKKFKVEYHAGGSTQNSIKV AQWMIQQPHKAATFFGCGIGDK FGEILKRKAEEAHVDAHYYEQ NEQPTGTCAACITGDNRLIAN LAAANCYKKEKHLDEKNWM LVEKARVCYIAGFFLHVSPESV LKVAAHASENNRIFTNLAPFI SQFYKESLMKVMPPYVDILFGK* DRSWPTFAREQGFETKDIEIA QKDTSPCKMNSKGQRIRDLHP KGRDDTVMATESEVTAFAGLGI KTQKEINDTNEAGDAFVGGLS QLVSDKPLTECIRAGHYAASIII RRTGCTTFPEKPDFH
20257	50625	A	20373	1	201	
20258	50626	A	20374	15	304	
20259	50627	A	20375	51	283	TWVKEAQNDGLCVYIFINCO MTGLDIEKD/QIEMACLITDSD LNILAEVRDAHVQSFLKGTG NITIFSSFFI
20260	50628	A	20376	2	520	QRRLRDWGRGWSRVMLGGS LGSRLLRGVGGSHGRFGARGV REGGAAMAAGESMAQRMVW VDLEMTGLDIEKDQIEMACLIT DSDLNLAEGNSVHEDKKFLD KYMPQFMKHLHYRIIDVSTVKE LCRRWYPEEYEFAPKKAASHR ALDDISESIKELQFYRNIFKHK
20261	50629	A	20377	2	206	EFGTRRHVPCLINFFKDQGS* LARLVSNWPQVIHPPWPPTVL GLRGVGHCPWPLGNSSVWV GGH

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20262	50630	A	20378	1	1401	MRSQKTSLVFSLEAKFYCSLRN ERIASCDIINDAGIQTKTLMKRS HVAYAIKKPVEQGDSFELISK GFMAITIAVCIEQNLRHSSSLFIC MSSTGGSGTTNASSLIPSYVFT PPHFNLDDKQGRTAGKSHCGE DRKEHNNACHQEEAAPDYNPL HGLQASGSPGKTQRIKSQALEG TRLVSHSEETRSGLIRLLRLRQR RLRDWGRGWCWRDMLGGSLG SRLLRGVGGSHGRFGARGVRK RGAAMAA\GESMAQRMVWVD LEITGLDI*KVQIEMACLTDS LILAEQPNLI\KQPDLLDSMS\ DWCK\EHGKSGLTAKVKEST NYHCQQA\VEFPALWYDQPD SLPGLCPTCQEIKFHE\DKKFP* QNTCPQFMKHLHYRI\DVSHC* KELCQTAGYP EYEFA\PKKAA FSIGPLDD\ISENLKVPFFPEN NHLPRKKIRMKRKEGKL*KMG ENEKTVS
20263	50631	C	20379	180	248	
20264	50632	A	20380	455	1133	GIEGWRGEADTLPAEQDQDGR RVSKGDI FSGGAETAQWGVGM GPFQAAPSKRAGREHRRGQRR VQHVGVWYPRPGSDKGHGKGT QDSRPVQLPPHPPIHLVSRHRG KLRRHGLRPMPEPRGLESKGTG NCFGELQH\RTSP*GRSGPREGG PRNIAQQGGCRGSACGRSSH\IE ALRPRVWCGEGPQWTW\CAVC PNRSAPGAGLAD\RHHPGESRA WGETRLGEAGGAE
20265	50633	A	20381	214	412	
20266	50634	A	20382	3	257	PATVIHTVNTTWSAALISRESAL RSFPVKAAALSPSREGGSVTAT PNVRSMTSAVPIMRVSVQ\SKR *PEEQN*QETYPQITTSR
20267	50635	A	20383	1	1569	
20268	50636	B	20384	15	1744	

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20269	50637	A	20385	2	7205	QASGSCWSSPFFSASTPSAAAT GVPGPTDMAAVLQQVLERTEL NKLPKSVQNKLEKFLADQQSEI DGLKGRHEKFKVSEQQYFEIE KRLSHSQERLVNETRECQSLRL ELEKLNQKALTEKNKELEIA QDRNIAIQSQFTRTKEELEAEKR DLIRTNERLSQELEYLTEDVKR LNEKLKESNTTKGELQKLDEL QASDVSVKYREKRLEQEKELL HSQNTWLNTELKTKTDELLAL GREKGNIELEKCNL
20270	50638	A	20386	120	7384	GWTRFPRVPPRESPAGGRARAT ERGDRGGGPGVWVLLVFAFLL RFYPVGRCHWGPWAPPTWAA VLQQVLERTELNKLAPKSVQNK LEKFLADQQSEIDGP*RGHGGE I*RWSEQQYFEIEKRLSHSQER LVNETRECQSLRLEKLNQK KALPEKNKELEIAQDRNIAIUQ SQFTRTKEELEAEKRDILRTNE RLSQELEYLTEDVKRLNEKLKE SNTTKGELQKLDELQASDVS KYREKRLEQE
20271	50639	A	20387	2	433	
20272	50640	A	20388	2	181	GFRRVSLF*FPGVRWGMRLK GAPDLA PFSQM*SGGRAPCVAS *PPCRGLRLMRTGSR

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20273	50641	A	20389	1	2422	MAGALAGLAAGLQVPRVAPSP DSDSDTDSDEPSLRRSAGGLLR SQVHISGHFMVSSPHSDSLPRRR DQEGSVGPSDFGPRSIDPTLTRL FECLSLAYSGKLVS PKWKNFK GLKLLCRDKIRLNNAIWRAWYI QYVKKRKS P VCGFVTPLQGPEA DAHRKPEAVVLEGNVWKRRIE VVMREYHKWRIYYKKRVSSG GPGRPQSFPFAAAGYRPPRKIPG KGILTPELAPLGFISQSRADSAT VWPQRLAASLPRGRRLKPSRE DDLAPKQAEGRWPPPEQWCK QLFSSVVPVLLGDPEEPEGGRQ LLDLNCLSDISDTLFTMTQSGP SPLQLPPEDAYVGNADMIQPD LTPQLPSLDDFMDISDFTFNSRLP QPPMPSNFPEPPSFSPVVDLSFSS GTLGPEVPPASSAMTHLSGHSR LQARNSCPGPLDSSAFLSSDFLL PEDPKPRLPPPPVPPLLHYPPP AKQETVPEPCTFLPPTAPTTP RPPPGPATLAPSRPLLVPKAERL SPPAPSGSERRLSGDLSSMPGPG TL SVRVSPQPILSRGRPDSNKA LLGSFLGSPNSLLPETENRRITHI SAEQKRRFNILGFDTLHGLVS TL SAQPSLKVSKATTLQKTA EY ILMLQQERAGLQEEAQQLR\DE IEEL\NAAINLCQQQLPATGVPI\ THQRFDQMRDMFD\DYVRTRT LHNW\KFWVVS LKPMAGGLQ
20274	50642	A	20390	315	387	
20275	50643	A	20391	570	1017	FCLHILQVPHTLAGHSPCAHG/R PPLPRF/HDRLPEEIQQIVRETF HLVLKRDDNICNFLEGGSLIGG SDYKLIYRHYATLYFVFCVDSS ESELGILDILQLEQFKKDNEETG FGSGTRALEQALEKTKANIKW VKENKEVVLQWFTENSK
20276	50644	A	20392	1	1128	
20277	50645	B	20393	62	130	

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20278	50646	A	20394	99	718	ENRGWQSMIQAILVNNHGKPK RLVRFYQRFPEEIQQIVRETF HLVLKRDDNICNFLEGGSL/L GGSDYKLIYRHYATLYFVFCV DSSESELGMLDLIQVFVGNWSWIS CFENVV*IWJ*TFHMDKVHYIL QEVVMGGWMVLETNMNEIVAQ IEAPNRLEKSEG/LSAAP/ARA VSAVKNNLPEIPRNINIGDLNIK VPLNSQFV
20279	50647	A	20395	3	370	SLHLAAILGETSTVEKL/YAAGA GLCVAERRGHTA/LHLACRVG AHACARAL/LQPRRRPREAPD TYLA/QGPDRTPTDNTHTPVAL/Y PDSLEKEEEEESHTPLHVAVIH K/DVEMVRLLRDAGADLDK
20280	50648	A	20396	2	1097	SRQSPATGGRLRWAPDAALAM AVVACLQQAADSKWGD SRLS SLGPDAAA PGGPGLGAELGPGL SWAPLVFGYVTEDGDTFSAGT EYMDLQNDLRQVSHGWCRA WGP GFFP*LPTACPLLLQTALH LAAILGETSTVEKLYAAGAGLC VAERRGHTALHLACRVGAHAC ARALLQPRRRPREAPDTYLAQ GPDRTPTDNTHTPVALY PDSLE KEEEESEEDWKLQLEVENYEG HTPLHVAVIHKD VEMVRLLRD AGAIDLKPEPTCGRSPLHLAV EGPRQADVLELLALRAGANP/A ARMYGGRTPLGSAMLRPNP/I LARILLRA/HGAPEPEGEDEKSG PCSSSSSDSRLSPSAWSPLPPG
20281	50649	A	20397	47	478	LRLRLKAIMLAFGRGKTRNSE ESSDSQEVWIKDTWMFTALGH CGISMFGLDRELTLTNYELFIS SSPTPS*VPORLCYVVSTFLMYL SLDHLTYTGEMKAFHLVLDTS VNSDFAFFVRLSFQYFYKLLCV LWQGTVNKEFI

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20282	50650	A	20398	1	1992	METFFVIGWQPAVTVWTIGVAP PPTLEITSQHEIWVAQHNPYIIS VKQESPAAMPWTAVALDSHRS MNTIVNCAREGSTLHAPYESLM PDDLRLWNSFILKSSPSPHSRSM KLSSMKLVPGAKYIRDHCLVK EALTIHKSPILLAIDLLGNLSG FTDYQSYVIHGCLENNPTLERSI ALFNGISKWVQLMVLKSPTPQ QRAEVITKFINVAKGATAELNL WQHPKIIMLSQVVPGVFSQEHS LIRSLHANLHFTVCFPEDPLAM VAGMVQESTCPCEHLQLPTTGQ LANWNEMTELVSNGNYCNRYR KPFTCDGLKIPILGVHLKDWA VHVNFDPWTTEEIKVNIVKMHQ LSVTLSELVSLQNASHHLEPNM DLINLLTV/DGLQPADLMHAISL FRTSHRPQGLFL*IKGTSPAHS DRSCQHFRV*KCSSWESWHGG/ WLSLEE*MSSFLLRSF*KI/YCSR KNVACQTRAVCTNLDALLSSS QMSNNHHFSLPAQDEVFEFFG VTAGHRDLDSRAITLVTGSSRK ISVRLQRATTSQATQTEPVWSE AGWGDGSGHTFFPKMKSKFHDK AAKDKGFAKWENKPRVHAG VDVVDRGTGTEFELDQDEGEETR QDGEPAEAVSVGAVAAPGMSE KELLQVDGRTPTRVLRLMADLV GISEFRGEPAFV
20283	50651	A	20400	1	417	
20284	50652	A	20401	2	94	

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20285	50653	A	20402	190	2189	AFCPAGTRSA PCRPRTMTMTL HTKASGMALLHQIQNLEPLN RPQLKIPLERPLGEVYLDSSKPA VYNYPEGAAYEFNAANAANA QVYGGTGLPYGPGSEAAAFGS NGLGGFPPLNSVSPSPMLLHPP PQLSPFLQPHGQVPPYILENEP SGYTVREAGPPAFYRPNSDNRR QGGRRERLASTNDKGSMMESA KETRYCAVCNDYASGYHYGV WSECGCKAFFKRISQELPTLC*I GWYWYQNRDIDQWNRTEPSEI IPHIYNHLIFDKRDKNKKWGKD SLFNK*CWENWLAICRKLKLD HFLTPTYTKINSRWIKDLNVRTK TIKLEENLGNTIQDIGMGKDF MSKTPKAMATAKADKDWLIK LKSFCSLLGYLKTENTAKETTIR LNRQPTWEKIFAIYSSDKGLIS RIYKELKQIYKKK/GNPINKWV KDMNRHFSKEDIYAANRHMKK CSSSLAIREMQIKTTMYHLTP VRMVIRKSGNDRCWRCGGEIG TL LHCWWDCKLVQPLWKT VV RFLRDLQLEIPFDPAILLGIYPK DYKSCCYKDTCTRMFIALFTI AKTWNQPKYPTTIG*IKKMWHI YTMEYYAAIKKDEFI/SLVGTW MKLETIILSKLTQEQKTKHHMF SFITGSRTMRTHGCREGNITHW GLLRDSVNMVMTQAH
20286	50654	A	20403	2	907	RVPAMATSSFALPRILGAGARA PSRWLGFLGKATPRPARPSRRT LGSATALMIRESEDSTDFNDKIL NEPLKHSDFNVKELFSVRSLF DARVHLGHKAGCRHRFMEPYI FGSRLDHDIDDLAEQTATHLQLA LNFTAHMAYRKGIILFISNRQF SYLIENMARDCEGYAHTRYFM GGMLTNARLLYGPTVRLPDLMI FLHTLNNIFEPHVAVRDAAKM NIPTVGIVDTNCNPCLITYVPVG NDDSPLA VHL YCRLFQTAITRA KEKRQQVEALYRLQGQKEPGD QGPAPHPGADMSISL
20287	50655	B	20404	70	1477	

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20288	50656	A	20405	153	688	AHPLLRSSEPTSRSRKPRCATT NGFLRIPEKTTIPVSPEVAIHRNR VITPNKPPTVKSLKVFCLDKE AQKEKESQK*KGPRVMPKTL RITTRKTPACGE/GSKDRWDRF QIEISQSRLLH*LCTSPF*DLFKQI TFHQYLSPGV*GEKSPFADALS QISIHTIDDDQFVKKKKKKKW
20289	50657	A	20406	26	603	RPRGTLREYKVVGRCPAHSK CHTPPL\YRMRNFAP\NHVVA KS/RAFVYFVSQKDKDEESLPG EIVYCGQGV*ESSPCGSKNFI WLR\Y\DSRSG\THN\MYRE*PGP *PTAGGCSPCYPRHGVARHAG PEAHFHFRFIERLEEJAGQQNC RRPGCSKQFPRISRKFPLAPP SLRRQDKPRF\TTKRPNFTF
20290	50658	A	20407	161	418	
20291	50659	A	20408	1	2580	
20292	50660	A	20409	3	264	
20293	50661	A	20410	3	302	ALALLSPWVVDGTRHRGAGGG AHPGGSGRTGAHRGGGRLRHG GLQVSPAPAREGS*GPARNRAQ RRAVDRTO*ECSSKEVYT*RLV PPPLGLHSHSSPE
20294	50662	A	20411	2	415	
20295	50663	C	20412	1	1230	
20296	50664	A	20413	238	1765	VTAYHAATMNEVSVIKEGWLH KRGEYIKTWPRYFLKSDGSF IGYKERPEAPDQTLPLN\NFSV AECQ\MKTERPR\NTFVIPC QLTNHRTGL\HTLVSPNQRE\W NPPYQVVPQPSRGGPKARTP WNNKCGSPK*LSHD*ENGSGGS ASHG/RKVTMNDSTYLNLLGK GTFGKVILFRKKTAGR*FA\MK NFRKKVINAKD*VAHNIQPRAG VLPEHPGNPFLQLR*KYAFDP TTRPVPL*MEYA\NGGELFF\HL SRERVFTEERA\RFYGAIVSA SEVTWHSRGRGNTRDNQSWKT LMLEQKMAHIK\ITDFGL\CKRG ASSDGAT\MKTFCEP\EYLAHE NLEDNDYGRAVDW\WGLGVVM YEMMCGRLPFYNQDHERLFELI LMEEIRFRTLSPKAKSLLAGLL *KDPKQRLGGGSDAKEVME HRFFLSINWQDVQKLLPPFK PQVTSEVDTRYFDEFTAQSITI TPPDRYDSLGLLEAGPADPASP QFSYASISIRE

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20297	50665	A	20414	192	866	LSCRMRLVLGQNPTLDSIDRS GVRSKCRIFNKLRESFHNSAE LTISVNNMYNCCSGNFSSRSCG DYLRYPPASSRGFSYPSNLVYST DLCSPTCQLGSSLYRGCEIC WEPTSCQTSYVEVQAPAKTSC YRPKNLPCASAPCKTTYSGSLG FGSSSRSLGYG*GSCYSVGC SSGFRSLGYGGCGFPISLYGVG FCRPTYLASRSCQSSCYRPTGCS
20298	50666	A	20415	312	1420	RSHSNAPSVVWNLTLPLDSGPH QSPASTTGPCNTIERSVPMSCS PPACPTQCVLCSCTEGQIYCG TTCPGPGCAPLPLPDSCCQACK DEASEQDEEDSVQPLHVVRHP QDPCSSDAGRKRGPPTAPTGL SAPLSFIPRHFRPKGAGSTTVKI VLKEKHKKACVHGGKTYSHGE VWHFAPRAFGLPCILCTCEDG RQDCQRVTCPTETPAC/RHPREK WPGKCKKICPEDKADPGHSEIS STRCPKAPGRVLVHTSVSPSPD NLRRFALEHEASDLVEIYLWKL VKDEET*GSGEVKYLAQGHATA RIFHLTQIKKVRKQDFPERGTA LPTARWPPRRSLERLPSDPGAE GHGQSRQSDQDITKT
20299	50667	A	20416	17	1008	KSGARSLQPFRLAPEDGGPLS LPNAAMARGPKKHLKRVAAP KHWMLDKLTGVFAPRPSTGPH KLARECLPLIIFLKDQTLNALT GDIEVKKICMQRFKIDGKVRT DITYPAGFMDVISIDKTGREFF VL/YLIDTQGVRFCL*HRIYTLR EGQSTSLCKVRKILLWAPKGIP HLVTHDARITRVPDP/LIQGE MNTHSRLI*KTGKI*FSPKFDH LVTCVMVTGGANLGRNWVLI TQQRRTSLGS*PLVHVKIDAN GNKLLATSDFSNIF/VVIGKGNK PWISLAPRGKIPPHHLEERDK RLAAKQSSVVKWGPVWTVSD
20300	50668	A	20417	1	1377	
20301	50669	A	20418	1	2178	
20302	50670	A	20419	158	250	

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20303	50671	A	20420	1	860	MDQTVKSLMASEEEYSTKEEK YEKEMKLLLEEKLEAEETRAEF VERSVAKLEKTTDDLEETLASA KEETWRFIRPGTRPYWNSATCF LLPGHKMAAEVHKLNPNVSEH DQERWHDAFGNGGADNHSKL QASTRRGGPLSQELLQSLAASL AAGGLTALSAEFTIGKGELMAH DVLWGCAPEYDDLISGTCSHL PKGKTHDVLGTGDDGRHSNTS LA WGAGVQFNPTESVAIDIA YE GPGSGDWRTDGFIVGGLFCGV NMAVKISGV LKDG TGKPVQN* TIQLKAKRNTTVVNTLASEN PDEAGRYSMDVEYGYQSVILL VEGFPPSHAGTITVYEDSQPGTL NDFLCAMTESIDARPEALGRFG LYWWKEVARNASIAVGQNTA AAKKSASDASTSAREAAATHAV DAGGFKNAQARTSSPDKAGSA GFKQGFPRGGNGINKRAT*RIK KVACR*SLMASEEEYSTKEEKY EKEMKLLLEEKLEAEETRAEFVE RSVAKLEKTTDDLEETLASAKE ETWRFIRPGTRPYWNSATCFLL PGHKMAAEVHKLNPNVSEHDQ ERWHDAFGNGGADNHSKLQA STRRGGPLSQELLQSLAASLAA GGLTALSAEFTIGKGELMAHDV LWGCAPEYDDLISGTCSHLPK GKTHDVLGTGDDGRHSNTSLA WGAGVQFNPTESVAIDIA YEGP
20304	50672	B	20421	34	800	
20305	50673	A	20422	130	368	RQVITTLYIPYRRRLSPDPPEQ PLNHKQNRKVNHHGTEFQVVV LPFPKMKINCYRRNQFFLFFFST VKVPVGWSMVPLQAATAGAR L*NSDISPLKSQQTQDKFPSSKP PHIYIKK
20306	50674	A	20423	1	57	

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20307	50675	A	20424	85	874	GPRGLVSMAGGSVEVTPSTFTC YLPPASPTTPPSHPGLLPRSPA LCSLHTGARTLPLFGGRCSSA VLPPRPGP/RAGSGGQRERFHR FQPTYPYLQHEIDLPTTISLSDG EEPPP*QVPCHLQVR/DPKQQLA ELNRE/SVGAPPNR TIFDSDLMD SARLGGPCPPSSNSG/ISAPTCYG VSGGRMEGPPATYSEVIGHLPG GPSFQH/QSSGPPSLLEGTR/L HPHTHSRP*RSAAIWSKEKDKQ KGHPSLGSPGGPGLGLRR
20308	50676	A	20425	3	250	ESVSATEDLAPDAAQGEDNSEI KELLARENELPACNGPAQAQPS PTTERAKSQEEVLPSTTTPSPGG ALSPSGQPSSSVDA
20309	50677	A	20426	2	393	
20310	50678	A	20427	1066	1824	
20311	50679	A	20428	3	902	
20312	50680	A	20429	1	2163	
20313	50681	A	20430	1	1890	
20314	50682	A	20431	1	2882	MKQQLPVSYLQVIFNH WASRJS GARGAGWGPVRLGRLCADRAL DGESRPGGGGQSGVPASEASQ KAAHGRRLPVPARLLRCAHSA LEPGRGSAASSPRNSTSDNDQPP DYSFSKRCDSHSLGFSLVWESR NLTLPTSKLLHFSAFHFFIYKC RAEGHKLKDKLNFLSAVKVM HESSKRVSSETLQFIYY/SEWYGH EELKAIVWNNDLLWEDYEKEL ADQAVRTMEIYYAQFSEIKERI AKRGRKLVDYDSARH

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20315	50683	A	20432	1	1791	MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEKVLQKLG KAVETKDERFEQSANNFYQQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSETLQEIYSSWDGHE ELKAIVWNNDDLWEDYEELK ADQAVRTMEIYVAQFSEIKERI AKRGRKLDYDVSARHHLEAVQ NAKKKDEAKTAAEEEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMSKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPSTSLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEDEPLPA CNGPAQAQSPPTTERAKISQEE VLPSSTTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSEIRPKKT ASIQRTSAPRRPPPPRATASPRP CSGNIPSSPTASGGGSA/TSPRAS LGTGTASPRTSLEI*PNPE/PPEK PVRTPEAKENENIHQNQPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE

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20316	50684	A	20433	158	1830	QLQSKMKLFWLLFTIGFCWAQ YSSNTQ/SKGRTSIVHLFEWRW VDIALECEERYLAPKGGFGVQVS PPNENVAIYNFRPWERYQP VSYKLCTRSQNEDEFNMVTR CNNV\GVRIYVDAVINHMCWN AVSAGTSSTCGSYFNPWKLRTF PAIP\YPGWDFNDGKC\KTGSGD IENYNDAQVRDCRLTGLLDL ALEKDY\VRSKIAEYMNHLIDI GVAGFRDLASKHWPBGDIKAI L\DKLHNLNSNWTFPAGSKPFIF QEVIDLRVGEPNLKASDYFGNG RVTEFKYGA\KTGVIR\KWDGE KMSYLKKWG\EGWGF\MPSDR ALVFVDNHDNQRGHGAGGASI LTFWDARLYKMA\VGFM\LAHP YGFTRV\MSSYR\WAKHSFKKG NDVNDW\VGPTQINNG\VIKEV TINPRH*LVGND\WV\CEHRWR IQIRNMVNVFRNGSGMAQPFLLQ NWYDNGSNQVAF\GRGNR\GFI VFNK*WPVIFI*LCKPGLPAGSY CDVISGDKVIGNCSAIKIPVSVD GKAHFSMSNSAEDPFLAIHAES KIVKFKIKCKSAKQKKKKKKG RPF
20317	50685	A	20434	3	383	
20318	50686	A	20435	1	378	CASGSSGWRPVLWAGAFTMAS AELDYTIEIPDQPCWSQKNPSPP GGKEAETROPVVILLGWGGISK DKNLVKYSAIYHKRKLLELLFD YEIEKEPPAFSLSSATVASCCTA TCWSSCRPVASAAACV
20319	50687	A	20436	1	558	CASGSSGWRPVLWAGAFTMAS AELDYTIEIPDQPCWSQKNPSPP GGKEAETROPVVILLGWGGCK DKNLAKYSAIYHKRGCIYRYT APWHMVFFSES LGIPSLRVLAQ KLLELLFDYEIEKEPLLHVFNSN G\VRHAVPLTCWELLQTRRFCR LRVVGTFIDSPGDSNLVGGSA GLGSHPGARG

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20320	50688	A	20437	78	1237	CWSHSDTYWPRTPRPPPGRPG PVVHLAQPVLHPEAGIPEFWES GSPGQTRGAALVLTVHICVSEN SPSPGGKEAETRQPPVILLGWG GCKDKNLAKYSAIYHKRNTAT LQPPLTYMRGWGLFTGAPAD QYLIQIKRISQWLRGCIVIRYTA PWHMVFFSESLGIPSLRVLAQK LLELLFDYIEKEPLL FHVFSNG GVMLYRYVLELLQTRRFCRLR VVGTFIDSAPG*QQPG*GLSGP GQPSWERRARPMRLRLLLVAF ALGGSSCFHVLLAPITALFHTHF YGQAYRTRALAWPELYLYSRA DEVVLARDIERMVEARLARRV LARSVDVSSAHVSHLRDYPY YTSLLCRTSMRKL RPLLKAIAPS HLCSQKINALKPSP
20321	50689	A	20438	3	427	
20322	50690	B	20439	101	1099	
20323	50691	A	20440	733	2228	

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20324	50692	A	20441	582	2595	PPPPVRRRDGPAAVRPAGAMA KKSANGIYSVSGDEKKGPLIA PGPDGAPAKGDGPVGLTGG RLAVPPR/ETWTRQMDFMSCV GFAVGLG\NVWRFPLYCYKNG GGVFLIPYVLIALVGGPIFFLEIS LGQFMKAGSINVWNICPLFKGL GYASMVIVFYCNTYYIMVLA GFYVLVKSFTSTLPWATCGNY/ TWKHSPTCVEIFRHEDCANAS LANLTCDQLANR/RSPVIEFWE NKVLKLSGGLEVPGALNWE/V TLGLLACWVLVYFCVWKGK STGKIVYFTA/THYPYVVLVVL LVRGVLLPGALDGIIYYLKP DW SKLGSPQVWIDAGTQIFFSYAIG LGALTVLGSYNRFNNCYKDA IILALINSGTSSFAGFVVSILGF MAAEQGVHISKVAESGPGLA FI AYPRAVTLMPVAPIWAALFFF MLLLGLDSQFVGVGEGFITGLL DLLPASYYYRFQREISVALCCA LCFVIDLFMGTDGGMYYVQLF DYYSASGTLLWQA/FWECVV VAWVYGADRFMDDIACMIGY RPCPVMKR/CWSFTPLVC/MGI FILNVVYYEPLVYKQN/TYVYP WWGEAMG/WPFAIS/SMLFVP L/HLLGLPSLRAKGHPWLKRW QHLLTQPIWGLHPL/EELPRFRD ADVQGLTHP*TPVSESSKVVV
20325	50693	A	20442	I	363	MGKRGLILLIEACIAIQPLQRW FVVPFRAGMPVTYD/HSNSAAG SPPV*NARLCSPGEKVLCSQT GNFPHTPQEQA/VPSAWNALPV QP*SH/GPSPMLVP/CRVCVCMET RVQGSASPGGQG
20326	50694	A	20443	747	1389	LGAVQLCPPPCRPCCHRAALPGG LFPPPRPPHSPQAGLPHQWQTQ* PGSVGSPTQLSPEASRPQWPPT A/GSPRAGVHPGHGQA*SADISS AKQWTQVGPAGQGGSKFGKT KVPWQSGPLGWDPGARAGQG VG*ETRGPQLQAWSDEGV/P GWRGSYRGHRRGP*PPAPWPW SGGHPGSPMEWPCPGTELQMR NRAGSRDLHSLGRAPPAATAPS

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20327	50695	A	20444	90	1181	RAEPLQVPGVPGSAQKPQGT QMAPVSPRRGPQRGWHTLGAQ RLLPQAALSSPAFPQHPGGRWA PRRRGQSSQGHSPESLPSERAQP HWNHPQLLSPCTPLSCP*GGPR QA/EQAGDSSGSGTWVGLGAAP SERGAPMSARHWLRAPGRPIF LLSALW*TPAWGGGPAASRSP GGPSSRVVGCPLCLAPGPVPS VE*RPMTSKDLPPSPR*K/P APV*/SPKAVGIPAWERPPT PETEGAGGSCAERLLAPVEMAP VSRGQRRDPFEGSRHG/DPPTDT AALGGPRPPQHLPRTRQHWI* GPGAPPTDTAALGDLRPQSPGL LMELGPISRDPHGRGPWQGPV GKLWPGGQSGSCPQSPPV
20328	50696	A	20445	2	957	IPSRKDHEKAEFEVHEVYAVDV LVSSGEGKVRVPELAKRGD*E CSPDQMLLKLLFQAKDAGQRT TIYKRDPKQYGLKMKTSRAFF SEVERRFDAMPFTLRY*AMIVL GTSLTRPYTQEHFSLPA*TC SVHVLTPSLSLPISFSLKVM*K NPKHDFCLRVGAILKYEQNGK T*WGVKDTSEYHLPCQAFED KKARMGVVECAKHELLQPFNV LYEKEGEFQKELHFGFPDYKISF L*VQKS*V*QRNFLSKHIFIFAIG EFVAQFKFTVLLMPNGPMRITS GPFEPDLYKSEMEVQDAELKA LLQSSASRKT
20329	50697	A	20446	85	266	

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20330	50698	A	20447	207	1759	LSQRALRLSPRARFSLSAPCLPCLLALLSLSSRIEGLTTACGWGRETEAAAQGGKRGCSGGSRKMSGEDEQQEQTIVD/DSL VVT KYKMGGDIANRVLRLSLEASSSGVSVLSLCEKGDAMIMEETGKIFKKEKEMKKGIAPTSISGTIN*PI/CHFSPPERSD/QDYIPPRKGD LVKIDLGVPCWGMGFIANVASH/SFVV DVAQGTQVTGRK/ADVIKAAHILCAEAA/LRLVKPGNQNTQVTEAWNKVVAHSFNCTPI/EGMLSHSLKQHVIDGEKP*FQNPTDKQKRAHEKADFEVHEVYAVDVLVKPQERARPKDAGQRTTIYKRDP SKQYGLKMKTSRAFFSEVERRFDAMPFTLRAFEDEKKA RMGVVVECA/KHELLQPFNVLYEKEGEFVAQ/FKFTVLLMPNGPMRITS/GPFEPDFYK/SEMEV/QDAELKALLQ/SSAKSEKPKKKKK/KASKTAGEWPLVAFSAVLETFRRKWKLGGLGVGPISPAACCSCLHPPSHQTPRLCEVQFFST
20331	50699	A	20448	1	3825	ARERSLRGSPAREEREKERKCTALSE*GEQMERKTN*TKQTE*N RNEIGPRGAGPPGDAGSGRQPA LRPHVHKQTEKTRVRTVLNE KQLHLTRLTCYANPRPDALMK EQLVEMTGLSPR VIRVWFQNK RCKDKKKSILMKLQQQQHSD K/SGEQLGRRLSEGGCASAASVACPF LGEPWEIQGELGAPDG VCLYLHASKASLGFEASYFVWD RGFSLSQWQPRVAGSGRCAEP KAAWQCAAPASRAGGLCTPSA AAERSPVEKEGSSDAIECAPPR KAMQTLNHSRPGAPVSKVAEK ARPNSTYCLLLAPQSLQGLTG TPLVAGSPIRHENA VQGSAAVEV QTYQPPWKALSEFALQSDLDQP AFQQLGLLSAGGRSPRDTFRLG ARGPGAPARVPLHLPLPGVSAA PVSFSESGSLGSSGSDVTSLSL QLPDTPNSMVPSPVET
20332	50700	A	20449	1084	2429	
20333	50701	A	20450	133	276	WDTSS*SLRTPRSRQVSTRPRR KKEKLPSKGMFSSVSLPQVL.TQ RHQRPTCSWSL.CWQPQLHLLR S
20334	50702	A	20451	2	205	

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20335	50703	A	20452	182	411	GRAWPAPPTSVTPRLRSPAESP RWPSAEERSSLP/VRGRRPGYG* VSCCGPRAPPGVNGDALRSARP AQLPA*RPQRH
20336	50704	A	20453	786	1208	GVHRTHTGRQKWRFCAPRAQ HSWGPGGRLPAGCRG*AGSCA/ PSLGL*CGAGPQGWGRDP*TR RRTPRRPPRGPRPRVWMAAPPAR SHPWRAAPRSAGAAPRPLGLG GRSGRETRPAPGGELQRPAAAG PPLMSCGWRVVLA
20337	50705	A	20454	385	727	KAMSPVFPRIHSKWDLDSLRLPF TSAALLSACKILKLVKDNKMK VATSGVKKSYI*STV*TTREDW TAGRQRTWRCIYSTTEEKEDSG *SPSKGNGEGRGDAT*TTER*RS DTGL
20338	50706	A	20455	568	3382	HPGWVARGPAGEGHAAGCG PARCQAGGPLQDGGCGGQGH FGGGHVPEIKGGFFPHAGACAL EERQPR*QP*GVGKRGGGLFHA SSSPSSGGSRTEPAEG*GGA VCR AGDLGHIDDAGDHGDSGK/KE RVEEEGGKPKHVLSTSGVQSD AREPGEESSQKADVLEGTAEALP PIRASGLGADPAQAVVSPGQGD GVPGPAQAFPGHLPPTKVEAK APETPSENLRTGLELAPAGRV NVVSPSLEVAPGAGQGA
20339	50707	A	20456	762	1245	LRQYSVKMRIVPTILLNFGADP DLRDIRYNTVLHYAVCGQSUS LVEKL/LEYEADLEAKNKDGYT PLL VARY*QLIPKLVKFLLE/KG ADVNASDNYQRTALILAVSGEP PCLVKLLQQGGEICNEG/MVD SQLRNMFISMVLLHRYPQFTAS HGK/QKHAK
20340	50708	A	20457	346	608	PKRRGAPLPVIPSQAS*KPKLPM GRPPPPVPSVPGPLPGSLAIA HSLEPHLVQSSCLVVPPTKQS KRKPGRGAQAPTLPNATEFSVC RNDPKEGGRSP*FPNRLLEPE APPRPSAGESPRPAA/SPLPCSE EK/PTPQLCARERLAPSAAPPPP PRCGAPLLEPSAWTPELARRA

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20341	50709	A	20458	340	889	SAPFSSGERTPGCEASFPFGGG GGNARPSGPAHPSPSSAS*KPKL PMGRPPPPVPSVSPGPLPGSLAI APHSPEPQLVQSSCLVVPKTK QSKRKPGRGAQPTLPNATEFS VCRNDPKEGGRRSP*FPNRLLE PEAPPRPSAGESPRPAAA/SPLPC SEEK/PTPQLCARERLAPSAAPP PPPRCGAPLLEPSA/EAEEGGW GAGPLGRALPPPPGKGLASGQ PGVRSPEKGADQRPQSPGPRLC SAPAPPRRS/PPRRRRPSNFVPED QPHYVPGSASAGPRRSRPPRR ELGAPSHLP
20342	50710	A	20459	148	397	GHKELVTGTEAIELAHAYETCH AVPRTIAKLVPKTHLMSESEW RNLGVQQE/RQGVVHYMIHEP EV*HFGCSRRLTQGTQRK
20343	50711	A	20460	139	272	VLKPGGSYSFGSPSCNSSH*LIG FQKWKDVPCEDKFSFVCKFKN
20344	50712	A	20461	440	1167	ARDSLQLSMAQTSSYFMLSCL MFLSQSQGQEAQTELPQARUSC PEGTNAVRSYCYF*WKTRET WVDADLYCQNMNSGKLGVC GSPRAEGCLFWPQLI*GGVGT* WTFNVLDLGLQ*PPKTRRW/H WEQWGPLVSLQSSWGHWEPPS RCLNPGVY/CVSLDLQSTRSRN WKDVPFVKDKFSFVCKVQKT RGQAGKIQCLELTPAITNGVQK LNRTISPTQLNLVTLSAEFALLI FNSFT
20345	50713	A	20462	3	322	
20346	50714	A	20463	1	420	DLVELVQYAGNIIPRLYLITVG VVVYKSFQSRKDILKDLVEMC RGVQHPLRGLFLRNYYLLQCTR NILPDEGEPTDEETGDISDSMD FVLLNFAEMNKLWVRMQHQG HSRDREKRERQVSWRCKCG TLQIQIVLTG
20347	50715	A	20464	1	1446	

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20348	50716	A	20465	3	2564	LGAGAACCRLLWGVAMPTTQQ SPQDEQEKLLDEAIQAVKVQSF QMKRCLDKNKRIGVRHKTML RNMLGIELRTSMLSPKSYELY MAISDELHYLEVYLTDEFAKGR KVADLYELVQYAGNIYPQGF YLLVHSLSCNNVKSPQSRIRDI LKDLVEMCRGVQHPLRGLFLR NYLLQCTRNLPEDEPTDEETT GDIRDSMDPVLNFAEMNKLW VRMQHIGHSRDREKRERERE LRILVGTNLERLSQVE/WCKCG TLRQIVLTGILEQVNVCRDALA QEYLMCEIIQVPDEFHLQTLNP FLRACAEHLQNVNVKNIIIALID RLALFAHREDGPGIIPADIKLFDI FSQQVAVTVIQRQDMPSEIDV VSLQVSLINLAKMKYPRVAD YVVDKVLGNNGRIFNKLNLH ATSSAVSKGNFTRLGLKLPVGH FTNNILTVLKLKHFHPLFGYFD YESRKISMSCYVLSNVLADYNT EIVSQDQVDSIMNLVSTLIQDQ PDQPVEDPDPEDFADEPEALV ARFIHLLRSEDPDQYVILNLTAR KHFGAGGNQRIRFTLPPLVFAA YQLAFRYKEISKVDDKWEKKC QKIFSFCTKTISALIKAE/LAQE LPLRTFSFKGGT*LA/AGELGFG NHGTVAYEFMSQGIFSVWKD/ EKSDFPKAQLGWPTFGSIGA LFRERVEVLSVEEDSNWNLRTQ
20349	50717	C	20466	23	385	
20350	50718	C	20467	16	435	
20351	50719	A	20468	1	436	
20352	50720	A	20469	1	747	
20353	50721	A	20470	1	864	

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20354	50722	A	20471	2	2138	VGRAAAAAA AVAVPLAGGQE GSPGGGRRGSRGTTMVKKRRKG RVVIDSDTDSGSDENLDQELL SLAKRRSDSEEKEPPVSQPA A SSDSETSDSDEWTFGSHKHKK KGQARTLEQKGTMKKQANKT ASSGSSD/RTDSSAESSA PEEGE VSDSDSNSSSSSDSDSSSEDEE FHDGYGEDLMGDEEDRARLEQ MTEKEREQELFNRIEKREVLKR RFEIKKKLKTANKKEKKEKKK* QEEEQEKKKLTIQIQESQVTSN KERRSKRDEKLDKKSQAMEEL KAEREKRNRATAELLAKKQPL KTSEVYSDDEEEEDDKSSEKS DRSSRTSSSDEEEFEIIPPKSQP VSLPEELNRVLSRHKLWRWCH MFFFAKTVTGCFVRIGIGNHNS KPVYRYAEITGVVETAKVYQL GGTRTNKGLQLRHGNDQVRFR LEFVSNQEFTSEFMMWKEAM FSAGMQLPTLDEINKKELSIKEA LNYKFNDQIEEIVKEKERFK APPNYAMKKTQLLKEKAMAE DLGDQDKAKQIQDQLNELEE RAEALDRQRTKNISAIYINQRN REWNI VESEKALVAESHNMKN QQMDPFTRRQCKPTIVSNSRDP AVQAAILAQLNAKYGSGVLPD APKEMSKASVGQGGKDKDLNSK SASDLSEDLFKVHDFDVKIDLQ VPSSSEKALAITSKAPPAKDGAP
20355	50723	A	20472	438	709	FLSQSWIFQIRASRTLFLVAFS SNTFTSCRSFCSSEAMGAGSG RSPLEQPRRRNRK PRAEPSNR AQPTPRTS/LRRCSLRPHRPCAR SR
20356	50724	A	20473	2	1315	ILQKRIGFLDALVRNSQPARYI NDYQLSNYGLDMLGPSLDPAP MASEELQKDLEEVKVLEKAT RKTEKSKIETIKNKLQKQSQK KAELL DNEKPAAVVAPITTYGT KGGGGEERGGEAPTSNEAQAT EVRGGAGGGKDKDDGDRER/P RKTRGGGRARTE*NNRHEQ*IQI KKRRRETEKERRNEKGRRRHKT ATQKRRRREARRRVGEGTRK REQPAHEQEHATTTHTRPPAP/R RTRKTQTHNRKERKKEE
20357	50725	C	20474	43	162	

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20358	50726	A	20475	2	363	YEPLDSNKRIGTSSSYVLC LCS SLAIFSNFMGNLLSFCGVLK LK SLACIH*RFFN*A**VFIIHSSRE Q*FINVCSSCPAFFNPERRNELY ASLLSFVPSALVPFEDNVSYLF VKSF
20359	50727	A	20476	505	2294	VYSDAKSIYCLLFAHSQRPPCV FNENDPQNSGTVHTVFLVGLTD HRHARAKIESWAGEAAPFTLV AASADKLFGLDHIISKYCGRIAV SVFQFQQYCGLCDSTS/SLQY CGLCGST*HSGSTVASVAGLHI VAVPWPLWQDFTLWQYRGCL/ AQDFTLWQYHGLCGRTSRVAV PWPLWQYFTLWQYCGLCGRIS HC/GQYRGCLCGRTSHCGSTVAS VAGLHVWQYCGLCGSTSRC/E QYHGLCGRTS/RLWQYHGLCG RTSYC/EQYRGCLCGSTSRCG/MY RGLCGRTSH/WWQYCGLCSTST YCSRTVA/LWQYFIL/CSTSY/W QQYHGLCGNTSYCGIL/QIQY SGLCSSTSYWGSTVASVAVLHI AAVLWPLRQYFILQONRGFCG NTSYCG/SYFILWQYHGLCGST SYCG/SYFILQQYHGLCGSTSYC /EQYRGCLCGSTSYC/TQYCGLCG SSSYC/AQNCGFCGNTSYCGSTS /VLQQYHGLCGSTSYCGRTV/V FCGSTSYWGSTSYCGSTVASLA VLHIVAVLCPL*QYFTTNKTKN KTKPGSCHLTYFGGAAGGPSL* APGGVAGTVGSASRSASWGLP EWICCLRDPKSLSFYPWGFVW
20360	50728	A	20477	2	554	LSSTGGLHAGRLCCSPCLLVIPL KSSQHIFRVLNTNIRLGRRKNS PLPITAHLRVWARRYAHVVL R KADIDLTKRAGELTEDEVER VITH/ILQNPRQYKDPKTGFFEQ DKKDVK/DGKYSQVPSQLVWD NKL P*KTWEPTERRFRAH*/RGL RHFLGAFVRVQQAHEPLGRR GRHRWVCPRRK

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20361	50729	A	20478	50	774	LFGVVYTGFC LGVW TAGVGGV PGPNFPRM LTLVRGP*GKGVG WVAGPQLRPTGPWSI*VSHPT PPGPLSISYRAQAAGGQGPAP/I THPQGRQEP*RQLPPGGPLA/RH PPKAPDPARPHP/RQHRGPS/ST APKGRCWQHKQEPSGHAPAGHT PGRPG/PPQAPRPSPWVGP GPQ TPTPCP*DEPHRPPGLQPWRPFS PLAMAPMGR LQALPGLDQRGQ TVSPLRL LGALES LAWLPSAFIA
20362	50730	C	20479	156	908	
20363	50731	B	20480	1	804	
20364	50732	C	20481	278	551	
20365	50733	A	20482	169	1144	INYSLEKHV GALGRVFLSL*RA GCPGMGSTRE RGLYL GKHRGS GGIW*ALAGP*KSRGDSVSLTQ GHTHVCSRSPR*ADSPPG/SHLS PVPHSVEVAGHVLVPATRAA V PCSASAGA*QSTYRTGVHQGNP TV*TK/PSRRPSGGVAK*FLPSA VRGEPGAKPLVDDLLPGWSLA THGQPPPLVAAPGSLWGRPAD A*GCETAGGSPCPRSTSRPSGPS GVQGCP LG*AGSGASASRSEPP GSTSCCPRAP/T*PAAPCVDPWP AGDQWRSHGYLPPSREL*/G/W MPSPRPATLPQLAFARQRQGNR FDAAFESSGEDFHQMPRVGRM
20366	50734	C	20483	31	90	
20367	50735	B	20484	48	197	

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20368	50736	A	20485	5447	5642	PRDMESCYNPGLDGIIEYDDFK LNSSIVEPKEPAPETADGPYLV VEQPKQRGFRFRYGCEGPHGG LPGASSEKGRKTYPTVKICNVE GPAKIEVDLVTHSDPPRAHVAHS LVGKQCSKLGICAVSVGPKNM TAQFNNLGVLHVTKKNMMGT MIQKLQRQLRSRPQGLTEAEQ RELEQEAKELKKVMDLSIVRLR FSAFLRASDGSFSLPLKPVTSQP IHDSKSPGASNLKISRMDKTAG SVRGGDEVYLLCDKVQKDDIE VRFYEDDENGWQAFGDFSPDT VHKQYAIIVFTPPYHKMKIERP VTVFLQLKRRKGGDVSDSKQF TYYPLVEDKEEVQRKRKALP TFSQPFGGGSHMGGGSGGAAG GYGGAGGGSLGFFPSSLAYSP YQSGAGPMRCYPGGGGAQM AATVPSRDSGEEAAEPSAPSRT PQCEPQAPEMLQRAREYNARL FGLAQRSARALLDYGVTADRR ALLAGQRHLTAQDENGDTPL HLAIHQTSVIEQIVYVIHHAQ DLGVVNLTNLHQTPHLHAVIT GQTSVVSFLLRVGADPALLDRH GDSAMHLALRAGAGAPELLRA LLQSGAPAVPQLLHMPDFEGLY PVHLAVRARSPECLDLVDSGA EVEATERQGRTALHLATEME ELGLVTHLVTKLRANVNARTF AGNTPLHLAAGLGYPTLTRLLL
20369	50737	A	20486	3	346	PQTITDELWVTLTVEVWDIST/ LFPGN*SHA/TLPSH*NLITLPL NANI/AIPQHALKGLKPVITRLL QHGLLKPINSPYNPILPVQKLD KSYRLVQNLRLINKIVSIHPVV PN
20370	50738	A	20487	1	808	YGTSLLLPWLITCPLPSH*NL TLTPLNANI/AIPQHALKGLKPV TRLLQHGLLKPINSPYNPILPV QKLDKSYRLVQNLRLINKIVSPI HPVVPNPPAFTSQITQAVSQAL GIQWNLHIPYHPQSSGKVERTN GLLKVHLTKLSLQLKKDWTVL LPLALLRIRACPRDATGYSRFEL LYGRTELLGPNLIPDTSPLGDYL PVLQQAQAANLLPTPDQPH EDTLAGRSVLVKNLTPTQTLQPR WTGPHFIYSTPTA VCLQDPPH

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20371	50739	A	20488	2	513	CCPIASEAQ*TITDAELVWTLTV EAQSLLRVFLSYLPTLTHKYGT SLLLWPWQITCPLPSR*NLITLTP LN/GQYPIQPHALKGLKPVITRL LQHGLLPINSPYHSPILPVLP DKAYKLVQNLRLIYQIVLPIHP VVPNPYTLSSVPPSTTHYSVL DLKHAFFTIPLQP
20372	50740	A	20489	1	1893	
20373	50741	C	20490	1	1806	
20374	50742	A	20491	1	645	MTSGPQINQPKKHLTNFKSEPS DL/FPSSPGCSLPAED*RCPIALE AP*TITQA/RVTLIVEGKSVPLV NTEATQSTLPSFQGPVSLASITV VGIDGQASKPLKTPLLWCQLG QHSFMHSFLVIPTCPVPLLGRDI LTKLSASLTIPGLQPHLIATLLP NPKPPSCLPLLSPHLNPQVWDIS TSLATDIMPITIRLKNHPYPAQ RQYPIQPHALKD
20375	50743	A	20492	113	328	LGSAGWGGGDLWEINPLSSCS LLREKDLLTTS GPQT VTS PRNISP ILNRDPTVQLTWQPLPELELW PKAL
20376	50744	C	20493	183	254	
20377	50745	A	20494	1	511	MWKGPKGLDMYGKSSVSPKTS DILGRDTELLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLWEINPLSSCSLLHE KDPPTASGPQT VTS PRNISPILNR VSEVSDHAGTPALVLHP
20378	50746	A	20495	1	1108	MWSELELPGNIFNGFDQNADN DMDDEIEAQEIVSDGDEEFVGN WNKPRDLVPCILATLALTRKGQ DTAQTMASEGARPKHWQLPGG VGPVGAQKSRIEVWEPLPIFRR MYGKACMSRQKFAAGAGFSW YVPVAVVGAKVHDVNLHMLS FPSKWKLHTCMKFGAVTQIVTS LGRSSCSLLLEKDPMPVLRPTSP RNISPISNLTKETRFIRGPKTPAP VTDWEGSLPLVFNHCRDASLII HPGFRGVRPRRDACLSPLAN LINLTFKVYNNRKKLQFLAFTV RQTSAMSPAHNKFTPEPQRPG IPPEPPPGACYKC/HEIRPPGQG MPAAQDSS*ATS/LSVRDPTGN WTVQLTWHPLPELELWPKAL

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20379	50747	A	20496	128	302	TAAARHSSRTSSPRSLQVLEI WPSQGGMPPAAWDSS*AASHL WQPLPEP/LELWPKAL
20380	50748	C	20497	80	106	
20381	50749	A	20498	196	575	
20382	50750	A	20499	1	505	TKETRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIHPGFRGVR PRRDACLSPSPLANLINLTFKVY NNRKKLQFLAFTVRQTSAMSP AHKNFQTPEPQRPGIPPEPPPG ACYKC/HEIRPPGQGMPPAAQDS S*ATS/LSVRDPTGNWTVQLTW HPLPEPLELWPKAL
20383	50751	A	20500	372	563	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT/TSRNPISPLN/PEK KETRFIRGPKTPAPVMD
20384	50752	A	20501	96	505	WS*QP*GLGSHRHHRRHRHSS SSSSSSSSSSKSNSDWQPLPEPL ELWPKAL
20385	50753	A	20502	79	207	
20386	50754	A	20503	583	736	
20387	50755	A	20504	99	246	DLIFHQRHSVSAESLTMHGLNN *QTSAKRVVQGTWQPLPEPLE LWPKAL
20388	50756	A	20505	654	719	
20389	50757	A	20506	71	951	LRSGLDPWEI/NPLSSCSLLREK DPPTTSGPQT/TSRNPISPNR/ PKETRFIRGPKTPAPVTDWEGS LPLVFNHSDRTSLIHPGFRGVR PRRDACLGPPLAASPTFLGKG PAAPRQTELGPNSSSASAPPPYN PFIASPPHTWSGLQFPMSTSPPP PAQQFTLKKVAGAKGIVKDLIN LTFKVYNNRKKLQFLASTVRQ TPATSPAHNQFTPELQQPGVP PEPPPRGACYKFQKSGHRAKEC LQPRIPPKPHPICVGPWKSDCP THLAATPRAPGTLAGGSLTPSQI

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20390	50758	A	20507	1	1010	CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSSQQLHPLDPWHE LLRAQELQCATNHKGYSHAEH EHAGLVQGGNGALAFSNSGH RHAVPTISSGTGRRTSPSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLRFGSDWLPSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKKNGEKRTLL QKRKKGMPHPAYEDLNIAAIT LPANVVLHQPSGFRSTGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTTSRNISPINRQRRQV LSMDPKLRHRSRTGKAAPWC LIAGTPL
20391	50759	A	20508	3	539	IVDDCGGAFTMGVIGGGVFQAI KGRNAPVCRLLEAPLFIYSCS RSVSPTVNVSSERAESRPTLFM AVSLHMAWCLAHIIRHRLRG SANAVRIRAPQIGGSFAVWGGL FSTIDCGLVRLRGKEDPWNISIT GAILTGA/VLAARSAPLAWVGS AMMGILL/ALIEGVSILL/TR* ATV
20392	50760	A	20509	3	778	GEQRAALPPAPKECTHPNVTNT LVQAESSDAGVRLRWGRGLTA RPDASAMEEYAREPCPWIVD DCGGAFTMGVIGGGVFQAIKG FRNAPVIRHRLRGSANAVRIR APSTTGSFAVWGGLFSTIDCGL VRLRGKEDPWNISITSGA/VLTA VLAAP/SGPLAMGGLQQ*WGG ILSAPHLRAFGILL/TR*TA/QQF RKWAPNSLEDPSQLPPKDVTP APGYPSYQQYHLRKLPLATMGA TSSVPFPDGSGLKGAGFPF
20393	50761	A	20510	1	231	LRWRVWSLSLMFRCVRSFFLL VGSWSRWRSEAADLGCCEYS S*GSTSGVVRFSRWACGLAGLR SEAADLAPPTSC
20394	50762	A	20511	318	494	

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20395	50763	A	20512	1	1234	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPQQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNAAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGSLRSQM PCADLSILKEAAETLDSSTRNS AFLGNTHDEAPIVHVFIPLAYS TNIWSLIFNPTTMMMCSDWL SSCENKRVDLAFGLVYSGTPVQ KLEQMKFSPQLGCNHFESKDR NDFLFAPEEIEKDPQGESLLCDF MTKTPKAMATKAKIDKWDLIK LKSFTAKETTIRVKNQPTWE KNFAIYPYDKGLISRIYKELKQI YEKKIKQPHQKVDERLLNLTT DRLTGEKAYRFIKVQVLRVTQ GMKIQRRARSKEQLQGDGDEIQR WKRLHSPPLLGEPEPHRIIFKLD SANDMHKSAPFSSQLQSPLWHQP VMQEVERQYKEKKDLVREGG KCRQCGRPCKVVLTELSLEAR GGWMEDIPSRRTSKCGPWELV SHCVQNWVVLGLTDFKNEAS DPRGVKLQFTTVSVTALKAAR LELLVLPGLLVVSLASGVKLQT FAVSVTAHKRSVDPKTEGAGS GLGQPRKGLSQCSSGPKG*YPE STKNLNKFRKKSNNPIKRLMK
20396	50764	B	20513	1	531	
20397	50765	A	20514	1139	1562	GALQPTAALWEPLSGLAKARA GTLSQLGSVEGVA*AGTGAAC GACGPDGVPGGRGLGGPRTGS SRPALSHFITEEDKDQRVQDQL GGVWHRMEIHEQHVKGQEE GDVEDHIPGEDHEGGGEERHIV PKQLLVLDVDRFLPK
20398	50766	A	20515	1	1597	
20399	50767	A	20516	461	1601	

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20400	50768	A	20517	1	914	MNNLRRAALRAVLTAKVCSF TPEPARPQTHQKEETPNTSEHQ KEQTPDTPPLRTVTLTARVHGF LEVSETKNPPIPDTPATREAEGL RSRLAVYSTRDSPCVACSGSYT QAQSLGRKFQDPVSLFEDLTK NTPEPNLRPITSKPVLVQETLSN FALFLKESNGPVVKVWGSJ/KG LT*KALHGFHVHIEFGDNTAR LYQVQGPHFNPLSQKTTVGPK DEESHCH*DLGQCDCLTKNGVA DVSIRFCESHSSGDHCIIIGRTL VVPWKKPDDFGQRVGNVESSK TGNAGKSVWPCGVNWIAQ
20401	50769	B	20518	8	173	
20402	50770	C	20519	13	180	
20403	50771	A	20520	3	486	VTETWKCAGIPHYRSFESC/IW NPVINSRMDYAGPVCFKNADI GRCAHEKLRED*DGAAPGEIGI QPEADATPYFATPTPVLTHGPC AAESEPALIGSKQFGLSRNSHI AIAFDDTKVKNRLTIELEVRT AEFRLLFYMARINHADFATVQL RNLPLY
20404	50772	A	20521	1	459	
20405	50773	A	20522	2	239	SDSSGSREVDPAATTMPGAA GVLLLLLLSGGLGGVQAQRQ QQRQSAHQQRGLFFAVLNLA SNALITTATCGEKGPEMYCKL VEHVPGQPVVRNPQCRICQNSS NPNQRHPITNAIDGKNTWWQS PSIKNGIEYHYVTITLDLQQVFQ IAYVIVKAANSRPGNWILERSL DDVIEYKAWQ*HAAVTDTEAL TP*PN*SPELGHRQNAQD*EVI CTSFYSKIHLENGEIHIHLINGR PSADDPSPELLE
20406	50774	A	20523	2	445	
20407	50775	A	20524	1	2765	MGRRRLLVWLCVAAALLSGA QARGTP/PWRGLR/LPGASRYSL YTTGWRPRLRPGPHKALCAYV VHRNVTCILQEGAESYVKA RQCRWGPCKPGTVTYRTVLRP KYKVGYKTVDLAWRCCPGFT GKRCPEHLTDHGAASQLEPEP QIPSGQLDPGPRPPSYSRAAPSP HGRKGPGFLGERLERLEGDVQ RLAQTYGTLSGLVASHEDPNR MTGGPRAPAVPVGFGVIEGLV GPGDRARGPLTPPLEILS

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20408	50776	A	20525	2	363	RFTKVMEMKEK\MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAHL
20409	50777	A	20526	1	1566	
20410	50778	A	20527	1	1604	MAILFEMRLGQSSAKFPGFQS SFFPVIPVKNKPSGKFKRDRAHFS STRLLWPDCQISQLWGGYLRK KGSSPSQGLIDKTPSPWKKAPR ERGCGGRSFSRFXHPCLTALKR AADLPAQHSSAKDTSQKGPTD TSYRRALAGIWQVPPPLGRSFQK KDQAAIFAVVQPLQVPRQTGS GVDLQQTSADWQQRGLTVRR KTNKQKGIACSLKDPIRGHQHQ RPKDNHNSPAREQNWTENEFD KLTEVGFRRRVITNSSELKKHV LTQCKDAKNLRSLEELLTRIPS VEKNINDLMELKNTARELREA YTSFNSPIDQAERISVIEDQFN KINREDKIREKRIKRNKQSLQEI WDYVVKRPNLQLIGVPESDKEN GTKLENTLQNIQENFPNLAREA NIQIQEIQRTPQRYSLRRATPRH IISV/RFTKVMEMKEK\MLKAVRE KGRVTHTHGKPIRLTTADLSAET LQARRQSGGQYFNIL*RGKIFQP R\ISYPA\KLSFISEGEIKYFIDK\Q MLRDFVTTTRDWPALKEHQAC
20411	50779	A	20528	58	1081	SSMAKPCGVRLSGEARKQVEV FRQNLQFEAE\EFLLR\FLPQKII Y\LNPA SFQEDFFFNVA*/LLNLS SGAPLGHPPIPRPLHPKDDME TDKAGRRKEVP*SVGFFPWGN* GKFLSLVCPGLKPE\WDFSKR NCILGDLHWIQTDPDSRPFEDGN DFGGSQSRKKVLEKG*MPVKT KVIEAFQITISKY/FSSERGDAC GPRPPKETHVMDYRALVHERD EAAYGELRAMVLDLRAFYAEI VKSSGIGAHVSFKVQNIHSSYC SGPTVSPCTVTGLPASQSPDSG AQLASSSGSHTCAAGGAACQS RALRLHSSALGWSMGLGTVEQ GAALIEEVQAAQEPTIEG

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20412	50780	A	20529	1632	1932	KEGCELCRCCCRPGPPASSHGQ PHHVFPF/VLSMASPWA VSPSS VNVSQFFIC/TQDAKTEWLDLDC KHVVFGKVKDGMNIVEVMEHL LGSKNGKISNQEDHHC
20413	50781	A	20530	245	740	GAWKARSDCSSNP*NYVNRLE LFADKVPKTAEFQALSTGEK GFGYKGLVFRHPIPGF/TCQSGD FTRPYSIGGKSHLPGRNLMTRT FILKHTGPGILSMANAGPSVNV SQFFICPAKMPRTIEW/LDCKHV VFGKVKDGMNIVEVMEHLGSK NGKISNQEDHHC
20414	50782	A	20531	135	1427	GKPTFASRQQPLAECPASSAL QRRWLWRRWWLRRRRRQR RSSGSCQGPAGPLGGPPANRG AAPQGSMMANNYNKDEVDGG PPCAPGGTAKTRRPDNTAFKQQ RLPAWQPILTAGTVLPFIIFGLI FIPIGIGIFVTSNNIREIEIDYTG EPSSPCNKCLSPDVTPCFCTINF TLEKSEFEGNVFMYGLSNFYQ NHRRYVKSRRDSDQLNGDSSAL LNPSKECEPYRRNEDKPIAPCG AIANSMFNDTLEFLIGNDSYPI PIALKKKGIAWWTDKNVKFRN PPGGDNLEERFKGTTKPVNWL KPVYMLDSDPDA*WIHK/DDFI VWMRTAALPTFRKLNRLIQRK SDLHPTLPAGRYSNLVNAAYYP VHYFDARKRMMSAISWMGGK NPFLGMA YFVGAISFHLGVAL LGINHKYRNSNTADITI
20415	50783	A	20532	1	370	
20416	50784	A	20533	1	1104	LREFANFDIWRKKYMRWM NHKKSRVMDFFRRIDKDQDGK ITRQEFIDGILSSKFPTSRLEMSA VADIFDRDGDGYIDYYEFVAAL HPNKDAYKPITDADKIEDEVTR QVAKCKCAKRFQVEQIGDNKY RFGDSQQLRLVRILRSTVMVRV GGGWMALDEFLVKNDFPCRAK GRTNMELREKFIADGASQGM AAFRPRGRSRPSSRGASPNRST SVSSQAAQAA'SPQVPAITTPK GTPIQGSKLRLPGYLSGKGFHS GEDSLITTAAARVRTQFVADS KEGLPSRPGSSLEAKFGSR/AS SRRGSDASDFDISEIQSVCSDVE TVPQTHRPTPRAGSRPSTAKPS KIPTQRKSPASKLDKSSKR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
20417	50785	B	20534	527	4627	
20418	50786	A	20535	37	315	
20419	50787	A	20536	1314	1577	HGSGSAPTCRWPRQTGRCREIC ADGFSGVMRNCTG*EAASGR* CKSFVHVYLQLRCACSVCHSA GSDSFQLQRSPTSTCTHALV
20420	50788	A	20537	1	1652	MQATKTESGRNGKPGQPSNRC HYLLNQGWVANSKGGRRTNIP DKELKSGDDPENVHITSFYLA LAAFPGRGRARDLQAMTEPPHP SVGSCAARASLTSAAPCSTAPSP INHPKAEECGCTARDWQAAPP AARVRDPLGEASWAPSEYVC NCSVVGSLNVNRCNQTGTQCE CRPGYQGLHCETCKEGFYLN TSGLCQPCDCSPHGALSIPCNSS GKQCQKVGVGISICDRQCQDGY YGFSGKNGCLPCQCNRSARCD ALTGACLNCHENSKGNHCEEC KEGFYHSPDATKECLRCPCSAV TSTGSCSIKSSELEPECDQCEDG YISPNCNKCENGYNFDSICRK CQCHGHVYLISTPKICKPESGEC INCLHNTTGFWCENCL*GYVH DLEGNCIKKEVILPTPEGSTILVS NASLTTSTPTPVINSTFTPTTL* TIFSVSTSENSTALADVSWTQF NIHILTVIHGVLLMGFEGAGY MYRENQNRKLNAPFWTIELKE DNISFSSYHDSIPNADVSGLVED DGNEVAPNGQMTLTTPHNYK
20421	50789	A	20538	1	177	
20422	50790	A	20539	1	480	
20423	50791	A	20540	410	896	FSCLKRMHIKAMPEDAKGQDW IALVKAAAAAAKNTGSKPR TSANSNKDKDKDERKWFVKPS KKEETSTCIATPDVEKKEDLPTS SETFGLHVENVPKMVPQPEST LSNKRKNNGQNSFQAKRARLN KITGLLASKAVGVDAEKKED YNETAPMLEQV

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20424	50792	A	20541	1	1526	LKDEEDFFDFKAGEEVLARWT DCRYYPKAKIEAINKEGTFTVQF YDGVIRCLKRMHIKAMPEDAK GQVKSQHPLSWCCPIDPAGSCN QSMGSEDWIALVKAASAAAAA KNKTGSKPRTSANSNKDKDKD ERKWKVPSPKKEETFNLLATP DVE/RRKEDLPTSS/EKHL*GLH VRRNVPKMVFPQPESTLSNKRK NNQGNV/FQAKRARLNKITGLL ASKAVGVGDAEKKEDYNETA PMLEQA/ISPKPQSQKKNEADIS SSANTQKPALLSSTLSSGKARS KKCKHESGDSSGCIKPPKSPLSP ELIQ/VEDLTLVSQLSSSVINKTS PPQPVNPPRP/KH/SERRRRSQR LGTLPMPDDSVKVVSSPLSSPL D/EGKVFS/LSSSSKISQESS/PE VPDVA/HICPLEKLGPCLP/LDLS RGSEVTAPVAS/DSSYRNECPRA EKEDTQMLPNPSSKAIDGRGA PAAAGISKTEKKVKLEDKS/STA FGIRSWDFSALLMKIPSYSPISLS GLPES
20425	50793	A	20542	363	1187	FHITMCGICCSVNFSAEHFSQDL KEDLLYNLKQRGPNSSKQLLKS DVNYQCLFSAHVLHLRGVLT QPVEDERGYNVFLWNGEIFSGIK VEAEENDTQILFNYSLSCKNES EILSLFSEVQGPWAFIYYQASS HYLWFGRRDFGRRSLLWHFSN LGKSFCLSSVGHPIWNWQISG KKFQHLDDFRIDLKSTVISRCIIL QLYPWKYISRENIIEENVNSLSQ ISADLPAPFVSQVMEGQTVSL EKPVVPLNMDVATSWHWETH AVFFPCATYR

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20426	50794	A	20543	1140	2372	CCHKLHWRLIAVIFPMCHLQER YFKSFLMYT*KEVIQQFIDVLS VAVKKRVLCPLRDENLDSQME VLENV**GKANVGNPFWGGGL D/CPWLLATLLDRHIIPLDEPLVL LNVAFIAEETMPTTFNREGNK QKNKCEIPYPKNFSKDVA ADSPNKTCCQPDRIITGRAGLK ELQAVSPSRIWNFVEINVSME LQKLRRTTRICHLIRPLDTVLDD IGCAVWFASRGIGWLVAQEGV KSYQSNKVVLTGIGCRWSNL QGYSPSSVSFAKSHGLGRIGKE IMMELGRISSLEILGRDDRIVIG DHGKEARFPFLG*/RMLSPFLNS SARFGEKANLDTFPRGIGEKL PFNALQPVELGLTASALLPKRAM QFGSRIAKMEKINEKASDKCG RLQIMSLNLSIEKGTKL
20427	50795	B	20544	70	464	
20428	50796	A	20545	18	552	
20429	50797	A	20546	1	1257	
20430	50798	B	20547	223	342	
20431	50799	A	20548	9	5293	KIHRHRLSPATEKGAASSGEGD KDPPPPAHEDIAVKGTATAAGT GPGTGAAAAAATAVPPHPNI RALQTQAQQIIPRGVPVQPLED RIFTPAVSAYSTVTQVARQPG TPTSPYSAHEINKGHPNLAATP PGHASSPGLSQTPYPSGQNA TTLVYPQTPQTMNSQPQTRSPF FPKGLKIOPPRATIPNSKSPFV PGAQTPAVYQG*FRHIMM/V NHLPLPYVPVQGPQYCIQYRH SGPPYVGPQQ
20432	50800	A	20549	1	78	
20433	50801	A	20550	1	2805	MAKGFYISKSLGILGILLGVA VCTIIALSVVYSQEKNNKNANS PVASTTSPASATNPASATTL QSKAWNRYRLPNTLKPDSYRV TLRPYLTPNDRGLYVFKGSSTV RFTCKEATDVIIHSSKLNLYTL QGHRRVLR/PPDIDKTELVEPTE YLVVHLKGSVKDSQYEMDSE FEGELADDLAGFYRSEYMEGN VRKVVAATTQMQAADARKSFPC FDEPAMKAENITLIHPKDLTAL SNMLPKGPSTPLP
20434	50802	A	20551	1	239	
20435	50803	A	20552	1	654	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
20436	50804	A	20553	161	3193	GSLRLPTITMAKGFYISKSLGI LGILLGVAAVCTIIASVVYSQE KNKNANSSPVASTTPSASATTN PASATTLDDQSKAWNRYRLPNT LKPDYSQVTLRPYLTPNDRGLY VFKGSSTVRFTCKEATDVIIIHS KKLNFPLSQGHRVVLRGVGGS QPPDIDKTELVEPTEYLVVHLK GSLVKDSQYEMDSEFEGELAD DLAGFYRSEYMEGNVRKV VAT TQMQAADARKSFPCFDEPAMK ARFNITLIPPQGT
20437	50805	A	20554	3	429	
20438	50806	A	20555	3568	4012	VLSTSPGTELPPIISPLAVNSTE LLKGELSLSSLGVLSLSDTSVPN SVSNSFLGLRKRLLGRGVGISC NALSALDLAACNFSLMRPLME NSAKPVLEVEGIGG/TAFDAGA GIALSDHFIKLISWYDNEFGYSN RVVDLMAHMASKE
20439	50807	A	20556	1	1211	QTAASSFASPGEPHRSNTMGKV KALVNGDFDRGLRVTRAAFNSSG KGDIVAINDPFIDLNYMVVMFQ YDSTHGKFGHTVKAENGKLV NGNPITIFQERDPSKIKWG*H/G AEYVVESTGVFTTM/EKAGAH FAGGSQKGHSSFAPSTEAIMFM MKVNYEKYDNLKIIISNASCTT NCLAPLAKVIHDNSGIVERLMI TVHVITTTQKTVDDGPCRKL RPD GHRALQNIIPASTSTAKAMVKV IPELNKLTGMA SHVPTAKVLV VDPTCH/LGKPAKYVDIKMM KQASEDPIKGILGYTEHQVSSD FNSDTSQSTFDAGAGITLNDHF VKLISWYDNEFGYSNSVVDLM AHVASKELSGYSLKVSVFVQK LFLSIRSNLSIAFDAIVFGVFVM KSLPVSICRM
20440	50808	A	20557	1	300	PTANVSVDLTCRL*PKAPYD DIKKVVKQASEGPKLGILGYTE HQVVSDDFNSDTHSSTFDAGAG IALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
20441	50809	A	20558	1	3399	
20442	50810	A	20559	1	3126	
20443	50811	C	20560	298	435	
20444	50812	A	20561	1	888	
20445	50813	B	20562	1	4536	

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20446	50814	A	20563	37	3900	LGLGLSMLVGQAGPLGPAVV TAAVVLLLSGVGPAHGSEDIVV GCGGFVKSDVEINYSLEIKLYT KHGTLKYQTDCAPNNGYFMIP LYDKGDFILKIEPPLGWSFEPTT VELHVDGVS DICTKGGDINFVF TGFSVNGKVLSKGQPLGPAGV QVSLRNTGTEAKIQATATQPG GKFAFFKVLPGDYEILATHPTW ALKEASTTVSVTNSNANAASPL IVAGYNVSGSVRS DGEPMKGV KFLFSSLVTKEDVA
20447	50815	A	20564	1	310	EEETVPTTAGASPGPPRNKKNR ELRPQRPKNAYILKKSRIKKPQ VPKKPREWKNPEPSAAAS*GGE GQAHHGPAICPGQICALSQTPG LPGNSLSPRPVGK
20448	50816	A	20565	3	267	
20449	50817	B	20566	267	560	
20450	50818	A	20567	1	429	LIGLDPEPLAEVDVISLEQGRRK QIERLGYDPQAKAPFQPKPKQK GRSSTASLVKRRKRVMD EENR VK*TIGNGGLPKGCTLPACAL CPCQPAHFLTLCVSLSPVPQD KVRQSLQQQHHKEAK/APKPTG ARPSALDRFVR

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20451	50819	A	20568	2	1951	FKPTVWQLRGV LHVDR LFWWA SMETAPKPGKDVLSKKDKLQT KRKKPARRYWEEETVPTTAGAS PGPPRNKKNR LRPQRPKNAYI LKKSRSISKPKQVPKPREWKNP ESQRGLSGAQDPFPGPAPVPVE VVQKFCRIDKSRKLPHSKAKTR SRLEVAEAE EETS IQSLLRSEL LLAEEP GFLEGE DGTAKICQ ADIVEAVDIASAAKHFDLNL RQ FGPYRLNYSRTGRHLAFGGRRG HVAALDWVTKKLMCEINVME AVRDIRFLHSEALLAVAQNRW LHIYDNQGIELHCIRRCDRVTRL EFLPFHLLD TASETGFLT YLDV SVGKIVAALNARAGRLDVMSQ NPYN AVIHIGHSNGTASLWESS YGREPLAKVLC\HRLGSGAVA VDSYRHVTWATSGP*DHQLED LDFFARGRY\QPLEHSGCPMG AGHLAFSQRELL/VLAGLGDVV NIWAGQGKASPP\SLDRPYFTH RV*GPVHGLQFCPFEDVLGVG HT*GUTSMLVPGAGEPNFDGL\ ESNPYRSRKQRQIEWEVKALL EKVPAELICLDPRALAEVDVISL ETGKR RKQIERLGYDPO\AKAP FQPKPKQKG\RSSKA\TLVKRK RKVMIEDHKG/DKVRQSLQQQ HHKEAK\AKPTG\ARPSALDRF
20452	50820	A	20569	1	437	
20453	50821	A	20570	157	425	

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20454	50822	A	20571	207	1562	LVIVFFYPQHTAPGPPLTVLNQ AMHARGPHGQLSPALPLASSVL MLLMNLAHLQGPWMLGPLTW HISPFSLPVHRLTHALGHTALP GILLLLLLPTVGWQQECHLGT LRLFLHASALLALASGLLAVLLA GLGLSSAAGSCGYMPVHLAML AGEGHRPRRPRGALPPWLSPW LLALUTPLLSSEPPFLQLLGLL AGLACILCLSPGPVGMCGFCG WVPGKEVAQRGEGPSNTKEPC THIAWPAWAHPWLLLVFLDR PPCPGQTDAAGAFRWLEPSERR LQVLQEGVLCRTLAGEGMPVQ VVGTVAGLPVRPSSLP/SSSRPPI PGPPYVASPDLWSHWEDSALPP PSLRPVQPTWEGSSEAGLDWA GASFSPGTPMWAALDEQMLQE GIQASEVSGPIGAGVALTLPTS PPTPNRLQLERMGFTEQAVV ALAATGRVEGAVSLLVGGQ
20455	50823	A	20572	460	916	AHSPRDHPWTVLNQAMHARGP VHGQLSPALPLASSVLMMLMST LWLVGAGPGLVLAPELLDPW QVHRLTHALGHTALPGALLS LLLLPTVGWQQECHLGTLRFLH ASALLALASGLLAVLLAGLGLS SAAGSCGYMPVHLAMLAGEG HRPRRPRGALPPWLSPWLLAL TPLLSSEPPFLQLLGLLAGLAY AAGAFRWLEPSERRLQVLQEG VLCRTLACGWPLRLLATPGSLA ELPVTHPAGVRPPPGPPYVASP DLWSHWEDSALPPPSLRPVQPT WEGSSEAGLDWAGASFSPGTP MWAALDEQMLQEGIQASLLAD GPAQEPQSAPWLS/KSSVS/*MR LQQLERMGFPTTEAAVVALA\ ATGRVEGAVSLLVGGQSGTNET LVTHGKGGAHSEGP/GPPWAN CPQHCLLASSVLMMLMSTLWL VGAGPGLVLAPELLDPWQVH RLTHALGHTALPLAPEPAAP AHCGLAAGVPPGHAIEIPACLSP ARPGFWAAGSAAGRPWAVQCS RQLWIHACPPGHAGWGRTTP
20456	50824	A	20573	174	401	CTVVFVSLAEISCTSRFCPNMW TPLREPMTENGRWGLSVRVLE HGGNQSNSACGPEPPEGEMGS* LEED*LPALIP

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20457	50825	A	20574	450	1029	ATQLPPQPWQTPAALGWAAAT SLMPYRAPSPPARAQHPALCL APPPPLWLQPLHLEASHSLVEA RPNPPVSTLAQQGIQSPRHLPR CPSLRPRQQPPQQVP/PQPAAPT PTATITSTGPSLFASIATAPTSSA TTGLSLCTPVTAGAPTAGTQGG FSLKAPGAA/PAPPQHPPLPPP PPPPPPAAAPPALP
20458	50826	C	20575	115	276	
20459	50827	A	20576	3	307	ASRLPGREGGARKNPGGCSAT QYISVSP/GAASFVVLGSQSLLT TVSPPLPA*/P/LAMAL*PRPLCA PGSPSRSPRLRSPLPSFFSRGRR RLSLLPQWSE
20460	50828	A	20577	2	388	
20461	50829	C	20578	244	487	
20462	50830	B	20579	5	569	
20463	50831	A	20580	204	676	RTDQYPORGETEEGLEQLLPH RQLPGGLGAHRGPDACGLRD SSRGVPLAGSPLRV*/GRGHDL RQSGGVPRPGGGSNRGLVVGAD ARGRAAPLAGGVPAADRSRL PGVPAAREPHGPTAPDPDSAA EPGAVSTLRAEPTQPVPVSTGC CSSTWN
20464	50832	B	20581	1	1413	
20465	50833	B	20582	60	224	
20466	50834	B	20583	8	2469	
20467	50835	A	20584	841	1436	HHQVPLPVGRERGGKRGPGSW ETCLSVLGAIPPSEWPVSPSW VHSLVPGEQALPLICSQPPMAP QWPETGPGPHLVHRTCRVCLN WQGMTRTRGYQAGPSSRRTIPT PAQLPAPLASLPPRQDPSPSPAE PPSGRFSMEPW/EPARHPGPGSP AAPCSSHRIT/APPTPSLAAQPG/ PVGSNPPLSPEGLCLAGTPACG W
20468	50836	A	20585	1799	5195	SKGNGPSSTTQTTPRAAPDGS LSEETPAGPTCSVPPASALPRQ QYAKSLPVSPVPWGFKEKRTE ARSSDEENGPKPKPASVDANTK LTRSLPCQGSLLKRAATSCERAGK AVGEEVSGYSLHGCSKERRRRP RLKKEGSGEPGVGYLFISVLV NSNSELIRLINNAIKNDLASRNP TFMCLALHCIAVGSREMGEA FAADIPRILVAGDSMDSVKQSA ALCLRLLYKASPDVLP/PMGEWT ARVVHLNDQHMVG

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20469	50837	A	20586	8	268	SRSSRTWSPPEKEKTKLQKQR EDELIQKIHLVQKRDFLVDDA EVERLREQEEDKEMADFLRIKL KPLDKVTKSPPI*QSQRAHL
20470	50838	C	20587	50	196	
20471	50839	A	20588	16	1263	SLSSRCMMVAEQGCALEPCQG LSHGAALGVLVVFP/VSSLQQ DQLDIISMAETT/MMP/EEIELE MAKIQRLEVLVRRESELRFMS FEEQYNEDHKKGVIDLFTADSL KTMTRLVVTGVWLAATASN PLQEGEHAGEQIGAGGCRSL GGALTWDPVLLPPVRISRMLLL LLIPGELPGIAFKLMNPTKAEPM HMFIIIEPFDLRKLMDDIQLCK DIMDLKQELQNLVAIPGCTRSM MLVSAQLEGLRKLIIAEDKG ADMSRAQSRSKRPPKMLICLLV DVFFPEKEKTKLQKQREG*AN PRRFHKLQKRDFLVDDAEVE RLRIEQE/EDKEMADFLRIK/LKP LDKVTKSPASSRAEKKAEPPPS KPTVAKTGLALIKDCCGATQC NIHVSPHVGCGPGWGPPTLLS
20472	50840	A	20589	31	339	
20473	50841	A	20590	1	1179	
20474	50842	A	20591	1	1167	PARSMAATSLMSALAAARLLQP AHSCSLRLRPFHLAAV/RGNLSL GQVGVCNHHGLLP*PPGLK* SSHLSLNEAVVISGRKLAQQIK QEVREQEVEWVASGNKRPHLS VILVGENPASHSVVLNKTAAAA VVGINSETIMKPAISIEEELLNL INKLNNDDNVGDLVQLPLPE HIDERRICNAVSPDKVDVGFHV INVGRMCLDQYSMLPATPWGV WEIHKRTGIPTLGKNVVVAGRS KNVGMPIAMLLHTDGAHERPG GDATVTISHRYTPKEQLKKHTI LADIVISAAGIPNLITADMIKEG AAVIDVGINRVHDPVTAG/PGL VGNVDFEGVRQKAGYITVPVG GVGPMTVAMLMKNTIIAAKKG AEA*RSEKVLKSKELGVATN

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20475	50843	A	20592	1	1963	MAASDVNCGACFAELQGNATA NTPGGTSHHTHLAIHGSCHDSQ AKEAGRKRPWPDPGRSEPAP DSHPHLSPEALGVFRRALSALK EAPETGEERDLMVHNIMKEVE TQALALSTNRTGSEMIQELLGF SPLKPLCRVWAALRSNLRTVAC HRCGVHVLQSALLQLPRLGSA AEEEEEEEEEDGKDGPTELEEL VLGLAAEVCDDFLVYCGDTHG SFVVRTLLQVLGGTILESERARP RGSQSSEAQKTPAQECKPADFE VPETFLNRLQDLSSFLKDIADV ITDKISSFCLQVALQVLRHKL QFCAHICNAVIGYLSARGSSVD GKPLLLFLRDQTSFRLLQVLL VLEPPRLQSLFEEHLQGGLQTL AAHPPIANFPLQRLLDVTTPEL LSPVFEELSPVLEAVLAQGHG VVIALVGACRRVGAYQAKVLQ LLLEAFHCAEPSSRQVACVPLF ATLMAYEVYYGLTEEEGAVPA EHQVAMAAARALGDVTVLGS LLQHLLHFSTPGLVLRSLGALT GPQLLSLAQSPAGSHVLDAILTS PSVTIPSCAAVCLQNLKGTNIVA LACKSP*QPRVLKCHLEWSSLE GP/RRKIAAELGEQNQLKEPP FGHHVARNVALTTFLKRREAW EQQQGAVAKRRRALNSILED
20476	50844	A	20593	55	393	
20477	50845	A	20594	150	379	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
20478	50846	A	20595	1	2408	MGVWGIRTPFMVVGLESVPVGS SPRGQGSCVRLPQRRDPKSHAG ARTGPETLRERAQQSNKLPEW AEKGSHPARWSPNRGGRWTLF TARERRPSRALKARAAGRQA KVADFRLPAAAPPEGAALRLD SERLPHQDEKEPSSYRGSCGSCP VTLRKMPYLGSEDVVKELKKA LCNPHIQADRLRYRNVIRVIR YMTQGLDMSGVFMEMVKASA TVDIVQKKLVLYMCTYAPLK PDLALLAINTLCKDCSDPNPMV RGLALRSMCSLRMSKLDQWQG AEVLNFFLLRYQPRSEELFDILN LLDSFLKSSSPGVVMGATKFLFI LAKMFPHVQTDVLRVKGPLL AACSSSESLCFVALCHVRQIL HSLPGHFSSHYKKFCSYSEPH YIKLQKVEVLCELVDENVQQ VLEELRGYCTDVSADFAQAIF AIGGIARTYTDQCVQILTELLGL RQEHIITVVVQTRFDLVWLCPO CTEAVCQALPGCEENIQDSEK QALIWLGVHGERIPNAPYVLE DFVENVKSETPAVKMELLTAL LRLFLSRPAECQDMLGRLLYYC IEEEKDMAVRDRGLFYRLLLV GIDEVKRILCSPKSDPTLGLLED PAERPVNWSWDFNTLVPVYG KAHWATISKQGAERCDPKLP KTSSFAASGPLIPEENKERVQEL PDSGALMLVPNRQLTADYFEK
20479	50847	B	20596	330	2458	
20480	50848	A	20597	2	171	
20481	50849	A	20598	32	1040	LQLAKLGDWRMQALRHVHCR FTEG*FMYSL*LTFFPAGYQVT GVFMKNWDSLDEHGVCTAD KIDCEDAIYRVCQILDIPFHHQV SYGTEVIFFYSSDFLNEYEGRT PNPDIVCNKHIFKSS*SLCSKNL TGADAIATGHYARTSLEDEEVF EQKHVKKPEGPASWRNCLSVG WFLYTLGQRANIGGLREPWYV VEASPPSHILQAPRTDHPALYR DLLRTSRVHVIAEPPAALVRD KMMECPPPRAPLFYYPVCVLTL NQDGTVVWTVATVPDARVSPQL FAVYKGDDECLGSGKILRLGPS AYTLQKGQRAGMATESPSPDS PEDGPMGLSPLL
20482	50850	A	20599	12	432	

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20483	50851	A	20600	2	509	RLHSLGDDYYQAIVKLVLENIDLS TKSMYSRVPECQVTTYVVYVGF AYSMRCYQDAIRVFASILLYI HRTNSMFQRTKYKYEIMILN EQMHALLAIALTMYPMRIDESI YLHLREKYVDKMLRMQNGDL QVYEELFRYSCTKFL*PVPNNY DVTVAHYHTESFLQSLRR
20484	50852	B	20601	8	1188	
20485	50853	A	20602	1	257	
20486	50854	B	20603	210	312	
20487	50855	C	20604	49	288	
20488	50856	A	20605	13	446	IPVRPTRPADDYSEEAAYDPYA YPSDYDMHTGDPKQDLAYERQ YEQQTQYQVIPEVIKNFIQYFHK VSDLIDQKVYELQASRVSSDVI DQKVVEIQDIYENDAVFLILYK ELYRHHYAKVSFQSFQYRCK TAKKSEEEIDFL
20489	50857	B	20606	77	611	
20490	50858	A	20607	1	1956	SLVDPRVPRVRLASEAAMS YPADDDYSEEAAYDPYA/PSD YDMHTGDPKQDLAYERQYEQ QYQYQVIPEVIKNFIQYFHKTVS DLIDQKVDELQASPCQVIVID QERLYEDSRTIY*EQA WTKL/TE RFFKNTWPWGGWKPLVPQGLA MDA/VSLDFYPKNYTYRHHYA KVSOGPSL/EQRFESYNYCNL FNYILNADGSRPLNYPNQWL WGYLSMEFIYPVFSHF/SQYRW *DLPKKSEEEIDFLRSNPKIWN VHSLNVLHSLVDKSNINRQL GGYTQAGGDP*ECGWGSMGR HSLYMMMLHYFSLVR/GFSRLHS LLGDDYYQAIVLENIELNKKKS MYSRVPRVPRSPYTY/VVGFAY LMMRRYQDAIRVFANILLYIQ RTKSMFQRTVYKYEMINKQIE QMHALLAIALTMYPMRIDESI HLQLREKYGDKMLRMQK/GD PQVYE*LFISYSCPFLAA/VVP TYDNVHPNHYHKEP/FLQQLKG VFLDEVQ/QQGAFAKPIRSFLKL YTTALLAKPGLASLDPHRGRE FRDPRFLCLSNHQQ*RNVLVLP AGISSPWIGESVSPQRVDLPTL NKDMIPHRGTPKVPQAVMGDF LHPVRSRSHKFGGA*SEPLKEGWG QRPWMIFTTTHREPVFVDHQQG
20491	50859	A	20608	2	413	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
20492	50860	A	20609	232	621	
20493	50861	A	20610	1	3590	MAPRKRGGRGISFIFCCFRNND HPEITYRLRNDSNFALQTMPEA LPMPVVEELDVMFSELVDEL DLTDK HREAMFALPAEKKWQIYC SKKKDQEENKGATSWPEFYID QLNSMAAGILEGVFVHIVITHC LQNQQQLLHDKQGGRHFICCL RSHQHPMLPACSNVHLSSFDRK TLCKDALCPLPASHVSRYLKRS LLALEKEEEEERSKTIESLKTAL RTKPMRFVTRFIDLGLSCILNF LKTMDYETSESRIH
20494	50862	A	20611	203	3480	SHQEIEQNSAMAPRKRGGRGI AFIFCCLRNNDHPEITYRLRNDS NFALQTMPEALPMPVVEELDV MFSELVDELADLPDKHREAMFA LPAEKKWQIYCSKKKDQEENK GATSWPEFYIDQLNSMAARKSL LALEKEEEEERSKTIESLKTALR TKPMRFVTRFIDLGLSCILNFL KTM DYETSESRIHTSLIGCIKAL MNNSQGRAHVLAHSESINVIAQ SLSTENIKTKVAVLEILGAVCLV PGGHKKVLQA
20495	50863	A	20612	1	338	PGGALRVPDAPAGAEGQELCR SDFPVGGAGVGDEEGVQCPAP AAHRDDTDLRGAH*EVQDAAG RRKQPDREQPAGAEEGAPHLPE RVPPG*RHGTCTDRGQARACG GPLAPE
20496	50864	B	20613	610	6429	
20497	50865	B	20614	28	280	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=/possible nucleotide deletion, \=/possible nucleotide insertion)
20498	50866	A	20615	160	1397	VKMSAQESCLRLIKDFLFVNL FFFALGSLIFCFGIWILDKTSFL SFVGL/AAFVPLQIW/SKVLAIIS GNLSPWGIALGLCWGALK/EL RCLLGVLVFGMLLLFATQITLE KSSSSNQRIAQLESLR/IDVVGK TIQKYGINPEETAPEENWDYV QSNLRWCGWHYGRDWFVFI RGNSEAH/RVTRS*YNFMAT* NSTILNKVIVHQLTRLEHLARSR HSAD/ICAVPAESHITRKGCAQ GIQK/WLHNTLIF*/WAICLGVG LLE/LGFMTLSNIPVEETVDHGL PTGSARYRLGPAPQSRAPPPVS VRWALPVLPNICLIPRLAVEPS GVHISPGDTTWLRAPAAVTSPT GPGAFVHSFLSPSVGLPPPTRLF FTQTSNKPAPFLVNDHKKGGRS KKALEGPNVTRA
20499	50867	A	20616	290	492	
20500	50868	A	20617	1164	2134	NNYNHHHHHHHHHDYYNHH/ HHYHHHHHHHHNNYHHHHHDH HHNYKHHHHHHYHQHHNNYNH HHHHHHSYNHHHHHHHHHHN YNHYHHHHHHHHHHHREYHH HH/HHHHHYHHHHHHNNYHH HYHHHHHHQYHHNNHHHHHHH YNHHYHHNQYHHYHHYHHHD YYHHH/HYHHNNYYLYNRYH HYHHYHQSNNHYRHHHHHHQY HHN/HEPFA/HHT*ILFCS*KQDR NLHCAWPPFFFFNCHHHCHH HHQQQQHSGVKTKQSRPESLLP ERCYLVHQKHPLHRPGAPQHQ KTASWRGQAREAAGSSPSGLSS HTADHEVEAFKRCFYSRF
20501	50869	B	20618	164	1526	
20502	50870	A	20619	1	762	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
20503	50871	A	20620	69	1054	AISCHVVHAGHQQTQITGNDPF PVVITYSKGPNLQSSRSDMDST EREQSRLTCLKKREEMKLKEC VSILPRKESPSVRSYKDGKLLA ATLLALHACCLTEVSFYQVAA LQGDALSLRAELQGHHAELP AGAGAPKAGLGGSSCSPRDLK IF*TTSSREKAI/PGSEQQK*GVP FQGPETVTQDCLQIADSETPT IQKGSYTFVPWLLSFKRGSAL EKENKILVKETGYFFIYQGVLY TDKTYAMGHLIQKKVHVFG DELSLVTLFRICIQNPETLPNN SCYSAGIAKLEEGDELQLAIPRE NAQISLDGDTVFFGALKLL
20504	50872	A	20621	3	855	LQNSHGHTMIRTLTLLSTLVAGA LSCGDPTYPPYVTRVVGGEAR PNSWPWQVSLQYSSNGKWHYHT CGGSLIANSWVLTAAHCISSSR TYRVGLGRHNLYVA/ESGSLA/ MSSVSKIIVVHKD/WNFNQISKG/ NDIALLLKANPVSLTDKIQ/LA/ CFPPAGTILPNNY/PC*VTGLGE SCRNTG/AVPDVL/QQGRLLAV DYATCS/SSA/WWGSSVKTSMIC A/GGDGVISSCNGDSGGPLNCQ A/SDALWQVHGIVSFGSRLGCN YYHKPSVFTRVSNYIDWINSVI AYN
20505	50873	A	20622	19	414	SVCWEDRYLKARMEESPLSRA PSRGGVNFNLVARTYIPNTKVE CHYTLPPGTMPASDWIGIFKP/ GYLPKPGAQLYQFRYVNRQQQ VCGQSPFQFREPRPMDELVT EADGGSDILLVVPKATVILQNO
20506	50874	A	20623	1	393	AKSWQEEQSAQAQRLKDKVA QMKDTLGAQAQQRVVSAPWQ QETGNSKGKL*RSR/V*REGER HG*RLNNTTPSPNAVWRER/IT SLADE*FTRNCDLHLLSPEAEL EPLKEQLRGAQELAASSQQA TLY
20507	50875	A	20624	56	416	NRPLALVADSTQPLHHTHTH TPLSDAPKPIGA/HLP/CSYLEF PLTSVPHPSLFHNLRYSVWRGF LYF*GFLYSVSSPRISHGKK*CI CAFCEEWGEQVVP/PIKAPLP LQVPPQQ
20508	50876	A	20625	115	392	
20509	50877	B	20626	1	3388	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
20510	50878	A	20627	3	1889	SSPREKTS DSSHRPSRHGFLFLR LVGLSPF SYLCVPPSRPVPGSPR SLSAMRLLPLAPGRLRRGSPRH LPSCSPALLLLVLGGCLGVFGV AAGTRPNVLLTDDQDEVL GGMTPLKKTALIGEMGMTFS SAYVPSALCCPSRASILTGYPH NHHVVNNTLEGNCSSKSWQKI QEPNTFPAILRSMCGYQTFPCR GNI*MKYGAPDAGGLGHVPL GLGVTWYALEKNSKYNYTL FYSMGKARKHGENYSDVLT DVLANVSLDFLDYKSNF*PFF MMIATPAPHSPWTAAPQYQKA FQNVFAPRNKNFNIHGTNKH LIRQAKTPMTNSSIQFLDNAFR KRWQTLTLLSVDDLVEKLVKRLE FTGELNNTYIFYTSDNGYHTGQ FSLPIDKRQLYEFDIKVP LLVRG PGIKPNQTSKMLVANIDLGP TIL DIAGYDLNKTQMDGMSLLPILR GASNLTWRS DVLVEYQGEGRN VTDPTCPSLPGVSCFPDVCVE DAYNNTYACVRTMSALWNLQ YCEFD DQEVFVEVYNLTADPD QITNIAKT FDP ELLGKMNYRL MMLQSCSGPTC RTPGVDPGY RFDPLRMF SNRGSVTRRRFSQT SSCSDPHTASADGSLHALFLMK
20511	50879	A	20628	132	253	
20512	50880	A	20629	1	1269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20513	50881	A	20630	1	1920	MDEAEFSSFFVVRTNTCGELRSS HLGQEVTLGWIQYRRQNTFL VLRDFDGLVQVIIPQDEVINFL LLSKSFFDAIAGSAASVKKILCE APVESVVQVSGTVISRPAGQEN PKMPTGEIEIKVKTAE LLNACK KLPEIKNFVKKTEALRLQYRY LDLRSFQMQYNLRLRSQMVMK MREYLCNLHGFDIETPTLFR TPGGAKEFLVPSREP GKFSYSLP QSPQQFKQLLMVGGLD RYFQV ARCYRDEGSRPDRQPEFTQIDIE MSFVDQTGIOSLIEGLLQYSWP NDKDPVVVPFTMTFAEVRPP YGTDKPDTRFGMKIIDSDFR NTEIGFLQDALSCKPHGT VKAICI PEGAKYLKRKDIGSIRNFAADH FNQELPVFLNANRNWNSPVAN FIMESQRLERLRLMETQEEDVV LLTAGEHNKACSLGKLRITGN VAGPSRKQEGVVLRDPTLFSFL WVVDPLFPQGRKKIQESWDR GQHPFTAPHPR*ITLLYTEPKK ARSQHYDLVLNGNEIGGSGSRI HNAELQRYILATLLKEDVKMLS HLLQALDYGAPPHGGIALGLD RLICLVGTGPSIRDVIAFPKFRG HDLMSNTPDVSVP*GTEALSYP SLQANRLQSRKSSLNHAYHAES
20514	50882	A	20631	1	425	KEPVGCVNNISFLASLAGSTSR NRLQSTRGAGRLQNSGTGLSTN LQHFQEEENFRKSSPQLEHT/WSF FGECTTHLPPVKAPLQTKKKT TNHCFLCGKKTGLASSYECRQ VGELEKLRCLCDNPAGWLCKI KYNLCLFITSL
20515	50883	A	20632	1	1647	
20516	50884	A	20633	1	3096	
20517	50885	A	20634	1	419	
20518	50886	A	20635	558	1070	SFRFGHSHGLWKRKKVA*GSN AIQHNMLQKGQNFGAALWY KGNSTQSKRPQRA*ESSTTKR GLQLSRQTLQLDPGGTVPCSEE YCICQ*EGPASRNRYNGVPSHF PSPTCIRESSHSKILKSLRCW GWPTDPWSVLPMDPRTSPLCA AGSQAVVAHSGRQQKYPAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
20519	50887	A	20636	3887	4573	KKTTLLTLTKTRNINPFKVVVK KKAYGSRKHLRQ/HLAINPAAL LPTAASQISEVKPVLPELAFPS EHRRSHGLESVPVLPQSSEAGV SFDLPAQADTLHSANKSRVKM RGKRRPQTRAARLLAAQESSEA EDMRSPEDPLHSGLMAPFPQM AIGHSSEQPVKETA LRPPWQLP LHLGKVVLCLEWTQAPLQSLW VIPEGRLTFLIGTFFPRALDLSP WREQNPRQR
20520	50888	A	20637	1	2988	MATAPSPMMLTLAPAWLCPAT TTPRDHSEASLEALPGDPPAHP AAAAATAAAVIPALEPHTPVYA IFVNHSLLDLYIDRPLPYLIGSK LFMEQEDVGLGELSSEEGNADE QSSGLEGACKVNLLELLTNAD KGLKAPEQHLKHVAGVNLGES VETSVLNYRELSPHKNRLLSPL RCSAPMSLHNSLVKPERQSKCF EFGKLPSSSSQSLDVQNTDSSF SRTTCFQGVKVDLSLGRKSDVIS KVEARDITEMTNKA
20521	50889	A	20638	1	1176	
20522	50890	A	20639	2	367	
20523	50891	A	20640	124	441	RYPRVPENRCFSELLFFQAPLG VGMARGNQRIELARQKNLKET QELSRGKGKEDSLTALSRKQD S*IIAKKQKAA\NEKKS/MQTRE NVMGTGYLENPGATAQLGVS
20524	50892	A	20641	32	232	
20525	50893	A	20642	1	256	
20526	50894	C	20643	133	509	
20527	50895	A	20644	88	685	QKRGRLFKIILKVVLVLMKVVI HRKMFQRAQELRWRAEDYHK CKAFSDHPLCKKASLQLQGNG GSGASSFFRIALLALPHS*NFKK QDGPPTSSNSTTFYN**LPEPQ DTSRMSSYSLSLSSSTLRG**S QDSSLSSYSGRGRKITETQAE VE*AEENRSLHSSLGNKKKSVSG TKEKNQKTKQNPHSKNKLTKN
20528	50896	A	20645	42	946	
20529	50897	C	20646	1	453	
20530	50898	C	20647	771	1223	
20531	50899	C	20648	324	659	
20532	50900	C	20649	427	654	
20533	50901	B	20650	343	1774	
20534	50902	B	20651	23	525	
20535	50903	B	20652	2354	5689	
20536	50904	B	20653	448	3506	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
20537	50905	B	20654	12	182	
20538	50906	C	20655	210	422	
20539	50907	C	20656	145	357	
20540	50908	B	20657	1	327	
20541	50909	B	20658	1	2595	
20542	50910	B	20659	122	472	
20543	50911	B	20660	163	418	
20544	50912	C	20661	86	517	
20545	50913	B	20662	334	2946	
20546	50914	B	20663	11	700	
20547	50915	B	20664	184	2372	
20548	50916	C	20665	267	467	
20549	50917	B	20666	131	268	
20550	50918	B	20667	18	255	
20551	50919	B	20668	100	356	
20552	50920	B	20669	120	839	
20553	50921	B	20670	355	504	
20554	50922	B	20671	1	1524	
20555	50923	B	20672	175	366	
20556	50924	B	20673	436	792	
20557	50925	B	20674	94	1347	
20558	50926	B	20675	865	1189	
20559	50927	B	20676	241	423	
20560	50928	B	20677	124	352	
20561	50929	B	20678	1	847	
20562	50930	B	20679	262	4624	
20563	50931	C	20680	76	297	
20564	50932	B	20681	1	702	
20565	50933	B	20682	1	1347	
20566	50934	B	20683	78	2874	
20567	50935	B	20684	133	7317	
20568	50936	B	20685	294	1449	
20569	50937	C	20686	139	367	
20570	50938	C	20688	154	445	
20571	50939	B	20689	1	1086	
20572	50940	B	20690	111	440	
20573	50941	B	20691	303	462	
20574	50942	B	20692	1	2905	
20575	50943	C	20693	349	453	
20576	50944	C	20694	233	376	
20577	50945	B	20695	1	2016	
20578	50946	B	20696	1464	3022	
20579	50947	B	20697	1	1059	
20580	50948	B	20698	1	933	
20581	50949	B	20699	1	930	
20582	50950	C	20700	129	215	
20583	50951	C	20701	283	408	
20584	50952	B	20702	1	1134	
20585	50953	B	20703	1	525	
20586	50954	B	20704	146	556	
20587	50955	B	20705	1	675	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20588	50956	B	20706	1	1107	
20589	50957	B	20707	1	774	
20590	50958	C	20708	52	156	
20591	50959	C	20709	1	420	
20592	50960	B	20710	1	1347	
20593	50961	C	20711	1	411	
20594	50962	B	20712	169	248	
20595	50963	B	20713	63	1321	
20596	50964	B	20714	1	359	
20597	50965	C	20715	1195	1674	
20598	50966	B	20716	964	1290	
20599	50967	B	20717	51	389	
20600	50968	B	20718	108	232	
20601	50969	B	20719	425	3545	
20602	50970	C	20720	35	226	
20603	50971	B	20721	1	387	
20604	50972	B	20722	1	1926	
20605	50973	B	20723	523	1242	
20606	50974	B	20724	42	2346	
20607	50975	B	20725	63	287	
20608	50976	B	20726	59	200	
20609	50977	B	20727	1	1176	
20610	50978	B	20728	1	769	
20611	50979	B	20729	1	2009	
20612	50980	B	20730	219	3045	
20613	50981	B	20731	195	1739	
20614	50982	C	20732	126	435	
20615	50983	B	20733	2752	4108	
20616	50984	B	20734	1	1104	
20617	50985	B	20735	24	230	
20618	50986	B	20736	1	1292	
20619	50987	B	20737	1	7977	
20620	50988	B	20738	157	2627	
20621	50989	C	20739	165	533	
20622	50990	B	20740	35	87	
20623	50991	C	20741	68	202	
20624	50992	B	20742	83	2670	
20625	50993	B	20743	162	276	
20626	50994	B	20744	104	245	
20627	50995	B	20745	66	2768	
20628	50996	B	20746	14	3115	
20629	50997	C	20747	69	203	
20630	50998	B	20748	1	2152	
20631	50999	C	20749	114	387	
20632	51000	C	20750	56	250	
20633	51001	B	20751	53	3398	
20634	51002	B	20752	642	2386	
20635	51003	B	20753	1	1242	
20636	51004	B	20754	51	601	
20637	51005	B	20755	192	463	
20638	51006	B	20756	125	1254	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20639	51007	C	20757	208	333	
20640	51008	B	20758	155	4443	
20641	51009	B	20759	1	2529	
20642	51010	B	20760	63	321	
20643	51011	B	20761	226	645	
20644	51012	B	20762	1	1395	
20645	51013	B	20763	258	475	
20646	51014	C	20764	126	263	
20647	51015	B	20765	1	1429	
20648	51016	B	20766	51	3256	
20649	51017	C	20767	83	403	
20650	51018	B	20768	1	621	
20651	51019	B	20769	1	463	
20652	51020	B	20770	1002	3594	
20653	51021	C	20771	107	403	
20654	51022	B	20772	51	401	
20655	51023	C	20773	46	398	
20656	51024	B	20774	1	513	
20657	51025	B	20775	1	531	
20658	51026	C	20776	1	423	
20659	51027	B	20777	52	670	
20660	51028	C	20778	43	375	
20661	51029	B	20779	1	1629	
20662	51030	B	20780	1	1713	
20663	51031	B	20781	1	5154	
20664	51032	B	20782	37	585	
20665	51033	B	20783	1	3789	
20666	51034	C	20784	149	367	
20667	51035	C	20785	89	234	
20668	51036	B	20786	113	278	
20669	51037	B	20787	1	1632	
20670	51038	B	20788	1	762	
20671	51039	B	20789	230	3411	
20672	51040	B	20790	95	1150	
20673	51041	B	20791	1	1230	
20674	51042	B	20792	74	3123	
20675	51043	B	20793	1	1719	
20676	51044	C	20794	206	402	
20677	51045	B	20795	302	424	
20678	51046	B	20796	60	80	
20679	51047	B	20797	1	1248	
20680	51048	B	20798	8	1910	
20681	51049	B	20799	124	807	
20682	51050	B	20800	43	618	
20683	51051	B	20801	7	328	
20684	51052	B	20802	244	385	
20685	51053	B	20803	850	970	
20686	51054	C	20804	97	360	
20687	51055	B	20805	551	3159	
20688	51056	B	20806	861	1110	
20689	51057	B	20807	1	876	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20690	51058	B	20808	1	849	
20691	51059	B	20809	1	1443	
20692	51060	B	20810	508	2398	
20693	51061	B	20811	53	185	
20694	51062	B	20812	50	633	
20695	51063	B	20813	1	444	
20696	51064	B	20814	58	262	
20697	51065	B	20815	27	1005	
20698	51066	B	20816	1	4860	
20699	51067	B	20817	1	3489	
20700	51068	C	20818	52	363	
20701	51069	C	20819	347	499	
20702	51070	B	20820	1	4140	
20703	51071	B	20821	85	3930	
20704	51072	B	20822	848	3116	
20705	51073	B	20823	41	1211	
20706	51074	B	20824	248	4307	
20707	51075	B	20825	67	3180	
20708	51076	C	20826	229	467	
20709	51077	B	20827	71	1827	
20710	51078	B	20828	1	1045	
20711	51079	B	20829	1279	1479	
20712	51080	B	20830	1	2460	
20713	51081	B	20831	62	3691	
20714	51082	B	20832	1	1062	
20715	51083	B	20833	1	873	
20716	51084	B	20834	1	1041	
20717	51085	B	20835	161	5445	
20718	51086	B	20836	199	343	
20719	51087	C	20837	86	229	
20720	51088	C	20838	1	225	
20721	51089	C	20839	34	165	
20722	51090	C	20840	238	455	
20723	51091	C	20841	200	322	
20724	51092	B	20842	59	164	
20725	51093	C	20843	1353	1793	
20726	51094	B	20844	1	1329	
20727	51095	C	20845	43	324	
20728	51096	C	20846	223	435	
20729	51097	C	20847	212	307	
20730	51098	C	20848	386	529	
20731	51099	B	20849	300	995	
20732	51100	B	20850	876	3312	
20733	51101	B	20851	153	306	
20734	51102	B	20852	39	3131	
20735	51103	B	20853	29	136	
20736	51104	B	20854	112	333	
20737	51105	B	20855	31	474	
20738	51106	B	20856	26	1716	
20739	51107	B	20857	27	1234	
20740	51108	B	20858	1	6390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
20741	51109	B	20859	1	1014	
20742	51110	B	20860	128	837	
20743	51111	B	20861	1	931	
20744	51112	B	20862	357	4629	
20745	51113	B	20863	1	1017	
20746	51114	B	20864	1	1908	
20747	51115	B	20865	224	9448	
20748	51116	B	20866	1	1209	
20749	51117	B	20867	138	359	
20750	51118	B	20868	1	1567	
20751	51119	B	20869	226	9033	
20752	51120	B	20870	20	2689	
20753	51121	B	20871	1602	2647	
20754	51122	C	20872	72	452	
20755	51123	C	20873	64	423	
20756	51124	B	20874	33	363	
20757	51125	B	20875	131	1675	
20758	51126	B	20876	37	219	
20759	51127	B	20877	1	564	
20760	51128	B	20879	1	651	
20761	51129	B	20880	44	424	
20762	51130	B	20881	28	202	
20763	51131	B	20882	1	3403	
20764	51132	B	20883	110	970	
20765	51133	B	20884	70	485	
20766	51134	B	20885	482	2943	
20767	51135	B	20886	469	1480	
20768	51136	B	20887	156	308	
20769	51137	C	20888	218	348	
20770	51138	B	20889	1	5130	
20771	51139	B	20890	21	1139	
20772	51140	B	20891	1	1302	
20773	51141	B	20892	1	1028	
20774	51142	B	20893	1	858	
20775	51143	B	20894	1	2001	
20776	51144	B	20895	1	546	
20777	51145	B	20896	1	1167	
20778	51146	B	20897	1	1299	
20779	51147	B	20898	1	1260	
20780	51148	B	20899	1	771	
20781	51149	C	20900	155	337	
20782	51150	B	20901	1	1251	
20783	51151	B	20902	106	543	
20784	51152	B	20903	57	2279	
20785	51153	B	20904	905	1120	
20786	51154	B	20905	145	2277	
20787	51155	B	20906	1	1384	
20788	51156	B	20907	1	4775	
20789	51157	C	20908	99	251	
20790	51158	B	20909	1	693	
20791	51159	B	20910	77	2173	

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20792	51160	B	20911	140	313	
20793	51161	B	20912	1	392	
20794	51162	C	20913	1	222	
20795	51163	B	20914	1	951	
20796	51164	B	20915	45	1244	
20797	51165	B	20916	166	2544	
20798	51166	C	20917	279	449	
20799	51167	B	20918	1	1250	
20800	51168	B	20919	229	2094	
20801	51169	B	20920	94	434	
20802	51170	C	20921	253	336	
20803	51171	B	20922	1	1314	
20804	51172	B	20923	6	327	
20805	51173	B	20924	163	3060	
20806	51174	B	20925	20	385	
20807	51175	B	20926	22	58	
20808	51176	C	20927	141	287	
20809	51177	B	20928	37	1063	
20810	51178	C	20929	261	401	
20811	51179	B	20930	66	3148	
20812	51180	B	20931	223	4149	
20813	51181	C	20932	21	278	
20814	51182	B	20933	158	1283	
20815	51183	B	20934	8	896	
20816	51184	B	20935	240	387	
20817	51185	C	20936	312	512	
20818	51186	B	20937	451	611	
20819	51187	C	20938	160	428	
20820	51188	B	20939	110	294	
20821	51189	B	20940	121	1764	
20822	51190	B	20941	1	423	
20823	51191	C	20942	74	316	
20824	51192	C	20943	136	255	
20825	51193	C	20944	79	381	
20826	51194	B	20945	282	1180	
20827	51195	B	20946	63	371	
20828	51196	C	20947	193	672	
20829	51197	B	20948	85	898	
20830	51198	B	20949	35	1055	
20831	51199	B	20950	1	870	
20832	51200	B	20951	103	1189	
20833	51201	B	20952	501	594	
20834	51202	B	20953	39	1694	
20835	51203	B	20954	489	4797	
20836	51204	C	20955	31	153	
20837	51205	B	20956	259	699	
20838	51206	B	20957	4	231	
20839	51207	B	20958	50	520	
20840	51208	C	20959	322	456	
20841	51209	B	20960	163	1152	
20842	51210	B	20961	33	745	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
20843	51211	B	20962	210	3519	
20844	51212	C	20963	34	294	
20845	51213	C	20964	301	381	
20846	51214	B	20965	71	675	
20847	51215	B	20966	1	873	
20848	51216	B	20967	118	1618	
20849	51217	B	20968	424	2415	
20850	51218	C	20969	106	231	
20851	51219	B	20970	71	756	
20852	51220	B	20971	1	1049	
20853	51221	C	20972	94	327	
20854	51222	B	20973	339	2589	
20855	51223	B	20974	89	273	
20856	51224	B	20975	1	2514	
20857	51225	B	20976	472	5831	
20858	51226	C	20977	247	300	
20859	51227	B	20978	1	2487	
20860	51228	B	20979	55	243	
20861	51229	C	20980	207	377	
20862	51230	B	20981	642	4117	
20863	51231	B	20982	44	2127	
20864	51232	B	20983	48	1127	
20865	51233	B	20984	1	3411	
20866	51234	B	20985	74	469	
20867	51235	B	20986	39	1251	
20868	51236	B	20987	223	378	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
20869	51237	A	20988	1	2577	MPPNRHRMRGETTLWNPGCDH AGIATQVVVEKKLWREQGLSR HQLGREAFLEQVWVKKEKG DRIYHQLK/KLGSSLDWDRA CF TMDPKLSAAVTEAFVGLHEKG IIYRSTAFVNWPCITLSAISDIE VDKKEITGRITLSVPGYKEKV EFGVLVSFAVKVQGS*/DDE EVVVANKLGSKTMLGDVA VAV VPPPKDTRIVYQHL/KGKNVIH P LSRSLSPSSSEDFVDMDFGTGA VKDHPRHQNDYEVGQRHGL EASIMDSRGA/PIKCASAFPGPA AGLRPGKRCWWR*RNRLFRG IEDNPMVVPLCNRSKDVEPLL RPQWYVRCGEMAQAASAAVT RGDLRLPEAHQRTWHAWMD NIREWCISRQLWGHRIPIYFV TVSDPAVPPGESEDLVSFYPGT LLETGHILFFWVARMVMLGL KLITGRLPFREYVLPSPCENAH GRK/MSKSLGNVIDPLDVHL/Y GISLQGLHNQLNSNLDPSEVE KAKEGQKADFPAGVPECGTDA LRFGLCAYMSQGS*K*TWNVN RIMG*RFQCNKLWKCTKFALR GLGKGFVPSDTSNSAGHESLA DR*IRNLLTEAVRLSNQGFQAY DFPAVTTAQYSFWLYELCDVY LECLKPVNLNGVDQV/AQAECA R QTLTYLTPWTLGLRLLSFMPFV TEELFQRLPRRMPQAPPSLCVT
20870	51238	A	20989	2	4083	SQRGEHVGAGCRGGDLRELGS PGEPTVSARSTPPPGPLGGSQ P RPAPGCEVDSPAQSDHLPVFP LRSDLLITMSTLYVSPHPDAF PS LRALIAARYGEAGEGPGWGGA HPRICLQPPPTSRTSFPPRLPAL EQPGGLWVWGATAVAQLLW PAGLGGPGGSRAAVLVQQWVS YADTELIPAAAGATLPALGLRS SAQDPQAVLGA/LGRALSPLEE WLRHTYLAGAAPTADLA AAV TALLLPFRYVLDPPAR

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20871	51239	A	20990	1	756	MDMGAIKEGESRRPGDRMTVA GTKLLHLQSTHLDLDFISLGPSPG ALELSKAQPAHAQDTRVLMKMM VIIWDLQVPLQPGHDGHSFRIH DYLVFQVLSPGDIRYIFTATPAK DFGGIFHTRYEQIHLVPAEPPEA CGELSNGGFIQDQIALVERGGCS FLSKTRVVQEHGGRGGDHL*Q RS*QMTASTW/QMIQDSTQRTA DIPALFLLGRDGYMIRRSLEQH GLPWAIIIPVNVHQHSPPSLSCC NRPFLFW
20872	51240	A	20991	2	393	
20873	51241	A	20992	1066	1824	
20874	51242	A	20993	3	902	
20875	51243	A	20994	1	2163	
20876	51244	A	20995	1	1890	
20877	51245	A	20996	1	2882	MKQQLPVSYLQVIFNHWSRIS GARGAGWGPVRLGRLCADRAL DGESRPGGGQSGVPASEASQ KAAHGRRLPVPARLLRCAHSA LEPGRGSASSPRNSTTSDNDQPP DYSFSKRCDSHSLGFSLVWESR NLTLPPTSKLLHFSAFHFFIYKC RAEGHKLKLDLKNFLSAVKVM HESSKRVSSETLQFIYYSEWYGH EELKAIVWNNDLLWEDYEELK ADQAVRTMEIYYVAQFSEIKERI AKRGRKLVVDYDSARH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \-possible nucleotide insertion)
20878	51246	A	20997	1	1791	MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKSRAQEKVLQKLG KAVETKDERFEQSANNFYQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSETLQEIYSSWDGHE ELKAIWNNNDLLWEDYEELK ADQAVRTMEIYVAQFSEIKERI AKRGRKLVYDSARHHLEAVQ NAKKKDEAKTAKAEFEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMSKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPSTSPSTLSKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEDEPLPA CNGPAQAQSPPTTERAK/SQEE VLPSSSTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSE/RPKKT ASIQRTSAPRRPPPPRATASPRP CSGNIPSSPTASGGGSA/TSPRAS LGTGTASPRTSLEI*PNPE/PPEK PVRTPEAKENENIHNNQNPPELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSSEGQDQLQV SMVPENNNLTAPEPEEVESTSE
20879	51247	A	20998	3	273	RRPRQRPTDQTQWFSILPDFSLD LQEGPSVESQTHSDPHIPPVDP TTHLTFNHLSIVCVSLTLSLPHL GSPCLWSPALVSQEAASHQDRR
20880	51248	A	20999	309	1310	RHRQRAPEQGPDAWKMMLDSL ALGG/LVLL\RDVSVE/WEGVRSLL K\ALVKKSALCGE/QVHILGCE\ VSEKEFREGFDS**STIRLVYHD FVRDPLNWSKTEEGL/VPGGPL GALRS\WCKR/TDVPVPTIALDS LS\WLLLRLHCTTL\CQ\ALHAV EPSRTLVLGDSSSVGKVSVLGL LHERLPRPAPVVALSSLAQTKV TLGGYHGARP\SAHIL\CRRPQ\ RPMYQQTQWFSILPDFSLGSPRG ALCRVPALIPPHITPGGIPHNSF *PFNLHL\SKKEREARDSLILPFQ FSSEKQQA\LLRPRPGQATSHIF YEPDAYDDLDQEDPDDDLNILP

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20881	51249	A	21000	418	1304	GLVMEIGMHHEHHHLLQAPNK EDILKISEDERMELSKSFRVYCII LVKPKDVSLLWAAVKETWTKH CDKAEFFSSENVKVFESINMDT NDMWLMMRKAYKYAFDKYR DQYNWFLARPTTFAIENLKY FLLKKDPSQPFYLGHTIKSGDLE YVGMGGGIVLSVESMKRLNSL LNIPEKCEQGGMIWKISEDKQ LAVCLKYAGVFAENAEDADGK DVFNQICWAFY*R/WQ*LITPN QVVEGCCSDMAVTFNGLTPNQ MHVMMYGVYRLRAFQPYFSM MHVFSYQLQMVLTMTTEKW
20882	51250	A	21001	1	1092	
20883	51251	A	21002	130	397	EGVHSQVNLFFPIKGNQTHVPAS HGTDSALPPTLQMDYRALVHE PD*AAYGELRAMVLDLRAFYA ELYHISSNLEKIVNPKGEEKPF
20884	51252	A	21003	11	805	SSMAKPCGVRLSGKGRKQVEV FYRNLFQEAEEFLRLFLPPESHI P*NRLQEDFPFNVA*/LLNLSS GAPLDIPSPDP/PP/KDDEMETD K/QEKKKEVPKCDLPGNEKCP PCLPLVKPRSLDLSEKCCILV/ TWGSRHLDPPRFEDGK*FWG* AIPGEGAWRG*NA/VKDPKWE AFPAIPISQVLSSEGDACGPRP PQETHVMDYRALVHERDEAA YGELRAMVLDLRAFYAELYHII SSNLEKIVTPRGEEKPIYVLEP
20885	51253	A	21004	352	670	AKRSRIHGVVIVDSGDAELGR DAAALSEKPPSLTIGLHMLVGS MGGEPAITATPANCPEYPAKPS SI/EQQ*QSQVQ**Q*QVRHGS PLHRTPRQLFLCSRQFAL
20886	51254	A	21005	3	222	SPEESPACPRQVFLYHLQRG QGKRVQVG*GGSLWITTKTRL PGGVGDNEVAPGSWHLALVFR LLSSGRP

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20887	51255	A	21006	1	3639	MSEETLQSKLAAAKKKIQDILN VLVSDLNRSNGVVLPITLTKWK DAPEAWDLCLALRSICGLAIQL LGAAPLTRAANFSAEVTIDVR DSARRWETRKAPYLSRIALRM NEAAVFRHLVPGVYFPRCDQG CQLTAALGCGAGVQSHVGPVT VTITGPDVTAADAAGLCRVL AVVGWGGSECLTPHPYKFHVE PYGGRLLVPRLSDPGSSRREA TSKVAVDLLVDAAGADGPVS QSPVWKEAAGVVSQLRGGQ
20888	51256	A	21011	137	944	KPRCCHSATMFEVPLVQGSILK KVLAEALKDLINACWDISSGV NLQSMDS/SHVSLQFTLPSEGF DTYRCDNLAMGVNLTIMSKIL KCAGNEDIVTLRIEDNVNTLV VFEASNQEKVSDYEIKLMDLD VEQLGIAEQEYHYVVKMLSGE FASIC*DLSHIGDAVVISGVKDG IIFSASGDLGNKNKLSQTSTVD KEEEAVTMEMNEPVQLTALR YLNFLTAKATPLSSMVTNMSA DIHLVVDYKIADVHGLKYLLA PKMEDEEGP
20889	51257	B	21012	205	1309	
20890	51258	A	21013	189	410	
20891	51259	A	21014	1767	2158	RAQPHLYPEAARTGRGK*LHFC APSSAPRAPVSERR/CAGRFLSW CPVAAWDPARWARRARRRRR AAARRRRPPRWRRLSARGR RRSLNSSKTKNTKCLNSINQRL KILSLQKDLMCGTAGRCKTLTE Q
20892	51260	A	21015	1	1710	
20893	51261	A	21016	132	522	
20894	51262	A	21017	1	1386	
20895	51263	A	21018	331	3101	SFSEANISTAKKTFLYNELVYV NTRKDTWTKVDIPSPRRCAH QAVVVPQGGQLWVFGGEFAS PNGEQFYHYKDLWVLHLATKT WEQVKSTGGPSGRSGHRMVA WKRQLILFGGFHESTRDYIYYN DVYAFNLDTFTWKSLSPGTVP TPRSGCQMSVTPQGGIVVYGG YSKQMPPHSGQSRGRKPGSCLL LLLLLLLLLLLLLVCVPLGYSL IELSSSYRI.HGNEPVPATFHGLN SHMGLVATILDNVNP

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20896	51264	A	21019	2	2911	VRGPRARCRRRSSKTEPRKGPS RTSTRKLELGAGSDSISVRRAP PHEHLFPSSGERGPFSLVSRRL GPGKMGKKGKKEKKGRAEK TAAKMEKKVSKRSRKEEPGVC RRIRPDLGVECSAAAAHGFPNR GQFYGLPCARHSSLGFTPEQE DLEALIAHFQTLDAKRTQTVEV PCPPSPRKCRGSQFVVTEDSVR KGTALRLNASLSVHPEKDELIL FGGEYFNGQKTFLYNELVYVNI RKDTWTKVDIPSP
20897	51265	A	21020	1	208	DGYRHEMLPASLIQAQRDYFG AH/TYELWAKPGQFIH/TNWTG HGGTVSSSYNAFALFSVQFFK SVVRDS
20898	51266	A	21021	3	316	
20899	51267	A	21022	2	578	LIGLAVMGQNLILNMNDHGFV\ TVSKVDDFLANEAKGTKVVGA QSLKEMVSKLKKPRRIILLVKA GQAVDDFIEKLRRCRDLKAKGI LFVGSQVSGGEGARYGPSLMP GGNKEAWPHIKTIFQGLAAKVG TGEPCDWWGDEGAGHFVKM VHNGIEYGDMLICEAYHLMK DVLGMAQDEMALCPIFCVSF

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20900	51268	A	21023	3	1758	AYANLGRTRFWREPLRVFPSLVL RASPLFGSALSAAMAQADIALI VLFVMGHNILNMKDHGFEVC AFNRTVSKVDDFLANEAGTK VVGAQSLKEMVSKLNKPPRDQ YLLC/VKAGQAVDDFIEKLVPL LDTGDIIDGGNSEY*GTPQDG CRDLKAKGILFEGSGVSAGEE GDRYGPMSLMPGGNK\EA WPHI KTI FQGI A\AKVGTGEPCCDWV GDEGAGHFVKMVHNGIEYGD MQLICEAYHLMKDVLGMAQD EMAQAFEDWNKTELDSFLIEIT ANILKFQD TDGKHL LKPIQGT S AGARRGNRGSGT/WPFGSGPKY GVPVTLNGEAVFARCLSSLKD ERIQASKKLGKPKVQFDGD* EHSWEDIRKALYASKIISYAQGF MLLRHAA\TEFGWTLNYGIGIA LMWRGGCHRSVFLGKIKDAFD RNP\ELQNLLLD\DFFKVQLFEN CQDSWR\RAVSTGVQGWAFP MPLFYRLPLSI*TGTSHEMLPAQ PSSRLQRGLLSGAHTL*NSWAK PGAVLFHTNWTG\HGGTVSSSS YQCLDHAAPVTLHDSTVPGHSI GLNGTAHLALCPIFCSVFVFSKSV
20901	51269	A	21024	317	885	MRWRSKSAWRAEPKSRRTNSGT ASNVSPSRPLEC*R/FLRLVSGE LILALIAFICITIMACSPCEGLY FFEFVSCSAFVVTGVLLIMFSLN LHMRI PQINWNLTDLVNTGLSA FLFFIASIVLAALNHRAGAEIAA VIFGFLATAAYAVNTFLAVQK WRVSVRQSTNDYIRARTESRD VDSRPEIQRLDT
20902	51270	A	21025	4761	5127	LGSGDL PWEINPLSSCSLLREKD PPTTSGPQT\TSPRNISPISNPHTR TSKRLNRSQGAF\QNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL

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20903	51271	A	21026	174	2238	LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQT/TSRPNISPSINPRQR RHILSMDPKLRRRSWTWVGSLLP LVFNHCRDASLIHPGFRGVRPR RDVCLGPSPLATITDAELYVT TVEGKSIPLIDTEATHSTLPSFK GPVALASIHVQNVQIKRDKEGH YIMVKGSIQQEELTILNMYAPN TGAPRFIKQVLNDLQRDLDSHT IIMGDFNTPLSLDRSTRQKVN KDIQDLNSALHQADLIDIRYTL HTKSTECTFFSAPHRTYSKIDHI VGSKALLSKCKRTEIINCLSDH SAIKLELRIRIKLTQNHSTTWKL NNLLNDYVWHKEMKAEIKM FFEINENKNTTYQNLWDTFKAV CRGKFIALNAYKRKQERSKIDT LTSQLEELKQEQTRSKASRRE EITKIRAELEIETQKTLQKINES RSWFFKINKIDILLARLIKKKR EKNQIDAINKDKGIATDPTIEIQ TTIREYYKHLCPNKLLENLEEMD KFLDTYTLPRLNQEEDESNNRPI TGSEIVAIINSLPTKKSPGPDGFT AKFYQRYKEELVPFLQYKEEL VPFLKLQFQIEKILPNSFSEA SIILIPKGRDRTKKENFRPISLM NIDAKILNKILANQIQHIKKLI HHDQVGFIPGMQGFNIRKKSIN VIQHINRTKDKNHMISIDA EKA FDKIQQFSC
20904	51272	A	21027	1	181	MEEKERKRRRKRKRRREEGR DGERKRMEKQKENQDPKDPPT TSGPQT/TSRPNISPSINP
20905	51273	A	21028	167	408	LGSRTPPWEINPPSSCSLLREKD PPTTSGPQT/TSRPNISPSINLVS GLFLLSSPTSLTIPQLSSFNLDD TLQSLPSLNF
20906	51274	A	21029	449	663	LGSGDLPWEINTQSSCSLLCEK DPPTTSGPQT/TSRPNISPSINPDP TGNRTVQLTWQPVPEPELWPKAL
20907	51275	A	21030	79	381	LGSGDLPWEINPLSSCSLLREKE PPTTSGPQT/TSRPNISPSINPELA TLAGNLATGPRNARSPGFLSH VLSVWDPDENQTVQLTWQPLP QPLELWPKAL
20908	51276	A	21031	122	334	LRSGDLLWEINPLSS*SLLEHKD PPTTSSPQT/TSRPNISPSINPDPT ENQTVQLTWQPLPEPELWPKAL

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20909	51277	A	21032	109	320	LGSGDLP*EINPSSCSLLREKDD PPTTSGPQVTSRPNISPINPDPT GNRTVQLTWQPLPQPLELWPK AL
20910	51278	A	21033	620	717	
20911	51279	A	21034	3	678	GGGFSDRDRITALQPGQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGKEFYFIPKAMG AMEGSGQRRITLDPGAHRNPS GGYSATDCGSRPAPGEINSHA SHITKPVWWFFTQTRMKFGAVT RIGGLPWEVNPILLSCSLLRE/KD PPTTSGPQSNQPRKHPISINPEL VHVPEIWPLQGGMPPAARIPPKP RPICVGP*KSTVQLTWQPLEP LELWPLSD
20912	51280	A	21035	339	1098	LGSGDLPWEINPLSSCSLLREKDD PPTTSGPPTVTSRPNISPINPGET KETRFIRGPKTPAPVTDWEGSL PLVFNHCRDASLIHPRFKGVPR RRDACLGPSPLAASPTFLGKGQ RLKTDITARLPKPPRPSRTLSFS TAPRILSIVVPGSGHTLAFDVT RHRLYRESKPVVGEEDVYSEW LSDVGKSEWSFSTCASSTSVNK HDTGRRLLGKRGGMCECSKGL CNFITMTKNIRSLAQMTIWQYL SPCREPV
20913	51281	C	21036	1	438	
20914	51282	A	21037	174	483	LRSGDLPWEINPLSSCSLLHEKDD PPTTSGPQVTSRPNISPINRQR RHILSMDPKLRRRSWTWVGSPL LVFNHCRDASLIHHPGRGVRPR RDVCLGPSPLA
20915	51283	A	21038	590	824	PNSSWMRGEPPKDPPTTSGPQT VTSRPNISPINPGRLLSDYSPRFQ RCQTTQGRPLPWSFTLSGKSRFS GEGATWGLKT
20916	51284	B	21039	1	1596	
20917	51285	B	21040	155	2206	
20918	51286	B	21041	1	831	
20919	51287	B	21042	75	474	
20920	51288	B	21043	38	1009	
20921	51289	C	21044	335	481	
20922	51290	B	21045	66	652	
20923	51291	B	21046	1	673	
20924	51292	B	21047	1	451	
20925	51293	B	21048	74	3516	
20926	51294	B	21049	783	3463	
20927	51295	B	21050	1	807	
20928	51296	B	21051	41	1700	

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20929	51297	C	21052	18	381	
20930	51298	B	21053	1	3147	
20931	51299	B	21054	1	2586	
20932	51300	C	21055	756	1403	
20933	51301	B	21056	42	205	
20934	51302	B	21057	40	420	
20935	51303	B	21058	303	1170	
20936	51304	B	21059	1	2631	
20937	51305	B	21060	19	3093	
20938	51306	B	21061	23	241	
20939	51307	B	21062	84	1775	
20940	51308	B	21063	68	1542	
20941	51309	B	21064	74	2566	
20942	51310	C	21065	730	1023	
20943	51311	B	21066	67	1159	
20944	51312	B	21067	294	929	
20945	51313	B	21070	68	336	
20946	51314	B	21071	1	1992	
20947	51315	B	21072	1	4188	
20948	51316	C	21073	44	535	
20949	51317	B	21074	983	2636	
20950	51318	B	21076	289	1693	
20951	51319	B	21077	364	2393	
20952	51320	B	21078	471	590	
20953	51321	B	21079	1	1026	
20954	51322	B	21080	343	4253	
20955	51323	B	21081	1	819	
20956	51324	B	21082	648	894	
20957	51325	B	21083	1	1236	
20958	51326	B	21084	1	822	
20959	51327	B	21085	211	363	
20960	51328	B	21086	193	264	
20961	51329	B	21087	1	1260	
20962	51330	B	21088	143	3158	
20963	51331	B	21089	85	353	
20964	51332	B	21090	221	598	
20965	51333	B	21091	1	4878	
20966	51334	B	21092	171	362	
20967	51335	C	21093	320	408	
20968	51336	B	21094	1	1218	
20969	51337	B	21095	1	1761	
20970	51338	B	21096	315	1224	
20971	51339	B	21097	526	3482	
20972	51340	B	21098	41	4858	
20973	51341	C	21099	38	250	
20974	51342	C	21100	157	225	
20975	51343	C	21101	191	415	
20976	51344	B	21102	42	507	
20977	51345	C	21103	71	367	
20978	51346	C	21104	231	439	
20979	51347	C	21105	207	459	

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20980	51348	A	21106	1	429	
20981	51349	A	21107	184	544	VRLKILQLQRFKMYVQQLDL TYFLRKIKCTLENGIVMSNTEA ESGVQLKPGRWGASALYSSHHI IH*A*LLVPR*VSNVVCSSRNDT* TKNKDTKNRRK*PKSSSTRRGK* KRERKEKEVT
20982	51350	A	21108	3	1200	LSQKEEEDTFIEEQLEEEKLL ERERQLRHEEWLLREKQAQEE FRIKKEKEEAACKRQEEQERKL KEQWEEQQRKEREEREEQKRQE KKEKEKTFMWKPSVDLFSHLA SLRTPICQDKGNAYQEHPFEK KKKRSSLAIPEGAFGYPHLL AILGLRCSRKHNFPTSSPTLLIKS MFTTFGMEQCRDDYDPDASL EYSEETYYQQLDFYEDVLPF KNVGKVIQF/KGLFEIQQCPRGK HCNFLHVFRRPNNEFWAERDI YLSPTDRTGSSFGKNSERRERM HHDDYYSLRGRNRNPSPDHYS KRNGESERKSSRHGRGKSKRT SKSRERHNSRSRGRNRDRS SRGRGSRSSRSRSTRSRSSRSQ SSRSRSRGRRRSGNRDRTVQS
20983	51351	A	21109	789	907	
20984	51352	A	21110	236	1823	CPIQRQSPGPAQTGRWEPLPCT VPITLRMSEGGGAGKMAALE KMTFPKKMTFPEKPSHKYRA ALKKEKRKIRQELARLRDSGL SQKEEEDTFIEEQLEEEKLLE RERERLHEEWLLREKQAQEEFR IKKEKEEAACKRQEEQERKLKE QWEEQQRKEREEREEQKRQEK EKEEALQKMLDQAELENLGT TWQNPEPLDFRVMEKDGVN CPFYSKTGACRFGDRCSRKHYP FPTSPTLLIKSMFTTLGMEQC RDRDDYDPDASLEYSEETYYQQL DFYEDVLPFKNVGKVIQFKVS CNLEPHLRGNIYVQYQSEEEC QAALSFLNGRWYVAGRQLQC EF*TGDRWKMAICGLFEIQQCP RGKHCNFLHVFRRPNNEFWA NRDIYLSPTDRTGSSFGKNSERRE RMGHDDYYSLRGRNRNPSPD HSYKRNGESERKSSRHGRGKSH KRTSKSRERHNSRSRGRNRDRS RDRSRGRGSRSSRSRSTRSRSS RSQSSRSRSRGRRRSGNRDR
20985	51353	A	21111	289	366	

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20986	51354	A	21112	1	1289	
20987	51355	A	21113	60	367	EELGYAGRGMGARQPPARKA VSPQLQERAEPVGGSPG*GWRSRP STHGIAISHGGPACSLCSLHFTFF VDFPSLFSPICLPEGWDWQQEQ PCLLYLSSPRCTQA
20988	51356	A	21114	1	653	RRRGSAAAGGAAERKAEVGA MNMAGGKAGKDSGKAKAKA VSRSQRAVLQFPVGRHRLK TRVTSHGRVVGATAAVYSAAI LVEYLTAEVLELVAGYAS/KDLQ SKSVSLPRHLQLAIPWVIEELDS LIQGLP*AGGGVIPSHPHKS/LIG KEGDSKKTALEGMILLTQPLSLP RHLYCNWDKKNNGDMWNFLP PVKWKSIDNYCRHDKRNICMF LDSEV
20989	51357	A	21115	1	1019	SVCWAGGAPRAHSTRTHAWLG RPAMEPGSVENLSIVYRSRDFL VVNKHWDVRIDSKAWRETGRP EPIQVASVEESGSDSGLC/HHSR FCHQLDFSTGALCVALLV/LGG LPGSTGLPRELRAILPLLQLRGH IQESRVSIVRWGGPGPRVSPTNL TPAFCAPCENPKPSLTGWSWG R*VWIGPAPSLIRHRPHAPGRTH QLRVHCSALGHPVVGDLTYGE VSGREDRPFMRMLHAFYLRIFT DTECEVECTPDPLPSLDACWS PHTLLQSL/DQL/VAGLGKQPPD P*TRG*GGPRPGSPSALLPGHGR PPPTTKPPEAEARQPGCLQWL SEWTLPEDS
20990	51358	A	21116	698	1472	RWAFRRGLSVDLGGSSAPLCP PATTARLDAEPHGSPLNSCLWE CSCLLQGIWAAGPSGLSLHYPP LSPLGSSPPSRPQRLVLRAGR GGWVGSGVGETMTSSYGHVLER QPALGGRLDSPGNLDTLQAKK NFSVSHLLDLEEAGDMVAAQA DENVGESSRTRGGGAGLGKGL SGVQTORASAVWESSRLKMLS RVGRASLGQRMATA*GRLQLYP HAPKSVTDRSPCSSQVTKSWNR GALQHSMIFTKRCLFQTLKE

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20991	51359	A	21117	50	1226	KMAEEVVVAKFDYVAQQEQ ELDIKKNERLWLLDDSKSWWR VRNSMNKTGFVPSTYYVGR/EN SARKASIVKLNKDTLGIGKVKR KPSVPDSASPADDSFV\DPGERL Y\DLNMPA\YVKF\YMAERED ELSLIKG\TKVIVMEKCS\DGW WRGTYNGQVGW\FPSNYVTEE\ GESPLGDHVGSLEKLA\AVVN NLNTGQVLHVQALYPFSSN DEELNFEK\GDVMDVIEKPEND PEWWKCRKINGMVGLVPQKL W*PLLQSIQLTSLGLTLTFQCGF IRPYIPGKFVGNPWYYGKVTRH QAEMALNERGHEGDFLIRDSES SPNDFS\SLKAQGKNKHKVQ LK\ETVYCIWQRKSCTME*LVE HYK\KAPNFYNVNGEKL\YL
20992	51360	A	21118	132	428	
20993	51361	A	21119	3	337	AKLAGAAVPPVCARGRAAPLAA AALPAARL\PSGAGPAGLVSDV RRRPFARE/PEPRVP/SQPPALSA LGALALKLFSSPPSCWSFSVKT GVLVPWIMCISWPYFLSGNLLT MMW
20994	51362	A	21120	438	1066	LNQKGKGGRGALKNDLVVAP PPSPRRGVRE*EALHVPDTPGPK KPRKRK*NQRQREAEK*TFPR EEEEARRETHGLPAPRPPPLCP/ PAASSAPRPGKGR*LLSAE GRARRRSAGASGGAGAAATAA AAAAPEHPRGSEPRQPAAPQ RERPRRPAPRLPPQCPRPKSGRA WTLQTTTGQKVCTGAGTRRA WRRAGAVRRRAFWA
20995	51363	A	21121	1	924	
20996	51364	A	21122	1	435	
20997	51365	A	21123	1	524	
20998	51366	A	21124	1	602	MKGKSPAHAQGPSFLHGGAG DQGRGRPITLYEDRGFGQRHY ECSDHPNLQAYLSRCNSVRVD SGCWVLYEQPNYSGLQ*FLRR GDYADHQWMGLSDSVRSCR LIPHASSHRLRIYEREDYRGQM VEITEDCSSLHDFHLSIHSFN VLEGSWVLYELPNYQGRQYLL RPGDCRW/CQDWGATDARVGS LRRARELY
20999	51367	A	21125	1	1239	
21000	51368	A	21126	298	408	
21001	51369	C	21127	92	241	

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21002	51370	A	21128	33	191	RDDPRVRPPPNST*PQEGPL* LIKCTSPQAPAPRTVHGPFY MRLIKMF
21003	51371	A	21129	3	1285	
21004	51372	A	21130	3	3468	QPGHTIYLLPTVICNLLPCELD FVYKGPMPINGTLKPGKEAALH TADTSQNIELGVLENFPLCKEL LIPPGTQNYMVRMLYDVNRR QLNLIRIVCRAEGSLKIFISAPY WLINKTGLPLIFRQDNAKTDAAG QFEEHELARSLSPLFCYADK EQPNLCTMRIGRGIHPGMPGW CQGFSLDGGSGVRALKVIQGG NRPLGIYNIIDVKKGRGRIIDT CMVIFAPRYLLDNKSSHKLAF QREFARGQGT
21005	51373	A	21131	3	451	
21006	51374	A	21132	2	107	LEGLEES/VRDRCKKEFTDLMI MDSRLLGPTSKVK
21007	51375	A	21133	2	158	PGIPVL/DYRTYTDGFFSLPSKD GDKDVMITGKLDILKPQNQHR VFTVESVI
21008	51376	A	21134	2	5632	FVRRTRCRESRCWPAETELDH WSLGEVVRGAMALQLWALT LGLLGAGASLRPRKLDFFRSEK ELNHLAVDEASGVVYLGA VNA LYQLDAKLQLEQVATGPALD NKKCTPPIEAS/QCHEAEMTDN VNPLLLVDPPRKRLEVCQQLLK GICALRALSNISRLFYEDGSG EKSFVASNDEGVATVGLVSTG PGGDRVLVFGKNGPHDNGIIV STRLLDRDTSREAFAYTDHAT YKAGYLSNTNQFVAAF
21009	51377	A	21135	168	5568	AREKCGGAMGAGSSTEQRSP EPPEGSSTPAEPESGGGPSAEA APDITADPAIAASDPATKLLQK NGQLSTINGVAEQDELSLQEGD LNGQKALNGQALNSQEEEE VIVRQVDHIDSESDVSRDSDTE MTTKSAVVHDI/TDDGQETPDI IEQIPSSSNLELTQPTESQAND IGFKKVKFVFGFKFTVKKDKTE KPDTVQLLTVKKDEGEAAGA GDHQDPSLGAGEAASKESEPK QSTKEPTELKREQ

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21010	51378	A	21136	807	1162	ISYHGRRRRRPQ/PVGPLGSCRS *SSRRWSTTGRTTFRAGWKSCS TPPSTSSLPTSTGTW*GPGTSAL LPPTPLPPPRAAATPCACACASE SRMPAARALGLRVRRRLLEGRS GKDTQG
21011	51379	A	21137	1	562	
21012	51380	A	21138	1	423	
21013	51381	A	21139	1	1871	MTTFKEAMTFKDVAVVFTEEE LGLDLAQRKLYRDVMLENFR NLLSVGHQAFHRDIFHFLREEK IWMKMTAIQREGNSGDKIQTE METVSEAGTHQEWFSQQIWEKI ASDLTRSQDLVINSSQFSKEGDF PCQTE/ARTICNSHKTEI/FPRA/I GYKPSFSDVSHDFHQQLHSGE KSHTCDECGKNFCYISALRIHQ RVHMGEEKCYKCDVCGKEFSQS SHLQTHQVRVHTGEKPFKCEVC GKGFRRSALNVHH
21014	51382	A	21140	1056	2988	FCILIGDKIQTEMETVSEAGTHQ EWSFQQIWEKIASDLTRSQDLV INSSQFSKEGDFPCQTEARTICN SHKTEIFPRAIGYKPSFSDVSLF DFHQQLHSGEKSHTCDECGKN FCYISALHMHQVRVHMGEEKCYK CDVCGKEFSQSSHLQTHQVRV TVEKPFKCEVCCKGFSRRSALN VHHKLHTGEKPYNCEECGKAFI HDSQLQEHQRIHTGEKPFKCDI CGKSFCGRSLNRHSMVHTAE KPFRCDDCKSFRQRSALNSHR MIHTGEKPYKCEECGKGFICRR DLYTHHMHVHTGEKPYNCKECG KSFRWASCLLTSSESHSGIEKP FKCEECGKGFYTISQCYSHQR SHSGEKPYPKCEECGKGYKRRRL DLDFHQVRVHTGEKLYNCKECG KSFSRAPCLLKHERLHSGEKP QCEECGKRFTQNSHLHSHQR/V HTGEKPYKCEKCGKGYNSKFI LTHQVRVHTGERPYNCKECGK SFGWASCLLKQRLHSGENPFK CEECGKRFTQNSQLHSHQVRV TGEKPYKCEECGKGFWSST/R LTHQVRHSHRETPKCEQHGK NIVQNSFS/EKLPEKVHQC*KK PYKCEDL/CGKGYNNRL*ILDM HQR/VHMGECTWKRECDMCF ISQASSLRLHQN/VHVGEP

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21015	51383	A	21141	154	1470	KDGDHMGYTYKVIERILEIGAF RPHMSLGQLQSARGVACLGCK GTCSGFEPHSWRKICKSCINAA KRTTA*HLT*KNDRLGRWLR DSKYSTLHLLG*KAGTASGFYK RNP ^M MILTNPATGKDPFTDTIT YEWGSPWEFTQETGDCSYMGA HSPREEGSQLTGHQRGAFYRA ARPAHAPGLPIYDQDPLALPVD FWRNELKTEWKEFVKIKYKSE GPSALGEVALPGQWGLAPRKE GE/GSRKKPEGGRPR/PAATTNG SLSDPSKEVEYVCELCKGAAPP DSPVVYSDRAGYNKQWHPTCF VCAKCEPLVDLIYFWKDGAP WCGRHYCESLRPR/CAPACDEI\ IFAEDYQRVEDLAWHRKHFC EGCEQLLSGLGVHRHPGVQLL VPQLAASPKRSLKGCTPQPESP GIPTKDKPGCARDPSLRVPDV TSKPSEINQ
21016	51384	A	21142	1	1332	
21017	51385	C	21143	147	272	
21018	51386	A	21144	160	374	ETPVSSRCEKHVSSPHLCPGIHR AVSLSSHSTCGRSWRSELHGPQ STNLSGNTLPLHFLFGAWQTG VFKM
21019	51387	A	21145	3	4366	LGAQQRELOEALGARAALAL LGRQLQAERRGLDAHERDVRE LRARAAASLTMHFRATGPAA PPPRLREVHDSYALLVAESWRE TVQLYEDEVRELEALRRGQES RLQAEEETRLCAQEAALRREA LGLEQLRARLEDALLRMREEY GIQAEERQRAIDCLEDEKATLT LAMADWLRLDYQDLLQVKTGL SLEVATYRALLEGESNPEIIVW AEHVENMPSEFRNKYYHYTDS LLQRENEWNLFSRQKAPLAS
21020	51388	A	21146	1	4617	RVIDCLEDEKATLTAMADWL RDYQDLLQVKTGLSLEVATYRI VEHVAVEGVSKLWKPLWQKS QSLVISSGVSTGGRLNLERLRR GPTPLASTESVKQVLVNNRMII DDEMVKTLAMSRTCAPNPLT ADVKTWSRSYSEDAATGPVL GVASTVALLEGESNPEIIVWAE HVENMPSEFRNKSYHYTDSL QREINERNLFSRQKAPLASFNI SSALYSNLSGHRGSQTGTSGG DARRGFLGSGYSSSATT

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21021	51389	A	21147	2	435	
21022	51390	A	21148	1	1233	MCEEETALVCDNGSGLCKAG FAGDDAPRAVFPSIVGRPRHQG VMVGMGQKDSYVGDEAQSKR GILTLKYPFIEGHITNWDDMEK KKEAEELARNMAIQQELEKEK QRVAQQKQQQLEQEQFHAFEE MIRNQELEKERLKI VQEF GKVD PGLGGPLVPD/SGEALLRCVPHL NSLIHTAFRLSHNCKAS*ATCG GQVLETWSTEQLRKYSHNRWI APCGGA WAAVPTVSPVSCQH CPGSGDMWNSLWKTDEE*YH YPCSHPPAKCWV*LLQHRERR RTFPHGTSGAGPHHTGLDSCQF *AVREHGVRI/GIHETTYNSIMKC DIDIRKDL YANNVLSGGTTMY GIADRMQKEITALPSTMKIKII APPERKYSVWIGGSILASLTFQ QMWISKPEYDEAGPSIVHRKCF
21023	51391	A	21149	2	1273	PRVPRVPRVPRVSLGEEPLIPSV LRSPAHSATHMCEEETALVC DNGSGLCKAGFAGDDAPRAVF PSIVGRPRHQGVVMVGMGQKDS YVGDEAQSKRGILTLKYPFIEHG IITNWDDMEKI WAPLLTLMEL RVSTWKRHPITL TEAPLNPKAN REKMTQIMFETFNVPAMYVAI QAVI.SLYASGRITGVLDSGD GVTHNVPIYEGYALPHAIMRLD LAG/RDLTDYLMKIL/AKRGGY SFVTTAEREIVRDIKEKLCYVAL DFEK*WATAASSSSLEKSYELP DGAGLSPIGKWTLP/CPETLFQP YFISNGVPLEFNDDNLTPSMK\ CDIDIP*GLICPTMFLSGGTTTHV PWALLDRIQKENPSGPPGTMK IKNAPPEREVTSVWD/LGGSILA SLSTFQA\MWISKPEYDDAGPSI VHRKCF
21024	51392	A	21150	95	674	

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21025	51393	A	21151	1	1536	MGGGEQGLTLRTAENQGLQVCP GEAGSSLGFSGNTPTNGLPARG DQTSYRDFWSGPQFPDLSLRTA APGAREQCCTHGGEGSTLEGS PDVPQDLFSPTLGFYGSTYPELE QGMLGGH*G/PAENQGLQVCP GEAGSSLGFSGNTPTNGLPARG DQTSYRDFWSGPQFPDLSLRTA APGAREQCCTHGGEGSTLEGS PDVPQDLFSPTLGFYGSTYPELE QGMLGGHVEASREYQMLSHV GNPDYPHALATEQATSPSTESG SAGFKGVALAMLSKITMCVRIG ILVFQDDQGSCKAFSTTGMG LVTYLLTCRAW SRLQCGASYR AHDVNVLPGCSGPAALLGDW FSLHSSDAVLPAGQGMLSQG EADACITLPHLPPSREVVFLLGL EAGGLIPGAEGPPDMGLVRGP PAVAAGPPRWLSPEFCLLQYS EEEGCKEPLWLKVEAEVSTLYR FMPTGFTRGPFNIEHREWNTT ATWTRMISNHNKHSQRGRKMT ARLPCGGAPHFSDRTDDKWRR SSLLTRSGCQTERLLTSQTEPLP AGGSPHFSNGETGQRRSSPPQR GCDRPQALLTSKTEQQRKSASH ISYDERPGKDAPHFLDGMVAG KRRSSLRLGSQA

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21026	51394	A	21152	689	2176	PATSPTRAMAPQPSAPAAASMLL PCPECPSPGPRFMTCCLSVSTFCS PSLRRPPGSIKSSGLGGGSSRT SCRLSGV\ALGAGSCRLGSAAGL GSTLGG\NSYSSCYFSGSGGGY GSSFGGV\DGLLA\GGEKA\TMH NLIDFLAS\YLDKVP\CPWKEAN TELEV\KIRD\WYQR\APGPAR DYSQYYRTIELQNKILATVD NANILLQIDNARLAC\ADDFRT K\VFETEQA\RLVSVEADINGL\A RVL\DELTLARADL\EMQIENLK EEAWPTLKERTTEGRRLNALR GQVGW*\RSMLEMDAA\PGVDL SRILNEM\PCVDHRVTRCINRP GAELKLGSGGWTEELKREVAT NSELVQSGKSKISEL\RRMTQAL EIELQSQLSMKA\SLEGNLGGD RATAYCVQLS\QIQGL\IGSGED QLAQLR\C\EMEQQ\NQDYKILL DVKTRLEQE\IATYRRLLE\VED AHLTQCKKEPVTTTRQV\RTIVG KRSRD\GKVILLPRSRFHQTTR
21027	51395	C	21153	58	252	
21028	51396	A	21154	2	190	
21029	51397	A	21155	2	432	KMADGV\DHIDIYADVGEFNQ EA\YGGHDQIDLYDDVISPSAN NGDAPEDRDYMDTPPPVPGYG PPPGPPPPQGGPPPPPGPPPRPP GPLGPPLD\TLAPP\HLP\G\PP\PG \APPPA\PHVEPSFLFLPPINS\GH GLHSDRPRFH
21030	51398	A	21156	1	1070	MGGIGARAAAAGKRRRRARA PPGLPPTSDGGGGA\AAASLR RLHAAPP\PGPSAAGSASRVPTI GSEAAPAREDRRLQHSGRV\RAS GSPRLTRPRPVKRRGRTRGGGA PRQGSAA\PRGGKGAHSAVAS ARAAAGPGSASRPHGAASAAG TWALTYLV\ELFADIRVNVYV HAVRILPSACAAAAAA\SCRF ALVGVGSEASSKLMDLLPKR ELHGQNPV\VTCPNKQFLSQFE MQSRKTTQSGQMSGEGKAGPP GSSRAAFPQGGRG\RG\PGGA VPGGDRFPGAPGGPPPPPFQD PSVNSDPVCGTFG/EH*\PPGYQT PSNLSVRPMAKPKPEGTDLSRS REGFFKSRFAPN

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21031	51399	A	21157	63	1750	MKMAGGVNHIDIYADVGE*FN QEAIEYGGHDQIDVHDDAISPS ANNGDA PEDRDYMDTLPPITVG DDVGKGAAPNVVYTYTGKRIA LYIGNLTWTTDEDL TEAVHS LGVNDILEIKFFENRANGQSKG FALVGVGSEASSKLMDDLKPK RELHGQNPVVTPCNKQFLSQFE MQSRKTTQSGQMSGEGKAGPP GGSSRAAFPGGRGRGRFPGA VPGGDRFPAGPGGPPPPFPA GQTPPRPLGSFQGGPGPPGPP PGQVLPPLAGPPNRRDRPPPPV LFPQGPFQPPPLGPPGPPPPV PGYGPFPFPFPQGGPPPPGPF P\PRPTGSLGHPLTLAPPASFP GP\PPGAPPPSPHVNPAFFPPPT NSGMPTSDSRGPPPTDPYGRPP YDRGDYGPGRMDTARTPLS EAEFEIMNRRNAISSAISRAV SDASA/GVDYGSATETLVTASLI KTIPKYPADD/CTKFLISSLDQ CLHGIESKSYGSGRRRERSRER DHSRSREKSRHRKSRSDRHH YYRERSRERER\HRDRDRD\RD RERDREREYRHR
21032	51400	A	21159	1	96	TNFKSGLLGLAED*HCPIASE AP*TTTDAEL
21033	51401	A	21160	1	1056	MWKGPGLDMYKGSSVSPKTS DILGRDTELLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPFCQ FTRAWNRTQVPDETAAGTY AAQSGDLPEINPLSSCSLLHE KDPPITASGPQTDQPKHLTNFK SGFRGVRP/LQGRPLPWSFTLSGK SRFSGEGASTPTSLCVSTSPFP WGARTQPLLLHPEWQ/CPLF* RSKYPNVLSCPSLFPRLDLS L/SAQSLISAPQLISLCPNPLFPC PDLLSLHPNPLFRPNPFAFLE GACYKCKQSGHQAKECLQPGI PPKLRPICAGPHWKSDCPTHLA ATPRAPGTLAQGSLTASQIFLA
21034	51402	C	21161	283	408	

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21035	51403	A	21162	3	505	ILNPVSGFLFLFSSPLSLNLSL NLFLLSILAPHFNLSILLISIPFIFP LEIELNSPGSHSQSPWNSGPR SDSFPDLLGLAAEE*HCP IASEA FSQTYRAYLSLSLSLSPEPPT AGDGVTHSSPVASTTITVLGQT /SKPAQCWPLPKVCCCHSLTSD YVHPRP
21036	51404	A	21163	164	420	LANFCEESGAGEPGSHSQSPWN SGPRLSDSFPDLLGLAAEDRHC PIASEAPLLQKSLYKSPCTSTI S*CCIPRSGISELSVN
21037	51405	A	21164	50	298	
21038	51406	A	21165	49	433	SSSGIWPSHSQSLRSPAKLLS RFRCSLSLLCLATLLLVWQP LPEPELWPKA/HLTDSFPDLG LAAED/W/HCP IPSEAP*TLTDAE LRVTLTVEGKSIFPGAGKEVTL ESYWVSLTLFLICYMII
21039	51407	A	21166	282	374	CDLFLPHPN*SMYFVISPTPKKV LCNSPHT
21040	51408	A	21167	71	333	I.RSGDLPWEINPLSSCSLFREED PPTTSGPQTNPQKEHLTNFKSA AED*RCQFASEAP*TITDAKLRV SLTAEGLLATLFLNPKPEY
21041	51409	A	21168	113	342	AFGCFITGVGRVTDSDGPLYTG PWAPGSHSQSPWNSGPRLSDF PDLLGLAAED*HCP IASEAPFLT LIFLLCVIQ
21042	51410	A	21169	301	608	TFTPLKSYIKAPSSAGPVAEQE MTPEGKVGAGPE*LTWKNQFL FY
21043	51411	A	21170	2	724	FLVSLMLPPAVVMLNHCYSLIF TNALVKRLFawnMLSELATCA GNLATGPRNARSPGFLSCVPS VRDPTGNQTVQLTWQPLPEPLE I.WPKA/HLTDSFPDLLGLATED *HSP IASEAPWAIMDAELRVTL TVEDRDS SSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSPCD LFLPHPN*SMYFVISPTLKKVLY NVTHP*EVS L*FSPPLRMVFVRS IPCQNIALNSTAYP
21044	51412	A	21171	442	501	

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21045	51413	A	21172	266	1003	SCMCLALDPCNHGEGHQPDFS GVKFRRHGADNHEASAAATATT AAATTVAIAAAAAAAAAAAR VTLTGSHFQSPWNSGPRLSDFS PDLLSLATED*RCPIASEVPWTI TEAELRVTLTVEGKSIPLIDTG ATHSTLPSFQGPVSLAPITVVG DGQASKPLAKTPPLW/CQLGQH SFMHSFLVIPHL/CPFLIRGRNII TKLSIASLTIPGSTANISLVAFFP NPKPPLCLPTSPQYHPLPQDLPS A
21046	51414	A	21173	2	245	LTALLRKS LDPRLISTGENTQTA ETMGPLSAPPCTQHITW/KGLLL TAETPKPSISSNNLNRPGGHGRL CALILLILEDSG
21047	51415	A	21174	3	324	
21048	51416	A	21175	3	552	
21049	51417	A	21176	3	435	
21050	51418	A	21177	3	1459	GAVRTWGRGFQTEKCCQASLLN FWNPPTTAQVTIEAEPTKVSKG KDVLLLVHNLPLNLAGYIWK GQMKDLYHYITSYVVDGQIIY GPAYSGRETVVSNASLLIQNVT REDAGSYTLHIVKRGDGRGET GHFTFTLYLIPWTLTYL*RSLA QVSHYETPGKTA PPGCSTA**L N*PPDLTLFSPVLFLKYVPVPGQ AFQYPKGLKTI GSSITHL*DV/LG KGSRENIPRAAK*D*N*EDSST ACSK*GPQVETPKPSISSNNLYP REDMEAVSLTCDPETPDASYL WWWNGQSLPMTSLQLSKNK RTLFLFGVTKYTAGPYECEIRN PVSASRSDPVTNLNLLPKLPKPYI TINNLNPRENKDVLAFTCEPKS ENYTYIWWLNGQSLPVSPRVK RPIENRILITQCSREMKQGPY QCEIQ/DRYGG/RSYPVLTLECP/ HIITKHSGLYACSVRNSATGME SSKSMTVKVSAPSGTGHLPGLN

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21051	51419	A	21178	3	1445	IRADPAHELENCSCPGKRLSTE RGRTAQLTAVLREFLDPRLISTE ENTQAAETMGTLSPAPCTQRIK WKGLLLTASLLNFWNLPTTAQ VTIEAQQPKVSEKGDVLLVHN LPQNLTGYIWKQGMRDLYHY ITSYVVDGEIIYGPAYSGRETA YSNASLLIQNVTRDAGSYTLH IIKGGDDGTRGVTRFTTLHLET PKPSISSNLPRETMEAVSLTC DPETPDASYLWWMNGQSLPMT HSLKLSSETNRTFLLGVTKYTA GPYECEIRNPVSASRSDPVTNL LPKLPKYITINNLNPRENKDVL NFTCEPKSENYTYIWWLNGQSL PVSPRVKRPIENRILILPSVTRNE TGPYQCEIRDYGGVRSDDPVT NLVYGPDLPRIPSFYTYRSGE VLVLSACSADSNPPAQYSWTINE KFQLQGQKLFIRHITTKHSGLY VCSVRNSATGKSSKSMTEVEV SGKWIPASLAIGF
21052	51420	A	21179	3	1380	TAQLTAVLREFLDPRLISTEENT QAAETMGTLSPAPCTQRIKWK GLLLTASLLNFWNLPTTAQVTI EAEPTKVSEKGDVLLVHNLPQ NLTYIWKQGMRDLYHYITS YVVDGEIIYGPAYSGRETAYSN ASLLIQNVTRDAGSYTLHIKGG DDGTRGVTRFTTLHLETPKP SISSNLPRETMEAVSLTCDE TPDASYLWWMNGQSLPMTLSL KLSETNRTFLLGVTKYTAGPY ECEIRNPVSASRSDPVTNLNLPK LPKYITINNLNPRENKDVLNFT CEPKSENYTYIWWLNGQSLPVS PRVKRPIENRILILPSVTRNETGP YQCEIRDYGGVRSDDPVTNLV YGPDLPRIPSFYTYRSGEVL LVLCGTLNPPAQYSWTINEKF QLPGQKLFIRHITTKHSGLYVC SVRNSATGKSSKSMTEVESAY SSSINYTSNGNRN

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21053	51421	A	21180	2	1341	TEGGRTAQLTAMLRQLLDPRLI STEENTQAAETMGPLPAPSCTQ RITWKGLLLTASLLNFWNPPTT AEVTIEAQPPKVSEKGDVLLLV HNLPQNLPGYFWYKGEMLDLY HYIISYIVDGKIIYGPAYSGRET VYSNASLLIQNVTRKDVAGTYT LHIIKRGDETREIRHFTFTLYL ETPKPYISSSNLNPREAMEAVR LICDPETLDASYLWWMNGQSL PVTHRLQLSKTNRTLYLFGVTK YIAGPYECEIRNPVSASRSDPVT LNLLPKLPYITINNLNPRENK DVLAFTECPKSENYTYIWWLN GQSLPVSPGVKRIENRILPSV TRNETGPVYQCEIRDYGGIRSY PVTNLVLYGPDLPRIYPSFTYYR SGENLDLSCFTESNPPAEYFWPI V*GKFQSQGKLFIPQITRNHSG LYACSVHNSAAGKEISVSLFRH
21054	51422	A	21181	1	1532	MTQFPMDKRGGRSRVAITNT AVTSLEWVPFHAFAIPRSTLVS QQLSTERGRTAQLTAVLREFL DPRLISTEENTQAAETMGTLA PPCTQRJWKGLLLTASLLNFW NLPTTAQVTIEAEPKVSSEKGD VLLLVHNLQNLGTGYIWWYKGA MRDLYHYVTSYVVVDGQIIKYG VPAYSGRETAYSNASLLIQNVAT REDVAGSYTLHIKGGDGTGRV GRFTFTLHLETPKPSISSNLNPR ETMEAVSLTCDPETPDASYLW WMNGQSLPMTHSLKLSETNRT LFLLGVTKYTAGPYECEIRNPV SASRSDPVTNLNLLPKLPKYITI NNLNPRENKDVLNFTCEPKSEN YTYIWWLNGQKPP/VSSPRVKR PH*KTGSLIPTVFTRNETGPVYQ CEIRARYGGVRSDDPVTNLVLY GPDLPRIYPSFTYYRSGGKSSY LSCFCGTSNPPAQYSW/TIN*K VFSLPGTKALYSRHITTKHSGL YVCSVRNSATGKESSSMTVE VSDWTVP
21055	51423	B	21182	28	29751	

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21056	51424	A	21183	158	1660	EASLLEDDDGMYVLRPLTSHQ YRTAQLRAMLRKFLDPRLSSSTE ENTQAAETMGPLSAPPCTQRIT WKGLLLTASLNFWNPPITTAQ VTIEAEPKVKSGKDVLLLVHN LPQNLAGYIWKGMKDLVYH YITSYVVDGQIHYPAYSGRET VYSNASLLIQNVTRDAGSYTL HIVKRGDGTRGETGHFTTLYL ETPKPSISSNLYPREDMEAVSL TCDPETPDASYLWWMNGQSLP MTHSLQLSKNKRTLFLFGVHK VHCRDPMECEIREPS*VASRS*P SSPWNLPLKLPKPYITINNLLNP REKKDVLAFCTCDPKSRNYTYI WWLNGQSLPVSPRVKRP/ENR DPSFLPSVTRNETGPYQCEIRD RYGGGIRSYPVTLNVLYGPDLP RIYFPISPIYHFREENLRTLSCFC GTFNPPGRVFLGTINGGSFQVIQ GQKALYSRPTTTKHSGA/LYAW LCSVTSRPLAWESSQIPWTVVKV SGSFQGTGTSSWGLNPL
21057	51425	A	21184	927	1378	QPPTLRSWDCWFAWGKRQLM SSP/STEPQVCFTEGHEIDFLLG TGMFAFSVLISCPG*LSSRSVTIR GILG*PVTRYFSHLLSCNWETLL FSHNAKTQGGTTLTPKPSKSH RPWAVRGLAPGAAA/VLNFSP GLSCLPTGQGLGPAAHHA
21058	51426	A	21185	1	221	ILLAQLESQDGDILRORDEFDLL VAGEICRFSALIEELEKNERPA RELLTVRPEPEPCPTCAVLRLLH LCLA

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21059	51427	A	21186	335	1963	VCDPALPPWAKQREWALEGSH SSRTSMGLLVASVTSLSGRWKF NCP/ICVQGTLEKAGSLNCG/H KNFCRACTRYCEIP/GPD/LEE SP/TCPLCKEFP/PSFRPNWQ LANVVNIERLQLVSTLGLGEE DVCQEHGEKIYFFCEDDEMQL CVVCREAGEHAHTMRFLDA AVAPYREQIHKCLKLRKEREI QEIQSRENKRMQVLLTQVSTKR QQVISEFAHLRKFLEEQQSILLA QLESQDGDILRQRDEFDILLVAG EICRFSALIEELEKNERPAREL LTDIRSLIRCETRKCRKPVAVS PELGQRIRDFPQALPLQREMK MFLEKLCFELDYEPAHISLDPO TSHPKLPLVPRITQRAQFS*QM GRTSPDNQ/RFDRA/TCVSRPT LGITGGRHTWVVSIDLAHGGSC TVGVVSEDVQRKGELRLRPEE GVWAVRLAWGFVSALGSFP/IR LTLKEQPRQVRVSLDYEVGVW TFTNAVTRPIYTF/TA/STRKVI PFFGLWGRGS/SFSLSSLRSSSY LLSSKYRTHINPSTMWT
21060	51428	A	21187	217	397	
21061	51429	A	21188	529	1526	YCGRVGELAAAGELVFLWSRVG PQNPRSSRLPPITLAMFLTRSEY DRGVNTFS/PEGR/LFQVEYDIEA IKLGSHSQLAPRHREGV/ALAV/ EKRIYLP/PLMGAQAGI*GKLLG DLMLHIGLLPIEWGLICLMLKT FNSIKSRVGRHR/YPW/GSPYNG GH*QWESFEPKLCPNLGFSFG EEDAESRVPM/SRPLGSSHLFIW EELYEKGT/PSLFP*GTPFWGPFV PVWMA/SQFGSGFQRGAPRAP LPRKFPTSPMTFERS/SPSSPHF SLKQVMGGRKLNANQ/TEIPRT VPALAE/NFPHCSQRKKLEEVQ GHFKESWILRTSLGTISVLNNVP
21062	51430	A	21189	211	382	TSVSPSPVPLPC*RHPGEPTGN NASNGTSSSRDESRRPPRVVPPP QTAVAITLSTA
21063	51431	A	21190	3	96	FFFPQKYD*DR*EHPFRHKT/LR NWRVGAQ
21064	51432	A	21191	1	1320	
21065	51433	A	21192	1	339	

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21066	51434	A	21193	289	3694	MAFVFPVPIESYSHVLAEFESLDP LLSALRLDSSRLKCTSIASVRK WLALGSSGGGLHLIQEGWKH RLFLSHREGAISQVACCLHDDD YVAVATSQGLVVVWELNQERR GKPEQMYVSSEHKGRRVTALC WDTAILRVFVGDHAGKVSIAIK LNTSKQAKAAAFVMPVQTIT TVDSVVQLDYLDRLLISSLT RSFLCDTEREFWKIGNKERDG EYGACFFPGRCSGGQQLIYCA RPGSRMWEVNFDEGEVI
21067	51435	A	21194	2	128	
21068	51436	A	21195	1041	2238	LLHPAQRSLSKDGTGESLEDA LMGEEGKPEINQQLSLESME ELALEKYPIAAPLPYPEKSS GVGNPEAKILSGTPPYKRRV LVTIENHTPLVELSEYLGNTLS EILDSPWEGAKNVYKCECDQ NFSHSHYLVHLQKIHSGEKKHK CGDCGKIFNHRANLRTTHRIHT GEKPYKCAKCSASFQSHSLSR HMNSHVKEKPYTCSICGRGFM WLPGLAQHQKSHSAENTYEST NCDKHFNEKPNLALPEETFVSG PQYQHTKCMKSFQSLYPALSE KSHDEDSERCSGCGDNFFFSK FKPLQCPDCDMTFPCFSELISHQ NIHTEERPH*CKTCEESFALDSE LACHQKSHMLAEFFKCTVCGK TFKSNLHLITHKRTHIKKHVK
21069	51437	C	21196	156	389	

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21070	51438	A	21197	1	2466	<p> MLSRLFRMHGLFVASHPWEVI VGTVTLTICMMSMNMTGIAG LFTIFSSFVFSTVVIHFLDKELTG LNEALPFLLLLIDLRASTLAKF ALSSNSQDEVRENIARGMAILG PTFITLDALVECLVIGVGTMSGV RQLEIMCCFGCMSVLANYFVF MTFPPACVSLVLELSRESREGR PIWQLSHFARVLEEEENKPNPV TQRVKMIMSLGLVLVHAHSRW IADPSPQNSTADTSKVSGLDE NVSKRIEPSVSLWQFVLSKMIS MDIEQVITLSALLAVKYIFFE QTETESTLSLKNPITSPVVTQKK VPDNCCRREPMLVRNNQKCD VEEETGINRERKVEVIKPLVAET DTPNRAFTVVGNSLLDTSSVL VTQPEIELPREPRPNEECLQIL GNAEKGAFLSDAEIQLVNAK HIPAYKLETLMETHERGVSI RQLSKKLSEPSLIQYLPYRGY NYSW*WGACCENVIGYMPPI VGAGPLCLDEKEFQVPMATT EGCLVASTNRGCRALGGGAS SRVLADGMTRGPVVRPLPRACD SAEVKAWLETSEGFAVIKEAFD STSRFARLQKLHTSIAGRNLYIR FQSRSGDAMGMNMISKGTEKA LSKLHEYFP*NCRF*AVSGNYC TDKKPAAINWIEGRGKSVVCET VIPAKVVREVLKTTTEAMIEVN INKNLVGSAMAGSIGGYNAHA </p>
21071	51439	A	21198	236	3022	<p> GEGSFRSATALTGARLSVGAGV RWPLVRSGGKDSVATMLSR LFRMHGLFVASHPWEVILGTVT LTICMMSMNMTGNKICGWN YECPKFEEDVLSSDIJLITRICA ILIYIFQFQNLRLQSGKYILGIA GLFTIFSSFVFSTVVIHFLDKELT GLNEALPFLLLLIDLRASTLA KFALSSNSQDEVRENIARGMAI LGPTFTLDALVECLVIGVGTMS GVRQLEIMCCFGCMSVLANYF VFMTFFPAC </p>
21072	51440	A	21199	1	450	<p> CKSRGSNLRVHFKNTRETAQAI KGMHIRTATKYLKDVTLQKQC VPFRRYNGGVGRCAQAKQWG WTQGRWPKSAEFLVIEHIQV NKAPKMRRRTYRAHGRJNPYM SSPCHIEMLTEKEQIVPKPEEEV AQKKKISQKKLKKQKLMARE </p>

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21073	51441	A	21200	1	876	
21074	51442	A	21201	1	1725	
21075	51443	A	21202	278	889	SVKMMVRYSLDPGGTPRKSC/KS QRGSNLRVPFKDHS*KLPQAHQ RVCHIRKSPTKYVKDVLHTRN QCVPIPDRYNG*QLGQVCCRHK QMGP GTTKGRW/PQKGV LKFL PAHALKTAE/SNAEL/KGLDVDS LVIEHIQVKNKAPKMMRRRTYR AHGRINPYMSSPCH/EMULTEK EQIVPKPEEEVAQKKKISPEETE RNKNLLARE
21076	51444	A	21203	1	1923	
21077	51445	A	21204	1	280	
21078	51446	A	21205	1	109	
21079	51447	A	21206	1	638	
21080	51448	A	21207	1	396	
21081	51449	A	21208	26	969	HGVGCRDGLPMECRFLCQIFM AFMQMNSYCARHKKATRRTV* /CRNQDMTESSQKWTGKGS AV EHLVESGEWTMHPARPVSACR CPSDCHVPLSPGACWPKLECLS EGSSYISDGKEYLFYLNVCGET EIQFCNKKQAAV/CQVKKSDTS QVKAAGRYHNQTLRPSESSWS LLFVVLVFFPGVHSPFSLDEALT LCPQNCLPPGTVSAPLNCVYPL ALSAVALAAGSELMECHRLV NSLEVSTAAQGSSTQFYACL CRLSTHLWKYSEESGRRLVCSF YQPSLNPALNLSFLVGTRLQE GAALLFIQSGFTIV
21082	51450	A	21209	1	465	
21083	51451	A	21210	217	453	
21084	51452	A	21211	1	840	
21085	51453	A	21212	1	663	
21086	51454	A	21213	176	957	DEPIGVLLSAPPAGTTT KIKADQ LHLQGAAPKICPCLQDGS LGQH YCFPVFSFRYYINLCQKIYKGPL GCSERASICRRTTTGDVQVLGL VHTQK/LGVIGPRVVVTTSKRY PCGGNKTASSVIELTCTKPVGR PAFKRFEIDSTCYFSDWSGAA CAVKPQEVQMVNGTITNPINGK SFSGLDIYFKLFRASGDMRTNG DNYLYEIQLSSTSSRN PACSGA NICQVKPNQDHF SRKVGTSDKT KYYLQGNPWLP TKFHI

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21087	51455	A	21214	3	7616	SPVEPRSPRAPAPSPPPPLPWRR DPVPGAAPSSRAPLASRPPRSSG PGAMGAAAGRSPHLGPAPARR PQRSLLLLQLLLVAAPGSTQA QAAPFPELCSVTWEAVDTKNN VLYKINICGSVDIVQCGPSSAVC MHDLKTRTYHSVGDSVLRSAT RSLLEFNTTVSCDQQTGNHRVQ SSIAFLCGKITLGTPEFVTATECV HYFEWRTTAACKDIFKANKE VPCYVFDEELRKHDNLNPLIKLS GAYLVDDSDPDTS
21088	51456	A	21215	2	184	VNCQPLGMISLMKR\PPGFSPFR SSRIGEIKEETTSHLRSEYKGR PPKAGAEPAEREVS
21089	51457	A	21216	1	203	
21090	51458	A	21217	1	1107	
21091	51459	A	21218	1	915	
21092	51460	A	21219	1	1932	
21093	51461	A	21220	2	746	

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21094	51462	A	21221	1	2157	MGFPLRPSPAHLSGRQQFPAK EERLLLSLTQESQSEEDCNDKD LFKAVDAALKKYNSQNSNNQ FVLYRIEATKTVGSDTFYSFK YEIKEGDCPVQSGKTWQDCEY KDAKAATGECTATVGKRSST KFSVATQTCQITPGGWFLWHC PGGKLTISDYPNSSRVLHCTQC VQGLNRRTRRHKTCPLQAAS QIEERIGFEGRPGLESFRAPCLL ASPFPCLEKGAEGPVVTAQYDC LGCVHPISTQSPDLEPLRHGIQ YFNNNTQHSSLFMLNEVKRAQ RQAAP/GREFSSMDTFEGYEGA EDMEKLAGPFPVG*QSRNLFQ IRFPGEERKHPGRKRRT*GSN GDRQHGEQACWGVHAG*LLR GRRLVSRRGARGPPPRRAAL PAVAPAPRLQSARIPERGDGDD GVRRWGHREAGS*GQS/LS/CN GIILIKEERLPCPFHCISLMKRPP GFSPFRSSRIGEIKEETTVSPHT SMAQAQDEERDSGKEQGHTRR HDWGHEKQRKHNLGHGHKHE RDQGHGHQRGHGLGHGHEQ HGLGHGHKFKLDDLEHQGGH VLDHGHKHKHGHGHGKHKNK GKKNGKHNGWKTEHLASSED STTPSAQTQEKTEGTPIPSLAK PGVTVTFSDFQSDLIATMMPPPI SPAPIQSDDDWIPDIQIDPNGLSF NPISDFPDTTSPKCPGRPWKSVS
21095	51463	A	21222	207	424	HHINCVLlyLQSHLRS/CEYQQA RPPKAGAEPAEREVSLTNWA ESSTPRHIAPTTASNLEMEGQE ERWDRI

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21096	51464	A	21223	170	1487	IMKLITILFLCSRLLLSLTQESQS EEIDCNDKDLFKAVDAALKKY NSQONQSNQFVLYRITEATKT GSDTFYSFKYEIKEGDCPVQSG KTWQDCEYKDAAKAATGECT ATVGKRSTTKFSVATQTCQITP AEGPVVTAQLRTCLG/CVWHPI IQRQSPDLEPILRHGIQYFNNNT QHSSLFTLNEVKRAQRQVVAG LNFRITYSIVQTNCSKENFLFLT PDCKSLWNGDGTGECTDNAYIDI QLRIASFQSNWDIYPGKDVVQ PPTKICVGCPRDIPTNSPELEETL THITITLNAENNAISYFKIDNVK KARVRVVAGKKYFIDFVAR\ET TCSKVESNEELTESCTKKLG/Q RLG/CNAEVVYVPWAEKKIYPT/ VFNCSTTGEWIFT*WKRPPRVF SPFRS/SRIGEIKEETVSHLRSC YKGRPPKAGAEPASEREVS
21097	51465	C	21224	21	281	
21098	51466	A	21225	204	441	QISQVLIHCNQK*VILTGNFLDT YF*TTFINKKIDELRLCA/CAVA HSYNTTLCKKPRWKDCLRPV QDQPVQHSETLSL
21099	51467	A	21226	333	604	SSDRITKPPSAEFLPLQRTFLHSL QDTVIELLH*DLETPLTVLQNH PSLPRIPAPPITLCPQTRWPHLR GHQGILAAASHILETALAIF

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21100	51468	A	21227	846	3269	GFMEVLRLDPIKKNSSSEKPAQS GFSRGNSPLSCPESVEASPAVNE KSVYSTHNYGTTQRHGCGRGLP YADHNYGAPPPPTPPASPPVQTI IPRSDLNGLPSPVEERCSDSPNS EGETVPTWPCGLSQDGFLLNC DKCRGMSRGKVIRLHRRKQDN ISGGDSSATESWDEELSPSTVLY TATQHTPTSTILTVRRTPKPKR KKSPEKGRAAPKTKKIKAFREG SRKSLRMKNPSSEAQNLDENTT EGWENRIRLWTDQYEEAFTNQ YSADVQNALEQHLHSSKEFVG KPTILDINKTELACNNTVIGSQ MQLQLGRVTRVQKHRRKILRAA RDLALDTLIIHYRGKVMLRQQF EVNGHFFKKYPYFVLFLLQNL NGVEMCDARTFGNDARFIRR SCTPNAEVRHMIADGMIHLICIY AVSAITKDAEVTIAFDYEYSNC NYKVDCACHGGRNCPIQKR S*CYRTATPTTSSKPTHHWSRD *T*KSIRRKELEMEQNEASEEN NDQSQSEVPEKVTVSSDHEEV DNPEEKPEEEKEEVIDDQENLA HSRRRTREDRKVEAIMHAFENLE KRKKRRDQPLEQNSDVEITTT TSETPVGEETKTEAPESEVSNSV SNVTIPSTPQSVGVNTRRSSQA GDIAAEKLVKPPPAKPSRPRPK SRISRYRTSSAQLRKQKQANA QQAELSQAALIEGGNSLVPTPT
21101	51469	A	21228	2	197	CRPPSPRPVRAARPARPQASF EPPRRMAP*SKRRRQSGRGPV RPSRVWARIKAPYSCCCQL
21102	51470	A	21229	4	488	GSYDINRQDTFQKDRQRVGP ASQKTEGFLRLLYSGLIAHCS LEILGRNDPPASASKVAETTDS GSLSLANT*PPTPR/VTSQTANA TSQAAPALPLGVSVPGRRAADPR PLLAWAPAPPGPGTSRNTHPAP DGLDMLVPIGDGVLGGNCFRN QCKSVSTS
21103	51471	A	21230	124	293	

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21104	51472	A	21231	239	1393	IYPQISFQKKFVFFSEALCTA RAEEDPIGLLNNPRTSRYSRL KPNSSLGGSESRTQMGLPPP PKSPDGARVPVPGCIKEAGPARG RSRLAPNPGALRRG/VGLGR*S ARI*GLVSKAAAGQGEARRGE AT*ARGALGRTTAGSFNAGWL TLDGARQQGRQTPTRIPSCVA DNAAGPSRTTTPD/EALRPLRG GPACTAPASFSDRAPYSASSAPS EGRWPSRGFPPI/PLYSQLPETR SHEWQAASKIQPRKASTSQ*SA RMEAT*QQWAGPPAEP*SLWFP RLARRSVVHWRTPY/ISSSITSLP PVAAGIPEDSGPGSTQSSSRPGN TSSSSRPPPPPPPP/QPLPPPPA GLASRPVRRRRPARPQASFSR EPPPRRMAP
21105	51473	A	21232	107	234	
21106	51474	A	21233	224	227	LPQPGPGRRRACLQASPRQYS RLPGRPPPSG*SW
21107	51475	A	21234	67	607	QRSWAGPGAAGTRPPARG RRRQPGNVDPRRRAPQLRSQM QVAMARATTATGNRLWPGLLI MLGSVCHRGSPCGLSTHVEILL LEHQDAYQAGIVFPDCFYPSIC KGGKFHDVSESTHWTPLNAS VHYIRENYPLWEKDETEKLVA LFGITSHMAADVSWSHLGLEQ GFLRTMGA
21108	51476	A	21235	54	193	
21109	51477	A	21236	1275	1764	STKCQFYSHLLLLFSASESKQLL LYSAFFRYVPVKDLLGIYEKLYI CFISLLQTGL*RYQE*YHIHFIS FSLP*LYPTYSTKSPFLVEQFQE YFLGGLDDR*NSCL*RSR*MAN SFDCLSDSVLQGVVFSVVTSL FLFLFNSCKMQKNDFHRNLTT S
21110	51478	A	21237	297	428	QCQRGPGCSRGHGI*IEHWTA FGLDLRLQWFARGSWASGHGP

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21111	51479	A	21238	3247	5958	QRSWAGPGAGPEAGTRPPARG RRRQPGNVDPRRRAPQLRSQM QVAMARATTATGNRLWPGLL MIVMASLCHRGSSCGLSTHIEIG HRALEFLHLHNGHVNYKELL EHQDAYQAGTVFPDCFYPSLC KGGKFHDVSESTHWTPFLNAS VHYIRENYPLWEKDTKLVA LFGITSHMVADVSWSHLGIEQG FLRTMGAI DFHGSYSEAHSGD FGGDVLSQFEFNFLARRWY VPVKDLLGIYEKLYGREVITEN VIVDCSHIQFLEMYGEMLA VSK LYPSYSTKSPFLVEQFQYFLG GLDDMAFWSTNIYHLSTFMLE NGTSDCSLPENPLFIACGGQQN HTQGSKMQKND FHRNLTSSLT ENIDRNIN YTERGVFFSVNSWT PDSMSFIYKALERNVRTMFIGG SQLSQKHVSMPLRHHYFLSPY ARLGWAAMTSADL INQDGVHGD LRGWGAPGLTAAPAHIPHSGR VYLIYGN DLGLPPVDLDLKEA HRILEGFQPSGRFGSALAVLDF NLDGV\PD LAVGAPSVGSEQLT YKGAVVYVFGSKQGGMSSPN ITISCQDIYCNL GWTLAADV N GDSEPD LVIGSPFAPGGGKQKG IVAAFYSGPSLSDKEKLNVEAA NWTVRGEEDFSWFGYSLHGV T VDNR TLLLVGSPTWKNASRLG HLLHIRDEKKS LGRVGYFPFN
21112	51480	A	21239	2	403	VVAEEDTEL RDLLVQTLENSGV LNRIKAE LRAGVFLALEEQEKV ENKTPLVNESLKKFLNTKDLQ GLEGRENLARDLGIIIEAGTVG GPLLLEVIRRCQKQKEGPTTGE GALDLSDVHSPPKSPGK TSAQ
21113	51481	A	21240	3	1699	

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21114	51482	A	21241	3	1812	APRLKMGHHPNKPVSQSRVVN DGQCKLHAAVDSRDPDGTGR RVSSGGTGLPGGRGPGLPAGA WLSAEGRGAGSGDCGPSSGS AEPTQRPPRPSALPGAIPPLHLG LAPFRLEASEAVAEQAPPPAPTLS FGAQWSGAPQGSVSSVNPGEA GPARCASGRGFGCVGRVARAR SVPCCGRWPLARLRRLSWRSK MAATAAAVVAQEDTELRLDL VQTLNENSGVLNRKAELRAAV FLALEEQEKVENKTPLVNESLK KFLNTKDGRVLVASLVAEFLQFF NLDFTLA/VFQPEPETS/TIF*LLF*L QGLEGRENLRDLGIIEAEGTV GGPLLA/LEVIRRCQKEKGPTTG EGALDLSDVHSPKSPGKTS QTTSPKIPRYKGQKKKTSQK AGDKKANDEANQSDTSVLSL PKSSSLHLLSHETKIGSFLSNR TLDGKDKAGLCPDEDDMEGDS FFDDPIPKPEKTYGLRKEPRKQ AGSLASLSDAPLKSGLSLAG APSLKDSKSRGNTVLKDLKLI SDKIGSLGLGTGEDDDYVDDFN STSHRSEKSEISIGEEIEDLSVEI DDINTSDKLDLTDQTLTVSGLS DVADYLEDVA
21115	51483	A	21242	419	651	TNIFSRNLNPQTNVFCARQLSS* SVTI*GVLGQAVTRYFSQALSC DWGTLFSAFLIMPESPTPLLG RDILAKAGA
21116	51484	A	21243	555	888	RTSSRRTPNPCRIRKNYFKFH MEPKKSP/*PRQC*AKRTKLEA SCYLTSNYTTRLQ*PKQHGWW TIRSFSSHEAIFQTITWGKTLDN TRLRTEVPAAFHSALCPWFIEI
21117	51485	A	21244	728	1428	
21118	51486	A	21245	238	505	INVGRHHVILQGLSCPQLSSRS VTI*GVLGQAVTYFSQLSCD WRTLLFSHVFLIMPESPTPLGR DILLYVCIGRFPIFRADCT
21119	51487	A	21246	940	1434	QLAPCTLTPEPRVCLTIEGQEVN CFLDTRAAFLVLLSCPQLSSRS VAIRGVLGQAVT*YFSQPLSCD WGTLRFSHAFIMPESPTPLLG RDILAKAGAIIEKRAFMKRK EIKKQARSSKVHTSAASSCART APLGSFAEHLIKIADFTPPSSSS PCTTLFFS

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21120	51488	B	21247	747	1138	
21121	51489	A	21248	1685	2051	SSSRTEGARGKRQMPSP/STEP RVCLTIEGQEVNCLLDTGAAFS VLLSCPGQLSSRSVTI*GVLGQP VTRYFPQLSCDWGTLFNSAF LIMPESPTLLGRGILAKAGAIH HAVLVTAAL
21122	51490	A	21249	2	1014	GGAGPVVLRRAACSPGPAPR AARPPAMEPGPDGPAASGPAAI REGWFRETCSLWPGQALSLQV EQLLHHRRSRQDILVFRSKTY GNVLVLDDGVICTERDEFSYQE MIANLPLCSHPNPRKVLIGGGE GGVLAREVVKHPSVESVVCCEI DEDVIQVSKKFLPGMAIGYSSF EADTYMWGDGF*VSWKQKQD AFDVNIIDSSDPMGPAESLFKES YYQLMKTA/LLEDGVLCCQG \ECQWLHLDLKE/MRQFC/QSL FPV/VLAYAYCTIPT/YTPSGQIG FMLCSKNPSTNFQEPVQAVDN SSKVAKMQLKYYNYSERATAA AFVLP/FAHQGLE
21123	51491	A	21250	3	418	FSYEKLLNWQEFVADLEHHSY RSFLGLTCLKQISTRTDFIIDTL ELRRDMYILNESLTDPAIVKPL AEEMLSYARDDTHYLLYIDK MKLQMRERGNRQTVQLHVWV QRSRDICLKKFIKPIFTDESYLE LYRKLEK
21124	51492	A	21251	1	1704	
21125	51493	A	21252	1	3104	MFDTHQAARLLNLRHSLDHL LKLYCYNVDSNKQYQLADWRIR PLPEEMLSYARDDTHYLLYID KMRLEMWERGNQPVQLQVV WQSRDICLKKFIKPIFTDESYLE ELYRKQKHLNTQQLTAFQLL FAWRDKTARREDESYGYVLPN HMLKIAEELPKEPGIACCN PVPLVRQINEMHLLIQQARE MPLLKSEVAAAGVKSGPLPSAE RENKSKQPVQVHL*QRPVLT GRKLLPACTFYMPACWGL

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21126	51494	A	21253	2	2775	QALARRAVQAEKMAPPSTREP RVLSATSATKSDGEMVLPGFDP ADSFVKFALGSVVAVTKASGG LPQFGDEYDFYRSFPGFQAFC ETQGDRL/CFQCMSRVMQVPM GC/RSNIKDRSKVTELEDKFD LL/V/DAN/DVILERVGILLDEAS GVNKNQQPVLPAQLQVPKTVV SSWNRKAAEYGGKAKSETFRL LHAKNIIRPQLKFREKIDNSNTP FLPKIFHSNPMVQ/KPLPQALSK ERRERPQDRPE
21127	51495	A	21254	3	2668	QALARRAVQAEKMAPPSTREP RVLSATSATKSDGEMVLPGFDP ADSFVKFALGSVVAVTKASGG LPQFGDEYDFYRSFPGFQAFC TQGDRLQCMSRVMQYHGCGRS NIKDRSKVTELEDKFDLLVDAN DVILERVGILLDEASGVNKNQ PVLPAQLQVPKTVVSSWNRKA AEYGGKAKSETFRLHAKNIIR PQLKFREKIDNSNTPFLPKIFIK NAQKPLPQALSKERRERPQDRP EDLDVPPALADFIHQQRQTQVE QDMFAHPYQYELNHFPTADAV LQKPQPQLYRPIETPCHFISSL DELVELNEKLLNCQEFVLDLEH HSYRSFLGLTCLMQISTRTEFII DTLELRSDMYILNESLTDPAIVK VFHGADSDIEWLQKDFGLVYV NMFDTQAARLLNLGRHSLDH LLKLYCNVDSNKQYQLADWRI RPLPEEMLSYARDTHYLLYIY DKMRLEMWERNQGPVQLQV VWQSRDICKLKKFIKPIFTDESY LELYRKQKKHLNTQQLTAFQL LFAWRDKTARREDESYGYVLP NHMMLKIAEELPKPEGHAIACC NPVPLVRQINEMHLLIQAR EMPLLKSEVAAGVKKSGPLPSA ERLENVLFPGHDCSHAPPDGYP IIPSGSVVPQKQASLFPDEKED NLLGTTCLIAATVITLNFNPSAE DSKKGPLTVAQKKAQNMESFE
21128	51496	A	21255	98	286	HARPRHGPRLRCEVGLRCAPG YAGASARPTCEGDTTRYCPQDP NQT*SRPVPIAHRYCLTG
21129	51497	A	21256	1020	1280	
21130	51498	B	21257	153	3804	

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21131	51499	A	21258	159	579	PNVRWCPS\CYRNQDDHELQIT HGNKILCGIVWKIAQVEQMR KFSRLEKQRTHV\SCSDLQAVR RFRGVVSEGSFEMGEKVYKRK DMFQLSLLTEQHGDSTLGS SSYTQMPAENGSLVHTLVTAAPPF FAEKPHSITAG
21132	51500	A	21259	1	1290	MGASRSQKPGPSRDYSYTAGC DVDQRRRGAQKLSRSDTKRIV MSYGKKALKNDKFEIRAFSSSL EVRYRNQDDHELQIHTGTRFY VELCGFAVTRLRDP\PMRLHAA MALLPWRPPDYSASLLPDWLP VPSSKVITYYPGFTSIWAFSNT E/LCSEYKYCYCECRSKQE/AHK RRKV*KLPMLAP/HLKRFKYK DQLHRFTKLFRASLRGPRDER LKRVSRLFLSVVVTSRVFDVL LRILHRLGQYVSSEYVVALMCS EGHGPGEADVTELLQSHEKTE WMRSCFFWMTKSGVFDGIYLV NAFNQEGEDLYKENCKTLMKE VEDAQINGKTSYAHGSEYCK MSILPRILLQKISRDDCFKIVLKF CVDHQKTKKCCMITLKSSVVQ LAFTIKISVSEMCAREDFVVVIS FQHSEVPSRQLARCTFKEGYT
21133	51501	A	21260	3	142	
21134	51502	A	21261	1	1368	

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21135	51503	A	21262	1	2420	MEEVAEAPQPIDPKPLATQPQSI IITITITITITITITITITITITITITIT IITITITITITITITITITITITITITIT TITITITITITITITITITITITITITIT VITITITITITITITITITITITITITIT QADECWGEAEPLMSRQAHVW LRYRTGCREERPDQELIGSWG HGPRSTLVRAKAMAPPPPLAA STPLLHGEGFSGYPARGPRFALTL TSQALHIQRLRPKPEARPRGGL VPLAEVSGCCTLRSPSPDSAA YFCIYTYPRGRRGARRKATRTF RADGAATYEENRAEAQRWAT ALTCLLRGLPLPGDGEITPDLLP RPPRLLLL.VNPFGGRLAQWQ CKNHVLP.MISEAGLSFNLIQTER QNHARELVQQLSLEDWDGIPT VSGDGLLHEVLNGLLDRPDWE EAVKMPVGILPCGSGNALAGA VNQHGGFEPALGLDLLNCSLL LCRGGGHPLDLLSVTLASGSR FSFLSVAGWGFVSDVDIQSERFR ALGSARFTLGTVLGLATLHTYR GRLSYLPATVEPASPTPAHSLPR AKSELTLTPDPAPPMASPLHR SVSDLPPLPQPALASPGSPEPL PILSLNGGPELAGDWGGAGD APLSPDSTAGFTSWLSQGSSTLT RLRRGPRNSPILWAPTSHP*CPG RGLH/RGPPDHLLPPLGTPLPPD WVTLEGDFVLM.LAISPSHLSAD LVAAPHARFDDGLVHLCCVRS
21136	51504	A	21263	573	1025	RKQSHEDWRSTNKTGVGHPSA RLYEPWWAHTWTPPGGSKAP SDP/PLSHQLSPAGQPHFASPEP TSKTPDPWPNGVFSFPLPQSLP ELRHTLYLPMGTGKKPPGSSMIF YT*AQYPGTNSATICRLLSYKS GQVYPNTGQAPPQQRGR
21137	51505	A	21264	48	327	EELEALRR/QRLAELQAKHGDP GDAVQQEAKHREAMRNSILA QVLDQSARAR/VSEQGLIEILKK VSQTEKTTTVKFNRRKVMDS DEDDDY
21138	51506	A	21265	1	400	
21139	51507	A	21266	786	905	VSEQGLIEILKK*COLTEKSTV KFNRRKVMDSDEDDDY

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21140	51508	A	21267	907	1327	PRLQRSTPSPWRTEELALRR\QRLADAAGQNTGDPGDA\QQEAKAPGQAE MRNSILA QVPGSSPAPAPRLSNLSHLVKP*KNLKPVENYPYTRLARYVTT*VMTGIRNQG FN*KSLKKVKAQ/QTEKT TVVKFNQKKK
21141	51509	B	21268	1	828	
21142	51510	A	21269	317	2390	KWPKMNPQQQRM AIGTDKE LSDLLDFSAMFSPVNSGKTRP TTLGSSQFSGSGIDERG/GTTSWGTSQGPSYSDSSRGFTDSPHYSDHLNDSRLGAHEGLSPTPFMNSNL MGKTSERGSFSLYSDTGLPGCQSSLLRQDLGLGSPAQLSSSGKPGTAYYSFSA TSSRRRPLHDSAALDPLQAKKVRKVPPGLPSVYAPSPNSDDFNRES PSYSPKPPTSMFASTFFMQDGT HNSSDLWSSSNGMSQPGFGILGTSTSHMSQ/SSSYGNLHSHDRLSYPPHSVSPT/DINTSLPPMSSFHRGSTSSPYVAASHTVPPINGSDSILGTKGNAAGISSQTGDALGKALASIYSPDHTSSSFSPNPSTPVGSPSLTGTSQWPRPGGQAPSSPSYENSLHSLQSRMEDRLDRLDAIHVLRNHAVGPSTSLPAGHSDIHSLLG PSHNAPIGSLNSNYGGSSLVASSRSASMYGTHREDSVSLNG/NH SVLSTVTTSSTDLNHKTQENY *RWPCKSQSGTVVPQEIKTENKEKDENLHEPPSDDMKSDD*SSQKDIK VSSRGRTSSTNEDEDLNPEQKIEREKERRMANNARERLRVRDINEAFKELGRMCQLHLKSEKPTQKLLILHQAVAVILSLEQQVRERNLNPKAACLKRREEEKVSAVSAEPPTPLPGTHPLSETT
21143	51511	A	21270	2	153	QNASSPSKGSQLLTSKGTKLDGE*V**INRSRLQKVANNKLLWRKLKGQF

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21144	51512	A	21271	1	1230	MRKTQCKNAESSKNQNASFPFPKDHNSLTAREQNWIEFEGELTEVGFRRRLNQEEVEFLNRPI TGSEIEAIINSLATKK/GPEGFIAEFY*RTQCKNAESSKNQNASFPFPKHNSLTAREQNWIEFEGELTEVGFRRRLNQEEVEFLNRPI TGSEIEAIINSLATKKRTRGHISRLLEVI TSFYVERGGNAMSFMGKGVTKSTILCLLHLSHEMMAQAGSLEWMSLWFLPLGSHSEEHPTQQGLA WLPLWVDRDPEVRFTSLGLGSALTTLTGCVALANSQCQNISGGLWGTVVNILLDQSECSMVRRESQHHVDVAKVYHLHPPPEW WPCLYLGLDHSRELRSSVLECEMEQRLEVTLGTTYPFVSPISKFIQAVTTKCLR LGASRFSVCLAGLSAAPEQKIHPPTTQQFQQLPHD SVGFLQFSLHPKGNFGSGISSPD RSGDASHYSYPSLWQIRGTSRVKKQTWGSGLNKKWGIHKVQPQRLMMQNDDDEESI
21145	51513	A	21272	1	987	
21146	51514	A	21273	180	466	ARGSERAAASFASMYEGKKT KNMFLTRALEKILADKEVKKAHHSQLRKACRVALEGNKAETE KQSPPHGEAKAGISTLPVVKSTNFIEADKYF
21147	51515	A	21274	1	1224	
21148	51516	A	21275	251	5986	SCRCPRLQSPSTSTPFSLLFLPLLLLPPSSRWEPRVGRAAASFASMYEGKKT KNMFLTRALEKILADKEVKKAHHSQLRKS/CGRV ALEEIKAE TEKQSPPHGEAKAG SSTLPVVKSTNFIEADKYFLPFLACQSKCP/RIVVSTSLDCLQKLMA YGAL*LGNA PDSTTPGKKLIDRIETICGFCFGPQTDEGVQLQHIKALLTAVTSQHIEHGTVLQAVRTCYNIYLASKNLINQTTAKATLTQ
21149	51517	A	21276	46	214	KLRLTTTSVYAI PNRRRYDGFKLVQSCIFI*NFRS*DLRPPQYMPFLIEGGMTVSN SCRAAFSFTSLC RHRFSEAWLQNTNTGGFGSTF
21150	51518	A	21277	306	616	
21151	51519	B	21278	47	927	

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21152	51520	A	21279	660	890	GGKITASGSPVPRPSGA*ALPSG RCSTPRTSSCPRLPEPPGL/PSP PSAPANTTPDDSHAAP*GTRAH THRPPPH/TATPSRPPPTSPPVAT RTAPKAPQ/HHP/PTSCPTQRPT DSPSVHEPSQPLATQHSQTPI*P VIVTQ
21153	51521	A	21280	3	213	
21154	51522	A	21281	349	2616	TTAMAHRKLFESVGSGMLDHRV RPGVPVPHSQEPESDMELPLEG YVPEGLELAALRPESPAPEEQE CHNHSPDGDSSDYVNNTSEEE DYDEGLPEEEGITYYIRYCPED DSYLEGMDCNGEELYLAHSAHP VDTDECQEAEEWTDASAGPH HGHEAEGSQDYPDRQLPIPEDE PSVLEAHDQEEDGHYCASKEG YQDYYPEEANGNTGASPYRLR RGDGDLEDQFEDIDQIVAEIKM SLSMITSITSAFEASPEHGPEPGP EDSVEACPPIKASCSPSRHEARP KSLNLLPEAKHPGDPQRGFKPK TRTPEERLKPHEQVCNGLEQP RKQQRSDLNGPVDNNIPKTK KVASFPSLVAVPGPCEPKNLID GIIFAAANYLGSTQLLSERNPSK NIRMMQAQFAVSRVKRMQKA AKIKKKANSEGDAQTLTEVDLF ISTQRIKVLNADTQETMMDHAL RTISYIADIGNIVLMAARRRMPR SASQDCIETTPGAQEGKKQYK MICHVFESEDAQLIASIGQAFS VAYQEFRLRANGINPELSQKEY SDIINTQEMYNDLLIHFNSSEN CKELQLEKHKGEILGVVVVESG WGSILPTVILANMMNGGPAAR SGVKLSIGDQIMSINGTSLVGLPL ATCQGIKGLK*PDHR*SFNIV/S CPPV/TPRFLYSKRPDLYQLGF SVQNGHICSLMRGGIAERGGR

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21155	51523	A	21282	20	771	TTPNKHMMQTRAGSAWYLR SRGCSQGAPQKASSGSGSSW NRSVATVPGIVLGWRRPELLSE RGCAEARGAGVAGRQLQLTG VQGSVVVRGRLGRREWCR GGGAAPRPTAGTPVPRRPGTR AGPEEGEGAGAGARAAPEPRP HALSPPAFGADGQLRPLLLTS LRAHHPRGGLLLTSPGTHQPR RGRQGTTPPASPSA/PEEGALP GVLPL*PPSPSP/SESPPRPHG GGALAVTRRTAA
21156	51524	A	21283	1615	1985	LGSTRQAAPGQLRGHQAPAPN SDATAGQGRCCRSAD*GWGSR EQI*ALPLPSGPAPLLPPLL PVPPSPPPSPSPPLPP/GPP* PPLTFSVVTGGLWCPHHRKSL NPTSGVNEY
21157	51525	A	21284	3	501	
21158	51526	A	21285	1	2646	
21159	51527	A	21286	31	319	VIQDLHVPPREESAEQVDDPPE PVYRT*RGSPGLHRAPLQPPF PARCGRRTRTRAPGAPTTTTQT RELPPGSRPLRLRVPPAQPPPL PRWTAT
21160	51528	A	21287	3	147	
21161	51529	A	21288	20	600	PVTPRRITLPAWLSVSPALPLP* PHPPAGLVMSARTSRCSTPTTS LRSSG*GWRTPGSHSTIQTPT LFDGSCPRSLPLEASINPARM VTPQRPALQRRRSQQSWMRL GAGRKSLLPQLL*GPRPWTRQG CSIAPRRQTRESGSRSTGVPPG LCWRVAS*HSSRTQRRLQAA* GSLSPFPLSTQWS

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21162	51530	A	21289	383	1800	TCSTQTSRLRNPRRPRAASLPQT CSRSRPSRAHSLTGRPPRFQSQ MPSRSPCC*IC*NIRIDLCGS/TH SDGRFELVFSKKLALRASSQD EAEWLDRLVREALQKVRPQQE DEWVNVQYPDQPEEPPEAPQG CLSPDLLSEPAALQGTQFDWS SAQVPEPDAIKESLLYLMDRT WMPYIFSLSEALKCFRIKNE KMLSDSHGVETIRDILPDTSLG GPSFFKIITAKAVLKLQAGNAE EAAALWRDLVRKVLASYLETAE EAVTLGGSLDENCQEEKNNTK HTTARNAFEENDFMENTNMPE GTISENTNYNHPPEADSAGTAF NLRTPTVKQETETKWEYNNVGT DLSPEPKSFNYPLSSPGDQFEIQ LTQQLQSLIPNNVRKLIHVR TLKMDCSGTHVQVTCAKLISRT GHLMKLLSGQEVKASKIEWD TDQWKIENYNESTEASEQKE KSLEAASGTQDGVHVQEPRPQ APSPDLQQPVESTSSQPSSTV SETAREVGGNGLQKAQAHG AGLKLVSSTSPQVCKLWW SAGLHTPPVTSGLTGVGLQGPQ QRFPKFPDFHPLISCGKVA
21163	51531	A	21290	2	667	
21164	51532	A	21291	84	377	RMGKHCFENLLFRDGKAQRAC MGYTVCHSHIVGSGQKCWPA WPQVNLQPSRHQQVCCSLPRC AKCKTVFHQSCQAVVKKGCPR CAR*RYQQQNVFA
21165	51533	A	21292	2	1168	FVLPVVS GRE TASSARLRGCR SREPPSPRSSRLVSCDSLREQ REWRCPQWWRMDWTPRLPSR HIISELEHLTFVNM DVGRCAW LRLALNNGLM ECVLKL LQ/EQ ARLREYYQPTALLRDAE GEF LSFLQGLMSLSFELSYK SAILNE WTLTPLALSGLCPLSELDPLSTS GAELQRKESLDSISHSSGSE DIEVHSHGHKIRRNQKPTASSLS LD TASSQLSCSLNSDCLQENG SKSPDHCEEPMSYDSDLGTANA EDSDQSLQEVLLFESKAQAASG TQDGVHVQEPHPQAPSPDLQ QPVESTSGQPSTVSETAREV GGNGNLQKAQAHGAGLKL VSSPTSPNISSMIQSTRPVHFCIV STKHCTWEKVGMD

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21166	51534	A	21293	263	813	
21167	51535	A	21294	130	1094	NQPHRTKGCPNSSTCEKNGSLT CDFMQVPLEMGKLRPEGERRV QDRDSNPSPSAGLFQARWS* PPRPSFLLPAGKRRGCDGGGRG GGRVRAGGAPLRVHRQGRAPP QSTEHWVHVRKPGGRPFYLP AQYVRELPAIGNPAADAPP IGTRSP* AARLRLPVRERGGSG PQRPPSGAPRRGQLPVRPCAAR RREP/AAAAWRPACPPACTCGP GARAARAVPGRPDARRRLASR RQPRKQRQLQGLQRSGLLGVP AAPVAQRLRRLRGHPGGTRP AAVGDREAGTTPGAAGRLAE DSARREPGLEENHSAQRRRA
21168	51536	A	21295	2	3676	
21169	51537	A	21296	432	3453	DLAGEVLLCGGAADYGTGLGFS SPAQVEANRGALCSSIERGHIIS ELEHLTFVNTDVGRCRAWLRL ALNDGLMECYLKLLQEQAARL HEYQPTALLRDAEEGEFLFS LQGLTSLSFELSYKSAILNEWTL TPLALSGLCPLSELDPSTSGAE LQRKESLDSHSSGSEDIIEVHH SGHKIRRNQKLTASSLSLDTASS SQLSCSLNSDSLQENGSKSP DHCEPMSCDSDLGTANAEDS DRSLQEVLLFS
21170	51538	A	21297	64	2996	LCPPAQPAASQPQVELPAGWPQ PHALPLPHDHRAQHLLGCAHP GRAKPELQHHDCACAAQIPHI PVRQPYQHPDPLCQPRRPACP ALPIHGRQLLQEPLQAGTGGG PGCPPWPGQPHPPVTQVQQPHC GAPQPAFQPGVS AVVLGRGIVK LAPEDLANLTALRVLDVGGNC RRCDHAPNPCMECPRHFPQLHP DTFSLSRLEGLVLKDSLSWL NASWFRGLGNLRLVLDLSENFL YKCKITKAKAFOGLTQL
21171	51539	A	21298	1	320	PVRTPPPAFSPKLTLRIMSLHQF LLEPNCGRPQLCRGTMARKPAP RKH*KHISRQCRVVLFEYKIGES VGFFKAVIFLVFLRFHSILDQS FSLSSLLWKIVTLT
21172	51540	A	21299	1	443	
21173	51541	A	21300	1	1059	

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21174	51542	A	21301	116	1559	PRTARFSCAHARTVRAVATRRR RVHFRDL\$AAP\$GLSVLRPRPT EPVRVDCPESANPPVARPDSP DPRMFELLAASDARINGPFCAP RVLLAPLLGAFVTVSKI\$KIAL SPK*\$RRSHLLRRNGSQWVKV H\$ELKEHNG\$HITGID\$WAPKSD RICH\$CLGADRNC\$LMVW\$KQID GVWKP\$NPG*\$FLRNLIGG\$NFL* KWVPPRRTKFGCGG\$GARLISV CYFE\$ENDWV\$SKHIKPIRST VLSLDWHPNNVLLAAG\$CDFK CRVFSAYIKEVDEK\$ASTPWGS KMPFGQLMSEFGG\$SGTG\$GW VHGVFS\$ASG\$DRLGWG\$ATD STV\$VA*\$CLQKV\$VQSTLKT\$E FLAAP*\$VVSFVSREP\$ASGLPAH DC\$CPMLFNYG*\$PRAALTFRLP KLDIPK\$QSIQRNMSAHGNAFG NMADKRATTED\$RNTAL\$ETLH\$ QNSITQVLYLLRW\$DKQD\$CRKF CTVTGIDGEPWTIWD\$FQDPRSL PSQGLRIM

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21175	51543	A	21302	1	2223	MKHYTRVQSSISPPAERQETHA WASPAVTSLESAACHELQEAD LSELSYPRIVSSSLQYYVAQG GSFPCFGMPWNFISGGAESTNA VISFANATTAVPMAVLSRRESS LANNPGVVNYSALPENENVGP EMPERPANSSKNSTETANYPTL MGNYNGQNTASLSVFIPPYFAE KIILTEMPGTETNVENNSQTV YYPALSGNTSAPPYPASSYLPTS NFVLERVAEMPETAGTNVKN TQTVNYPSSGRGRSQGNASLS LSIPPKFGIERHLCFLVLAIRSK AAMNNIYHIGFV*TQAFISLRY/ MPKSAVAGSYGNALQNVLHIE MLFKTESGPQMSYGTMSYS MKNNCDDQDDASACLTPDFA LLPLNILVKVDNTNTNSVNTMN RSTLLDSDSGQDSSSSVCIPP YGYLGDPRKRVRLKIHLLAV QNMAMPKQAACYLVRILFSKEI LISSSVDIHLKDSQSLDPNKMA ALREYLATTFPTCDLHEHGKD WQDCISGINSMIYCLSEGKSTP KTVRKNNKRTNRVASASADR DQGRDGGEGCSWMFQPMNN SKMREKRNLQPNNSNAIPEGMRE PSTDNPEEPGEAWSYFGRPWRN IRMPCSVLTAKTKSCASLSAR YLIQKLFTKDLVLVQSNVYGNL KHGLCALDPNKISALREFLQEN YPICDLSNGRDWKSVCVTSINS
21176	51544	A	21303	1	297	
21177	51545	A	21304	1	162	
21178	51546	A	21305	11	212	KGKNCVAIAADRRFGIQAQMV TTDFQKIFP/MGAQRLKFRNL YELKEGRQIKPYTLMSMVANL LYEK
21179	51547	A	21306	37	554	SSIKFGRSNPDYWIAPSRNLDP AIMSIMSYNGGAVMAMKGN CVAIAADRRFGIQAQMVTRDF* KFFPMG*PACTPGMAGFAIDVQ TVAQRLKFRNLNELKEGRQIK PYTLMSMVANLLYEK/RDPDHL FETISQAMLNVDRAVSGMG VIVHIEKDKJITRTLKARMD

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21180	51548	A	21307	51	741	YTAIMSIMSYNGGAVMAMKKG KNCVAIAADRRFGIQARLLTTN FQKIFPMGDRLYIGLGGASPLD VQTS/VAQRLKFRAEPMVS*RE GRQKPYTLH*AMGGQPSLL*E KVFGPLTYTEPVHLPGLGPERP FKALSICFSKTLIRVGPMDLNL DFCGSSGNLAPNKMVG/MCESL WGGPTWDPDHLF*KPFSQGHG *MLWDRDGS/VSGMGSSLFHIE KDKIPRTLKARMD
21181	51549	B	21308	150	404	
21182	51550	A	21309	199	395	
21183	51551	A	21310	100	182	SFLFWIKR*SFPDALYFSSKSGA CSCN
21184	51552	A	21311	203	289	KCLALDIALATRRSAI*FPSVKG PGRGV
21185	51553	B	21312	166	411	
21186	51554	A	21313	232	317	KCPALDIAVATRRSAI*FPAVKG PGRGV
21187	51555	A	21314	129	278	FYSSVSGVSSKDDRRFGCSGYS AAVISFRQC*SQLPGCSATYQR ESTFS
21188	51556	A	21315	789	962	
21189	51557	A	21316	477	599	
21190	51558	A	21317	86	577	ATEPLAPSERREVSIPLVPAPL PPPPPPVPSRTRTRPWRP*AC FPMTLAASCGRTPSPWPSQQPIP QPAPVG/PGNIKTLGDAYEFAV DVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNTFAHKCQLPE DVDPTAVTSALRKDGSLTIRAR RDPHTEHV
21191	51559	B	21318	312	466	
21192	51560	A	21319	886	1338	GFWQVIRALRGGEVHREGTSA PGRHRRRCGRSAWNRCCCTAC SHVWPPRQMWPPQG/PDVAMKT GNIKTLGDAYEFAVDVRDFSPE DIIVTTSNNHIEVRA/REA/ERPD GTVMNTFAHKCQLPEDVDPTS VTSALREDGSLTIRAWKHPHTE HVQ
21193	51561	A	21320	3	605	KKLTPVVRSRVERDPRVRRGLR PHPVLSLRLPPGQGPAPSVDEPQ NLFHLPSEGEKIPFLFLLLFTPP PRPPVLSRPRTRPWRP*ACFP MTLAAICGPTSPWPSQAPV/V AGNIKTL*DAYEFVVVDVRDFSP EDIIVTTSNNHIEVRPEKLAADG TVMNTFAQQQLPEDVDPTSV TSALREDGSLTIRARGHPHTEH

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21194	51562	A	21321	3	450	SSAAEFVQEPGRGAPGSPSPISASR PGPAPRPASLPPSQMQAAALPE EIRWLLEDAEEFLAEGLRNENL SAVARDHRDHILRGFQQIKAVG GDIGQDSSDDNHSGLGLSLTY DAPFLSDYQDEGMEDIVKGAQ ELDNVVKQGYLEKKS*DH
21195	51563	A	21322	1	399	IGQDSSDDNHSGLGLSLTSDA PFLSDYQD/EG*VHQISDHWEK LRTWC*VYCDKGMEDIVKGAQ ELDNVVKQGYLEKKS*DHFFG SEWQKRWCVVSRGLFYYYANE KSKQPKGTFLIKGYSVRMAPHL RRDS
21196	51564	A	21323	3	1189	RLPARPPPDQGRPVVPLSRPAK CRLAVLPEEIRWLLEDAEEFLA EGLRNENLSAVARDHRDHILRG FQQIKARYYWDFPQGGDIGQ DSSDDNHSGLGLSLTSDAPFL SDYHDEGMEDIV*GAQELDNVI KQGYLEKKS*DHFFGSEWQK RWCVVSRGLFYYYANEKSKQP KGTFLIKGYGVRMAPHLRRDS KKESCFFELTSQDRRSYEFTATSP AEARDWVDQISFLKDLSSLTIP YEEDEEEEEKEETYDDIDGFD PSCGSQCRPTILPGSVGIKEPTEE KEEEDIYEVLPDEEHDLEDES GTRRKGVDYASYQGLWDC YGDQPDLSLQRGDLILFLSKE YNMYGWWVVGELNSLVGIVPK EYLHHLPLKWKERWKPREIYFF
21197	51565	A	21324	47	225	NSHHVVRGRPCADSSSPSGDRG QPEAQAPDSSAPEHAQEPGRA AVKRPDL*SHMTRRP

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21198	51566	A	21325	66	725	AILILLSSSEGLWSSDQHRLLVGV QDSPPQGS LGCYFSAMATSEQS VCQARASVMVYDDTSKKWVPI KPGQQGFSRINIYHNTVSNTR VVGVKLQDQV VINYSIVKGL KYNQATPTFHQWRDARQVYG LNFASKEEATTFSNAMLFALNI MNSQEGGPPSQRVQNGPSPD EMDIQRQVMEQHQQQRQEF ERRTSATGPILPPGHPSSAASAP VSCSGPPPPPPVPPPTGA/TP PPPPLPAGGAQGS SHDESFHV QDWPLAISWGPSLRRVPNGPED ASGGSSPSGTSKSDANRASSGG GGGGLMEEMNKLLAKRRKAA SQSDKPAEKKEDESQMEDPSTS PSPGTRAA SQPPNSSK\AGRKP WERSNSRGYFCVLD SVQNPAL WPKSPES*EPPSVSSL/ISRMKPA GSIVSDMA\LD AFDLD/IRMKQEI LEEVVRELHKGERKEIID\AIRQ EA*SGISRKKNLGHRAP\PTRTS FICSQRPLM
21199	51567	A	21326	301	390	
21200	51568	A	21327	72	415	
21201	51569	A	21328	395	697	RVMSPVHVNTICSPHPSDGDV IVPIVLSNERYHWPVLGWVGG VDCDEFFRVVLGEARLHLDGV AHQH*TKGTISNLFQ\ATSVSH LVEVVPQKLSWVI
21202	51570	A	21329	36	399	VEILTSKRAGDWFKEELRLGG LDHIVDKVKECVDHLSRDEDEE KLVASLWGAQRCLRVLSVTV HNPENQSYLIAKYDSQLIVSSA KALQHCEELI*QYNRAVDTLCL ADCKPLPHPTVL
21203	51571	A	21330	1	177	
21204	51572	C	21331	198	350	
21205	51573	A	21332	113	228	
21206	51574	A	21333	1	466	

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21207	51575	A	21334	1	4133	ASGCWRKEVAGSANGVEMV QGVPVQTPALTHRRKRRRRRRR RPSGGTQQALLPAPAVAASES* ARARPAALEAGREVAGPPSCPP NRASYLPKASLASLGSHPAL LSRARVPRPPAGRKERE\RRKRP \VAKAPARLURGEYETGVKMTS RFAKTYSRKGGNGSKFDEFVS NKRTTLSTKWGETTFMAKLGQ KRPNFKPDIQEIPKKPKVEEEST GDPFGFDSDDESFPVSSKNLAQ VKCSSYSESSEA
21208	51576	A	21335	3	221	
21209	51577	A	21336	1	580	
21210	51578	A	21337	2	1095	ARGNRPPPPRTERGVLESRTS RHRAPRLPPAMPAPRAPRALAA AA\PASGKAKLTHPGKAILAGG LRGGUQICMTFPTEYVKTQLQL \DERSHPPRYRGIGDFVRQTVRS HGVLGLYRGLSSLLYGSIKAA VVRFGMFE\FLSNHMRDA\QGR L\DSTRGLLCSLGAAGRP*\VV VCPMETIKVKFIHQDTSNPKY RGFFHGVREIVREQGL\KGT YQGLTATVWLKQGSNAIRFFVM TSLRQWAYPRGTTPNKAHEPF*I TWGSFGA\IASASQVSFGNTPLD VIKTRMPGPWRPHKIYR\NTWD \CGL\QILKKGGGSRAFYKGT V\PPGPGLAWDVA\VFV\YDEV G*SCFNKVWKNGIKA
21211	51579	A	21338	3	375	TACDSGAEDGPASRVSQMPTLP PPMPWNLPAAGVDCITTSGLAL TALFFKMEEANLASRAKAQELI QATNQILSHRKPPSSLGMTAP VPSTLGLPPGPSSYLLSGSPPLG GC\GSTPTTPGLAA
21212	51580	A	21339	51	3789	GRGHPHGGGELLPASPRGSP EGDQPGQGDPEEKEGRVVRGGA PDVPSAHALVPEQTVLGLHQ RVTAPQGRHGAH*LGDRDLHSG RPORPTHGTWAPCLPYPTLGS G*RRHHGNPAGTPRSLFPFPEK ELEAPPPAPRFDIYDPFHPTDEA YSPPPAPEQKYDPFEPTGSNPSS SAGTSPSEEEEEEEEEEEEEED EEEEEGLSQSISRISETLAGIYDD NSLSQDFPGDESPPDAQPTQP TPAGTPPQ
21213	51581	A	21340	286	393	
21214	51582	A	21341	64	610	

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21215	51583	A	21342	1	4433	MWAQLLLGMLALSPAIAEELP NYLVTLPARLNFPVSQKVCLDL SPGYSQDVKFTVITLTKDKTQKL LEYSGLKKRHLHCISFLVPPAG GTEEVATIRVSGVGNNISFEEL KKVLIQRQGNFTFVQTDKPLYT PGQQVYFRIVTMDSNFVVPND KYSMVLELQDPNSNRIQWLEV VPEQGIVDLFSQLAPEAMLGTY TVAVAEGKTFGTFSVEEYVLS FLLLLSSVLPKFKVEVVEPKELS TVQESFLVKGGL*)
21216	51584	A	21343	3	522	ELRTWIEGLTGLSVGPDFQKGL KDGTILCTLMNKLQPGSVPKIN RSMQNWHQLENLSNFIKAMVS YGMNPVDLFEANDLFESGNNMT QVQVSLALAGKMGNTKNCASQ SGMTAYGTRRHLYDPKNHILPP MDHSTISLQMGNTKNCASQVG MTAPGTRRIHYDTKLGTDKCD
21217	51585	A	21344	1	1230	MHQEDLRAWYLDLGLPSHQNE TTDVSVVYERFSLDTATYPKQA KQWDFPFLRVSTAQPTAWKCC RAPSPYTHQDTALIPSPTARWL SPEKEPKQGEVGEKSLLPDPTLP LTDPRLTGSTEQKKDLAAGPVG SALRRRPPAVSSTQFNKGPSYR LLADVQNRLLPKYDSQKEAEL RSWIKGFTGLSIRPDFQKGLKD GIILCTLVNKLQPGSVPKIN\ASV *NWH*LENLSNFLKAMVSYGM /NPVDLFEANDLFESGNNMQVR VSLLALAGKAKTKGLRSGVDIR DKYSKKQNFDDTTMKASQCVI RLQITNKCASQSGMTAYGTRR HLYDPKNRILPPMDNSTISLQM GTNKYASQVGMTAPGTQRHIY DTNLGIDKCENSSMSLKMGYT QVANHSGQVFLGRQIYEPKY
21218	51586	A	21345	2	389	

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21219	51587	A	21346	1	1113	MHQEDLRAWYLDLGLPSHQN AQPTAWKCQRAPSPYTHQDMA LIPSPARWLSPEKEPKQGEVG EKSLLPDPPLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRLADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIICTLVNKLQPGSV KINVASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANNLFESG NNMQVRVSLALAGKAKTKGL RSGVDIRDKYSEKQNFDDTTM KASQCVRILQITNKCASQSGMT AYGTRRLHYDPKNRILPPMDNS TISLQMGTNKCAQVGMTAPG TQRHIYDTKLIDKCESSMSL
21220	51588	A	21347	353	1260	SCWCLKLALAVSST/QFNKGPS YRLLADVQNRLLFKYDSQKEA ELRSWIKGFTGLSIRPDFQKGLK DGIICTLVNKLQPGSVKIN*AS V*NWHQLENLSNLKAMVSYG M/NPVDLFEANDLFESENNMQ VRVSLALAGKAKTKGLQSGV DIRDKYSEKQNFDDTTMKARL CVIRLQITNKCAQVGMTAYVT RRHLYPDKNRILPPMDNSTISLR MGTNKCAQVGMTAPGNQWH IYDTKLIDKCESSMSLKMGY TQVANHSRQVFLGRQIYEPKY QPGGPVAHGAPSAAGCPGGE
21221	51589	A	21348	3	530	
21222	51590	A	21349	1	853	MPESWLAAPFPYGDIKKVVGL QLKEGLHQNLTMQDSIQIFDFQ LPGLLRPSSVLWTLKPYHTAGL ASDRDSYKILACMPCMFGRSR SPLRDIKSHQADLELVKNSLD TIHRLESELKKQSKIQSQMKVE KAHLEEEIAELKKSSQAQDKAKL LEMQESIKDLSAIRADLANKLA EEERAKKTSAGAFGP/LIAQAN SRDEGTATITQLELERDVHQRE LKDLTSSLQSVKTKHEQNIQEL MKHFKKEKSEAENHIRTLLKVPL LNPDDTEGIFLVAHEVNKA

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21223	51591	A	21350	1	652	NTSLINTKKKLETDISQIGEME DIIQEARNAEEKAKKAITDAAM MAEELKKEQDTSALHERMKKN LEQTVKDLQHRLEAEQALAK GGKKQIQKLEARVRELEGEVES EQKRNVAVKGLRKHERKVKE LTYQTEEDRKNILRLQDLVVDK LQAKVKVSYKQAEAEQSNV NLSKFRRIQHELEADFRADIA ESQVNKL RVKSREVHTKIISEE
21224	51592	A	21351	21	5868	PAAMSSDSEMAIFGEAAPFLRK SERERIEAQNKPFDAKTSVFVV DPKESFVKATVQSREGGKVTA KTEAGATVTVKDDQVFPMPNP KYDKIEDMAMMTHLHEPAVLV NLKERYAAWMIYTSGLFCVT VNPYKWLVPVYNAEVVTAARG KKRQEAAPHIFSISDNAYQFML TDRENQSILITGESGAGKTVNT KRVIQYFATIAVTGEKKKEEPA SGKMQGTLEDQIIANPLLEAF GNAKTVRNDNSSRFGKFIR
21225	51593	A	21352	54	399	
21226	51594	A	21353	441	1585	VPPMGGGPPFVGPVGFPGDRS HLDSPEAR EAMFLRRAAVAPQ RAPILRPAFVPHVLQRADSALSS AAAGPRPMALRPPHQA LVGPP LPGPPGPPMMLPPMARAPGPPL GSMAALRPPLEPAAPRELGLG LGLGLKEKEEAVVAAAAGLEE ASAAVAVGAGGAPAGLAVIGP SLPLALAMPLPEPEPLPLEVV RGLLPPRLRITELSLRPRPRPR PEPPPGMLMALEVPEPLGEDKKK GKPGIEHRCIATA/AQGASWE DPPTCWKWD AE*LSRVFGDL GNEVND*HLGHAASARFPISL KAKVIR*QSAQAPKGYG/FVS FKDPISDYVRPMREMNGKYVV LAPPIKLRKSMWKDRNLDVFR KKQKEKKKLGRL

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21227	51595	A	21354	1	1122	MPGGKIGFLIEKGATEQSSTGN DFDELREEGGRRSNYSLEQEDI QTKGKEVENFEKNLEECVTTIS NTEKCVKELMELKTKARELRE ECRSFRSQCNQLEERVPAKDE MNEMKREGKFREKRIKRNEQS LQEIWDYVKRPNLPLIGVPESD RENGTKLENTLRDIIQENFPSLT RRGQPFRIEMENTENAPKDNLLE KEQLPRHNNCLELTQEEPAWD LQFDLLDLNDISSALKHHEEKN LISLLPQRGADYLSFRSHFQKNF VCVENCSLQERTVTGTVKVKN VSFEKKVQIRITFDSWKNYTDV DCVYMKNVYGGTDSDTFSFAI GLPPVIPTEQKIEFCISYHANGQ IFWDNK*WGRKYKNCVIVQW
21228	51596	A	21355	71	1124	GPPLCLMSCTRMIVLDPRPL TSSVMPVDVAMRLCLAHSPPV KSFLGPYDEFQRRHFVNKLKPL KSCLNIKHAKSQNDWKCASHN QAKKRVPVFADSKGLSLTAIHV FSDLPEQPAWDLQFDLLDLNDI SSVALKHHHEEKNLILDFPQPST DYLSFRSHFQKINFCVLAENCSL QERTVTGTVKVKNVEF*GRKF QIRYHFSDSWEKLTLDVDCVY MENVY/GVGTGSDTFSFAIDLPP VIPTEQKIEFCISYHANGQVFW DNNDGQINYVIVHVQWKPDG VQTQMAPQDCAFHQTSPKTEL ESTIFGSPRLASGLFPEWQSWG RMENLRLLCDELSNNVTGLDLS YSPMQS
21229	51597	C	21356	204	273	
21230	51598	B	21357	1	1062	
21231	51599	A	21358	1	397	QRPI*PTKPIGQRVSKGHQP/TR HDFDTQFLAAHETISRLVGFS AQVQYLDLIK'DPSKLFNEER LIDKTKVTYLLKWLPESESLFLA SHASGHLVLYNVSHPCASAPPQ YSLKQGEFVSVAAYNDLF

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21232	51600	A	21359	71	1736	FRTSLKDVWHTPLTPFLPPLKSI DLNKPDKRIYKGTQPTCHDFN QFTAATETISLLFGSFSRRTWA WCGPAV*AGPCPTAFLGTLRLI DKTKVTYLLKWLPESESLFLASH ASGHLVLYNVSHPCASAPPQYS LLKQAWGFSFYAAKSKAPRNP LAKWAVGEGPLNEFAFSPDGR HLACVSQDGLRVFHFDSMLL RGLMKSYFGGLLCVCWSPDGR YVVVTGGEDDLTVVWFSFTEGRV VARGHGHKSWVNAVAFDSLY TTTAAEEAATAAGADGERSGEE EEEEPEAAGTGSAGGAPLSPLP KAGSITYRFGSAGQDTQCLW DLTEDVLYPHPLARTRLPGT PGTTPPAASSSRGGEPGPGPLPR SLSRNSLPHPAGGGKAGGPGV AAEPGTPFSIGRFATLLQERRD RGAEKEHKRYHSLGNISRGSG GSGSGGEKPSGPVPRSRLDPAK VLGTALCPRIHEVPLLEPLVCK KIAQERLTVLLFLEDCHITACQE GLICTWPRPGKAFTDETEAQT GEGSWPRSPSKSVVEGISSQPG
21233	51601	A	21360	2	467	LMQ/NWDAAMEDLTRLKETID NNSVSSPLQSLQQTWLIHWSL FVFFNHPKGRDNIIDFLYQPH MLADKLNMTPEEAERWIVNLI RNARLDAKIDSKLGHVVMGNN AVSPYQQVIEKTKLSFRSQML AMNIEKLNQNSRSEAPNWAT QDSGFY
21234	51602	B	21361	1	909	
21235	51603	A	21362	3	3617	YWKERTQKVIPRATENHGLKS YLQKTKLSIDEAAFLPDNLK SELLELLTHWLQGVPMTPSLG SINLLGWLTELRETHYICWFIV KETTRDTDEEMCRTEPALACSI SHYDDGGCIQMLNTPETLQCSA KDSKHFIPKECSPGENRPPSDT GKTVKFLSLNIFNLQLAESTDA EQRANCILRCFLTETTLNYQKIL SVRPGTKLATASHVSLGLQTP PFGLAQHLIRPHAFAPKDPLTS FTERNRSG

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21236	51604	A	21363	75	2141	GPRLGLTTMWHEARKLGRRLR GLLFDSRRKAERRREYEEKIKK DPAQFLQVHGRACKVHLDLSA VALAAESPVNMMMPWQGDENN MIDRFDVRAHL\DHIPDYTPPLA HHHFSQNPQESDERKCNERYR GLVQNDFAGISSEQCQLYQIYIDE LYGGLQRPSEDEKKKLAEKKA SIGYTYEDSTVAEVEKAAEKPE EEESAEEESNDEDEVIPDIDV EVDVDELNQEVADLNKQATT YGMADGDFVRMLRKDEKEAE AIKHAKALEEEKAMYSRRSR RQRREFREKRLGRKISPPSYAR RDSPTYDPYKRSPSESSSRSR SRSPTPGREEKITFITSFGGSDFE AAAAAAAAAASGVTTGKPPAP PQPGGPAPGRNASARRRSSSS SSASRTSSSSSRSSSRSRGG GYYSRGRHARRSRSSWSRSLR SRRYSRSLRGRHSGGSRDGG HRYSRSPARRGGYGRPRRSLR SHSGDRYRRGGRLRHSSSR RSSWSLSPSRSLTRSLRSHSPSP SQSRSLRSLRSPSPSPAREKL TRPAASPAVGEKLLKTEPAAG KETGAAKVPKLTPEKLLKLRM QKPLNRQFKADKKAQRKR*S QAEHERQERKDEA\RAMARKIG MKERER\REKEREWEWQYSRQ SRSLP/RDYSREYSSRRSLR SRSPHYRH
21237	51605	A	21364	1	609	
21238	51606	A	21365	1	1227	
21239	51607	A	21366	1	1626	
21240	51608	A	21367	370	4388	GFIWNRITPTEDGQTRELQNH GLSAPVPRGRGKKVKQTQSS DIQKAEWLRYNPEQLQDEG YKKHIKHHCNKVLLRVMLYY LKQEVIGNECQKVFDDVDASDI DVWVPEPDHSEVPAEWDFD ADKSLIGVFKHGYEYNTIRA DPALCFLERVGKPKDEKAAAE QRANDYMDGDVEDPEYKPAPA IFKDDIEDDVSSPGDLVIADG QLMEGDKVYWPTQSALTTRLR RLITAYQRTNKNRQIQIQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
21241	51609	A	21368	1	530	AEADAIHQMVREGQRRRRQQQ AATSESSQSEASVRREESPM DV DQPSPSAQDTQSIASDGT PQGVE KEKEERPPELPLLEQLALDEL WDMLEGECLKELESHDQHAVL ETHRTVLNQILRQSTTHLADGP FAVLVDYIRVLDFDKRKYFR QELERLDEGLRKEDMAVHVRR DHVF
21242	51610	A	21369	1	217	
21243	51611	A	21370	274	599	PVSKESRVAPLCDFCLPFIQSES SQSEASVRREESPM DVDPSPS AQDTQSIASDGT PQGEKEKEER PPELPLLEQLSDELWDMLEGE CLKELEESHDQHAVLVLQPA
21244	51612	A	21371	2	731	TPTPTAPTPTVTSAPALVAATAI STIVVAASTVTPTIATITTVSI SPTTKGSKSPAKVSDGSSSTD FKMVSSGLTENQLQLSVEVLTS HSCSEEGLEDAANVLLQLSRGD SGTRDTVLKLLNGARHLGYT LCKQIGTLAELREYNLEQRR AQ CETLSPDGLPEEQPTTKLK GKMQSRFVSGLSASSIQA AVR QLEAEADAIHQMSSESSQSEASVR REESPM DVDPSPSAQDTQSI A
21245	51613	A	21372	208	423	LYVKPTAPPK*AL*SEGLE*MSP QCLWQGLQQGAQKKLLEVP NKLTQTIN*PANVLILA*GGSSS YRPPHK

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21246	51614	A	21373	1	2002	MPQLPGISLPEGVDPFLAALPD DIRREVLQNQLGIRPPTRTAPST NSSAPAVVGNPGVTEVSPEFLA ALPPAIQEEVLAQQTAEQQRPE LAQNASSDTLMDPVTLIQTLP DLRRSVLEDMEDSVLAVMPPDI AAEAQALRRREQEARQRLMH RLFHSSSTSALSAILRSPAFTSR LSGNRGVQYTRLAVQRGGTFQ MGSSSHNRPSSGNSVDTLRL RGRLLDHEALSCLLVLFVDE PKLNTSRLHRVLRNLCYHAQT RHWVIRSLLSILQRSSESELCT PKLTTSEEGKSKSGSSSHE NRPLDLLHKMESKSNQLSW/L SSVMDAALGFR/TNIFQIRSG GRKHTEKHASGGSTVHIHPQA APVVCRHVLDTLIQLAKVPF FTQQRKTETNCESDRERGNKA CSPSSQSSSGICTDFWDLVK LDNMNVSRKGKNSVKSVPVSA GENKVSEAQANSAGSSTTTA TSTSTTTTTAASTTPPTAPT VTSAPALVAATAISTIVVAAST VTPTTATTTVSIPTTKGSKSP AKVSDGGSSSTDFKMVSSGLTE NQLQLSVEVLTSHSCSEEGLED AANVLLQLSRRPARMLAMHW PSLYNVETEKTLALPNLIALQTS PFASGVIAKSSDRLINQCAPV WRWR
21247	51615	A	21374	1	6384	MVSPPEKTHGHSIRNWLDELKDL PILHAYSNLPSPAVDLAIHSSK EGRMDWTEGQVTGPVVSAAAT SGAGSTTSGVVSGLSREINYI LRVLGPAACRNPDIFTEVANCC IRIALPAPRGSGTNGSGSRIPRES APEMATAESLVEELSEDAAGG ASPGVELPALGCSELPAAEVSP TASSKNLETICEYAYCMAMLP TGLEDYPKRGFLDLTQERIWTD IPSPGNIPTHPLMVRHADHSS LTLGSGSSTT
21248	51616	A	21375	1	1356	
21249	51617	A	21376	80	608	

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21250	51618	A	21377	298	1374	GRGDWPDLNLQTATASWTPR WCLLRKPVEAPSGGATEERTLS LTSGLSMPADPCEGGARSCLV TESARGGLQNGQSV DVEETLPS EPENGALLRSERYQGPRRRACS ETLAESRTAVLQQRRAAQLPG GPAAAGEQRASPSKARLKEFLQ QCDREDLVELALPQLAQVVTV YEFLLMKVAESLGITEFLRKKEI HPDNLGPKHLSRDM DGEQLEG ASSVKREREAAEEGLASVKRP RREALSNDTTESLAANSRGRE KPRPLHALAAGTIVSQEEDIVT VTD/GRGACLRMGPLEGVPLEA VESVVTVEPEPSQ*NGVRY*NS SDFIQRRSMASNVYFSNVNIAQ MNLFLIKNNVFL
21251	51619	C	21378	354	530	
21252	51620	A	21379	1	1272	MVLSEKASGTLRGCTEERTLS LTSGLSMPADPCEGGARSCLV TESARGGLQFLQQCDREDLVEL ALPQLAQVVTVYEFLLMKVAE SLGITEFLRKKEIHPDNLGPKHL SRDM DGEQLEGASSEKRERE AAEEGLASVKRPRREALSNDTTE SLAANSRGREKPRPLHALAAES HTTTVSGGNGSVFQAGPQLQA LANLEARRGSIGAAALSSRDVSG LPVYAQSGEPRLTQAQVAAPF GENALEHSSAQDTWDSLRSPPGF CSPLSSGGGAESLPPGGPGHAE AGHLGKVCDFHLNHQQPSPTS VLPTVEAAPLEKILSVDSVAV DCAYRTVPKPGPQPGPHGSLLT EGCLRSLSGDLNRFPCGM EVHS GQRELESVVCLSAETMAF*NFP MGAIMSYCLRD/RSRFLFRLPM GLSCPLQVQ
21253	51621	A	21380	90	204	
21254	51622	B	21381	13	423	

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21255	51623	A	21382	1513	2405	RRAQYRRWRRRWRRRHREPE KEKRRHSRSHSRRRTLIF* TQSRSRRE*LHCQSRSR** FKSPRQRRSHSRERGRSTARHYRST KERQQRSSRSGTRSPKKSRC PKRKL SLSPSPGKHKKKKKDKERNRY ERERSTSKKKSKDREKDKERKS ESD TDVVKVTRVYDEEEQGYDT SQE IEMHADNPAAIQTVVLQRD DLQNGLLSTCRELSRATAELER AWREYDKLEYDVTVTRNQMV EQLDHLGEVQCWCYRTEKYV MERGPEQDPKRAFLDFVQERIQ GESAVQSESKFIKTVKK
21256	51624	A	21384	1	180	
21257	51625	A	21385	3	115	
21258	51626	A	21386	3	312	LPTALLRSTMALHSGRVLPGI AAAFHPGL/AA/ASARASSWW THVEMGPPDPILGVTEAFKRD TNSKKMNLGVGAYRDDNGKPY VLP SVRKFFVTQTISGTGAL
21259	51627	A	21387	3	395	STMALHSGRVLPGIAAAFHPC LAAAASARASSWWTHVEMGPP DPILGVTEAFKRD TNSKKMNLGVGAYRDDNGKPY VLP SVRKAE AQIAAKNLDLLPLLNVC SLSSH TVSPAQQGTRKEDILGFACC
21260	51628	A	21388	1	303	
21261	51629	A	21389	2	425	RPE*WKEIATVVKRNLFALFD MAYQGFASGDGDKDAWALHH FIEQGINVLCQSYAKNMGLYG EHVGAFTVVKDADEAKRVES QLKILISPMYSNPLNGAQIASTI PNT PVGLKVVVMGGLHDHPQ VMSDEKETTLRA

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21262	51630	A	21390	3	1508	HEAGAGSLCVCAPRPLLRPAAA HCPYSVRSTMAHACTSGRVLP AAA\FHPGLAAAAARASSWW THVEMGPPDPILGVTEAFKRD NSKKMNLGVGAYRDDNGKAL PCCPSVRKAEGPRLPQKIWDKE YLPIGGALAEFCKASAEALALGE NNRSLERVGRFVTVQTHFWEL GALRLGASFLQRFFKFSRDVFL PKPTWGETHPSFRDAG/MQL QGYRYYDPKTCGFDTGAVED ISKIPEQSVLL/LHACG/HNNPTG VDPREQWKEIATVVKKRNL AFFDMAYQGFASGDGDKDAW AVRHFIQGINVCLCQSYAKNM GLYGERVGAFTMVCKDA/DES KRVESQLKILIRPMYSNPPLNG ARIAAILNTPDLRKQWLQEVK GMADRLNGHAGLQLVSNLQGR EGSTHNWATHSPTKLGMFCF HRG*KLEQVERLKEFSIYMTK DGRISVAGVTSSNVGYLAHAIII QVTKYVSLVRGNGDNLVLSL
21263	51631	A	21391	1	184	
21264	51632	A	21392	70	253	
21265	51633	A	21393	1	351	VMEFYCQSCETAMCRECTEGE HAEHPTVPLKDVVEQHKASLQ VQLDAVNKRWGTLPKPPTGCL YLRPGLMASCQLTNQKASI/VD DIHSTFDELQKTLNVRKSVLLM ELEVNYYGLKHK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
21266	51634	A	21394	208	2546	WLHCMQQQRAGSKTAGPPICQ WSRMASVEGTNIPISLVVVGQNDK QFLICSICLERYKNPKVLPLCHT FCERCLQNYIPAHSLTLSCPVC RQTSILPEKGVAALQNNFFITNL MDVLQARTPGSNAEESILETVT AVAAGKPLSCPNHDGNNVMEF YCQSCSETAMCRECTEGEHAIEH PTVPLKDVVVEQHKASLQVQLD AVNKRWGTLPKPPTGCLYLRP GLMASCQLTNQKASIVDDIHST FDELQKTLNVRKSVLLMELEV NYGLKHKVLQSQDLTLLQGQE SIKSCSNFTAQLNNGHTETEVLL VKKQMSEKLNELADQDFPLHP RENDQLDFIVETGLKKSINH GTILTTNAVASETVATGELRQ TIIGQPMSTVITTKDKDGELCKT GNAYLTAELSTPDGVSADGEIL DNKNGTYEFLYTVQKEGDFTL SLSLYDQHIRGSPFKLKVIRSAD VSPPTGKRRVKSPGSGHVQK KAVKRPASMYSTGKRKENPIED DLIFRVGTGRNKGFTNLQGV AASNTGKILIADSNQCVQIFSN DQGFKSRFGIRGRSPGQLQRPT GVAVHPSGDIIADYDNKVVSI FSSDGKFKTKIGSGKLMGPKGV SVDRNGHIIIVDNKACCVFIFQ PNGKIVTRFGRNGDRQFAGP HFAAVNSNNEIIITDFHNHSVKV FNQEGEFMLKFGSNGEGNGQF
21267	51635	A	21395	1	591	
21268	51636	A	21396	3	608	LEGDQRWINTVSQALHLLSTLY GPFPCNYGIGRCAKMAVELWR NLEEEEDGETKGRRPEIGHIFLL DRGKLCPAFLSSFSRRHGNME GVVAKLS*S*GCESQL*GAWV LGPMSIKAALGHAV*KAGSGR TFMVRDLCPDVFVTALCSQV VYEGLVDDTFRIKCGKCYGPLH LGKMDGSSALAPATWGRVCGR DPHPE
21269	51637	A	21397	268	402	
21270	51638	A	21398	139	452	

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21271	51639	A	21399	1	2497	MGPVAAPLGLSLPATDGAHSV RGNSVLVPSGLIPKDYRSCLKTQ YLQSYGPEHLLTFSNLRRAGLL TEQAPGDTLTAVESKVSCLVTD KAAGKITDAFSSLAKRSNFRAIS KKLNLIPRVDEYDLKVPRDM AYVFGGAYVPLSRIIEQVLER RSWQGLDEVVRLNCSDFAF DMTKEDKASSESLRLILVFLG GCTFSEISALRFLGREKGYRFIF LTTAVTNSARLMEAMSELPGK KDLFIETDLMSPLDRIANVSLLK QHEVDKLYKVENKPALSSNEQ LCFLVRPRIKNMRYIASLVNAD KLAGRTRKYKVIQSPQKPYACE MVL EEEGIYGDVSCDEWAFSL PLDVDLLSMELPEFFRDYFLEG DQRWINTVAQALHLLSTLYGPL SQTICYGIGRCAK\ MAYEFVEGT WEEEEEDGRNPRARREGFG\HIF LL\DR\DVDFVDSTLLPKLVYEG LVDDTFRIKCGSVDFGPEVTSS DKSLKVLNNAEDKVFNEIRNEH FSNVFGFLSQKARNLQAQYDR RRGMDIKQMKNFVSQELKGLK QEHY\LLSLHIGVACESIMKKKT KQDFQE\LIKTEHALLLEGFNIRE STSYIEEHIDRQVS\PIESRLMC LLSITENGLIPKDYRSCLKTQYLQ SYGPEHLLTFSNLRRAG\LLTEQ APGDNLTAVESKVSCLVTDKA AGKITDALSSSLAKRSQFRAISK
21272	51640	A	21400	1	216	
21273	51641	A	21401	2	270	
21274	51642	A	21402	1	600	SGRALHASWAAGVGAYSGRL RSDALEGESFALSPSSASDAEF DAVVGYLEDIIMDDFQLLQRN FMDKYYL\EFEDTEENKLIYTP\I FNEYISLVKEYIEEQ\LLQR\PEF NMAAFHHNITPSVPVCRHHKD EVAW*QYSAMLAPPFTRFSWA F*RNVFGTYRGRKKEGRGL\DL SSGLVVTSLCKSSSLPASQNNL RH
21275	51643	A	21403	1	297	

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21276	51644	A	21404	1	1419	MGAPLLSPGWGAGAAGRWW MLLAPLLPALLVLRPAGALVEG LYCGTRDCYEVLVGSRSAGKA EIARAYRQLARRYHPDRYRPOP GDEGPGRTPQSAEEAFLLVATA YETLKIVFPELKIVKELTTLMP SRAVWIIWSHKMSGGAGPEL DIGYVPVLLHMPKRIGSGMDTS RSTTVIPVEIRNKELIALLVKAQ DRQEEETNYKLRFNGLSYEVG YLVILQDEETRKDYDYMLDHP EEYYSHYYHYYSRRLAPKVDV RVVILVSVCAISVFQFFSWWNS YNKAISYLATVPKYRIQATEIA KQQGLLKAKAKSKNNKVQR RNS*VEENIIKNIKSKIDIKGGY QKPQICDLLLLFIILAPFHLCSYI VWHCRWIYNFNKIGKEYGEEE RLYIIRKSMKMSKSQFDSLEDH QKETFLKRELWIKENYEVYKQ EQEELKKKLANDPRWKRYRR WMKNEGPRLTFVDD
21277	51645	A	21405	1	1266	
21278	51646	A	21406	1	739	
21279	51647	A	21407	1	428	

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21280	51648	A	21408	99	2338	MPEEVHHGEEVEVETFAFQAEIA QLMSLIINTFYSNKEIFLRELISN ASDALDKIRYESLTDPSKLDSDG KELKIDIIIPNPQEPYPGLWVDTG IGMTKADLINNLGTIAKSGTKA FMEALQAGADISMIGQFGDGFY SVANLVAKKVVVITKHPDDEQ YAWESSAGGSFTVRADHGEPIA VRGTQVILHLKEDQTEYLEERR VQEVVKKHSQFIGYPITLYLE KERKEKISDDEAEKKGEKEE DKDDEEKPKIEDVGSDEEDDSG KDKKKTKKIKEKYIDQEELNK TKPIWTRNPDDITQEEYGEFYK SLTNDWEDHLAVKHFSVEGQL EFRALLFIPRRAPFDLFENKKK NNIKLYVRRVFIMDSCDELVPEA YLNFIPIGVVDSEDPLNIFRKML QQNK/LWKVIRKNIVKKCLELF SELAEDKENYKKFYAFSKNLK LGIHEDSTNRRRLSELLRYHTS QSGDEMSTLSEYVS/RMKETQ MSIYYITGESK/EQVANSFAFVER VRKRGEFVVYMT/EPIDCYCQ QLKEFDGKKLVSVTKEGLELP EDEEEKKKMEESKAKFENLCK LMKEILDKKVEKVTISNRLVS SPCIGIKHKLGAQALIERDHE KPRALRDHPQGGIMMGKKAP *ESPDPHPHFVETRAGRKADAR QVMIRAVKD/LWVVLLV*NPP LLSSGFSLED/PQT/HTPNRIYRI
21281	51649	A	21409	1	426	
21282	51650	A	21410	1	1305	
21283	51651	A	21411	446	3180	VAVRLGSASQFPGARQLPRP PSWSSSIHPISTTGLSESTDSDS KSGLRGFSAYNPSSRIKSTTSS NSSDGAVTASNQDTGIPWVLV TGPITPVNSPVESLQGSASFSSGF STPRGLVKGPTLPPDSNLT/SVSD YTWIFVRGPPINDLSQVSIQAP PTPSNTPECQYKGLPHPCPASP GVWYQDHLYPITFPQCRHKHL LHPITSPQCQGRRLPPQCLTLR GVQYKNLLHPVILSSCRHKDIL NLITLAE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
21284	51652	A	21412	24	667	MLPWLNCITTGVPWTPTSKRW LRNSKVCDCCKDTPSNAFSLLS VPPTTTSPASLAWWSGCARLLD LGSSSLMMSPTMASPACRPWL GQRWRLISGSWAWAIVPT*VP VPEPSWKNRAG*PGCSSYESPH MRRPTRPSASCLFWAPRASLA MHLMATSFVLLSSARITSEKA PLSGEGIHKVKWNWNPSPASP FPMGVSVTAGPRTWMTLP
21285	51653	A	21413	1	304	RAQVLPARCYPGSTVSPLGFRG LPLPRGGSEIPRCATAATRP MPFLFYLFLLQQH AAVPGFWTSAHPA/CDVITYHGF PSLQALAGPPWQCI
21286	51654	A	21414	1	7629	
21287	51655	A	21415	180	423	
21288	51656	A	21416	17	753	QAHTRRAGGRAQVLPARCYPG STVSPLGFRGLPLPRGGSEIPRC ATAATRPHRMPFLFYLFLLQQH RPHHWHGGAAVPGFWTSAHPA /CDVITYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGG/RLAAAAATRVLI*GGP QGPHPAWSGHQGG*LHLPDG PRQAPGCARGCPYVAHCPT*LQ LAPYHVPGEGETPPDQGTGKL FPEPVGTLCWLGPSALSGHHHF YDLSRTP
21289	51657	A	21417	17	1087	QAHTRRAGGRAQVLPARCYPG STVSPLGFRGLPLPRGGSEIPRC ATAATRPHRMPFLFYLFLLQQH RPHHWHGGAAVPGFWTSAHPA /CDVITYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGG/RLAAAAATRVLI*GGP QGPHPAWSGHQGG*LHLPDG PRQAPGCARGCPYVAHCPT*LQ LAPYHVPGEGETPPDQGTGKL FPEPVGTLCWLGPSGWIRCLLK NYRLPLDLEGLLGNAFDGHQ LLRPLIFCQDHLREGPIGRGDS QGEELPQLPSSLSSIPYGFCDH CWTKDVEDPPLVTHPSGSRD GHMTQA/WPVKVVSPLATVIGH VMQASLLAL

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21290	51658	A	21418	3	1584	TQKNTAVRAHRLWGREGISRK EGAGPTPQESRRIGARSGALMT RKGRGMQVEEELSETGKVVKQ HRVGEALRVVVLVWAGSLG/D RRGLVLGRRGYYGAVPAVEMP ARALLPRRMGHRTLASTPALW ASIPCPRESELRLDLVLPSSGQSF WREQSPAHWSGVLADQVWTL TQTEQLHCTVYRGDKSQASRP TPDELEAVRKYFQLDVTLAQL YHHWGSVDSHFQEVAKFKQG VRLLRQDPIECFLSFICSSNNNIA RITGMVERLCQAFGRPLQLDD VTYHGFPSLQALAGPEVEAHLR KLGGLGYRARYVSASARAILEEQ GGLAWLQQLRESSYEEAHKAL CILPGVGTKVADICLMLADKP QAVPVDVHMWHIAQRDYSWH PTTSQAKGPSPTNKELGNFFR SLWGPYAGWAQAGLLGNAFD GHQLLRPLIFCQDHLREGPPIGR GDSQGEELPQLPSSLSIPYGF CDHCWTKDVEDDPLVTHPSG SRDGHMTQAWPVKVVSPLATV IGHVMQASLLAL

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21291	51659	A	21419	837	2785	WTRMLFAVSCNDGECQNSNVI LFCDMCLNLAVHQECYGVPIPE GQWLCRRCLQSPSRAVDCALC PNKGGAFKQTDGGRWAHVVC ALWIPEVCFANTVFLEPIDSIEHI PPARWKLTCYICKQRGSGACIQ CHKANCYTAHVTCQAQAGLY MKMEPVRETGANGTSFSVRKT AYCDIHTPPGSARRLPALSHSE GEEDEDEEEDGKGWSSEKVK KAKAKSRJMKMKARKILAEKR AAAPVVSVPICPPHRLSKITNRL TIQRKSQFMQRLHSYWTCLKRQ SRNGVPLLRRLQTHLQSQRNCD QVGRDSEDKNWALKEQLKSW QRLRHDLEARLLVELIRKREK LKRETIKVQIAMEMQLTPFLIL LRKTLEQLQEKDGTGNIFSEPVPL SEVPDYLDHIKKPMDFFTMKQ NLEAYRYLNFDDFEEDFNLIVS NCLKYNAKDTIFYRAAVRLRE QGGAVVRQARRQAQKMGIDFE TGMHIPHSLAGDEATHHTEDA AEEERLVLENQKHLVPVEEQLK LLLERLDEVNASKQSVGRSRRRA KMIKKEMTALRRKLAHQRETG RDGPERHGPSSRGS LTPHPAAC DKDGQTD SAAE SSSQETSKGL GPNMSSTPAHEVG/GEPQFCSP KRTRRQ/HGPPKRPGRPPKNRES QMTPSHGGSPVGPP/RAPHHEFP ASAQAG*EPQFCSPKTRRQLD
21292	51660	A	21420	I	2625	MENKITGYTTVDISQWHRKEHF EAFQSV AQCTYNQTVQLDITAF LKT VKKNKHKFYPAFIHILARL MNAHPEFRMAMKDGELVIWD SVHPCYTVFHEQTETFSWLSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGFENMFFVSANPWV SFTSFDLNVANMDNFFAPVFTM GKYTTQGDKVLMP LAIQRDSE DKNWALKEQLKSWQRLRHDL ERARLLVELIRKREKLKRETIKV QQIAMEMQLTPFLILRLK

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21293	51661	A	21421	164	1401	PPKGRGMQVEVEELSETGKVVK QHRVGEALRVVVLVWAGSLG/ DRRGLVLGRRGGYGA VPAVE MPARALLPRRMGHR TLASTPA LWASIPCPSELRLDLVLP SGQS FRWWREQSPA HWSGV LADQV WTLTQT EEQLHCTVYRGDKSQ ASRPTPDELEAVRKYFQLDVTL AQLYHHWGSVD SHFQEV AQKF QGVRLLRQDPICLFSFICSSNN NIARITGMVERL CQA FGPRLIQL DDVTYHGFP SLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGG LAWLQQLRESSYEEAH KALCILPGVGTKVADCI CLMAL DKPQAVPVDVHMWHIAQRDY SWHPPTTSQAKGPSPTNKELGN FFRSLWEPYAGWAQATPPSLQ VLFSADLRQSRHAQEP PAKRRK
21294	51662	A	21422	751	2107	SSEHPRELHRIPISWAMSELKDC PLQFHD\FKSV DHLKVCPRYTA VLARS\EDDGIGIEELDTLQLEL ETLLSSASRR\LRVLEAETQILT DWQDK\KGDRRFLKLRDHE FGAPPKHGKPKK\QKLE\GKAG HGP GP\CPGRPKSKNLQPKIQE YEFTDDPIDVPRIPKNDAPNRF WASVEPYCADITSEEVRTL EEL LKPPPEDEAEHYKIPPLGKHYSQ RWAQEDLLEE QDGA RAAAV ADKKKGLMGPLTELDTKD VDA LLKKSEAQHEQPEDGCPFGALT QRL LQALVEENIIPMEDSPIDP MSGKESGADGASTSPRNQKP FSVPHTKSLESRIKEELIA\QALL *AGDLLAKDSEDEVLAELRRK QG\EL\KALSAHNRTKKA\DLLR LAKEEVSRQ\LRQR\VRRAERE GMDAFRKIHGLPGRKRNSPPK K\EKDQA WKNS*KEREHP
21295	51663	A	21423	107	331	

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21296	51664	A	21424	387	1071	NNPEWRTLIYVDKENGEPGTR VVAKDGLKLGSGPSIKALDGR SQVSTPRFGKTFDAPTQPYLKL PRKALGTVNRITTEKSVKDPGD PSNKKQPKLFRPKKDGPEEGLL KAKKPLFPGLOD*CPPEIRKIPF PFNPS*TLRSF*PCPEEHPDCGTF PL*VGVLMIPLTREREL*KSW FQLGPPFHLWKDGLPPWGIPI LQFSFQGISVRTWGVLDLPVCC DIDI
21297	51665	A	21425	480	1270	RSVKKVGAQRPGSGGWGNG EGWVPQATAPGWAYTHVLFY LFVTTPIAALRADGFGDNPFY HCLVAEILPAPGKLLGKSTWPL EVHLSSRPQRSPHRLPEALLPFS LSQG/HCVVGYGIYYFIYSTWK GRTIYLEDIYVMPEY/RGYWAE AEAGVGAKHPTDPTVIPCPQSP AGVIF*SPSAQTIAIFCLFSTTG QGIGSKIHKVAEVALDKGCSQ FRLAVLDWNQRAMDLYKALG AQDLTEAEGWHFFCFQGEATR KLAGK
21298	51666	A	21426	182	797	LPFARPWDFGPRQRGSGWLPC GSREAKEGDCGDILRLIRVKA GPDLAEFEKLFSGGERSVEEAL ESRLAFGDNPFYHLFW*AEILP APGESYWG/HCVVGYGIYYFIY STWKGRTIYLEDIYVIAGNIGV QGIGSQK*SKKVAAEVALGIRGC SPNFRLARPLD\WNEGEPWDLY KAPRSPKI*RKLEGWHFFCFQG EATRKLAKG
21299	51667	A	21427	224	490	QAGFISARNITWR*ANRRSTWR SYRRKSGRTANCPISPACSRC SAPIFIPKNGWWRAMVAPLKW PSTGAFNRLFVPLLTWWRSPDR
21300	51668	A	21428	301	773	HGPGTQQRPRSIWRMPQ*ARPG GRSLAVGGGPRPRAAGGP*VA SRARRCQRAHGCHCAFSPSP ALLSQDAGLCQSRPLLLGQRR LSQEVVWSGLGNVHFCQPPEDA ATTPSCPEALTAQQQQAASVCDR VSHRFSTWSMVRCSDRTEGQR LQTLGD
21301	51669	B	21429	1	1380	

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21302	51670	A	21430	1	1660	AGVLASHPNSTDVHIINLSLTFH GQELLSDTKLELNSGRRYGLIG LNGIGKSMLLSAIGKREVPPEH IDIYHLTREMPSPDKTPLHCVM EVDTERAMLEKEAERLAHEDA ECEKLMELYERLEELDADKAE MRASRILHGLGFTPAMQRKKL KDFSGGWRMRVALARALFIRPF MLILLDEPTNHLDLDACVWLEE ELKTFKRILVLVSHSQDFLNGV CTNIIHMHKKLKYTYGNYDQ YVKTRLELEENQMKRFHWEQD QIAHMKNYIARFGHGS AKLAR QAQSKEKTLQKMMASGLTERV VSDKTLFSYFPFCGKIPPPVIMV QNVSFKYTKDGPCIYNNLEFGI DLDTVALVGPNGAGKSTLLK LLTGELLPTDGMIRKHSVKIG RYHQHLQEQLDLDSPLYEYMM KCYPEIKEKEEMRKNIGRYGLT GKQQVSPIRNLSDGQKCRVCL AWLAWQNPMLFLDEPTNHL DIETIDALADAINFEFGGMMLV SHDFRLIQQVAQEIWVCEKQTI TKWPGDILAYKEHLKSKLVD\

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21303	51671	A	21431	78	2022	NNSNLPVWIIIPSDLAKKAA KKKEAAKARQPRKGHEENG VVTEPQVAEKNANGRE/TTRE VDLLTKELED FEMKKAARAV TGV LASHPNSTDVHIINLSLTFH GQELLSDTKLELNSGRRY/GLIG LNGIGIGKSMLLFAIGKREVP EHIDIYHLTREMPSPDKTPLHCV MEVDTERAMLENEAERLAHED AECEKLMELYERLELDAD*AE MRASRIHLGLGFTPAMQRKKL KDFSGGWRMRVALARALFIRPF MLLDDEPTNHLDLDACVWLEE ELKTFKRILVLVSHSQDFLNGV CTNIIHMHNNKKLYTYGNYDQ YVKTRELEENQMKRFHWEQD QIAHMKNYIARFGHGSAKLAR QAQSKEKTLQKMMASGLTERV VSDKTL SFYFP CGKIPPPVIMV QNV SFKYTKDGPCIYNNLEFGI DL DTRVALVGPNGAGKSTLLK LLTGELLPTDGMIRKHS HVKIG RYHQHLQEQLDLDLSPLEYMM KCYPEIKEEEMRKIGRYGLT GKQVSPIRNLS DGQKCRVCLA WLA WQNP HMLFLDEPTNHLDI ETIDALADAIN EFEGGMMLVSH DFRLIQQVAQEIVCEKQTITK WPGDILAYKEHLKSKLVDEEPO LTKRTHNVCTLTASLPRP
21304	51672	A	21432	313	599	
21305	51673	A	21433	737	1006	DNPVVFVFGSVYMLDYVY*FS YVEPLHPWDEAHLIMVDKLF DVL L DSVQCYFIEDFCINVNQ YWSKILFCCISARLWYQDDAG
21306	51674	A	21434	1108	1260	GVNPNLSCFLWAFSAIHFLPH TALNVSRQFWYVVSFLVSK NIFISAF
21307	51675	A	21435	804	917	
21308	51676	A	21436	158	298	
21309	51677	A	21437	1	1068	
21310	51678	A	21438	1	1188	
21311	51679	A	21439	122	352	
21312	51680	A	21440	647	662	ICGVISEGSLVFH*SISLFWYQY HAVLVT/DSL VV*FEVT*HDASS FVLLA*DRRPEGSSPKSP
21313	51681	B	21441	53	692	
21314	51682	B	21442	1	925	
21315	51683	A	21443	606	900	

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21316	51684	A	21444	33	852	CWKFWARAN*AGGITLPDFKL YYKATVTKTAWKFHFTMFGV DLKETCTAPSLWKDLALNTVE LVCKLCVRQVEGARQIFQLNCT VSE
21317	51685	A	21445	3	795	
21318	51686	A	21446	475	1023	CWFSAGDGGLPDPDYQDFAA HPAGAGALYKCRDLINDNLR VSCQSHDDGDIRGMAFARQ*Q RPVQIDHNMARRG**AATFQPI NKTFSGIHWPHGMRTGGTNPN FENIECTNHIHTLGLPFSEVERN DCDGFNFQLHIFRQTRDLHTAP GRIGRLMLIEELLIDFVGGKII QIGDKHGH
21319	51687	A	21447	1637	2020	PSSEFTGGPARGFPERARAQL TGRTPGQRTQLDNDLLTKSTP WRGVMGPTLLPGLLAGPFQPL GHTGPFYPQGFWRQKTHWVRL AQAHWF*LGQFRGPKTADGG GSKGPGLSASHGAKHHVITYV
21320	51688	A	21448	1051	1185	
21321	51689	A	21449	1290	2025	
21322	51690	B	21450	1	1410	
21323	51691	A	21451	3269	3678	SLSIRLATAPCWLRYPASSRRFQ PTRSAGSVTDSSVTASASSPG*R *NASP*CRERSHRSSRGQARRSL HLWDRSDR*TLPCDHGRCCCHA NDQQVGFAGNYSTAGQT*RWT GFTAGHAGRDINKSADKLPA T AGKR
21324	51692	B	21452	2655	2825	
21325	51693	A	21453	1	896	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKLNLTQNHSTTWKLN NLLLSDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKA VCRGKFIALNAHKRQKERSKIDTL TSQLELEKQEQTHSKASRRQE ITKIRAELEKIEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITDTPTEYK LPSENTTNTSTQIN*KI*KKWIN SSTHTLSQD

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21326	51694	A	21454	23	559	TPGLRQSSLSPSAFASQNAAGVS GIGGFLVSLTSRMKPWTLAMFR CVVSWFFLLVGSWSCWLQE*SC RPSQ*VSQFLNSSASGVVCCSC LELFVPPGGFVSLASRVKLQT FTVSVTAHKGQVDPKSEQQQD LVQKAKEHSFCSVEADLSGLPL LAGAACFYSLMEPHPHADWSI LQRAD
21327	51695	A	21455	26	323	
21328	51696	A	21456	221	734	
21329	51697	A	21457	293	2103	PCHSALSSPLPHRDCIALCFLNS GTSFVAGFAIFSILGFMFQEQG VPISEVAESGPLAFIAYPRAVV MLPSPSLWACCCFFMVLLGL DSQFVCVESLVTALVDMYPHV FRKKNRREVILGVSVISFLVGL IMLTEGGMVVFQLFDYYAASG MCLLFVAIFESLCVAWVYGAK RFYDNIEDMIGYRPWPLIKYCW LFLTPAVCTATFLSLIKYTPLT YNKKYTPWWGDALGWLAL SSMVCIPAWSLYRLGTLKGPFR EVIIPVSIRMTKVAGTAGLSGN VGPRCDLSRIEELPDGGTRCGM DSRVSGTTSNGETKPVYPVME KKEEDGTLERGHWNKMEFVL SVAGEIIGLGNVWRFPYLCYKN GGVVGFYNSIKNIPILQRVILFV RIHNMLNKGQGVLAACDAK KIEEKEADAGSASVPGDVMRT KKLSFEGAWHPCLLVGLKLS ALELRGGFISARIAGPRAESDS VGLERELRVCIANKLPGEADAA GPGTTFWKHCSPITDGADAV EGRNTQEAFFRLNPEAAFLHF MEMVDTNALHVHGIHTRKNHP GQKEAAHSQHGTFPIRWTLNLL KRTFQKGNRAEPNSPAM
21330	51698	A	21458	1	419	MKLRTLAVSATALKVARLEFV PFDVRCSEFLSSGVKLQTFAY SVTALNALRLFLVPPGGLMVS LASGVKLQIFTVSVTAHKSSVD PKTLG/CVDGTGRRGAGGGGAH RGGLGRGTAHGGGGRLRHGGL QVSSPAPRKGS

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21331	51699	A	21459	24	1639	GGMDSRVSGTTSNGETKPVYP VMEKKEEDGTLERGHWNKMM EFVLVAGEIIGLGNVWRFPYL CYKNGGGAFFIPYLVFLFTCGIP VFLLETALGQYTSQGGVTAWR KICPIFEGIGYASQMIVILLNVY YHVLAWALFYLFSSFTIDLPGW GCYHEWNTGNWVDVVE/HGG* GEWCGNGSNTPHVCR/VTGWT W*SRWLKGMVWEWQHPTCV QGTGWTW*STWLKG/PGNRVD VVEHVAEGNGVGMDPHTHTCA GNRVDVVEQVAEGNEHCMEF QKTNGSLNGTSENATSPVIEFW DSPPGPQFVCVECLVTASIDMF PRQLRKSGRRELLITIAVMCY LIGLFLVTEGGMYIFQLFDYYA SSGICLLFLSLFEVV CISWVYGA DRFYDNIEDMIGYRPWPLVKIS WLFITPGLCLATFLSLSKYTPL KYNNVYVYPPWGY/SIGWFLA LSSMVCPVLFVVITLLKTRGPFR KVGVGESDLLKEGTERGWT WGRTHNWQGGADTNSECGAA LQSHRILTRTLKTSPIVAFQKCS
21332	51700	A	21460	1358	4787	RRCCGWSRYLLKRLWKWIS GEGWAEKSDARRRGICTFWLE FE/VTCLSWNSLF/YAHINVDISG MKVFWLYVGMCFSSFCWHIED HWSYSINYLHWGEPKTWYGVP SHAAEQLEEVMLRELAPELFESQ PDLHLQLVTIMNPNVLMHEGV PVYRTNQCAGEFVVTFFRAYHS GFNQGYNFAEAVNCTADWLP IGRCQVNHYYRLRRHCVFSHEE LIFKMAADPECLDVGLAAMVC KELTLMTEETRLRESVV
21333	51701	A	21461	1	5773	MEEKPLVKKGKDSSEKKRRRK LEKVEQLFGEGKQKSKELKKM DKPRKKLLKLGADESKELNKL AKKLAKKEERKKKKEKAAAK VELVKESTEKREKKVLDIPSK YDWSGAEESSDENAVCAAQN CQRPCKDKVDWVQCDGGCDE WFHQVCVGVSPMAENEDYICI NCAKKQGPVSPGSHKAVITVV VKAVSYLKFEESTSELMWLL AAFSSFVVVGKALDFVWPLA REEKEIGDNKDLERNKIGVNM

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21334	51702	A	21462	85	1333	STSRALSGAQRFGRLIDHGARV PALLLLLLLPVHVVSATTEPPE LDDEDFRVCNCFSEPPQDWSEA FQCVSAIVEVEIHAG/GLNL/EPF LKVRVDADADPRQYA/DTVKG PR/VRASQVGAAQVPA/QLLV GALR/VLA/YSRFKELTLEDLKI TGTMPPLPLEATGLALS/SLRLR NVSWATGRSWLAEL/QQWLK PGLKVLISIAQAHSAPFSCEQVR CFPGPSPA*DLSDNPGTGANAE LMAALCPHKFPAIQNL/ALRNT GNRRRQGVCAALAAAGVQPH SLDVSHINSLRANRNP/APRCM /WSNA/LNSPQICRFAGAGTGVP KGPAPAKL/RVLRSSACNRL/INR A/PQPWTSLEPVDNLGQLDGNP FPGSPGTGSPTEGSMN/SGVVP SLCNVTRCTRVGSGT/VLLQG ARGFA
21335	51703	A	21463	1640	5804	TITGSSPLAGGHSTCRGRMDM VENADSLQAQERKDILMKYDK GHRAGLPEDKGPEPVGINSSIDR FGILHETELPPVTAREAKKIRRE MTRTSKWMEMLGEWETYKHS SKLIDRVYKGI/PMNIRGPVWSV LLNIQEIKLKNPGRYQIMKERG KRSEHIIHIDLDRVTRTLRNHV FFRDRYGAKQRELFYILLAYSE YNPEVGYCRDLSHITALFLLYL PEEDAFWALVQLLASERHSLPG FHSPNGGTVQGLQD
21336	51704	A	21464	1	960	
21337	51705	A	21465	1	1317	
21338	51706	A	21466	1	3393	
21339	51707	A	21467	2745	6141	QGSKGTCHPQAQQPWDEGVW QEAPSQSEPWGQSQEPPTMPQR LPHARQHTPLPLGSADYRRVVS VRPQGFHRDPKDSRDAAREQ GSLAPRPVPASRGGTLCKGYR QAPPGPAAQFORPICSASPPWAS RFSTPCPGGAVREDTYPVGTQG VPSLALAQGGPQGSWRFLWK SMPRLPTDLDIGPWFPHYDFE RSCWVRASQEDQLATCWQAE HCGEVHNKDMSWPEEMSFTAN SSKIDRQKVPTKGGATGL
21340	51708	A	21468	65	320	
21341	51709	A	21469	3	505	

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21342	51710	A	21470	2	1756	CRCHSELGSSSL*/CCTRGIGGAI GAVGFRSQAASLAGQPPDNG VCVHAGNSRIFVPLPVGLEVKG FSHSAFTFGIESHSQSNINGTLV PPSALISILKGLQYVEAEISINK DGTVFDSRPIESLSLIVAVIPDV VQMRQQAFGEKLTQQQASAA ATEASAMAKAATMTPAAISQ NPPKNREATVNGEENGAEHINN HSKPMEIDGDVEIPPNKATVLR GHESEVFICAWNVSLLASGS GDSTARIWNLNENSGGSTQL VLRHCIREGGHDVPSNKDVTSL DWNSDGTLAMGSYDGFARIW TENAPALDWDQNNMTFASCS TDMCIHVCRGLGCDHPVKTFQG HTFCTCIESICFWGGLRKLTTM TEGKRLRPKTFCDGGALLPPA GRRPHLLTGPDIFFKRLSALFQN EVNAIKWDPSGMLLASCSDDM TLKIWSMKQDACVHDLQAHSK EIYTIKWSPTGPATSNPNSSIML ASASFDSTVRLWDVEQGVCTH TLMKHQEPVYSVAFSPDGKYL ASGSFDKYVHIWNTQSGSLVHS YQGTGGIFECVWNARGDKVGA SASDGSIVCILWQLSGKQ
21343	51711	A	21471	1	1647	
21344	51712	B	21472	4	267	
21345	51713	A	21473	1	1824	
21346	51714	A	21474	33	543	TFEGANNFVGDPVLPNPPKG LPPLHIYWMNIELEHIEQDERV YMSQKGDLYFANVGRKRDSRN D/YCCFAA/FPRIKGLLYRKMPM /RNLTVNSSSIKAKENPKLLLA SPLRSGSESSITLKGEILLLECF AEGLP TPQVDWNKIGGDL PKG REAKENYGKTLKIENVY
21347	51715	A	21475	197	516	TYLAAGRTPTLDPWNQERCTM PSGSIWILETHSSFGWVTVAH LSSDPKGCQF*VGSRIEGSATD PAFCASCATWTIRPSRSNGA*G VNG**VCWLEPLAGPHR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
21348	51716	A	21476	1	1766	MNVALTHIDTHHAEFEMALQA ALVWNTLRTAGGKKSVDHLASA LLVHEIHDGANLTSNVTLEDQ GIYCCSAHTALDSAADITQVT LDVDPDPENLILSERQNRSVRL TWEAGADHNSNISEYIVFEGN KEEPGRWEELTRVQKKTTVIL PLAPFVRVYQFRVIAVNEVGRSQ PSQPSDHHETPPAAPDRNPQNIR VQASQPKEMIIKWEPLKSMEQN GP/GLEVRVTWKPGGAPVEWE EETVTNHTLRVMTPAVYAPYD VKVQAINQLGSGDPDQSVTLYS GEDLPEQPTFLKVIKVDKDTAT LSWGLPKKLNGNLGTGYLLQYQ IINDTYEIGELNDINITTPSKPSW HLSNLNATTKYKFYLRACTSQ GCGKPIEESSTLGEQSVSLEKC ENKLIRNIGTKKGQTAIRIPENV EAAELRKQKQLEECGGFRRRRE NANEQQGVTEEFKQNEKLRF LLLKIVILAVAREMTWNGEGR DLSEPSLTVVFADLSSPAYSLHT TMAQEPGPGFLFLSLSTIPWISSI PMIHASVQVSWIPLLRNSLMVH IHSSLEQRNLKVHISKEQKLLNS VDSDLTDNPPTHTIVN
21349	51717	A	21477	1	1440	RAMEPLLLGRGLIVYLMFL.LLK FSKAIEIPSSVQVPTIIKQSKVQ VAFPFDEYFQICEAKGNPEPTF SWTKDGNPFYFTDHRHIPSNN GTFRIPNEGSHSHFGQKYRCFAS NKLGIAMSEIEFIVPSVPKFPK EKIDPLEVEEGDPVIVLPCNPPKG LPPLHIYWMNIELEHIEQDERV YMSQKGDLYFANVEEKDSRND YCCFAAFPRLRTIVQKMPMKLT VNSLKHANDSSSSTEIGSKANSI KQRKPKL
21350	51718	A	21478	266	3974	

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21351	51719	A	21479	1	2421	QAGAMASGSVAECLQQTTCF VCLQYFAEPMMLDCGHNICCA CLARCWGTAETNVSCPQCRETF PQRHMRPNRHLANVTQLVKQL RTERPSGPGGEMGVCEKHREPL KLYCEEDQMPICVVCDSREHR GHSVLPLEEAVEGFKEIQNQL DHLKRVTRLKFTDFLAQGEQA RAELLSLTHMEREKIVWEFEQL YHSLKEHEYRLRLARLEELDLAI YNSINGAITQFCNISHLSSLIAQ LEEKHQPTRELLQDIGDTLSK AERIRIPEPWITPPDLQEKIHFIA PKCLFLTESLKQFTEKMQSDME KIQELREAQLYSGGSIVGGHEP GEPRGIKAGYGTCNCFPEEEKC FCEPEDIQDPLCDEL CRTVIAAA VLFSFVVSLLSAFCIHCHYHKF AHKPPISSAEMTFRRAQAFFVS YSSSGARRPSLDSMENQVSVD FKILEDPKWEFPRKNLVLGKTL GEGEFQKVVKATAFHLKGRAG YTTVAVKMLKENASPSLRDL LSEFNVLKQVNHPIVILYKLYGAC SQDGPLLLIVEYAKYGLRGFL RESRKVGPGYLGSGSRNSSL DHPDERALTMGDLISFAWQISQ GMQYLAEMKLVHRDLAARNIL VAEGRKMKISDFGLSRDVYEE DPYVKRSQGRIPVKWMAIESLF DHIYTTQSDVVSFGVLLWEIVT LGGNPYPGIPPERLFLNLLKGTG

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21352	51720	A	21480	79	2253	PSATLSCTPSVAASLGEPVAFPL SLRGHRRRHPRGHSPKPSVRGRV WDTGPGGAALRPPGASQEQR GESAGELGSVQSSAPGMPVVRP RRPGAMASGSVAECLQOETTC PVCLQYFAEPMMLDCGHINICC ACLARCWGTETVNSICPQCR EITPQRHMRPNRHLANVTQLV KQLRTERPSGPGGEMGVCE/K HREPLKLYCEEDQMPICVVCDR SREHRGHSVLPLEAVEGFKEQ IQNQDLHLKRVKDLKRRRAQ GEQARAELSLVQTMEREKIVW EVEQLYHSLKEHEYRLRLARLEE LDLAIYNSINGAITQFSCNISHLS SLIAQLEEKQQQPTVRELLQDIG DTLSRAERIRIPEPWITPPDLQE KIHIFAAQKICLFLTESLKQFTEK MQSDMEKIQELREAQLYSVDV TLDPTATYPSLSDNLRQVRY SYLQQDLDPNPERFNLIFPCVLG SPICFIAGETIIWEGRGWDKAK WTIGVC*RLSCQEKGGVTSAP QNGFWAVSLWYGKIEYWALT SPMTALPLRTPFQIRVGIFLDYD AVEVSFYNVTERC/HTPFTFSS CLPFGGLVRPLSSLSYSGREK VQLPLINLP*SGIDGGFLAHVG INHGSPFWKTFPFEGRVNSGPK GLLAIVLRPGTRHLVCLANVLS KLGIUNHVPRPCSGRHGCPCLP SFFLPMQIVKCNEMYQDILEKT
21353	51721	A	21481	1	1068	

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21354	51722	A	21482	955	2548	MSLCGARANAKMMAAYNGGT SAAAAGHHHHHHHHLPHLPPP HLHHHHHPQHHLHPGSAAAVH PVQQTSSAAAAA MLNPGQQQPYFSPAPGQAPGP AAAAPAQVQAAAAATVKAHH HQHSHHPQQQLDIEPRPIGYG AFGVVWSVTDPRDGKRVALKK MPNVFQNLVSKRVFRELKML CFFKHDNVLSALDIL*PPHIDYF EEIYVVTLMQSDLHKIIVSPQP LSSDHVKVFLYQILRGLKYLHF RLGILHRDIKPGNLLVNSNCVL KICDFGLARVEELDESRHMTQE VVTQYYRAPEILMGSRHYSTAI DIWSVGCIFAELLGRRILFQAQS PIQQLDLITDLGLTPSLEAMRTA CEGAKAHILRGPHKQPSLPVLY TLSSQATH*TGHLFAECGFDP SKRISAKDALSHPYLDEGRRLRY HTCMCKCCLSPS/ TGRVNT/SDL EPVT/NPKFDDTFEKNLSPVRQV KEIHHQFILEQ/KQGNRV/PLWIN PQSAVFKSFISSTVAQPSEMPP/S PLVWE
21355	51723	A	21483	119	692	SYKSRLARKSVTGGKAPRKQLA YKKPASQECGPLTGGVKKPHR YRPGTVAAP*NLDGYQKSTEL MIRK'LRFRQLVREIAQ/DFKT DLRFQSAVIRWLCRMA/SEAYL VWPFKDTNLVCLSMKRVITY AKKTFQLSTPASRGERALRIHS WMGKHFILKKKKKFLFLL VVLNVRYFFFHGVKRYLSI
21356	51724	A	21484	2	363	RFTKVMEMKUMLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNLKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELKEALNMERNNW YQPLQKHAKL

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21357	51725	A	21485	1	1468	MRNLRNIQKAKATINLGISFDE GLKGFMSRIEAAPLPNTRWC LPHGYSGPANSGGCYYITTGMS CWLSLDLYPRHDGVHVLQGG DLEHDIPVDLGSRPVSVDPSRS APGPQGPAPVDSGSRTPPANP GAGPSPVDPSSRPAPVASGFRLL MIDQNTKLIPVPGWPLRLRLKI YLSRSASLDSGSRFAPVDTNFI PVPTDRGHSHAPEDPVDRLTSV DPTKEKNWMENEFDKLTEVGF RRSVITNFSELKEHVLTHRKEA KNLEKRLDEWLSRITCAEKSLN DLMELKTTVRELREAYTSFMS QFDQAEERISVIEDQINEIKLSL QAQEDARHRNTDQRSSSENRRS EPWSLEERKREQWNSLKQNA QQDTEAMSDYK/R/YSSET*RRR *LFCLLRKVHSEGP*KKDQRE TRNQKGLGFLDRPQWVSGKM KQECLQLGTPWP*IIIGWQYFP RDGMGVRTDFCRIFQLARMR LCEGCLMNS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
21358	51726	A	21486	1	2589	MSPVTLWVRTSSRGEDRCGMC TPGRDTGFAPISGMC SKYRSCTI NEDTGLGLAFTMPMSLDTKHIP NFGKVHGYIMRHHKNEDTIPW RRNTKKEEARGTQPLEADDQN PGWEDGKPGSLENEGRSSIRG NPAPDMPQPPKEDLFLPDEYK SCLRHKRSLLRSHRNEELNVET LVVVDKMMQNHGHENITTY VLTILNMERILKKTSTTHHPSA MERCVPVNLQIRDSLWNHCFSL ATTVHRFHPVGRHALKKMYKL PSAYINVSITKYTQRFALTYISC VFHRNAAFVAVPGEGRCCAGV DVPAPMSLRSPGPHWPQEHGA LWISCTVRGMASCLGQLCRVS MRVRANIGKVQKPRLRISNGK GLHTQSELSSGAYLEKGRWGA APGLDSRNEKGETEGARDSGTPG RQSQTQLRGPPGPVPGSSKIAPO TLTRQGSMTASRKLVLLEPFC ERTGEQSGQLYPPSPLLVEVW MPAGTSSTVDLLPELCRRWER QALSCLRLYRQRTSVSICALCD HTETRVALSTCQGLECNSSPA RKQNWMEFEELTEVGFRKS VITKFSKLKEHILTHRKEAKNLE KRLDEWLTRITSVEKSLNDLME LKTTVRKVLHEAYTSFNSRFDQ VEERILVIEHQNEIKQEDKVRE KRVRNEQSLQEIWDCVKRPN LCLIGVPESDGENGTKLNTLQ
21359	51727	A	21487	260	1292	RLCAFNKRMTFQNFNTIEDHLE NELTPIRDGALTLDSSKELSVSE SQKGEERDRKCSAEQFDLPQD HLWEHKSMENAAAPSQDITDSPL SAASSSRNLEPHGKQPSLRAAK EHAMPKDLKKMLENKVIETLP GFQHVKLSVVKTILLKENFPGE NIVSKSFSSHSLITGVYEGGLK IWECTFDLLAYFTKAKVKFAG KKVLDLGCGSGLLGITAFKGGG KEIHFDYNSMVIDEVTLPNV VANSTLEDEENDVNEPDVKRC RKPKVTQLYKCRFFSGEWEFC KLVLSEKLFVKYDLNLTSETIY NPDYYSNLHQTFLLRLSKNGRV LLAKAHVQRNLSRL

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21360	51728	A	21488	263	1466	RLCAFNRKMTTFQNFNTIEDHLE NELTPIRDGALTL\SSKEL\SVS ESQKGRKE\DRDKCSAEQ\DL P QDHLWGNISSMGK\WQAPS\QG HRTSSTSV\AASSSRNL\EPHGKT ALLAGAGQSRMAMPKR*\RR LEN*\SPLET\LPGFQHV\KLSVVK TILLKENFPGENIVSKSFSSHSDL ITGVVEYEGGLKIWECTFDLLAYF TKAKVKFAGKKVLDLGCGL LGITAFK\GASKEIHFQDYNM IDEVTL\PNVVA\NS\TLEDGGM DV\KWS\PDVEK\MPGNPKV\TQ\L YK\CRFFS\GEWS*\VL*\ALYSSE K\LFVKYDPHSSPSETIYN\PIDY YSNL\HQTF\RLRLSKNG\RVLLA SKAHYFGVGGGVHLFQKFVEE RDVFKTRILKIIDEGLKRFIIEITF
21361	51729	A	21489	2	367	
21362	51730	A	21490	2	376	QTYSLRRATPRHIIIVGFTK\VEM KEKVLRAA\NKPIRLTV\DL\SAET LQARKEGGPIFNILKEKNFPQRI SYPAKLSFISEGEIKSFTDKQML KDFVTT\RPALQELLKEALNME RNNQYQPLQKHAKW
21363	51731	A	21491	1	690	
21364	51732	A	21492	1	714	
21365	51733	A	21493	1	1536	
21366	51734	A	21494	1	765	
21367	51735	A	21495	1	972	
21368	51736	A	21496	1	2670	
21369	51737	A	21497	2	1178	
21370	51738	A	21498	2	827	
21371	51739	A	21499	1	777	
21372	51740	A	21500	168	1057	IRLKNHDH\GELRNKTCINRNL AEIKKFS\ENYENKETMYLNLW DVAKAVLR\GQFIALNARIKKE KSQVYNLISQLKELENQEQTNP KASRRQEITKIRAE\KEVETWK TLKKINESGRGVDCSS\DA\NGT KPDGE*L**VDKSR\PSEARQAN IIHQEIHGTPQR*\SLRRATPRH/II VRFTKVEMKEKMLRAARKKG WVTHKGKPIRLTADLLAETLQ ARREWGPINFILKEKNFQLRISY PAKLSFIREGEIKAFTEKQILRDF VTT\RPALQELLKEALNMRND RYQPLQKHAKL

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21373	51741	A	21501	3	1263	GRTIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRLSRSQCDQLEERV SAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIERQRTPORYS RRATPRHIVRFTKVEMKEKMG LLVPNWTNHSPLFRAILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSPGGGEGQSAVARLTGL IGVPESDVEKETKLETTLDQIIQ ENFPILARQANVQIEIQTTPQR YSSRRATPRHIVRFTKVEMKE KMLRAAREKGRVTLKKGPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK
21374	51742	B	21502	1	2356	
21375	51743	A	21503	2	484	
21376	51744	A	21504	2	902	ASFFSKKTSFGGWWGAGGPGD PGMGNHGGFRGGFSRGIRGW HSRGQGGQGGRAHRGKTKDK EWTSPKLGHLVKDMKIKFLEEI YLFLLAIKEFEIIDFLGASLKDE VLKIMPVQKQTHASQRTRLKG FIVIGDYNG/HVGLGVKCSKEV A/TAIRGAILG*LSIVPMCROY WGSKIGKPHITVPCKVTGHCGS VLVHFIPAPRGTGIVSVMP/KK LLL MAGIYDCY/ARSCATLIGN FTKATFD AISKTSYPTPNLWK ETVFTKSP/YEFRNSGQEFTDYL VKT/HIRVSVQRTQAPAVATT
21377	51745	A	21505	2	407	STISCGGNFPIRGGSGVASLER AESSSTEPAKAIKPIDRKS VHQI CSGPVVP SLSTAVKELVENS LD AGATNIDLKLDYGVDLIEVSG NGCGVEEENFEGLTLKHHTSKI QEFADL LSDVTSTCHVSAKVG
21378	51746	A	21506	362	490	
21379	51747	A	21507	3009	3889	
21380	51748	A	21508	1	504	LDLHKWFLSSFLTAISIGIKF LLKIHISRGSGVLLQLPGNPSP AAHGTEELEPKFLEQGYLRAVL PGPRVHATA*LEPTVTDQGYAR AGLPIQEVEDVLFGLVVLVLLHV IGQVAEDRNQVAAQGHQES/C PAQCWGDCTHLEIAGWRGIRRS DANPRSQRKFGF

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21381	51749	A	21509	2	1101	WTERRLGSGVRGDLRERSRPA VNRTPRMSRVSPGAPRGTPSSRR WMMMKCWDHQLPG*IPAPHV GPLAG/IRKKEWSEDEEEPEKE LAPEPEETWVVEMLCGLKMKL KQQRVSPILPEHHKDFNSQLAP GVDPSPPHRSFCWKRRE WWD ESESLEEEPRKVLAPPEEIWV AEMLCGLKMKLKRRRVSLVLP EHHEAFNRLLDPVIKRFLOWD KDLRVSDKYLLAMVIA YFSRA GLPSWQYQRIHFFLALYLAND MEEDDEDPKQNIIFYLYGKTRS RIPLVRNRRLQCRCLNPRARK NRSQIALFQKLRFQFFCSMSGR AWVSREELEENTGPRGDVDFQ QELYSNANGRQQRGEEFPVQI
21382	51750	A	21510	3	918	
21383	51751	A	21511	1	792	
21384	51752	A	21512	3007	3885	
21385	51753	A	21513	615	845	GHTASPPRSPQAQGRAPSVAP PPTTPQICPTTSSFSKKRTYAG GWDLPQQAQDC*SPCGAQGG WVTLAVASASS
21386	51754	A	21514	357	562	GSSTCGRETERVVLKKRKRSP HFQYRNSPTAEARPLE/PTQW GRRSHSPRPSAPLPCSCPQKSRK SV
21387	51755	A	21515	1	1335	
21388	51756	A	21516	537	1164	SSTPEAKAIKPIDRKSVMHICSG PVVLSLSTAVKELVENS LDAGA TNIDLKLDYGVDLIEVSDNGC GVEEENFEGLISPTLKHHHTCKI QEFADLTEVETFGFQGEALSSL CALSDVTISTCHASVKVGTSLV FDHDKIIQETPYPHRPGTTVS VKQLFSTLPVRHKEFQRNIKK/R ACFPFAFCRDCQFPEASPA MLP VQPAELMAV
21389	51757	A	21517	224	903	GFTWYIGMAQPKQERVARARH QRSETARHORSETAKTPTLGNNR QTPTLGNRQTPRLGIHARPRRR ATTSLTLLRAFGKKTQS/STEP AKAIKPIDRKSVMHICSGPVVLS LSTAVKKIVGNSLDAGATNIDL KLKDYGMDLIEVSGNGCGVEE ENFEGLS WDSGTGVDFDHDGKIIQ KTPYPHPRGTTVS VKQLFSTLP VRHKEFQRNIKKPVGEKYMRS VDTQACSCI

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21390	51758	A	21518	2	1321	VKSRAALLGPGA/LSPLEVSRRR PWTERRLGSVRGDRLRERSRPA VNRTPRMSRVSPGAPRGTPSRR WMMKCDHQLG*IPAPHV GPLAG/IRKREWSDEEEPEKE LAPEEETWVEMLCGLKMKL KQQRVSSILPEHHKDFNSQLAP GVNPPPHRSFCWKRKMEWW DQSEESLEEEPRKVLAPPEEIW VAEMLCGLKMKLRRRVSLVL PEHHEAFNRLEDPVIKRFLAW DKDLRVSDKYLLAMVIAYFSR AGFPSWQYQRIHFFLALYLAND MEEDDEDSKQNIHFYLRKNRS RIPLLRKRWFLGHSMNPRARK NRSRIPLLRKRRFQLYRSTNPRA RKNRRIPLLCRRRFQLYRSMN SRARKNRSQIVLFQKRRFHFFCS MSCRAWVSPEELEENTGPRGD VDFQQELYSNANGRHQAGGEE

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21391	51759	A	21519	1	2654	RSACGSPA WNFPSPRGSGVAS MEVRAESSSTEPAKAIKPIDQKS VHQICSGQVVLSTAVKELVE NSLDAGATNIDLKLDYGVDLI EVSDNGCGVEEENFEGTLKH HTSKIIEFADLTQVETFGFRGE ALSSLCALSDVTITCHASAKV GTRLMFHDHNGKIIQKTPYPRPR GTTVSVQQLFSTLPVRHKEFQR NIKKEYAKMVQVLHAYCSFQ QASV*VAPISLDK/RKRQPVVCT GGSPSIKENIGSVFGQKQLQSLI PFVQLPPSDSVCEEYGLSCSDA LHNLFYISGFISQCTHGVRSSST DRQFFFINRRPCDPAKVCRLVN EVYHMYNRHQYPFVVLNISVD SECVDINVTDPKRIQLLQEEKLL LAVLKTSLIGMFDSDVNKLNV QQPLLDVEGNLIKMHAAADLEK PMVEKQDQSPSLRTGEEKD SISRLREAFSLRHITTENKPHSPK TPEPRRSPLGQKRGMLSSSTSG AISDKGVLRPQKEAVSSSHGPS DPTDRAEVEKDSGHGSTSVDS GFSIPDTGSHCSSEYAAASSPGDR GSQEHVDSQEKAPETDDSFSDV DCHSNQEDTGCKFRVLPQPTNL ATPNTKRFKKEILSSSDICQKL VNTQDMSASQVDVAVKINKKV VPLDFMSSSLAKRIKQLHHEAQ QSEGEQNYRKRKRAKICPGENQA AEDELKREIKTMAEMEIIQGF
21392	51760	A	21520	238	413	
21393	51761	A	21521	288	467	
21394	51762	A	21522	1	3038	MDVGWDLGEDCWQEHHTAF SFDWCWPCSQNGDRVPSVNPVG GGAPRSYLQVASECWAAPAA VHVGEVPHAGGLHTEGADPV IGLYLVHRGACQPTPTVGNRQ TPTLGIHARPRRRATTSLTLL AFGKNAVRTPEAKAIKPIDRKS VHQICSGPVVPSLSTAVKELVE NSLDAGATNIDLKLDKESGLI KVQANWGWVKEETSKGLLKH HTSKIIEFADLTQVETFGFRGE ALSSLCALSDVTISTCHV
21395	51763	A	21523	34	256	ETGPPGSA PGRLEFTNIKRVVVP QERVELETLLVS YFSPTPRPTP PPFPHPCS*EDNVITVFSSIKNGP GSSR

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21396	51764	A	21524	727	2953	HVSgyDDVPLGTLSDIWPPAL FSVVSFAAFFFTTPIEAVLKSFSC LLVWYIGMAQPKQERVARARH QRSETARHQSETA/KTPTLGN RQTPTLGNRQTPrLGIHARPRR RATTSLLTLLRAFGKKTS/STE PAKAIKPIDRKSVHQICSGQVVL SLSTAVKKIVENSLDAGATNID LKLDYGMDLIEVSGNGCGVE EENFKGLTLKHHTSKIQEFADL TRVETFGFGEALSSLCALSDV TISTCHVSAKVGTRLVFDHDGK IIQKTPYPHPRGTTVSVKQLFST LPVRHKEFQRNIKKAQR/PQAR CYRCS*PNVSPGPGMAAATLS A*PRSQSSYFISCKA/EDNAICPI AEQKAEGKFSSRYRNHDSAEN RRDGSMTRPRTDWTLKRACTE KRRPQHASSFEWRGHSCLCWRD EQRDAETLKMLLDSGLSVQKK TKDRTETRFGEIMGQILGKIMMS HQPQEQEQSPQRSTSGYPLQE VVDDEVSGSPAGVDPSPPRRS LGWKRKRECLDESDDPEKEL APEPEETWVAETLCGLKMKAK RRRVSLVLPYYEAFNRLLDP VIKRLLAWDKDLRVSDKIPSEP TILGASPKTLPPASRICIRPSNTP PPRNFHMSTVTPMLSYLANDM FEDDEAPKQNIYFLYEETRSHI PLLRELWFQLCRYMNPARKN CSQIALFRKYRFHFCSMCRCA

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21397	51765	A	21525	1054	2349	SCPQIIFLSSCLQVASAECWAAA PAVHVGEPPVHAGGLHTERGAD PVIIGLYLVHRGGACQTPINGSR QTPTLGIHARPRRRATTSLTL LAFGKNAVRCALIGPGSLTSRT RPLTEPLGEKERREVFPPRP VEHNVSSRWEPRRRGACGSR GGNFPSPRGGSGVASLERAES SSTEPAKAIKPIDRKSVHQC SGPVVPSLRPNVAVKELVENS LDAGATNVDLKLKLDYGV DLIEVSG\NGCGVEEENFEGL /TSLALKHHTSKIREFADL TRVETFGFRGE/AL*ASLCAL SDVTISTCHVSA\VGTLTG VFDHDKIIPENPPNPH PRGTTVSVKQLFSTLPV RHKEFQRNIKKRA\CF PFAFCRDCQFPEAS PAMPLPVQPAELTP RSTPAPHPCSL EDNVITVFSS\VK NGPGSSKMICTNGSSPSS
21398	51766	A	21526	2	393	
21399	51767	A	21527	2	165	
21400	51768	A	21528	3	196	
21401	51769	A	21529	1	411	
21402	51770	A	21530	1	1727	GPQGVGRMAEGKAGGAAGLF AKQVQKKFSRAQEKVLQKL GKAVETKDERFEQSASN FYQQQAEHGLKYDLKN FLSAVKVMHESKR VSETLQFIYYSEWY GHEELKAI VWNNDLLWEDYEEL \AQDQAVRTMEIY VAQFSEIKE\RIA KRGRKLV DYDSARHHLEAV QNAKKKDEAK TAKAEFEFNKAQ TVFEDLNQEL LEELPILYNSRIG CYVTIFQNI SNLRLDVFYREMS KLNNHNL YEVMSKLEKQHS NKVVFVKGL SSSRSLVISPG VRTATVSSPL TSPTSPSTLSK SESESVA TEDLAPDAAQ GEDNSEIKELLE EEIEIEKES EAGSSEEDDPL PACNGPAQAQ PSPPTTERAK\SO EEVLPSSTTP SPGGALSPSGQL SSSA TEVVLRT RTASEGSEARPK KTASIQRTSAP PRRPPPRATAS PRPCSGNIP SSPTASGGGSA\T SPRASLGTGTAS PRTSLEI*PNP E\PPKEPVRT PEAKENIHNQ NPEELCTSP TLMTSQVASEP GEAKKMEDKE KDNKLISAD SSEGQDQLQVS MVPENNNLTA PEPQEEVSTSEN
21403	51771	A	21531	1	1530	

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21404	51772	A	21532	499	1587	HPRDPEAPSGPLWSASLPA YSQGHANEFDGNSNSTSHAVLVLV QKHIAVL SNKLC LSTSSLVQGG VNAHLGTLIWPQPRGYLSPRSA IPWFVSPTVTSGLHFPWEVQ*L FLLSCWGAHQSLPQRMPLLC CQGMWVPEGSMA TVGLSQQLF DSALLLQKAGALNLDITGQLR SDDNLLNTSALGR LIPEVARQF PEPMPVVLKVR LGATPVAHGS TQTATLRPA SPFVGGSWATGP PNSAFPSPPSCLVVNLRTPAS LSSKGEALREHVCAWWMSQL TVASSNVGFIDTQVRTLMTGTV FEKPLLDHLNGLSGHGLPSLV WVNLYVAPEIFVYEGYVVISS GTLLPEPEAKTTGRP
21405	51773	A	21533	1385	3111	IAPSEVKEHKMVLMLNP IHN ITSIVPEAMPAAITMPVLLTGLF LLVWNYEGTSSIPGPGYCMGIG PLISHGRFLWMGIGSACNYYN RYVGEFMRVVISGEETLIISKSS SMFHIMKHNHYSSRFSGKLGLQ CIGMHEKGIIIFNNNP ELWKTR PFLYERLCHAPASVRMVTVCA ESLKTHLDRL/EEVTT/ESGLCG TCLTLRRRVHGWDTSN TVFLG IPL/EESAIVVKIQGYFDAWQAL LIKPDIFFKISWLYKKYEKSVK DL/KDA/IEVLA/EKRRRISTE EK LEECMDFATELILAEKRGDLTR ENVNQCILEMLIAAPDTMSVSL FFMLFLIAKHPNVEEAIKEIQT VIGERDIKIDDIQKLKVMENFIY ESMRYQPVVDLVMAQSL*EG* C*SMGYPV/KKGITNIYSWNIGR VHRL*FFPKPNEFTLENFAKNV PYRYFQPFGFGPRGCAGKY/LS AMVMMKAILVTLRLTDTST*RT LPGTSVFESIQEGYTTCPWHPD/ ETKNML/EMDLYPKETSDRCLG TLRKAGQYLT LGAFSPVCS PNTNHPILCPLVFILHSGTLGSPMA
21406	51774	A	21534	129	378	IVCKFSVSTHKNIRAKKPDRLP ECGTQIRKDTLKRVRRTVLHYL CPPPSVPEIPAWRGDCSP/VGK EGKCTPDLPNPNIELRPV

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21407	51775	A	21535	1	474	MQKQIISVTEVEWYPKYNSNM KEYWSTQNHQFEQLSTHKNIR AKKPDERLPECGTQIRKDTLKR PCPLDRPLWPHITAEQGSKPST WPAPCDP/IF*ANIHLPSLHTGPC RSKVQAHSSRPQCQASSTCVPR LQDLPC*PRFLRLVDQDARPA APVYQGSRTYPADPDSRPAPVD SGCIISGQADW
21408	51776	A	21536	2	325	WAFSITERREFQVYYNSCPSSS WIGDARAFSPDPTGLYPIYSQ DTQTFRLLWNYNTDFPGSPAC KWQAMELLSPQSPFRVDRGEH LPFLVKGARYTLVPAGQEGAL AAWLEALRGQLGRRGAVVSM MDAEGLERSSPDCAMGLSDGE WQLVLNVWGKVEADIPGHGQ EVLIRLFKGHPETL/EKFDK/FTR HLKSEDEMKADELKHKMCH TVLTPLVGHILRE/KGHH*RQR FKPLGTSSSHCPSTKIPPLKVTL EFHLPGIAFIQVLAEQAIPEGDFG AECPGAQLKQRPWELFRKNNG LPTYKEAGAFQGARALAGFPTP THLGPPGFKKRAGV
21409	51777	A	21537	2	1011	
21410	51778	A	21538	157	322	
21411	51779	B	21539	1	975	
21412	51780	A	21540	218	388	RKLPLAGLPCINRQHS*SNVNIC FLTPV*KIQN*LQSEQFLPYPTIV IITLCFFAV
21413	51781	A	21541	663	933	GCAGPCLVNQMFQKYYLGKS HHPSLVSLNRGAHCTVGPKPQ PSGP*KLGYFVKVFPPCG*FWK YGPSWGMEERAWTGSPLGPGP PLKKV
21414	51782	A	21542	389	1033	NQGLRNLGLCRTCLVNKMFTS SILGKSHRHSLSVINQGNALW KAAGPLPLKAGYC/QGFSPCHS LKYGSWDEKDLTPQPDTLKG SVLRWISKRGKPLAVEIEEGHC L/LCLPLGTECLGIK/PIVHLFNSE IGENRPYGG*DMFCSNGCLG* FL*LPLRCLG/GEKHKSGL/HVHI PVIVPPELNYDIDSFAHMFV DLSLITLLSCYIFFC
21415	51783	A	21543	82	163	
21416	51784	B	21544	1	211	

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21417	51785	A	21545	71	1086	NMNLSTVLAFAFLGIASAVPKF DQNLDTKWYQWKATHRRLYG ANEEGWRRVWVEKNMKMIEL HNG/EKYSQGHGFTMAMNA FGDMTNEEFROMMGCFRNQKF RKGVVFREPLFLDLPKSVDW KKGYYTPVKNQKQCGSCWAFS ATGALFGQMFRKTGKLVSLSE QNLVDCSRPQGNQCGNGGFMA RAFQYVKENGGLDSEESYPYV AVDEICKYRPENSIVANDTGFTV VAPGKEKALMKAVATVGPISV AMDAGHSSQFYKSGIYF*PDC ISKNLQDQVLLVGYVFEAGANS NNSKYWLKNSWGP/EWGSIN GYVKAIDKNNHCIGIATAASY
21418	51786	A	21546	170	412	LWLSFLLMHWH*IPLAASVFT VSN/PILDFS*IQLKTPKHFGLNG NTGFLGKQLRLLRLSVSVRL HCLLYRRTQMPPL
21419	51787	A	21547	1	753	
21420	51788	A	21548	125	464	TAVFLTQSLFGGLFTRTRMKFG TMTRI/RGDLPWENPLSSCSLL HEKDPPTTSGPQTNPQKKHLTN FKSRKVERTKGLLTKLTKLSH QLKKAWTILLPLSLRIQACPR NAT
21421	51789	A	21549	1	753	
21422	51790	A	21550	291	671	
21423	51791	A	21551	10	453	TALLLTQSLFGGLFTRTRMKFG AMTRIG/DLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGQCTMQGCLPWSFTLSGKSR FPGAGASTPQPLLLHP
21424	51792	A	21552	740	1010	TAMLLKQSLFGCLFTRTRMKF GAVTRIG/DLP*ETNPLSSCSLLR DKDPPTTSSPQTHQPKKHLTNF KSGCSPGRARSQSFLSCSSTL
21425	51793	A	21553	134	358	TAMLLTQSLFGGLFTRTRMKFG AVIRIGDLLWEINPLSSCSLLHE KDPPTTSGPQTDQPKKHLTNFK SSCSSPG
21426	51794	A	21554	392	645	

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21427	51795	A	21553	1	1900	MQNALESLSNRIEQVEVRSNEL EDKFFELTQSNKDKKIRIRKYK QSLKEVWDYVYKGPNNRIISVPE EEENSKSLENIFGEIIEENLPSLA RHLDNQIQEAQRTLWKLIAKRS LPRHIVIRLSKVYKTERILRAVR QKHQVTHLTCKESYKLVKVG WKRHFQMMDTKNEQGKIKNEN HLIISIDVEKASDKIQRFMIKTL SKIGIQGKYLNVIAIYDKPTAN ITLNRK/LESIPSEKLKAFPLRT GTRQGCPLSPLFFNTVLEVLAR AIRQEKEIKIGIQKEEVKLSLF ADDMMYLENPKDSSRKLLEWI KESNKVSGYKTHVHKSVALLY TKQ*QAENQIKNRNPFIAAKK KKKKKKKKKRNRIYLTESK DLYKENYKTLKEIHDNMNKW KHIPCSWMGRISIVKKL*LQKA IYKLNAILIKIPPLFFTELEKTLK FIWKSNSIRIAKVLSKKNKSG GITLPDFKLYTIRKINSKWIKD LNLRPETIQILEDNIGKTLLEIGL GKDFMTKNPKANAKKKTINR WDLIKLSKFCTAKGTVSrvKRT HRVGENLPHYTSIHPTIYTIYTS DKGLISRIYNEFKQIVTRITTCVF LHPPHPKAKTTSYGDQLLGGN
21428	51796	C	21556	10	339	
21429	51797	B	21557	97	1458	
21430	51798	A	21558	1	387	
21431	51799	A	21559	3	604	GSVIAYYWSEFSIPQHLVEEAE RVMAEERVFMPPRARSLSKSFV VTSVVAFRESEGGQWAWDWPP FHGVGLGPGPLQGTGTTPRAQCP REKTTTCWPGTSL*IRKQE*GNG LYQEMLYSPSYSSATDSKTVQR TQDNSSCSFGLHARGVELMRFTT PGPFDPSPYPAHARCQWALRGD ADSVLSLTFRSFDLASCDEARS DLV

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21432	51800	A	21560	1000	2084	FRGTPVQRRGGGWADLPGRGCE LGRRLRSEEQARRVHKAPS/DF GTG/LKENTGKGVNGLEEGVEFL PVNNVKKVEKHGPGRWVVL AVLIGLLVLLGIGFLVWHLQY RDVRVQKVFNGYMRITNENFV DAYENSNSTEFVSLASKVKDAL LYSGVPFLGPYHKESAVTAFM WVWREGSVGCTPDWLGVGSG YSVWGTRKREMVLEVLDWRK EGPRCVLLLEGSVIAYYWSEFSIP QHLVEEAERVMAEERVVMLPP RARSLKSFVVTSVVAFPTDSKT VQRTQDNSCSFGLHARGVELM RFTTPGFPDSPYPAHARCQWAL RGDADSVLSLTFRSFDLASCDE RGSDLVTVYNTLSPMEPHALV
21433	51801	A	21561	3	2820	TGALILQKGEIRVINQTTCEPLL PQQTIPRMCMCVGLSGGVDS QVPPGQEGGRQFPLKETNNRK GRLPKRLRPHTWCCYSLEC SLRCTEDTWEDQKVNGL VEFLPVNNVKKVEKHGPGRWV VLA AVLIGLLVLLGIGFLVWH LQYRDVRVQKVFNGYMRITNE NFVDA YENSNSTEFVSLASKVK DALKLL YSGVPFLGPYHKESAV TAFSEGSVIAYYWSEFSIPQHLV EEAERVMAEERVVMLP
21434	51802	A	21562	111	465	
21435	51803	A	21563	2	197	
21436	51804	A	21564	359	405	EMQSRD*RK*YL*RIVNCVPL RERLGYVCGGLGERSKEGTLWI YQGLQKSQDTGRV
21437	51805	A	21565	208	287	IVSRSEKGVWVYVEGWEREAR REHYGYIKGYKNHRIHMMQSS KALV*LEDLRKH*IFRCVFSNP QVILML
21438	51806	C	21566	141	305	
21439	51807	A	21567	170	973	RMAACRALKAVLVDLSGTLHI EDAAVPG/AQEALKRLRGASVII RFTVNTTKESQDQLFKRLRKL G/VDISEDEIFSLTAARSL*AR KQVTPMLLDV*SGHYLIFKGIQ TSDPNAAVVMGIGTRTFSLSKF WNQAFRLLLGWSTSDSNSQSQ GFQEFKMGMLGPWTIL*LL*K YATDTKATVVGKPEKTFFLGSI AGHWLLNLEEAVMIG/DDCRG VDVGAQDVGMGLVKTGKYR ASDEEKINPPPYLTCESFPHAVD

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21440	51808	A	21568	42	211	
21441	51809	A	21569	92	366	AGSEMRPGLTWACSLARLLSP SFIKHWFLSCLSCSRSSGSYA QWCPPHQSAAGHCQTPAHA QAYLSPPQMDHSSVRSLEAC QTY*SASAAAGHCQTPAHQAQY LSSPPQMDHSSVRSLEACQTY
21442	51810	A	21570	1	834	
21443	51811	A	21571	3	835	
21444	51812	A	21572	1	1649	MPIVLVDWSDIREQKRLMVLV ASVALHGRSVTLYEKAFPLSEQ CSKKAHQFLADLASILPSNTT PLIVSDAGFKVPWYKSVKLG WYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKR LTKSNPISCQILLYKRSKGRKN QRSTRTHCHHPSPKIYSASAKEP WVLATNLPVEIRTPKQLVNIYS KRMQIETFRDLKSPAYGLGLR HSRTSSSERFDIMLLIALMLQLT CWLAVGVAQKQGWDKHFQAN TVRNRNGSLLTNWPSVPPTIKE EENSEEELAAATTSKEQEPIGTD LDAVRTPEPLEEFPKREDQEGS PPETSLPYKWVVEANLLIPAV GSSLSEALDIESDPDAWCDLS KFDLPEEPSAEDSINNSLVQLQA SHQQQVLPPRQPSALVPSVTEY RLDGHTISDLSSSRGELIPISPS TEVGGSGIGTPPSVLKRQRKRR VALSPVTENSTLSFLDSCNSLT PKSTPVKTLRFS/PSQFLNFWN KQDTLELESPSLTTPVCSQKV VVTIPLHRDKTPLHQKHAA

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21445	51813	A	21573	59	2384	PRPGSRSLCRRAGERGAVRAG GMSRRTRCEDLDLHYQDTS DVPEQRDSCKKVKWTHEEDEQ LRALVRQFGQQDWKFLASHFP NRTDQQCQYRWLRVLNPDLVK GPWTKEEDQKVIELVKKYGTK QWTLIAKHLKGLGKQCRERW HNHLNPEVKNKSCWTEEDRIIC EAHKVLGNRWAEIAKMLPGRT DNAGKNHWNFTIQK/RKGDGT GFLREYKD*KPPVYVLP/LEEDK DGLQSAQPTGQRSLLTNWPVS PPTIKEEEN/SEEELAAATTSKE QEPIGTDLDAVR/TP/EELEFP/K REDQEGSPETD/SLPYKVVVE AVNLLIPAVVS/SLYEALDLGS/ DPDAWCDLSRFDLPEEPSIEDSI NNSLVQLQAS/HQQILPPRQP SAILVPSVTEYRLDGHITISDLR SSRGELIPISPTSEVGG/SGIGTPP SVLKRQRKRRVSPVTENSTS LSFLDSCNSLTPKSTPVKTL/PFS PSQFLNFWNK/QDTLELESPLA DYPPQVCSQKVVVTTPLHR/DK TPLHQKHA/AFVTPDQKYSMD NTPHT/PTPFKNALKEYGPLKPL PQTPHL/EEDLKEVLRSEAGIELI IEDDIRPEKQKRKPLRRSPIKK VRKSLALDIVDEDVKLMMSTL PKSLSCRTTAPSN/SSTLTLGSIK EDNSL/LNQGLLAGPSRKAAC VPEGPESHFHGQLAPYVVPVGK
21446	51814	A	21574	190	889	SLPRRLESPGRLAMARGVIAP VGES/LCRYAEVPCSPSAKRDPDA DVDQQRVLRSLIAGVGQVAAL AFAG/RYALRIWKP/LE/QVITET AKGRFQTPRFSSY**GG/FLNII* LRREA/GLIGVSP/SAGKAKIRT IAHR/RVMILESPQIKGGSPYVA AKINEAKD/LLETTTKRLMLKD HTEGKKNEGTSKKKSPAKYS KTWSFLIFYMGFDHSLIFRPLSC ITNKMLIVLLFIIF

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21447	51815	A	21575	2	652	EGYIC/RHFTGSSALLTRTHITY GVIANVAVVRINSPNS/RMLAA CKTLQEVTLQSQEAQRIVEKLE KSTKPIVAAINGSCGGGLEVAI SCQYRIATKDRKTVLGTPEVLL GALPGAGGTQRLPKMVGVPAA LDMMLTGRSIRADRAKKMGLV DQLVEPLGPGLKPEERTTIEYLE EVAITFAKGLADKKISPKRDKG LVEKLTAYAMTIPFVRQQVY
21448	51816	C	21576	98	316	
21449	51817	A	21577	35	247	
21450	51818	A	21578	1	2391	LQLKMVACRAIGILSRFSAFRIL RSRGYICRNFITGSSALLTRTHIN YGVKGDVAADRINSPNSKVNT LSKELHSFFSEVMNEIWASDQI RSAVLISSPKPGCFIAGADITML AACK/TLQ/ETQLSQEVAQR/IV EKP*KSPQSLIVGCPNSGSCGLGR RTLRLPISSPQYRIATK/DSKTVI *VPPEV/VLGGPLPGRQGGHTK GCPKMGVCLPAFGHECLTGR SIR/ADRAK/KMGLVD/QLVGTP GTQGLKPEERTTIEYLEEVANTF AKGLADKKISPKRDKG/LVEKL TA/YAMTIPFVRQQVYKVKVEEK VRKQTKGLYPAPLKIIDVVKTG IEQGS DAGYLCE SQKFELVMT KESKALMGLYHGQVLCKKNKF GAPQKDVKHLAILGAGLMGAG IAQVSVDKGLKTLKDATLTAL DRGQQQVFKGLNDKVKKKAL TSF/ERDSIFSNTGLQDYQGF* KRPDMGELKAVF/EDP*LSHR VLKGVGSR*FPDHWYSLPSNT SALPISIEAAVQOKT*EG*LGMH YF/SPVDKMQLL/EIITTEKTSKD TSASAVA/VGLKQKG/VII/VVK DG/PLLVVTYQGVFAPMMS/VI RILQEGS/VDPKKLGPWTTTSFG FPVGAATLV/DEVGCGMLAK HVVAEDLGKVFGEFVGGNPE L/LTQMVS KGFGLGRKSGEGLLT SSGRVVVKRILNSTMD/SI*ASL
21451	51819	A	21579	119	387	VEDSKEIFSSA*DYLSTHSHKHP ASHESYHVNPNLCNPVAPTSGA HSIV*KWPSWLGTVAHSCNPNS FGRPRRADCLSSRSSRPAPWPT
21452	51820	B	21580	73	3177	

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21453	51821	A	21581	1399	5140	SGEPERALRGAAAMPSPGTAGA ALLALLAALCPASRALEEKVC QGTSNKLTQLGTFEDHFPQPS QRMFNNCEVVVLGNLEITLCER NYDLSFLKTIQEVAGYVLIALN TVERIPLNLQIRGNMYEYNSY ALAVLFNYDANKTGLKELPMR NLQEIHLHGAVRFSNNPALCNVE SIQWRDIVSSDFLSNMSMDFQN HLGSCQKCDPSCPNGS/CWGAG EENCQKLTIIICAQQCSGRCRG KSPSDCCHNQ
21454	51822	B	21582	82	305	
21455	51823	A	21583	122	219	YAKRIYDVVVYHTAYTCTFHA *KIRGMTQ*NW
21456	51824	A	21584	404	1228	GLAAFLARAGRRRKELPGSPR PLPQLPAGGSPRWARMRPSQR RPPTLPMAASPAHWPRESLVLY HWTQSFSSQKVRLVIAEKLVC EERDVSLPQSEHN/EMPWFMR NLGEEV/PVIIHRDNIQ/CTMDQ IHLTMWERTFHRERHVGALMP EVGSRAA/PRVLQYRELLDALP MDAYTHGCILHPELTTDSMIPK YATAEIRRHANATTDLMKLD HEEEPQLSEPYLSKQKKLMAKI LNEHDDVSYLKKILGELAMVLD QIEGGAGRRKKLENE
21457	51825	A	21585	3	1194	KNLSVKLSENGTLKNCVVADS ETDIDVYMYTRVYVYIPRIENS WNDTIKLVGTATISAVGGDIDA QGEWAFPLLGPISLSPGPEWKV RVVVPDKGLVCEERDVSLPQSE PKPEWFMRI NLGEEV/PVIIHRD NIISDYDQIIDYVERTFTGEHV ALMPEVGSQHARVLQYREL DALPMDAYTHGCILHPELTTDS MIPKYATAEIR/SDI*PNATTDL MKLDHEEEPQLSEPYLSKQKKL MAKILEHDDVSYLKKILGELA MVLDDQIEAELEKRLKLENGQK CELWLGCFAFTLADV/SLGATL HRLKFLGLSKKYWEDGSRPNL QSFFERVQRRFAFRKVLGDIHT TLLSAVIPNAFRLVKKRPPSFRR ASFLMGLSGMGMYFALHGTSR

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21458	51826	A	21586	1	929	MDPSIYFLPSKREGHLQAYIRDS VPEDPLILIFFSASSDQRPWLKA PHLPALRGFRGGGAGGGAQSR TTEDYVAWAKGNSPTSPSPRSR GGCSAKLSGPRRP RP RPGR LFN MAASANSVSRWRTESPEGLE SLHSTLSAISVSRPEGGAELSD TADTMGFGDLKSPAGLQV/PTI TWRTRATSRGMCHHKQMWQY LKPCPAHRLPTCVMPYV/GYNH IKSYEKEKASLPGVKKALGKYG PADVEDTTGSGATDSKDDDDID LFGSDDEEESEAKRLRE/DTSC TI*IKESQKTCTCCQVFHLTRCE
21459	51827	A	21587	1	2405	MALRVVRSVRVLCSLHVACE KVGMQIPRFCYHERLSVAGNC RMCLVEIEKAPKDQSMFMFGND RSRFLGKRAVEDKNIGPLVKT IMTRCIQCTRCIRFAEIAGVDD LGTGGRGNDMQVGTYIEKMFM SELSGNIIDICPVGALTSKPYAFT ARPWETRKTESIDVMDAVGSNI VVSTRTGEVMRILPRMHEDINE EWISDKTRFAYDGLKQRQLTEP MVRNEKGLLTYTSWEDALSRV AGMPALALQSAEIAASARPPP RLGSEEPCLCLAAHRLGCEEPLC LAASLESEERLCPAAIPPGNLRY VFISAKTDKYSKLAPVEWVTV EKVPENVEVTELEGNRQSRDR VSRI PGNAIWIWFTGFKWKKT TTLWFLNLAIDFIFLLFLPLYIS YVAMNFHWPFGIWLCKANSFT AQLNMFASVFFLT/GDQPGPLY PLDPSCLISSASNPQELSDCHYI HLAFGFSNWRSCPVLPGHCGV Q*SYSL*QFSEA*S*PHFDQAP CSDLGEIYHWLSLPFANNEYLL LVSHLQGEAEKHPDLQ*AFLDN SGCGGLCGLLDSLSPV*HLGA HHSPQ*LFPPCDAGWNPLHWF GIPQ*LLEPHPLCPN**EVPSSL VLSC*DTQVHTVGSQLFVQVL KEAKKPMVVLGSSALQRNDGA AILAAVSSIAQIRMTSGVTGD WKVMNILHRJASQVAALDLGY

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21460	51828	A	21588	1	2065	MLRIPVRKALVGLSKSPKGCVR TTATAASNLRVVFVDGQSLMVV EPGTTVLQACEVRIGMQIPRFCY HERLSVAGNCRMCLVEIEKAPK DQSMFMFGNDRSFLFEGKRAVE DKNIGPLVKTIMTRCIQCTRCIR FASEIAGVDDLGGTTGRGNDMQ VGTYIEKMFMSSELSGNIIDICPV GALTSKPYAFTARPWETRKTES IDVMDAVGSNIVVSTRTGEVM RILPRMHEDINEEWISDKTRFA YDGLKRQRLTEPMVRNEKGLL TYTSWEDALSRVAGMLQSFQG KDVAIAAGGLVDAAEALVALKD LLNRVDSDTLCTEEVFPATAGA GTDLRSNYLLNTTIAGVIEAD VVLLVGTNPRFEAPLF*CEFR KSWLHNDLKLVALIRAVPVDL TYTYDHLGDSPKILQDIASGK/ SHPFSQLKEAKKPMVVVLGSS ALQRNDGAAIALA VSSIAQKLR MTSGVTGDWKVMNHLHRJASQ VAVLADLGYPKPGVEAIRKNPPK VLFLLGADGGCITRQDLPKDCF IIFYQGHGHDVGAPIADVLPGA AYTEKSATYVNTGRAQQTQV AVTPPGLAREDWKIIRALSEIAG MTLPYDTLDQVRNREEVSPNL VRYDDIEGANYFQQANESKL VNQQLADPLVPPQLTIKDFYM TGEVTEINEALENPGLVNKSR YEDGWLKMTLSNPS

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21461	51829	A	21589	56	2352	ATRPPRGSSWCRQFSRTASAAP GRSNMLRIPVRRALVGLSKSPK GCVRTTATAASNLIIEVFVDGQS VMVEPGTTVLQACEKVGMQIP RFCYHERLSVAGNCRCMLVEIE KAPKVVAACAMPVMKGWNIL TNSEKSKKAREGVMEFLANH PLDCPICDQGGECDLQDQSM FGNDRSRFLEGKRAVEDKNIGP LVKTIMTRCIQCTRCIRFAIEIA GVDDLGTGGRNDMQVGTIIE KMFMSLSGNIIDICPVGALVTS KPYAFTARPWETRKTESIDVMD AVGSNIVVSTRTEVMRILPRM HEDINEEWISDKTRFAYDGLKR QRLTEPMVRNEKGLLTYTSWE DALSRVAGMLQSFQKDVAAI AGGLVDAEALVALKDLLNRVD SDTLCTEEVFPTAGAGTDLRSN YLLNTTIAGVEEADVLLVGTN PRFEAPLFNAWIRKSWLHNDLK VALIGSPVDLTYTYDHLGDSPK ILQDIASGSHPPSQVLKEAKKP MVVLGSSALQRNDGAAILAAV SSIAQKIRMTSGVTGDWKMNI LHRIASQVAALDLGYKPGVEAI RKNPPKVLFLGADGGCITRQ DLPKDCFIHQGHGHDVGAPIA DVILPGAAYTNKSAITYVNTG *ASASIMLAVTTPLGSRWDKI IRALSEIAGMT/LFPYDTL/DIQV RNQIGKSSPNLVIRYDDIEGVA
21462	51830	A	21590	246	761	MRLQGAIFVLLPHLGPILVWLF TRDHMSGWCEGPRMLSW/CPF LQSLICLLQTAIRYSVVG*VLVS HTWPWYPMGWQVLYI*ITYA VQLTISWTVLVLFFTVHNPGLV RHTVLSSRSNVGEGETTWLQK HILAALLLPYLAWLTVTSALT YHLWRDSLCPVHQPOPTKSD
21463	51831	A	21591	I	1497	
21464	51832	A	21592	I	1731	

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21465	51833	A	21593	1	6626	PRSLCFSLWAEAAVLADGGLR RRRRLLRGTMASAFVPGASLE DCHCNLFCLADLTGIKW*KYV WGGPTSAPILPVTEEHPILSSSS RCLTAHVLGVRRRDQRPERR L*IFWWGEDP\VLTLFTMTYQ KKKMECGRMDFFPMNAVLCFS KAVHNLLELRLMNRNFRIGK WVVKPYEKDEKPKNSEHLS FTFFLHGDSNVCTSV EINHQP VYLLSEEHITLAQQSNSPFQVIL CPFGLNGTLTGQAFK
21466	51834	A	21594	1263	1906	AVRGMVRNARAVLTKGGTFLS PALEPLVAGGSGG/EFSQLGAEE RKAIARF/AIDHVDRRVPVLI GG/TNARETIELSQHAQQAGRT ASTIDSV AHLRSMIHTVK/GAHP HFTVLCGYDDHLF/NTLLGGD GAISASGNFAPQSVNLLKAW RDGDVAKAAGYHQ TASIPDQLI HPYESRLFKCQHVLTRGITSF*L LCPPGSLRRQGISTYHSLHN
21467	51835	B	21595	113	484	
21468	51836	A	21596	300	780	KSGTNETIRRKARGGKIKMDD LRG\PRCQ*EPWKRLMTIMPS CLHLWAQNTTVSILSFVDKDLL EPGCSVLLNHKVHAVIGVLM D TDPLVTVMKVEKAPQETYAD IGGLDNQIQEIKESVELPLTHPE YYEEMGKPKPGVHPFGPTWPR VKPFCPRQ
21469	51837	A	21597	2	840	AIEHCQSGDNPESTRRGFLQW LGRNPALVPHPGRTGHSQPPVT FHRHPSDCQSPAGRKFKGPSH RGQPPPFHKSPMTTASHLARC ARTYHQDSEAAINR/QINLELY ASYVYLSMSYYFDRD/DVALK NFAKYFLHQSHEER/EHC*ENL MKACRTNEGWPNLSFQDIKET KTDDWESGLNA/ME/CALHFE KKC*KISLLELHKLAATDKN*PP ICVDFI*DTFTLNEQ/V*KAIKRI WGDH/V*PKLWRKMGSA PN LG FGEYLF*QSTPWGSDNES
21470	51838	A	21598	3	390	

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21471	51839	A	21599	1	483	FQLEVPQNITLNPFGGPPVFS WRDQAVLRQDGVVVTINKKR NLVVSVDGDTFEVVLHRVWK GSSVHQDFLGFYVLDHRMSA RTHGLLGQFFHPIGFVSDIHPG SDPTKPDATMVGILQKDYSKDP WHGAEVSCWFIHNNAGLIDG AYTDYIVPDI
21472	51840	A	21600	1	1521	
21473	51841	A	21601	1	837	
21474	51842	A	21602	3	310	EVANLSSQALRMWLDYGFVT PLTSMISIRGMADQDGLKPTIDK PSEDSPPLEMLGPRRTFVLSALQ PSPTHSSSNTQRLPDRVGTVDV* VVT*PYVLCWNL
21475	51843	A	21603	62	462	MPLPLPSAFVLSALQSPHSS NTQRLPDRVTGGFSVNGQLIGN KARSPGQHDGTYFGRLGIANP ATDFQLEVPQNITLNPFGGPP VFSWARDQAVLRQDGVVVTIN KKRNLVVSVDGDTFEVVLHR VWK
21476	51844	A	21604	37	2883	SMDGAMGPRGLLLCMYLVSL ILQAMPALGSATGRSKSSEKQ AVDTAVDGVFIRSLKVNCKVTS RFAHYVVTSSQVNTANEAREV AFDLEIPKTAIFISDAVTADGNA FIGDIKDKVTAWKQYRKAAS* EKA'GLVRASGRTEQFTIHLT VNPQSKVTFTLTYEEMLRNHN MQYEIVIKVVKPQLVHHFEIDV DIFEPQGISKLDAQASFLPKELA AQTIKKSFSKGKTSNGSHSRF QGHVLFRTPTVSQQQ
21477	51845	A	21605	1	1008	
21478	51846	A	21606	1	435	
21479	51847	A	21607	1	676	IRHQGAAQEGDAETPGSVERR GRRAGAEDGMSQAPGAQPSPP TVYHERQRLCAVHALNNVL QPAA'FSQEADEICKRLAPDSR LNPHRSLLGTGNYDVNIMAA LQGLGLAAVWWDRRRLVPS WPCPKGLG*ILNLPSPVSLGLL SLPLRRRHLRWPCARL/VTVS YNLDSKLRAPGPGGLRTE/LR GLSLAAALAQGLCEVLLVVT EVEEKGSLWRTD
21480	51848	A	21608	89	316	ELLSPLLVAAGPSDLTVTGLKSF SSPSLCSLNTLAGTSRLMVA*L YESLGQGEDLGLLTPGPEFLSIS SYCNFM

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21481	51849	B	21609	1	1920	
21482	51850	A	21610	1	1727	LPRVLGHSGRGGLSSRRSQGL VSRFRLRALCAGSDMWRLPG LLGRALPRTLGP/SLWRVTPKS SSPDGPQTTS/LLVPVNLDR SGPHGPGTSGGPRSHGWKDAF QWMSSRVSPNTLW/DAISWGTL AVLALQLGR/HHFQAF/LAAGPA KRVE/HCS/WHSP/LDRFFSSPL WHPCSSLRQHILPSPDGPAPRHT GLK/ENPRLGKE/EAQAQRNFS HNSLRGARPIQDPSEEG/PGDFG FLHASSIESEAKPAQPPTGEK EQDKSKTSL/EEAVTSIQFLQFL SVSIAFNFLGNQMDPAPRQEGT ENMKSGDHTAAFSYFQKAAAR GYSKAQYNAGLCHEHGRGT DISK/SV*KAGLYYQLAASQGH SLAQYRYARCLLRDPASSWNPE RQRAVSLLKQAADSGLEAQA FLGVLFTEKPY/LDEQRAVKYL WLAANN/SDSQR/HLGICYEK GLGVQRNLGEALRCYQQAAL GNEAAQERLRALFSMGA/ASPG APTNLTVTGLKSFSSPSLCSLNT LLAGTSR/LPH/ASSTGNLGLLC RSGHLGASLEASSRAIPHPYP LEKNVVRLGFG
21483	51851	A	21611	1104	1680	LATPDVRYCYLSTYTSLPNPAR RFFFLSLCCKFSHSHKTATVKK YNKSEYPWDLVK/AHLQGAFTS NITFDISELQNKILDNRHTQEF QPSLEDWTEFQEGLES/LNPWTY LKYHSNLYVVLGVMLFCLCLL FIVCKIGWTANRRMRAAQPG LTFQLIHKQGDMDQAEGPVDV TNSAFHWRLYDQTANCLS
21484	51852	A	21612	364	824	LCILFKQLSTWRTGCAQPTKR GYTELQTEGPM/KSMFLWLGE QVQILQL/HSNCIVILTLV/FCV TNLE*FIVCKIGWTANQK/MGA AKPGLTFFLLICKIQKQDM*GA KGPWDVINS/AFH*RM
21485	51853	C	21613	196	504	
21486	51854	A	21614	3	142	

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21487	51855	A	21615	1178	2285	IVWLMTGGQC*RY*LSALIKL* DR/WFQRLCIHVQRLRPVHAH LYLQPGMEDGNSFRQMFSTR SLHIPTRDLPSPDITVVLHQVY NVLLGLLSRAKLYVDAAVHGT TKLVVPYFSFMTYCLISKTEKLM FSTYFMDLWNLFPKLSEPAIA TNHNKQALLSFWYNVCADCE NIRLIVQNPVVTKNIAFNILAD HDDQDVVLFNRGMLPAYYGIL RLCCEQSPAFTRQLASHQNIQW AFKNLTPHASQYPGAVEELFNL MQLFIAQRPDMREEELEDIKQF KKTITISCYLRCLDGRSCWTTLS AFRILLESDEDRLLVVFNRGLIL MTEGKDVTFMIVCC*TTSLIIS SIYYAELQSTVKNLLKH
21488	51856	A	21616	1	436	
21489	51857	A	21617	369	508	
21490	51858	A	21618	2150	3120	DLRALALLSVHTPKQLNPALI PTLQELLSKCRCLQQRNSLQE QEAKERKTKALAWTTITFRV GGGNTLGVTLGRVVCSEAPPK YKC*KQN*LPTSPPNVILMTFRE VSLACVFTDDEGATPIKRRRV SSDEEHTVDSCISDMKTETREV LTPTSTSDNETRDSIIDPGTEQ DLPSPENSSVKEYRMEVPSSFSE DMSNIRSQHAEEQSNNGRYDD CKEFKDLH/CSKDSTLA/EEESE/ FPSTISAVLSDLADLRSCDQQA LPSQDPEVALSLSCGHSRGLFS HMQQHDILDLCRTIESTIHVV RISGKGNQAAS
21491	51859	A	21619	2	4049	EEENGREYKFDVSSLELWVH DNMQFLQDKNIFEHTYFGFMW QLCSCIPSTLPDKAVSLMTAK LSTSFVLETFIHSKEKPTMLQWI ELLTKQFNNSQAACEWFLDRM ADDDWWPMQILIK/CPNQIVRQ MFQRLCIHVQRLRPVHAHLYL QPGMEDGSDDMDSVEDIGGR SCVTRFVRTLLIMEHGVKPHS KHLTEYFAFLYEFKMGEEESQ FLLSLQAISTMVHFYMGTKGPE NPQVEVLSEEEEEE
21492	51860	A	21620	58	219	

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21493	51861	A	21621	195	1187	RVPRTWLLPSFCASRSRENEGL SEFGASQTVTPSPASSVQAW MEPEFLYDLLQLPKGVPEPPAE ELSGVCKKYLPTSRKDPKFE ELQKVQQEWINATLLPEHIVVR SLEEDMFDGLLHHLFRKWAAL KLEAEDIALTASQKHKLTVVL EAVNRSICSWRSGRPSGA/WEST WNKDLLSTLHLLVALAKRFQ DLSLP/D/HTNVQVEVITIEVAA NFVNQKLDRLGLSVQNLDTQV GTGVILLLLIGQLEGFFLHKEF YLTNPSPAEMVSFVTLAELL/I GRGPAQLPC/LALKVSAT/MDA KSTLRVLYGLFCKHITQKAHRD RTPHGAPN
21494	51862	A	21622	96	1350	AAGLLPPGLVPEDPRRTNLLP FGIQGPPFALSRLFCVSESGWA WEAMEPEFLYDLLQLPKGVPEPP AEEELSKGGKKYLPTSRKDP KFEELQKPA/VLMEWINATLLP EHIVVRSLEEDMFDGLLHHLF QRLAALKLEAEDIALTATNQK HKLHWCWRP*TGVCSSWRSGR PSGA/WESIFNKDLLSTLHLEA LAKRFQPDLSLPTNVQVEVITIE STKSGLKSEKLEEQLTEYSTDK DEPPKDVFDLFLAPEK/LNA VKEAIVNFVNQKLDRLGLSVQ NLDTQFADGVILLLLIGQLEGFF LHLKEFYLTNPSPAEMLHNVT LAELL/IGRGAQLPC/LALK/TI VNKDAKSTLRVLYGLFCKH KAHRDRTPPWSPELTLTASKAQ SLPVSPAGGPEAAGCPPTVPLFP
21495	51863	A	21623	1	87	
21496	51864	A	21624	45	277	
21497	51865	A	21625	171	511	GKFRYPALHSWATRLRTSTAA GHCCMNSSQNKLSKSWAMTR HALNVKRFITFQSHQCSLSKKV NLSLFQQAERLPSQELTHLL QEVRC*RDFFPEEATWTGLPV LPSQ
21498	51866	A	21626	276	387	
21499	51867	A	21627	1	218	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
21500	51868	A	21628	139	9009	ESSEDSVSGGLPFLVDLGFSSVC VSLFHVKNPVQWDQKLPKKKK PVRSYCGSKLLQREVIQPDVME EMVVSVCVVKHLNLVDALQSLN FQYQEEHAEEYDLCKIMGETF KKLNAMERQLQNKMELELLC SMKEVSFDGNDLENMVLRLRE KFLQEVNSLIQKPSHPAKTKT LVKSLMNRAELLHVITIAAQSG LTRSISGTPAETPACKSASETKV ISHAVRQPVFLRSMSPADLEMI GNEDLEFTRANQRR
21501	51869	A	21629	1697	2056	
21502	51870	A	21630	237	1545	KPENKKSRTGRNRTKSTPGYRA /RPAAATARISARSTK*WKNSL AGRWARHICWTLWALIPRITLR /HVMAGFPQRMQKDYRDAID ALCDANRFGQKKRLGFWRYKE DSKGVLGCLSYLLIGFYITDPKN GAAAMKAFVVTRVGDVFLAFA LFILYNELGTLNFRMVELAPA HFADGNMMLMWATLMLLGGGA VGKSAQLPLQTLADAMAGPT PVSALIHAATMVTAGVYLIART HGLFLMTPEVLHVGIVGAVTL LLAGFAALVQTDIKRVLAYST MSQIWLRCSSRLACRHGCGGSL ECLQHEGIPYSRMGRPHHTSAL RRFTSEFGMGSAFTLGYYFFMY KQAVILLMLFTASVSAACLTPI AIDHGTGPAELLTVALRYNLS SYDAAYLELALRLLEPIAKGSPN FAFRRAATGNEGIMHFLRNK GILWI
21503	51871	B	21631	1	1440	
21504	51872	A	21632	525	716	PKTPAGPVEPMHQVPSSKRVP RDKRTRGDSRHSQSKPTKRY NHAYEI*PRIKWFIPDAGC
21505	51873	A	21633	8	136	
21506	51874	A	21634	1476	1611	GCDPAPGLPAPPHT/QP/DH*NQ RQIGIG*FLTGTVPATHLRQLA AA
21507	51875	A	21635	461	827	AALQMRDTSADPCGEQSVCG YSEPVPEYACFHRIQDLHDTE AACFSHAGSGRTHV*SQSEHAA GSVLWSYRYRC*TTGATGYTDR FSQQRCHVRRGISPRCWPEYQS RSWCRLFPSPESAG

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21508	51876	A	21636	1	3735	MAEASVFQTVDPWRPGFATIPD FLKERYDKTTRIIIDFCFLIATGV CFLPIVLVYSGALALNSLPHVGES LQISHGAAIWLLVILLGLAGILY AVIGGLRAMAVADSSINGILVI GGLMVPVFGLIAMGKGSFMQG IEQLTTVHAEKLSIGGPTDPLP IGAAFTGLLVNTFYWCTNQGI VQRTLASKSLAEGQKGALLTA VLKMLDPLGLKPDLLAYNTAL RALIPQRLIAFDDAVRSTLKEEE KLVNSSDWGY
21509	51877	A	21637	840	1064	WSVENYIIRRGYGGHIPLPAASP AVAAQWCDAGR*VPPAARRW HRHQVYLYTILTLDRGLSRARF CIPSAHCSAY
21510	51878	A	21638	979	1409	RLVVDIFHDNRHAFPRRLVSDA AAHNACTQHRGLFRGFNVFGE FLRFAYILIVKENADQCAQFV GMRQRDKTFVQV*GFFTTKT GRSFNGFYCGDGGRI MF/LPLFV RP SL*RW*SSWWLQSCSVLVVP ASADVLLSSRRGR
21511	51879	A	21639	903	1397	LP TLPM MVCTTPTSSRKHWM *NPSTLT/HAWVPYTNFSPIYEG KCGMSGARVEGKVIYETQSTH KLLA AFSQASMIHVKG DVNEE TFNEAYMMHTAASPHYGIVAS TETAAMMMKGNAGKRLINGSI ERA IKFRKEIKRLRTESD G WFF DNAAGYIDTITLGGPS
21512	51880	B	21640	1	5305	
21513	51881	A	21641	129	723	LITARGQVADNRDLAPWV PDAPSRALPEMTLDSRVAAAV DLFVARIGHQADGRRIYIPQAI QGVAAIIIAEKDEATDGEIREM HGVPDIYLSQLNELLALAGRC YHEPSDNLRLVGVGTGTNGKTT TTQLLAQWSQLLGEISAVMGT VGNLLGKKKEKAAIQYNTLC KSC T LTHPKPHNESDH/IRCRC*

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21514	51882	A	21642	1	2230	MMRTSGGTRDNESSDDDERER ENRLSDEKSNEYANLVGGERY EPDEENPMLGFRGAGRYVSDSF LRLCSSLEIVKARETVAIQGLK HDL LADDTALRALIPQRADRF MNAVSTLKEEEKLVNSDDWG YDAQAFARWRPEYGYFAKQA GFTVKTSASLAALWQVVNQIG GKERYFFGNLWQTRALMDRAI GHKLAKGRPEREYLQTGDAVD SWKVIVVEPEKQLTLFGMKAP GLGRLCFSLEDKGDYRTIDVRA FWHPHGNRAEREKPRFPYSRR KSFIGNMLLPMSIMPPVFRRI CPLGVARLGKFRDPVYLVCVFT RQIFRYTSGDEF LQINTTGGED IDDIDDIKLFVYEESSYGISKESH WREAINAKAMGAMTLNWQEK RWQRRFFNSEEPGNIEPVYMLEK VENQNHAKWEVHNFTMGYQR QVTEDTYEYLLNVVGVVPVPD NIHPMTKDEAGVWSWRTPIK GNLYEYFFNVVDGVRSDTGTGA MTNPQRQVNSSMILVPGSYLDT RSVAHGD LIAITYHSNALQSER QMYVWTPPGYTGMGEPLPVLY FYHFGDTGRSAIDQGRIPQIM DNLLAEGKIKPMLVVIPDTETD AKGIIPEDFVPQERRKVYPLNA KAADRELMNDIPLISKRFNVR KDADGRALAGLSQGGYQALVS GMNHLESFGWLATFSGVTTTT

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21515	51883	A	21643	1	1549	MDASGHHVVRGFASGMGCCRV RRTMKRETGGGRLAGFRLVGT LGQHLGAHRSASKGHQILAA RHVDRDLAK/LQLA/NVSCHEVD LSWPDNLALLQDIDITVYFLVH SMGEGGDFIAQE/RQVALNVRD ALREVPVKQLIFLSSLQAPPHEQ SDHLRARQATQ/EIRSEGNVP/V TELRAEIIIVGAGS/AAL/EVMIRD MVYNLPVLTTPRWVRSRTTPIA LENFLHYLVALLDHPASEHRJF EAVAGPEVFSYQQQFEHMAVS GKR/RWFDPPSP/LPTRWISVWF LNVITSVPPTTARALI/QGLKHD LLADDTALRALIPQRLIAFDDA VRSTLKEEEKLVNSSDWGYDA QAFARWRPEYGYFAKQAGFTV KTSASLAALWQV/VNQIGGKER YFFGNILWQTRALMDRAIGHK LAKGRPEREYLTGDAVDSWK MIVVEPEQQR/LT/LFGMQAPGL GRL/CCFSLQEDKDYRTID/VRA FWHPHGMGP/L*F*WLLMIPAH LFIFRGMMAKQIARLAVPSTDLD
21516	51884	A	21644	201	363	SLRGSRTAASPCWAVP/VHVP HGAGEPAHHPGHP*/LPPPH VLLPLQPVLA
21517	51885	A	21645	3	440	PFSLPFSLGLTASLFMNTWLAIS SNCDGFIPASPAFCFSLMSSA L*RTKAM*IMC*FSGLSGSGKV YIR*ASHSL*NCAGLSSFP*MT SESLLTFVAF*APL/NPSKRASLS RFSLCISLSCSNWGSVPGNW VLPYSWGF
21518	51886	A	21646	359	543	VVTPDSGSSH*KANSFCLSGAN LMLKKASFRSKQVNLSSAGS NPSNMYGLTVGCKVTVA
21519	51887	A	21647	2	582	
21520	51888	A	21648	3	574	
21521	51889	A	21649	1	195	LCVFFVLVSFFLSPLDSQLAVV C*FDGTGIGMYLTS/AVSPPPRN GVVASVMAVAVTPMLNLFICS
21522	51890	A	21650	2	457	
21523	51891	A	21651	21	545	PPCTSLRPLHAFSGMKTHLNRG TLSLDSQLHNLI/ALQMTCFKD VEIPNFWEPSVTPSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGVGGYLGSDVSSSP RKRAVASVMYTVTPMLNPF YSLRNRDMKSVLRRPHSSAV

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21524	51892	A	21652	899	1039	LWTSSSLTAESSPMRAA*LRETSI VSAASRAFSALSSSALRAFSAC
21525	51893	A	21653	804	1390	QGTIILKVLRLRLRWTWIPSRASL RTGYCFCLTGWTPGLTSISTGA WLTANPGGLSSAHTLGHRLAR AGLISWPGSVKKSLSHSSRGSIR VIMTPVPGNFSKKEPCSVKEIVA LSLLSKSLPNKGKGQSGMYKN* *ITLCPPIVQVWGKQKACFAET PMAPMMSIVFLDKGATEAVTT ECSALVSTRKSMSPPTV
21526	51894	A	21654	84	730	HLSDSKSQVRYQPSADLSFLLG HYNPQSSRRVLSVLDQLHNLI ALQVTCFKDVEIPNFFCDPSQLP HLACCDTFTNKIIMYFPAIFGF LPISGTLFSYSRIVSSILRVSSG GKYKAFSTCGSHLSVVC*VYGT GVGGYLSSDDVSSSPRKAASV VMYTVITSMNLNPFYSLNRNDIK GVLRLQPHGSTVQFYLLICSIPF VVWVKKGSKVK
21527	51895	A	21655	1049	1979	
21528	51896	A	21656	2244	2901	LRCLSLPFLEAWKRDMLLSVM AYDRFVAICHPLYHSAIMNLC VGFLVLLSFFFFLSLSDSQLHN LIALQMTCFKDVEIPNFFWEPS QLSHLACCDTFTNIIMYFPTAIF GFLPISGTLFSYKIVSSILRVSS SGGKYKAFSTCGSHLSVVC*FY GRGVGGYLSSDDVSSSPRKGAV AAVMYTVVTSMLNPFYRLGN RDIKSVLRRPTEHLISKK
21529	51897	A	21657	1	2850	

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21530	51898	A	21658	1	1703	KKMALTSFLPAPTQLSQDQLAE AEEKARSQRSQPSLVSSRRPEP PYGYRKA WIPRLLED F*DRGA FPEIHVAQYPLDMGRKKKMSN ALAIQV DSEGIKYDAIARQQG SKDKVIYSKYTDLVPKEVMNA DDP DWQRP DDEAIIEITEKAIR VAL EKSVSQKVA AAMPVRAA *QIGPLLQYIPIHTISGKGVAIQ T SWS*TRR VIRVMVEMQKDPME PPRFKINKKIPRGPPPPAVM HSPSRKMTVKEQQEWKIPPCIS *LGKMAKGYTIPLDKRLAAD GEEGLQDSYTLNGKFSAKLAE ALYIADRKAREAVEMRAQVER KMAQKEKEKEEKLREMAQK ARERRAGIKTHVEKVYFSTVH TEDGEARERDEIRHRRKERQH DRNLSRAAPDKRSKLQRNENR DISEVIALGVNPRTSNEVQYD QRLFNQSGMDSGFAGGEDEI YNYVDQALIGGKYMAQSIYRP SKNLDKDMYGGDLEARIKTN RFVDPKGVFLVQTRRQREGREP VQFEEDPFGLDKFL EESPTAM GGSKRPSG*PAAPREHGAWKA RKRREKE
21531	51899	A	21659	2	1588	CLRRALPGSIESAPTAPPPPSGE GSQAYISRLPATLIVILERRQL LGVWRRARCCSLINLAHRRHC GMPTRSPCAILARRYEGRRSPS TVAQPPPPPIELAPSTSETPIQ ATRGAPHPAQPS/VPPA/PARPPE RPPVPEQGPSGTHPDPTP/PGPT NAPQRPSPAPNTTN*PTRMHM QLPDAA*TPYPA YGSDYL*AR* DATASHQASCTN/SPDAA*TPYP AYAKIERA*ENPVPSAIKIIGRSS SSGRQASPWGMA/SPHWRSWR MGPNNGSGKRPRRAAERISCCRN AQGRTHSQKAYIQQPQCCVN VHLQPPD/PTPAQ/PSQTLSPD S/PAPPLPAYPS/TQHPTAPPTSSP MSS/RIVKHPHQHCGARPQGGK ERDETERKDAKERNRRTATPTT RHTDRLPRTAHGPPPP/PPPPPP PPPPPPPPRDSRRRPRREKPEQQ KEGGQTGRTOQKETAARRGEER ETGRKKTRGAPPRPAAARRPH ETAETKRPPARQHRPPRRRPS DGETRTRHQLGFIMLGLLSWN

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21532	51900	A	21660	2	192	RVDICSTNYCWLYPMTSGPSF SYV*GP*EEDVRE*MCGRDGL* YLSIGVVCGFICQHHNRAQ
21533	51901	A	21661	783	2119	GSEMPVTVM LTLGEPGHFMSS LGVCWCGVEDEAAPSQSIYIQ RETQVRTPMAGVSPKKAHPCE MCGPILGDILHVADHQGTHHK QKLHRC EA WVNILYDSGNFHR RQNEHIGEPYRGSVEEALFAN RCKLHVSGISHLSSVRV/EKDFL LRSGLLQQAETHTGKSNKTEC VSLFHGGKSHYSCGCMKHFS TKDILSQHERLLPTEEHFVWCE CGKSSSKYDSFNHQGVHTREK PYTCGICGKLFSSKSHLLVHQRI HTGEKPYECEVCQKFFRHKYH LIAHQRVHTGERPYECSDCGKS FTHSSSTRVHKRVHTGQKPYEC SECCKSFAESSSLTKHRRVHTG EKPYGCSECEKKFRQISSLRHH QRVHT/NERAYECSESSLIKYW RIHT*VRSCDCSKCGK/CFQTRS ALLGYWRVHTR/KSPYK*NKFG QFCSHTSVFLQDYS
21534	51902	A	21662	84	437	KMTSTQPVKFSLFASHSVPCGQ SFPGRRAFAFAMPRRRIPSSDHL PEPGQSHQHVNRQRWACRELI AAFLPSSYRL*L VETGGEIGQRN RASCHSPFAGSSPGIFQTEIGKP CLLP
21535	51903	A	21663	69	446	
21536	51904	A	21664	880	1365	
21537	51905	A	21665	1705	2196	RQNQREGDDDDTDQPPRPGTQ MTELFLLIQLMCFMANALRQL VHPL/MGNVHEYFADLKMPAC AVSAFLCAMHRSITSMFE*DNG PGPADADAR/LDMRIQVFMFCA NTL/PARVLQRKNKPGQDHPET AERRAESQRIIEKGLKCIQGGKI VNSISMKEGVDAFIH
21538	51906	A	21666	1	1147	
21539	51907	A	21667	254	557	AADEIGGIAVETVTEDAHLLCG CTVVAIPRICVSAGGGAGDRK SSVRFHQNLAQVHITRGV/VWT MTNSHIITCCATAFGITTSPTSPT ESTGVPCGRRNQH

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21540	51908	A	21668	557	1031	SSRNASGAVRKISRGMPPDKKW NMALT*HSR*ANFSPLPVSGLS RRKICTIPRAQRJR*PICADRLSV ASPAACGIA YTRRYSHDGATA EK YAH LQSRFRQCCRQFH PAA YDESPHRNRRRKWRPTYRCHP APDHRTACLRSAFYGNAPGCV QTERS W
21541	51909	A	21669	572	825	QARISTSFRESLPSRHPVPRYR PLEAFWTPCTRGYYRFFFS PAR ENAEYRTL KHWAKFLLVRA SF PGASTLCCKSPGRITISV
21542	51910	A	21670	303	899	EDNYSGSSLYCFDDVASVQMP GSGNGCRR*CAGKTSG/TWRNS LVRQWLLTAQKKTLLHAYSNL PKTWAQILFSKQVR LRSPLNRH LIW*CAAVKL*LLVLYPAIRQSI SSKSIKSLSRRYFR LPIGDSM* NRW*RIFTIGMYIGTAL*SDGAI VVCRLCENLPGSFHQRHQRCD AASLAGGSEPIAFSRAGRTPGP
21543	51911	A	21671	1	1320	
21544	51912	A	21672	99	761	IDNAPPDQTTVHAFANSENHS PPQLPYETPDADPTHQAFSRW RHRPQAY SADALLRERLPPTHR HRGQSPDSL TSLPYWRGRKRY RAAPALT*TPPDTLFDSP*PAV PPPVAKELPVTAQRQVHNAMS ANSFVIFHPVKIRNNIVLQPAIAI QRRNGHGVTRCAALHSRHGS LSVARHRVHLPVCRQADDKPA PAPLRPARYCLCPNQSAAVRYL R
21545	51913	A	21673	62	680	SSRNASGAVRKISRGMPPDKKW NMALT*HSR*ANFSPLPVSGLS RRKICTIPRAQRJR*PICADRLSV ASPAACGIA YTRRYSHDGATA EK YAH LQSRFRQCCRQFH PAA YDESPHRNRRRKWRPTYRCHP APDHRTACLRSAFYGNAPGCV QTGPVRRSGAASAPVFLSG TSPWSEFARTIALVRGRSRKSTR RLWHISAHC
21546	51914	A	21674	411	481	

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21547	51915	A	21675	402	915	RLASKLFTTVTPRGGV GELQAT TRNAAVAGIKRKRNRGRPAEE PELTADRGGQGENEITEAATAAK ARRTMRPKTGNQNPDKHRTRG LQICHFTFNANGNRARCSAANA MAATISGLSSGLSGTWQETIR PPLAAIF*SSCASNDIHLPKSFLA LPNGTAPLNGLPSIAS
21548	51916	A	21676	1416	1832	GSAPRQRHLAGRPPVTTTRPKHV SHHGPQENSAHRLSHVDNESTC IVCGTLRLQHSARYFPSPLETL FLAPVNHVS/EYNWQAAVPK*I Y*HQTFPGRDCQHLLFHFVRKF GVRESI/AQVVAVRAATSAWRY SRSSAITL
21549	51917	A	21677	97	300	
21550	51918	A	21678	756	1179	RRRLSPYCRAAAGSSPSYECF AHQRSVASSRGHTGTTRQFYRE HWFLRCIRRLSGTRLLAYHRFC QPHLACSGKRAVSASSTRSADV AAWYRV/CAKPFSSSS*VQEDL SYLRFSA*P*TVIL*PACRKPCKR KRRGQRRWR
21551	51919	A	21679	3	1279	
21552	51920	A	21680	1	2448	
21553	51921	A	21681	317	1985	PNTPLTSKPLLLTHPLTLLTPSA SGWQKTTKLSCVF/PETEKYAH ERLAHHVAQGANQYAPMTGV QALREAIAQKTERLYGYQPD DSDITVTAGATEALYAAITLV RNGDEVICFDPSYDSYAPAIAS GGIVKRMALQPPHFRVDWQEF AALLSERTRLVILNTPHNSATV WQQADFAALWQAIAGHEIFVIS DEVYEHINFQQGHASVLAHPQ LRERAVAVSSFGKTYHMTGW KVGVCVAPAPISAEIRKVHGYL TFSVNTPAQLALADMLRAEPEH YLALPDFYRQKRDLVNALNES RLEILPCEGTYFLVDYSALSTL DDVEFC*SLTQEHGVAIPLSVF CADPFPKLRILRIQTAAINLLVN HERRANAVINVDHAEIPFLRIIL PFLRQRQHHAVIDHHPNAELL FQQIFHLHRRCPRRFRHGLRHA GHRINLTVDFQRQVDGMVRPQ FTVAMPAIFRFRTAAPSASVHQ SGVRLPYQFMALIASDNFCCW VHGGYITLAVNGNDAIGSVFNN QIVKCPRTQCLGEVINTLTDLP HFTGQLW

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21554	51922	B	21682	160	312	
21555	51923	A	21683	80	452	
21556	51924	A	21684	158	1980	REDTAHLPAVGFLLPQNPFRAIR ASGEMLLPLLLLPMCWAVEV KRPRCVSLTNHHFYRESKPTV CLDGSATIPFDQQRLLTYCDCK VDGS*RSQATAA/C/PNGQAFH/C HQTLLGL*SPL**SPSKPGSNDGV CDCCDGTDEYNISGVITCENC KEEGPVRRESLQQMA/VEVRE GFRLEEDPLFEGLGKKAREEK QKKLVELQAGK/KSLEDQ/VE LRTVKEEAEEKPEREAKQHQK LWE/ELAGFQGNPREQDARA ADAFKELDDMDGTYSVTLEQ THPELDTDGDGALSEAEQAALL SGDTQTDATSFYDRVWAAIRD KYRSEALPTDLPAPSPDLTEP KEEQPPVPSSPTEEEEEEEEEE EEAEEEEEEEDSEVQGEQPKA PPPLSPQPASPA/EEDEKMPPYD EQTQA/FIDAAQEARNKFEEAE RSLKDMESIRN/LEQ/ISFDFGP NGDV/FAYLYSQ/CARDLTTNE YV/YTRLCPFQVLLFAGNPNNG VFPTSLGHLGASW/VLGPDHGQ VSVAMKF*ARHGACWQGNPL QHP*RFWFGKET/MVTKHPQ*P SRCEYLHGS**TPAA/CPEPPAL KQPPQPK/DHDEVLSWMGARE
21557	51925	A	21685	59	359	LLRIGNDWCIPKGITPTTHIKLP IGEIRQPNATLDLSQSDNEY CLLLAKELGLNVPDAEIIKAGN/ GARVSGRTF*QALEC*ANGFTS LATGGYVSDI
21558	51926	A	21686	1	213	MSIAVTTTDPINTGVSTSSSSS TGSNAADLQSSFLTLLVAQLKN QDPTNPMENNELTSQLAQISTV SGIEKLNTLLGSSGQIDNSQSL QASNLIGHVMIPGTTVLAGTG SEEGAVTTTTFPFGVELQQAADK VTATITDKNGAVVRTIDIGELT AGVHSFTWDGTLTDGSTAPNG SYNVAISASNGGTQLVAQLQF ALVQGVIRGNSDITTFGVNMKL AHLGRQALMGVMAVALVAGM SVKSFADGELLNKKERGTLLV GLEGTYPFSPFQDDGKLTGFE VEFAAQ*FAHGQQRRTKQFS DFAGGAAEKPDPQSNKGQRA DVAIGTNQHGQRD

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21559	51927	A	21687	1	2339	MSGGQTEKQAQLIRDFQPDMI MVTSPYCLNIEELERQLGGDA SGCSLRVGVFGAEPWTQAMRK EIERRLGITALDIYGLSEVMGPG VAMECLETTDGPITWEDHFYPE IVNPHDGTPLADGEHGELLFTT LTKEALPVIRYRTRDLTRLPGT ARTMRRMDRISGRSDMLVLR RRHLCRPSACQLCRPPSLPATD RVLELFAQSGAQWLVLGDVL NHGPRNALPEGYAPAKVAERL NEVAHKVIAVRGNCDEVDQM LLHFPIAPWQQVLLEKQRLFL THGHLFGPENPALNQNDLV YGHTHLPVAEQRGEIFHFNPGS VSIKGGNPASYGMLDNDVLS VIALNDQSIIAQVAINPAPEKEG FLIMEQRRRLASTEWWDIVNEEN EVIAQASREQMRAQCLRHAT YIVVHDGMGKILVQRRRTETKDF LPGICATSKVRKLLCKSAALLP VSELLVLLTPVFGSAVIGKL GAFAIHIDGITVKRRLVRNTVL QFCGRSRQPLEYVSAGDTGPVL RALKRMAMMRHYMSQT VKG VTDTRAIDEVALSVAQVEEMY RYLAIANYEDRFVIPTSHREMA GDFAERNNGCGFTFGDGCHGS DSKFNLFNSSRIDAINITEILKVI GLLMEYPDELLWECKEDALALI RRDAPMLTDFTHNLLNAPLLD KQAEWCEVFDRGRTTSLLLFEH
21560	51928	A	21688	391	631	
21561	51929	A	21689	2779	3348	LMQLHNLPLVAGLRQFCQQLV IQRLYFFTTATAHQCTRHMCHR HRSLLTAHRQMALCFQYVDDL HHAFADVLIINACYPLLMGEQ GVFIYNGTQQLLHWVIIDSRQD HGFGGL*KSRIVCERRRL*SQH GQVFRHHVPDHRIDIAFNAL *TLVIREISSVPASVGVGIDFPGG AATWAGPVVIKPGQS

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21562	51930	A	21690	1	1239	MPNVDDVVGEMVNTMSASRSY QANVEVLNTEKAMSIAVTTTDP TNTGVSTTSSSLTGEQRRRFTK QFSDFAAGAAEKPRPDQSNKG QRADVAIGTNQHDAARILRKG TMTLLNPYFGEFGGMYVPQIL MPALRQLEEFVSAQKDPFQ AQFNDLLKNYAGRPTALTCKQ NITAGTNTTLYLKREDLLHGGA HKTNQVLGQALLAKRMGKTEII AETGAGQHGVASALASALLGL KCRIYMGAKDVERQSPNVFRM RLMGAIEVIPVHSGSATLKDAC NEALRDWSGSEYETAHYMLGTA AGPHYPYPTIVREFORMIGEETK AQILEREGRLPDAVIACVGGGS NAIGMFADFINETN/VSVGPOH AYLNSSVRAD*VSIIDDEDLQA FKTLTASYKTPAAAKTSLHVP
21563	51931	A	21691	32	1778	WDARVFSHSGWVLYLIRQYCSI SAVSSCGSTTGSAACSATSWATA TSDSVTHLRLFSYRGSDFRMR RFNHFRRLRFGNLGGFYDTGHF FNNWRANNRFDSGGDRDLSHH RLHMYFFLFALLFNLILRTYN WIADPDFARGQFRRRARYGQR HWRLGWITLVTIATTLTTYAQ VTRRAARTTRHATVTVVISIVL FLLFWCSLRYDWHYCILIRSTP SVLSQYPVGNELRRRLVHLHL LCTYSDDSDRDPYRQESRTRN GVVPVIVNIDVHRFGQTGDQH GAMIIPVIFLLNVAMHERASGHI PNGNRTYYLSRSQPPVFALMVE LFEEDGVA VARYLDHLKMEYA FWMDGAEILIPNQAYRHVVRM PDGSLHRYWCDCHTSCD*SW LEDVETAKHSGRPPNEVYRDLR AGAASGWYSSRWLRDTGRLA SIRTTQFIPIDLNAFLFKLESAIA NISALKGEKETEALFRQKASAR PMREYETGEQWDKPNGWAPL QWMAIQGFKMYGDDLLGDEIA RSWLKTVNQFYLEQHKLIK EY HIADGVPREGGGGEYPLAQDGF GWTNGVVRRLIGLYGEP

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21564	51932	A	21692	1	2514	MKTLIARHKAGEHIGICVCSA HPLVIEAALAFDRNSTRKVLIEA TSNQVNQFGGYTGMPADFRE FVFTIADKVGFAERHILGGDHL GPNCWQQENADAAMEKSVEL AVVIDLWSRAVIGWSMSPRMT AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK RHNLRGSMASAKGCCYDNACVE SFFHSLKVECIHGEHFISREIMR ATVFNIECDYNRWRHRSWIN LLSQKRNTQGRIEDGRQH
21565	51933	A	21693	1	1527	
21566	51934	A	21694	792	1602	HCLSARRYELVCQPK*AFVR*L LR*IAVLR/HLNIQHLLRRSHSLR HGRRHTRKGERGTINIVNGTPI HERSRNIDNRRSPSPYIRKGAH TELRSDDHPLLINQHWHHFAGM VAVTNGRIVAVIRHHDQAIJWL HRLNKPQKVTVNDLQTFGITCD VFCMTSEVGFNLVNGANKRRRM GVKFVEGDHNPALHJQLPAH AIRIVDDICHLTHQHGWHACFI QFLWHLHFFIDAIAMHMDLET VISARTRIDTNKAPFFAFCGIE
21567	51935	A	21695	1	1530	LSQQT VNTLQAQHQTHFFMG VIHQQRPTTHRRDVVIGHQWH CAVMSGTHSNVIEKTANIIGV VFTEIKSNNAKPVLAIESNAA ATDGEIVFDGEILKSACEINDSD KKIEVALGHYNAEQFRNIGERS PKIPFTIPLVNCMTGEIANILGS KPGTIFTMLRDTGGIKPHERKR AVAHLTLSEEEIRAGLSAKMS IRAIGYWR*IASPSTFSRE/VQRK GGHRVYKAVDANIRANRMAK RPKPCLLDQNVPLRKLVEKLE MKWSPEQISGWLRRTKPRQKT LRISPETIYKTLYFRSREALHHL NIQHLLRRSHSLRHGRRHTRKGE RGTTINIVNGTPIHERSRNIDNRR SLGHWEGDLVSGTKNSHIATLV DRKSRYTIIIVRLRGKDSVSVNQ ALTDKFLSLPSELRLSLTWDRG MELARHLEFTVSTGVKVYFCD PQSPWQRGTNENTNGLIRQYFP KKTC LAQYTHLDELVA AQLN NRPRKTLKFKTPKEIJERGVALT
21568	51936	A	21696	2	140	IITNSISRPDPPMSDPHS*SPAS SSAKTETKSLFNAFLV

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21569	51937	A	21697	1817	4083	KGLLTSTFHYIKTPEVPNLCVEG GTRLQIWPACSTSGGGTCWK APPQPPRPPTSSSPS/PAPPSEAF VLSAGAMQLEAGAYSLVIKES KNNVGVVDVKKRHCTAGGNV NQYNHYGKHCVLSCSGPASGA QPLYRMAQPPSPNMAAGIPPA ARISSSITSPLLKPSWLHLAHP VLQAHLTEEGLGRSHHVQRGQ CLVSKSVFTNACWEMQNVKRF TDFIPLHKNTRGPEPLCRRRNQ APNMACMQQHWQRRN
21570	51938	A	21698	247	281	KPGKQHSMLK*SALLPSAHGPT S/CKEARCHPVQILPELLF*MP KKICPPLCYLWTVKAWETTTFH AEV
21571	51939	A	21699	531	716	PRRLRAAPPDLGGFRLLPR/LPE ASGCSP*SQRLFQKAPSPAPCS WRRSRFCVKTCVLPMGGO
21572	51940	A	21700	202	606	ITCLHAHVTCQILPYLMLPAP LLRPLPTPLTVAGVGQSLPEIQL SVTLPLQPGRNQGSLESRHLVS WAEPP*DPASVALPLQPGRNQGS LESRHLVSWAEPP*DPASVAL PLQPGRNQGSLESRHLVSWAEP
21573	51941	A	21701	444	1167	FRLHGHLERGPFYFLSPLAVQS SQSCLRRFTTRYHLPIYVLNRK NSWHVAHIFRRHAKPEEQAPIY SHIHFTSDLDEVLNDPDVKLVV VCTHADSHFEYAKRALEAGKN VLVEKPFTPLAQAKELFALAK SKGLTVTPYQNRNRFDSCLTAK KAIESGKLGEIVEVESHFDYYRP VAETKPGLPDQDGFYGLGALFT NQQGFKSSLSIFADSSSSVAG RSPHNLVKKRGGIVAIASAFAG
21574	51942	A	21702	1	668	

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21575	51943	A	21703	1	1308	MRVYMDGRLIVSTRQRKVLAA GPMLYAATRAPAFTMSGDNLV RSHASIYMTSCHTLTGEQAGYA VFGALLPAITLLHLNSACCIVYV SCLLADAGHRDSLQQAGDKWT TTDSYSSSCTSETLGSACVRYA HSSRNHVRFALSDLDDEVLDPPD VKLVVVCTHADSHFEYAKRAL EAGKNVLVEKPFPTLAQAKEL FALAKSKGLTVTPYQNRFFDSC FLTAKKAIESGKLGIEIVEESHF DYYRPVAETKPLPDGAFYG LGVHTMDQIISLFGRPDHYRL* HPGALRNKSPWIWNPFEAQLFY G\DLKAIVKTSHLVKIDYPKFIV HGKKGSIKYGIDQQETS LKAN IMPGEPGAADDSVGVLEYVN DEGVTVREEMKPEMGDYGRV YDALYQTITHGAPNYVKESEVL TNLEILERGFEQASPSTVTLAK
21576	51944	A	21704	199	706	SHDVCRINADQRDRNRRQR RSLRVYKLGNNQQNNGIGPRIL FHHFTQYALNFRHMRTEHGFC HPCDTVHRHDGHTGTEDFVF/ WR*TRDWFWSG*\YQRPQQQH KHLNNQYHRQRFAAEGWTQV RISTKKGDSYDCPEENPHCQPV AGRYHYSLVGRVSNATLARLIR
21577	51945	A	21705	354	569	SRAVCVQVGTRLWAIFGVSE LQRHVLVVFAGFWIVKNSRNL FLVCRAEHKRSVVKGLLRQQG AGLLVPLS
21578	51946	A	21706	373	462	
21579	51947	A	21707	1	1293	

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21580	51948	A	21708	1	1371	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIHILTKTNPASISK NEVFRSGMIAIVAVYGIAWMA ETMFAPACYGYIILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPQSVKAD IATNPFKRPGGAFIRITQTFRVT QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAERETGKAALVMGC VGVTEGAIPFAAADPLRVIPSIM VGSVCGAVTAALVGAQCYAG WGGLIVLPVVEGKLGYYIAAVA VGAVVTLFV*TC*KVWRVKM GLRLMKKKTTWIWILKLI
21581	51949	A	21709	961	1116	
21582	51950	A	21710	228	388	RRGRNRYPALQ*TMFLPADGP ARCLSRQAAILKESVLPK*GRP DVVFSPAYPY
21583	51951	A	21711	1168	1851	LHRTGQRPAAQRTETHHPFFNH FARLQVDTVVINHHQHTVAFQ NRTFRSEI*RNNVDIFQPDVLPD ILLGPPVREREDADAFVNLVP VVVPQLRALIFRIPAMEAVTER VNSLFSAGFLFVTARTTEGGIKT VVFQRLFQAFSFHNIGMFRAAV HEWINPHRHAFRVFMHQFQAA VGFSSTIAELIHLAEFFAGIDMQ QREQRQTWIKRLARQMQHADG IFTDRVEH
21584	51952	A	21712	1	2653	
21585	51953	B	21713	632	709	

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21586	51954	A	21714	1	1214	MHDQQVIDAYHPDLRRTRAAS QSIIPVDTKLAAGITRFFPQFND RFEAIAVRVPTTNVTAIDL SVTV KKPVKTDVGGAGTVKLNRCQI ARISRQDVITPPGCVFEKALTLL IASGRNDTLARQNNHTKESLVE KPERKILVIKMRVYHGDMLLTTP VISTLKQNPDAKIDMLLYQDT IPI LSENPEINALYGISNKGAGTF DKIKNVLSLIKTLRANNYDLVI NLTDQWMVALLVRCLPARMKI SQLYGRHQHGIWKSFTHLAPI HGTHIVERNLSVLEPLGITDFYT DTTMSYAEDCWKKMRREDA LGVKDHVYVIQPTARQIFKCRD NDHISKVICMIRGSPTEGRWSVF FFYPADFTFVCPTELGD/GC*PL RRTAETGRRRIRSIYRSLHPQS
21587	51955	A	21715	25	1086	
21588	51956	A	21716	1	1113	
21589	51957	A	21717	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGILFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21590	51958	A	21718	1	2076	
21591	51959	A	21719	2742	3109	VWTEGTGNASRARR/WKGNQL LPVSLVKRKTTLPNTQTASPR ALADSLMQLARQVSRLEKRAV SATQLMAKAVKQGQSSLLPVSL VKKKNHHPGALIRKPPLPARWPI LLIQLARQVSRLETGQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
21592	51960	A	21720	174	1608	TAAKRKIPASIRSIND*KY*VC KRT*CVGQLAAIENADGTVAEY NGYHVVFALAGSPKADDDTSI YMFYQKVGDNISIDSWKNAGR VLMNPLMLVKIKLSLTLACH ALLDCKTLTLTELGRNLPKAR TKHNIKRIDRLGNRHLHKERL AVYRWHASFICSGNTMPVLVD WSDIREQKRLMVLASVALHG RSVTLYEKAFPLEQCSKKAHD QFLADLASILPSNTTPLIVSDAG FKVPWYKSVKELGWYWSRV RGKVQYADLGAENWKIPSNLH DMSSSHSKTLGYKRLTKSNPIS CQILLYKSRSGRKNQRSTRTH CHHPSPKIYSASAKEPWVLATN LPVEIRTPKQLVNIYSKRMQIEE TFRDLKSPAYGLGLRHSRTSSS ERFDIMLLIALMLQLTCWLAGV HAQKQGWDFHFQANTVRNRN VLSVTRLGMEVLRHSGYTITRE DLLVAATLLAQNLFTHGYALG
21593	51961	A	21721	1	3285	
21594	51962	A	21722	1095	1188	
21595	51963	A	21723	568	1263	
21596	51964	A	21724	2	1688	
21597	51965	A	21725	1456	2046	SKGKVAIVSSHQEVRASPRRSP LGSEERPGPHTSRQAAGQPHPG TCSSVHCQGSWGLQTQNSEVIH DGDVEAISVGEDAAPGPRVHG ADLGQEEEAFFR*VVMGGLPDR DSALAPVPEPMHRGWAVRAAE GAVQNDPVGGSERSWGAGSHS QPFSHRPAPHTRGLAQAQTEAA GEGAVPEVHRGAVLAGVRAPG WAQP
21598	51966	A	21726	335	595	AGLFKSRKVSSICIRFE*ILTSL GVRISTGKLVARIHGSFADAE*I LWTTGGDNESVS/MR*FFRPLER DLYNRIWHEIGLLLVSL
21599	51967	A	21727	80	428	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNGLWYCELS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21600	51968	A	21728	622	1281	

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21601	51969	A	21729	1066	1827	VPQAKGNNVVITSYMTNRGFF EDKKATFAPSLMNIKGNKTSV VKNSILEQGGQLTWLQVAKRAG LGGGQSGRTVLRERVRIEIAST HIALQHAIVTGDVGMDDIPQE ARQYRHNQAYAYSIOGDGAED DDERIAFASHTIQECRSQGPQG YPFKIYSSRKDRIPISQSLLSEHF TVHEETAPDLETTG*PGCKDHG NLCC/LSSVKLRYSMYRIKAGL WMTHPG*RTYWV
21602	51970	A	21730	1	1326	
21603	51971	A	21731	1	1971	
21604	51972	A	21732	1	1626	
21605	51973	A	21733	1	1810	
21606	51974	A	21734	305	442	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
21607	51975	B	21735	1	1938	
21608	51976	A	21736	531	669	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21609	51977	A	21737	80	428	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRIRCP YLLTGLISVSKNGLWYCELQSH YTVVLLL FMRKRSRFQSNVQR KLMTNF
21610	51978	A	21738	10	426	
21611	51979	A	21739	314	451	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21612	51980	A	21740	1	1139	MWIGSRTPYINILVYSSPEVS CEKPKYVKSQTSHTGTGFESHKR YIFYRLRVGKNLHVSAMGLGK SQERRKKALKSQPPQPADSFPS LPTVEGLTTSGEVAAGFWLSGE ALSSC*LLSASVHLLACLGMG KCSGFWLYF
21613	51981	A	21741	306	444	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE

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21614	51982	A	21742	189	1089	HHTAHQC*CW/L*S/DHGINPLRS WVGTV*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRKGR KNQRSTRTHCHHPSPKIYSASA KEPWLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWKHF QANTVRNRNGSLLTNWPSVPP TIKEEENSEEELAAATTSKEQEP IGTDLDAVRTPELPEEFKREDQ EGSPPETSLPYKWVVEANLLI PAVGSSLSEALDLIES
21615	51983	A	21743	1	1135	
21616	51984	A	21744	80	430	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
21617	51985	A	21745	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCPL LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21618	51986	A	21746	773	1015	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHG SFADASF STDLYHGTLKPA SLTMSGVLL GRMLARSARNWS
21619	51987	A	21747	391	527	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHG SFADAE
21620	51988	A	21748	671	1030	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHG SFADAE*I LG DGW*Q*VRVER*FFRPLERD LYNRILACPLINT*PTPVRLKP *TVWSMGPPVGT PARPIRTSGA CWWCW
21621	51989	A	21749	221	478	AEQDCTLPVL RHFTFFKSRKVS SICIRFE*ILTSCLGVRISTGKLV ARTHG SFADDQTLFFMTLAVS GELWTPSPWRPNISRTS
21622	51990	A	21750	590	940	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCPL LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21623	51991	A	21751	473	613	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHG SFADADT

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21624	51992	A	21752	342	1459	SFLWRFRLLRGGSERFCLAGIPSA SGV*NIPASASIRSIND*KY*VCKR T*CVGQLAAIENADGTVAEYN GYHVVFALAGSPKDADDTSIY MFYQKVGDNIDSWKNAGRVF KDSDFDANDPILKDQTEWS GSATFTSDGKIRLFYTDYSGKH YGGQSLTTAQVNVSKSDDTLKI NGVEDHKITFDGDKTYQNVQ QFIDEGNYTSGDNHTRDPHYV EDKGKHYLVFEANTGTENGYY GEESLFNKAYYGGGTNFFRKES QKLQSSAKKRDAELANGALGII ELNNDYTLKKVMKPLITSNTVT DEIERANVFKMNGKWYLFIDS RGSKMTIDAKSTLLESTEGSMT PPMTATEPFLRFLKGEIAQPKPH
21625	51993	A	21753	2094	2201	
21626	51994	A	21754	81	1080	HHTAHCQ*CWL*S/DHGINPLRS WVG TG*V/GVRGKVQYADLGA ENWKIPISNLHDMSSSHSKTLGY KRLTKSNPISQCILLYKSRSGKR KNQRSTRTHCHHSPKIYSASA KEPWVLA.TNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPA YGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQEHPLWSL ALVRRSPAQSPHVG TGSSGST GCSSQAPCMKSNALIVILGTV TLDAVIGLVMPLPGLLDIV HSDSIASHYGVLLALYALMQFL CAPVLGALSDFGRRPVLLASL LGATIDYAIMATTPVLWYPLV
21627	51995	A	21755	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVAIRCP LYLLTGLIFVSKNDLWYCELOS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21628	51996	A	21756	1	593	MGVNDLWQILEPVKQHIPLRNL GGKTIAVDLSLWVCEAHPVKK MMGSVMKKHLRDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AAYPIPDQVQSVLISMLLIAL MLHLTCGLAGVHAQKQGWOK HFQANTVRNRNVLSTVRLGME VLRHSGYTITREDSLVAAITLT QNLFTHGYYLGLK*GDL SVLSL
21629	51997	A	21757	410	547	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE

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21630	51998	A	21758	719	814	AGLFKSRKVSSICIRFE*ILTSL GVRIFNR
21631	51999	A	21759	1	1596	
21632	52000	A	21760	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCEIQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21633	52001	A	21761	1343	1480	AGLFKSRKVSSICIRFE*ILTSL GVRISTGKLVARTHGSFADAE
21634	52002	A	21762	2	151	
21635	52003	A	21763	258	396	AGLFKSRKVSSICIRFE*ILTSL GVRISTGKLVARTHGSFADAE
21636	52004	A	21764	1	3081	
21637	52005	A	21765	449	586	AGLFKSRKVSSICIRFE*ILTSL GVRISTGKLVARTHGSFADAE
21638	52006	A	21766	563	2042	
21639	52007	A	21767	1001	1093	
21640	52008	A	21768	1814	1870	
21641	52009	A	21769	2760	3723	HHTAHCQ*CWL*S/DHGINPLRS WVGTV*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSGKR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPEVIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL QLRHRTSSSERFDIMLLIALML QLTCWLAGVHIAQKQGWDKHF QANTVRNRNVLSTVRLGMEVL RHSGYTITREDLLVAATLLAQN LFTHGLFGPSVDAPPPKRGFKR PKLPELRLQRFFGGVITPPLESY SLPSDPVHLFPPRPPRQLTASP LRARAPYECSSCKDA
21642	52010	A	21770	860	3503	
21643	52011	A	21771	4597	6030	
21644	52012	A	21772	1513	3464	AGLFKSRKVSSICIRFE*ILTSL GVRISTGKLVARTHGSFADAE
21645	52013	A	21773	1	453	

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21646	52014	A	21774	1	1526	MSSSHSKTLGYKRLTKSNPISC QILLYKSRSKGRKNQRSTRTHC HHPSPKIYSASAKEPWVLAITNL PVEIRTPKQLVNIYSKRMQIEET FRDLKSPAYGLGRHSRTSSSE RFDIMLLIALMLQLTCWLAGV HAQKQGWDKHFQANTVRNRN CKMATLKEKLIAPVAEEVEANS PNNKITVVGVGGVGMALCAISI LGKVSWPDELALVGCWFWDK LKGNDGSPQHGEIIFQTPKN CGQDKGLFWGPPNS*RFVSW*L AGSPVQPRRGIRLKSWSVPEK WLMVFQIPLFLKIVKYSP*FAS* LVVSHPVADIPTYVTWETKVGL PKHRVIGSGCNLDSARFYLMA EKLGIHPSISCHGW/IFWGEHG DSSVAWCWNGVNVAGVSLQE LNPENGTNDSENWKEVHKM VVESAYEVIKLGYTNWAIGLS VADLIESMLKNLSRIHPVSTMV KGMYGIEVEFLSLPILNARG LTSVINQKLKDDEVAQLKSSA DTLWDIQDKDLKDL
21647	52015	A	21775	2	355	
21648	52016	A	21776	2	178	
21649	52017	A	21777	1	888	
21650	52018	C	21778	127	255	
21651	52019	A	21779	1	1824	
21652	52020	A	21780	330	476	
21653	52021	A	21781	452	500	

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21654	52022	A	21782	3	1584	DAWAAVSRGDEPGWGSWSR LLQHWGVSCWSDPKRFSSALQ GYIITDWCAPFNKRIWKREQPE ETFPNTEITNGEFGK\RPADME EEQAFKRSRNT\DEMVELRILLA QSKNAGAVIGKGGKNIKALRT DYNASVSP\DSVPERILCISA DIETIGEILKKIIPTEEGQLQSP TATSQLPLESDAVECLNYQHYK GSDFDCELRLLIHQSLGREGIIG GQRCLKSKELRGGLTQTITKLF QECCPHSTD\RVVLIIGKPKDRFV ECIKIILDISESPIKGR\AQPYDP NFYGWKPMYDYGFTMMFDD RRGRPVGFPMRGRGGFDRMP GRGGRPMQPYRRDYDDMSPRR GPPPPPPGRGGRGGSARNLPL PPPPPPRGGDL MAYDRGRPGD RYDGMVGFSADETWD\SAIDTW SPSEWQMA YEPQGGSGYDYSY AGGRGSYGD LGGPITQTQTIPK DLAGSIYKGGQRIKQIRHESGA SIKIDEPLEGSEDRITITGTQDQI QNAQYLLQNSV\KQYSGKFF
21655	52023	A	21783	211	1635	KNMETEQPEETFPNTEITNGEFG KRPAEDMEEEQAFIRSRNTDEM VELRILLQSKNAGAVIGKGGK NIKALRTDYNASVSPDSSGPE RNL\SISAD IETIGEILKKIIPTEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFCELRLLIHQSL AGGIIGVKGAKIKELRENTQTIT KLFQECCPHSTD\RVVLIIGKPD RV\ECIKIILDISESPIKGR\AQ YDPNFYDETYDYGFTMMFDD RRGRPVGFPMRGRGGFDRMP GRGGRPMPPSRRDYDDMSPRR GPPPPPPRGGG/RGLGSRARNLP LPPPPPPRGGDL MAYYKRRGP GDPYDGMVGFSADETWDSPID TWSP\SEWQMA YEPQGGSGY DYSY/AQGRGSYGD LGGPITTT QVTIPKDL\ALGSIYWKKGQR\IK QIPS*V\GELSIKIDEPLEGSEDR ITITGTQDQI\QNAQYLLQ\N SVKQYADVEGF
21656	52024	A	21784	860	1201	TISEPPALILLPIA VPSFSTTCRLP EDIIVSFAFP\LLIFCVPLLLIVP VAMP*LLIFCVPLIMVFAFPA TSITPPLSIRVASALALVKTDIVP LSLIIVLFAEPYAFMSK

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21657	52025	B	21785	1	3750	
21658	52026	A	21786	1	1350	
21659	52027	A	21787	189	1939	TAMAGRMPCAEVISGSATRPD GPKALFKPIGRPHQAIKPP AAPPKQAVTNGFMGRVPPKT LTPSESSLAPMTLVVIVVKEA LPPAKIFIPVVPYQPIRRAPDAE PLSASKTPSVYLVNFVVSPEDL RKLTVDVLPALRANTRALWQV EVSAPPSFMTQATPATQPLINAE PAAAPTEQNQVGVPMMPGVQ GADAPVVAQNGPSRDVKLTFA PIAPPGSMVLRGLNPNGLSLEFG MRSDEVVTKAMVQLELTPWH GYGCQCPLPVKYLAAIGFSV MIEALNQLAIFNRRRFLSANQT LRQRTTEAVMRLLSGQKEDAE LDAETASMLVDHGNQQIFNPQ ERRMIERVLNLRNQRVTSSIMTS RHDIEHIDLNAPEEEIRQLLERN QHTRLVVTGGDDAEDLLGVVH VIDLLQQLSGEPLNLRVLIRQP LVFPETLPLPALEQFRNARTH AFVVDFEGSVGEIVTSLSDVTETI AGNLNPEVEEIDARHDIQKNAD RSWTGN/GLLPLGDCRL*QASP TGCINRRGSHYGYPTLYEFKRK FLTPGTCKRCDDQRGDAMRVQ VQWVFYTYILPLANE
21660	52028	A	21788	558	1563	TNNRL*K*GNN**LTNQKKSR RWIHSRILPEAGC/GIASVGRNN CGLWRFTPAKAIWGGKIHPVFQ RQILRVLSQTLFPN/MSLGRNLG YGLKMFVGPRAELKPRFKEALP MVNLEGFEDRFVDQISGGQQQ RVALARALILPKVLLFDEPLS NLDAANLRRSMRDKIRELQKQF DITSLYVTHDQSEAFVSDTVL VMNKGHIMQIGSPQDLRYQPA SRFMASFMGDANLFPATFSDG YVDIYGYHLPRPLHFGTQGE MVGVRPEAITLSDRGEESQRCV IRHVAYMGPQYEVTVWHGQE ILLQVNATRLQPDVGEQYYLEI HPYGMFVLADAA
21661	52029	A	21789	201	312	CSWHDREFPDWKAGTHLLARG* QLSLPVWLCPVLLKLS
21662	52030	A	21790	925	2388	
21663	52031	A	21791	1	759	

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21664	52032	A	21792	1	1086	MEKKITGYTTVDISQWHRKEHF EAFQSPAQCTKNQTVQLDITAF LKTVKKNKHKFPYAFIHILARL MNAHPEFRMAMKGVPGGDSV KNTSRVWSGNERDQKLLTENA LNDLIPSFLLTGQQTALGRRVVS GVIEIADGSRRRKAAALTESDY RVLVGELYDEQMPLSRLGND YRPTSAHPQKRRYASRLQNEFA GNISALADAENISVRDVLNLL EVLGVDSVEKTRVWWSGNERD QELLMEDALDDLPSFLLTGQQ TPAFGRVSGVIEIADGSRRRK AAALTESDYRVLVGELDDEQM AALSRLGNDYRPTSAYERGQR YASRLQNEFAGNISALADAENI SRKIPRCINSALP
21665	52033	A	21793	1	935	MLRDLKKNVDLKGFEPPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMLVKNVRETDEVGKGQI RMRTVFEQAIDQRSSTDNEGAP VIPKHTLNTQPVEDTSLSTPAAP MVDSLIARVGVMMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWWSGNERDQELLTEDALDDL PSFLLTGQQTAPAFGRVSGVIEI ADGSSSRSKRRRGCEGGRR/V RQCGCPDQKHIPAFVSVGGKIHL SGRTPVEKRPLPQPRDLGARA FAACRGSRGRPWNLPAALRL HADLGCVRGGGGWPGANPY PAPASSTC
21666	52034	A	21794	181	923	QHAIVTGDVAGMHHPQEARQ YRHNQAYAYSIGDGAEDDDE RIVRFHTRCLTEAFEKLQCGGV VNQLSRRGNNQIHSTYDINRA DTQVRRRAVNNYDIIVMSNSFN ASRSIRCGSVGSLPSSNLPIINSVS IRCRAR/SG/EE*QAPASKWAL LHK*HRPFQDRKAGECLLHEY EDLVPIRDLRLFPGGRYLPRA KHVAPSEPDPEQDEQKLRFCR HLYGQQRSPVEIRLQHVAIAY PTHHAYD

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21667	52035	A	21795	178	798	IRLEPFKINVLEQITKHIEKLQCGGVVKQLSRRGNNQHISSTYDINRADTQVRRVAVNNYDIIVMSNSFNASRSIRCGSVGSLPSSNLPINSVSIRCRAR/SG/EE* CQAPASKWALLHK*HRPFPQDRKAGECLLHEYEDLVPIRDTLRLFPGGRYLPRAKHVAPSEPDPEQDEQKLRFCKRHLYGQQPRSPVEIRLELVAIA YQTHHA
21668	52036	A	21796	499	972	
21669	52037	A	21797	3	1141	SRVKLGQSSSEQVAALKTREPMNIATLEVLVLKGLRVCFVKVNHKPGPASMYPGWVPILYIHAEDPLLFPYLGEKEDVTYAIKPTCWPGLDIHPSCLALPRIETELMGKFD EGKLPDTPHMLMLRLAIETVAHDYDVIVDSAPNLGIGTINVVCAADVLIVPTPAELFDYTSALQFFDMLRPLLKNVDLKGFEPPDVRILLTKYSNSNGSQSPWMEEQIRDAWGSMLVKNVKEFAGNISALADAENISRKIITRCINTAKLPKSVV/ALFSPHGELSA\GDALQKAFTDKEELKQQASNLHEQKKAGVIFEAEVITLLTSVLKTSSASRTSLSSRHQFAPGATVLYKGDKMVLNLDRSRVPTCEKIEIAILKELE
21670	52038	A	21798	1	617	LEPASLSIPNLLHPRGLRAITIAVFGKQNTYIRLEPFKINVLEQITKHIEKLQCGGVVKQLSRRGNNQHISSTYDINRADTQVRRVAVNNYDIIVMSNSFNASRSIRCGSVGSLPSSNLPINSVSIRCRAR/SG/EE* CQAPASKWALLHK*HRPFPQDRKAGECLLHEYEDLVPIRDTLRLFPGGRYLPRAKHVAPSEPIILSC
21671	52039	A	21799	181	953	QHAIVTGDVAGMDIPQEARQYRHNQAYAYSIQGDGAEDDDE RIVRFHTRRLTFKINVLEQITKHIEKLQCGGVVKQLSRRGNNQHISSTYDINRADTQVRRVAVNNYDIIVMSNSFNASRSIRCGSVGSLPSSNLPINSVSIRCRAR/SG/EE* CQAPASKWALLHK*HRPFPQDRKAGECLLHEYEDLVPIRDTLRLFPGGRYLPRAKHVAPSEPDPEQDEQKLRFCKRHLYGQQPRSPVEIRLQHVAIAYQTHHAYD
21672	52040	A	21800	1	798	
21673	52041	A	21801	1	1782	

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21674	52042	A	21802	666	1131	KGRGTYGNERDQELLTEDALD DLIPSFLLTGQQTAFGRRVSGV IEIADGSRRKAAALTESDYRV LVGELDDQMAALSR LGNDYR PTSAYERGQRYASRLQNEFAG NISALADAENISRKIIITRCINTRQ LPKSVVGVFFSHPGELSARSGDA
21675	52043	A	21803	1	3297	
21676	52044	A	21804	1	898	
21677	52045	A	21805	1	1977	
21678	52046	A	21806	1	1929	
21679	52047	A	21807	181	755	QHAIVTGDVGMDDIPQEARQ YRHNQAYAYSIQGDGA/GMTM SALLDFIHGA***YIRCGSVGRL PSSNLPINSVSIRCRAR/SG/EE*C QAPASKWALLHK*HRPFQDR KAGECLLHEYEDLVPIRDTLFL FPGGRYLPRAKHVAPSEPDPEQ DEQKLRFCRHLVYGGQPRSPVE IRLQHVAVAYQTHHAYD
21680	52048	A	21808	181	456	QHAIVTGDVGMDDIPQEARQ YRHNQAYAYSIQGDGAEDDDE RIVRFHTRCLA*SRRVNNYDII VMSNSFNGQSEHQVWIGGQFT FIKFAH
21681	52049	A	21809	1	780	
21682	52050	A	21810	1	1050	
21683	52051	A	21811	5	735	PPAAP/MGNLLMARVGVKARG KAHYLPLLRGESVRKTSRVGSG NERDQELLTEDALDDLIPSFLLT GQQTAFGRRVSGVIEIADGSR RRKAAALTESDYRVLVGELDD EQMAALSR LGNDYRPTSAYER GQRYASRLQNEFAGNISALADA ENISRQIITRCINTAKLPKSVVAL FSHPGELSARSGDALQKAFTEK RTLKQQALTSEQKKRGI/YEAE EVSSSLSPQGRLLSNRSASKDMY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
21684	52052	A	21812	1	887	MNMNIKIVKQATVLTFTTALL AGGATQAFKENNQKAYKETK AVGSGNERDQELLTEEA WNDL ILSFLTGGQTPAFGRRVSGVIEI PDGSRRRKAAALPKSDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAFTDKELLKQASNLHEQK KAGVIFEAEEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMVLNLDERSVPTEC/IEKIEA ILKELEKPAP
21685	52053	A	21813	345	921	RWRQLNLSFCSSCSGSGSEGAT CFARGSA YELGQRYASRLQNA FAGKISALADAEIFSRKIITRCIN TAKLLKSVVALFSHPVELSARS GDALQKAFTDKELLKQASNL LHEQKKAGVIFEAEEVITLFTSV LKTSSASRTSLSSRHQFAPGAT VLYKGDKMVLNLDERSVPTEC IEKIEAILKELEKPAP
21686	52054	A	21814	1	1989	
21687	52055	A	21815	6	311	
21688	52056	A	21816	3	848	PGGDSVKNTSRVWVGNERDQK LLTENALNDLIPSFLLTGQQT LGRRVSGVIEIADGSRRRKAA LTESDYRVLVGELYDEQMPPLS RLGNDYRPTSAHPQKRRYASRL QNEFAGNISALADAENISRV VNLLEVLGVDSVEKTRFVWS GNERDQELMEDALDDLIPSF LTGQQTAPFGRRVSGVIEIADG SRRRKAAALTESDYRVLVGEL DDEQMAALSRLGNDYRPTSA YERGQRYASRLQNEFAGNISALA DAENISRKIIPRCINS/AKLP
21689	52057	A	21817	1	969	
21690	52058	A	21818	1	1614	

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21691	52059	A	21819	1	832	MDDIPQEARQYRHNQAYAYSI QGGDAEDDDERIVRFHTRVTV DSDTLASDAARLTCRHGLARD VKFTLEVLRGDSVEKTSRVWS GNERDQELLTEDALDDLIPFFLL TGQQTPAFGRRVSGVIEIADGS RRRKAAALTESDYRVLVGELD DEQMAALSR LGNDYRPTSA YE RGQRYASRLQNEFAGNISALAD AENISRKIITRCINTAQLAKSG VALFSHPGELSAPSGDAL*KAF TD*EEFL*PQGSNLYEQKKAG\ VIFGS*KKFSLFLTSVY
21692	52060	A	21820	678	1338	TLRQTKPDNSAEIADGSRRRKA AALTESDYRVLVGELDDKQM AALSR LGNDYRPTSA YER GQR YASRLQNEFAGNISALADAENI SRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFDTKEE LLKQQASNLHEQKKAGVIFEE EVITLLTSVLKTSASRTSLSSR HQFAPGATVLYKGDKMVLNLD RSRVPTIECIEKIEAILKEKPPAP
21693	52061	A	21821	1	1809	
21694	52062	A	21822	2	1010	
21695	52063	A	21823	284	2177	
21696	52064	A	21824	1	1296	
21697	52065	B	21825	1	1044	
21698	52066	A	21826	637	1073	IRLEPFKINVLEQITKHIEKLQCG GVVQKLSRRGNQHSISTYDIN RADTQVRRVNNYDIIVMSNSF NARSRSIRCGSVGSLPSSNLPS VSIRCRAR/SG/EE*QAPASKW ALLHK*HRFPQDRKAGECLLH EYEDLYPSVIH
21699	52067	A	21827	1	2403	

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21700	52068	A	21828	1471	3186	LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFTPI GVAAIKGTGTVVHVSSSLGG DHGSPSRIGGLLVCDYGPLVSS SGISGPTRIVGLIISLGPYHLCF RSDYRTGITDPLYIGDATIRVSL RVYSLPSRSRIEHV VANCMIPI KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGT AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNISDSWKNA GRVFKDSKFDANDPILKQDTQ EWSGSATFTSDGKIRLFYTDYS GVMARGNAITLPVCGRDVKYT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDPLIFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSA YERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFDTKEE LLMQQASNLHEQKKAGVIFEA EEVITLLTSVAKTSSASRTSLSS RHQFAPGATV/LYKGDKMVLN LDMSR/VQLECLDRLHACRSTL
21701	52069	A	21829	158	926	AGPVIQNYVNTQPV/EETSYSTP AAPMVDSLIARVGVMAPGNAI TLPVCGRDVKFTLEVLRGDSVK KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELEDDEQMAALSRLGNDY RPTSA YERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFDTKEELLKQGGSSRV GDNISDSWKTRGRVL
21702	52070	B	21830	1	3774	
21703	52071	B	21831	1	1495	
21704	52072	A	21832	556	1622	
21705	52073	A	21833	1	2616	

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21706	52074	A	21834	1412	3310	SVTSLCKVTSVCLTSAASCRS VLMRSTAEQLQCASTLRKRKA ARRLLSLMMTARKARKITRRW RIGEAADLVGVSSQAIRDAEKA GRLPHPDMEIRGRVEQRVGYTI EQINHMRDVFGRRLRAEDVFP PVIGVAAHKGNDPQGTASMYH GWVPDLHIHAEDTLPPFYLGEK DDVTYAIKPTCWPGLDIIPSCLA LHRIETELMGKFDEAQP NLGIG TINVVCAADVLIVPTPAELFDY TSALQFFDMLRDLKNVDLKG FEPDVRILLTKYSNSNGSQSPW MEEQIRDAWGSMLKNVVRET DEVGKGQIRMRTVFEQAIDQRS STDTSLSIPAAPMVDSL IARVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLLTGQQT PAFGRRVSGVIEIADGSRRRKA AALPEISNYGVLVAELDDEQMP AYPRLGNDYRPTSA YERQRY ATRLQNEFAGNISALADAENIS VITRCINTAKLPKSVVALF SHPG ELSARSGDALQKAFDTKEELLK QQASNLHEQKKAGVIFEAEVI TLLTSVLKTSASRTSLSSRHQF APGATVLYKGDKMVLNLD RSR VPTECIEKIEAILKELEKPAP
21707	52075	A	21835	783	2371	
21708	52076	A	21836	3236	4718	
21709	52077	A	21837	1	2481	

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21710	52078	A	21838	2450	3963	LLTAPITGGIGTINVCADDVMI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEFDPVRIILLTKYS NSNGSQSPWMEEQIRDAWGSM VLKNVVRETDEVGKAAPMVDS LIARVGVVMARGNAITLPVCGRD VKFTLEVLRGDSVEKTSRVWS GNERDQELLTEDALDDLPSFLL TGQQTPAFGQRVVSQVKEIADGI RRRKAALTESDYRVLVGELD DEQMAALSRLGNDYRPTSAYE RGQRYASRLQNEFAGNISALAD AENISRKIITRCINTAKLPKSVV ALFHPGELSARSGDALQKFT DKVEDLLKQASNLHGAEKSW GCYFEAEVITLLTSVLKTSSA SRTLSRRHQFAPGATVLYKGD KMLNLDRSRVPTERYGVFL NVLLPATKYQLHDPSLRNMEL NYSASEDLVLKGLRVLLVEG NDPQGTASMYHGWVDPDLHIHA EDTLPPFYLGKDDVTYAIKPT CWPGLDIIPSCALHRIETENYNG
21711	52079	A	21839	1573	2858	EPVFEQAIDQRSSTDTLSLTPAA PMVDSLIARVGVVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDL PSFLLTGQQTAFGRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISQ*ICWKYFCAG*C GKYFRKIITRCINTAKLPKSVV ALFHPGELSARSGDALQKFT DKEELLKQASNLHEQKKAGV ISPPEVITLLTSEIKTSSASRTSL SSRHQFAPGATVLYKGDKMFT VKIAKRSQAPCMKSNALVIL GTVTLDVVGIGLVMPVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPVLGALSDFRGRPVLL ASLLGATIDYAIMATTPVLWIY PLVNSPSC
21712	52080	B	21840	63	368	
21713	52081	A	21841	189	204	SLPSGIKQSSSKASSRIQVAPT M*SLPRQPLAWPSGHEACPQG
21714	52082	A	21842	153	370	LIAGAFRKASGGNNIFRRPKTL* LRRQPR*PQKSTPRRNKLGHYA IIFPLTTESAVKKIETNTLVFT VLV

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21715	52083	A	21843	842	1770	CTPEKCLPAVHRRNWLNRNAEPP VWKRHLSPICRKRQGRATKPK RRPWYTTPTRRVRDVALRPYS RH/GRQPHAKKIRMSLTFRRP KTLRLRRQPRYPKSTPRRNKL GHYAIKFPLTTESAVKKIEENN TLVFTVDVKANKHQIRQAVKK LYSDVDAKHTEERRHDEQNNIL TREAKNRNDNTRNRARTE TNT ETQKNSGYQALISFHSYYSDTS DNKAHLVSYQSQGCTYDRLG WNLLIRMTCSRSLQHTYDIQSTQ IASC FHPVSVRVNRLYCANYG GISA VFMPLRKELLILTRSSNSK VSQRLI
21716	52084	A	21844	353	605	EMAPKAKEAPAHPKAEAKAKA LKAKKAVLKGVRSHT/RKKKIR MSLTFRRPKTLRLRRQPRYPK STPRRNKLGHYAIKFPLTT
21717	52085	A	21845	301	946	PGSYLKPLSWTVALSRLPGFMS RWPCQRLTWQRRSVTQASGAS GASLCASRLPRDKTAPKAKEAP APPKAEAKAKALKPKKAVVER CPHTHAKKRIRMSPTFRRPKTL RLRRQPRYPKSTPRRNKLGHY AIHK/FPLTTEISAGKKNNKNT LVHCGC*RPTRHQIRQAVKKL YDSDVAKVTTLICPDKEKKAY VRLAPDYDALDVANKIGII
21718	52086	B	21846	12	115	
21719	52087	A	21847	1397	1489	
21720	52088	A	21848	519	747	SGSVISPIAA*YRIFAVL*SVQ* **AGPGDLSDGDEL*SVAIQPN VFIAVSSITCNWLPFGKCGSTY WMCQSM
21721	52089	A	21849	185	456	QHQPLEVASQWKVCSVSVKLL SQSSDVTRVPLEGLDRLSERSG SLSVL*SGILWALDAASQLVSL LP*LTRYHDP RVSSLSSTYV*SP
21722	52090	A	21850	789	1086	

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21723	52091	A	21851	1	766	SGRKEANYVYGS LTQAGTVSLG LDAEGQEVVFPFSAVLP MVAP NDLVFDGWDISSLNLAEMRR AKVLDWGLQEQLWPHMEALR P/LGLAVYIPEFIAANQSARA/D NLI PGSRAQQLEQIRRDIDFRS SAGLDKVI VLTANTERFCEVI PGLNDTAENLLRTIELGLEVP\A STLFAVASILGGLCLSFNGSPQ NTLVPGALELA WQHRILVGGD DFKSGQTKVKS VLVDFLIGSGL KTMISVSYNHLGNNDGEN
21724	52092	A	21852	2	2122	WKSWMVFTAMKLVKAHRLK LRLKGYLPVTCLEGRNQRIAA TIRHNRARGRHQITAMSEIVRE LSQLGWDDNKIGKELGMSDSE VLR LKQINGLQELFADRQYSRA WTLKLAQAFSCCQRRFL LGK TETNQFMWEGIGAKHRQRNRR YAVLLRQPLAKLNIIQARYPNQ HRQHAGECNP HCQAGGDIVDR CPARCFTKGD SKDGSP PQATWP FHNSATMTAKRLSEASQCGSK KSILRERIIRPSITRYPFQSTMN HPLPEQTLGCIATDYGSSPSFDR SPGPAHYYYWTDHSTANIRYQV AAEENGEYTYVERVKIPLDHGT LLIMERATQADWQLEQIRRDID DFRSSAGLDKVI VLTANTERF CEVIPGLNDTAENLLRTI/D/RSV WEVSPSTLFAVASILEGCAFLN GSPQNTLVPGALELA WQHRVVF VGGDDFKSGQTKVKS VLVDFLI GFRLQRP/SSIVSYNHLG\NNDG ENLSAPLQFRSKEV\SRSNVVD DMVA\SNPVL YTPGEEDHCV VIKYVPYVGDS*RAL\DEYTS MLGGTNTLV\AHNTCEDSL\A APIML\DLGAA*PSCCQRVTF LDIGTPSRPFHPVLVPAQAF KGA\TLSPGKP/VLVNAAFSAS AAAIENILRACVGLPPQN HMLL EHKMERPGPSLKR VWTWLP YPMLNKKGPGRSQCPMAAPVD
21725	52093	A	21853	1	1908	
21726	52094	B	21854	1	1833	

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21727	52095	A	21855	1	749	MFQLMKASSGGEEAACMPAGL MENYKHTTVLLDEAVNGLNIR PDGIYIDGTFGRGLGEEGRLLA IDRDPQAIAV/AKTIDDPFRSIIH GPFSALGEYVAERDLIGKIDGIL LDLGVSSPQLDDAERGFSFMRD GPLDMRMDPTRGQSAEAWLQT AEEADIAWVLTQYGEERFAKRI ARAIVERNREQPNDELEEFQA LKSSLNVLAPGGGVSIISFHSLE DRIVK/RFMREHQFCVVVRSGV GLKT*SVR
21728	52096	A	21856	532	1418	CFASGFIGELRKNIVGFIEQDHT RGLVFRLTPGRTRLAESLNLVIC LPMNFQPYDSADWITGVVPF DMATSGRAGGRHGPAAIRQVS TNLAWEHNRFPWNFDMRERLN VVDGCDLVYAFGDAREMSEKL QAHAELKLAAGKRMLSFGGDH FVTLPLLRHAHAKHFGKMAVH FDAHTDTYANGCEFDHGTMFY TAPKEGLIDPNHVSQIGIRTEFD KDNFTVLVDACQVNDRSVDDV IAQVKQIVGDMP/VYLTLYNCG GPS*QFHSRLPAQSPLDRCRAR YLAPQCVPDFRTLQR
21729	52097	B	21857	64	1842	
21730	52098	A	21858	1	503	MRWLVSPIEDTGHKALLFACL ALHRACVSGHCLSPKCVGVGD RSHEMVAPGLFLDWLDDGTGV WDGTSTNVEGAQEHAVLILLII TDGVISDMETGMPWCRLPSCP CPSSSGRGQCGLRCHGVPGWG RRMLRSHTGEEAARDIVSFPF ESSATMSEEVYDPRSLYERLQE QRTGSSRTARQEA VVGSKVTV SQPGHRQETT VLEHLVQY/FILL IITDGVISDMEE/TRHAAVQASK LPMIII/VGVGNADFAAMEFLD GDA/GMLRSHTGEEAARDI/VQ FVPFREFRNNVRGGL*PSISI
21731	52099	A	21859	2223	2363	

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21732	52100	A	21860	3	693	GDDGKWMVLVHRTEVIKYTLDP VWKPFYVPLVSLCDGDMKPIQ VMCYDYDNDGGHDFIGEFQTS MSQMCEARDSVPLEFECINPK KQRKKKNYKNSGIIILRSCKINR DYSFLDYILGQCQLHVSPLGID FTASNGDPLDPSSLHYINPMG TNEYLSAIWAVGQIIQDYDSDK MFPALGFGAQLPPDWKVSHEF AINFNPTNPFCSGVDGIAQAYS TCLPHIRFYGPT
21733	52101	A	21861	1	2231	MYSQEGNQFCNRTDCQELLPP PAPMAHIPSGGAPAAAGAPMG PQYCVCKVELSVSGQNLDRD VTSKSDPFCVLFTENNGRWIEY DRTETAINNLNPAFSKKFVLDY HFEEVQKLKFALFDQDKSSMR LDEHDFLGQFCSLGTIVSSKKI TRPLLLLNDKPAGKGLITIAAQE LSDNRVITLSLACRRLDKKDLF GKSDPFLFELYKPGDDGKWMVLV HRTEVVIKYTLDPVWKPFYVPL VSLCDGDMKPIQVMCYDYDN DGGHDFIGEFQTSVFKMCEAR DSVPLEFECINPKKQRKKKNYK NSGIIILRSCKVNQRGQARARG QVSGHTEGTDRLDLEPARPVF KSRLCHILALWPSLHLTRPQSP HLWNGDINEAEHVQGYSSLTFL CGGQGRHELTFQGLS W WENCH CELLPPTVGMQGAEDIGWGHF VLSGISVTVTPMINRDSYFLDYI LGGCQLMFTVGIDFTASNGNPL DPSSLHYINPMGTNEYLSAIWA VGQIIQDYDRPRSFLKPDWPAG TEAVTGQHVMSVYETHVEWG RQIGLPDVAQNTRHPVKFEFQ VSHEFAINFNPTNPFCSGVDGIA QAYSACLPHIRFYGPTNFSPIVN HVARFAAQATQQRATATQYFILL IITDGVISDMEETRHAVVQASK LPMSSIIIVGVGNADFAAMEFLD GDSPHAAALPTRGRRQPRDIVQF
21734	52102	A	21862	694	825	QPGLSINIEAGAVPRPFARRYW GNLG*FLFLGVLCRFFSPGSPH
21735	52103	A	21863	1032	1127	FYAKAEAGDRTVA*PHKPKMF LSIHHRVAKI
21736	52104	B	21864	1	564	

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21737	52105	A	21865	43	617	PIIQKVRSHTPKRAPCTACTYTVS GSFSLPSPGFFSPPHGTGSLSVS QEYLAL EEVSPHISARDCTCSG LLIELPSTGIFVYGAVTL YRAPF QTLPVTHALIQALGCSPFARRY WGNLG*FLFLGVLRCS*SSPGSP H*PMDSVNDSVSKHT/EVSPFG NPGYNGSYHLTDAYRRLARPS SPLTVGHPPLYG
21738	52106	A	21866	2969	3593	
21739	52107	A	21867	1219	1503	HFTDGGNNRQHGCGRVRQAG KQVVCVVEHQNQYNHRCVW* ESFQVRTHGTGEPVKNKTRTSQA VSHHNQSCQVDQCVCAVIAG NVFPRHNVCQGQH
21740	52108	A	21868	193	378	
21741	52109	B	21869	1	1473	
21742	52110	A	21870	3536	3926	PKMVRWLARKCWNTVSTVRC FWMAMPTPVFAPCAAIKTASA R*MSWASSR*PNRGCVKSATLR QFS*VAAMK*PPVAQ*WWLGR NASTAGGDSGAGRSLDDGEPTP CGMGLEQKRHGNPAGCVAPSR WS
21743	52111	A	21871	140	901	MAMSKVKSITRESWILSTFPEW GSLWNEEIEQEQVAPGFTFMW WLGCTGIWLKSEGGTNVCVNL WCGTGKQSHGNPLMKQGQQM PPMAGVKKLQPNLRTTPFVLDP FAIRQIDAVLATHDHDHIDVN VAAAVMQNCADDVPFPGPKTC VDSWIGWGVPKERCIVVKPGD VVQVTALEIHAPDAFDRTPIT WLADQKRRRTVKG/MDDAPL* QVSYRPSTPPRCYWSLSSSV YYSKRPFAGHYARLCIPFMD
21744	52112	A	21872	287	392	
21745	52113	A	21873	1	492	
21746	52114	A	21874	569	1061	SGTVLDM/SEYSRVQIRKQPYS KGYIPVRQKTKAAWLLKAVTFI DLTTLSGDDTSSNIQRLCYKAK YPIREDLLKALNMHDKVAAGF PAGQTHLKTREEIRLAVEDGA TEIDVVINRSLVLTGQWEG/LYS PVVYSALPCNI*HSRLFLPSGNA LLLWLWCLHS

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21747	52115	A	21875	2	1072	ARSNIRMVTAFRSLPAGSSGAA RAVMSAHNRGTGLDLSWISKIQ VNHPAVLARRAEQIQRRTVVK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGITVTAACVVIYP ARVICDAVKGTSRPAG/CVNIPV GISRAAGF/PAG/QTHLKTRLEE IRLA VEDGSLQKIDV/VINRSLG A*QAQWEALYDEIRQFIRKAC GEAHLKTLATGELGTLTNVY KASMIAMMAGSDFIKTSTGKE TVNATFPVAIVMLRAIRDFFWK TGNKIGFKPAGGIRSAKDSLAW LSLVKEELGDEWLKPIELFRIGA STLLSDIERQIYHSCGLGRYGS LFMDLSQCL
21748	52116	A	21876	3	221	
21749	52117	B	21877	49	342	
21750	52118	A	21878	1	828	
21751	52119	A	21879	1362	2405	RPPWRHWDGNSSVLVHFQLHF LLRPLQTLSLGLEEELLQRGIRA RLREHGISLAAYGTIVSAELKG GSRPCA VVWPSEPGAGRCPGN SFSCGNSQCVTKVNPEDDQED CSDGSDAEHCEGLQPAWRMA GRIVGMEASPGFEPWQASLRE NKEHF CGAAIIN/DQPLRS*NHR FQDPTKWVAYVVRPTS AARRP APCGPSKKA/WISGWGYLK/EG LP*ASRPAMVKPEVLQKA/DW ELLDQALCASLYGHSL/TDRMV CAGYLDGKVDSCSVLFLFRGTI SFFSEDRNLIRYVLLYSIFVFN CISGKPPQPPVLRALCQHPPQI DAGPQYRASCWVTVPKLQGIF
21752	52120	A	21880	600	904	SVSLLDEETALPFSWDELRLSA LLDT*AAFOEIELAFQDPQCVG LLTAP/YADAAFGSTDIAMFLL VPILSARKPASPRSS*TFSHLATE PLPASIK*AAA
21753	52121	A	21881	393	572	
21754	52122	A	21882	165	432	PGMAVSYEKISKYPVEFLPAQA NIAGHNDAPEREPEFQW*LWLL LPNF*LQEKCSPTLCHFLSRRTQ SEFPSSSTAAGNLSVSLLYPCKS
21755	52123	B	21883	1	1011	

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21756	52124	A	21884	783	1234	YYRRCGAASPHGRDPVQIG*TS SQPR*SAVRN/PASVIPVARHSA RAPAILRP*VVVAERSERSIPGL RATPAEIRTTAPSSAGVASSPE KPLIFTAIDSHGTSHWSDIHHVC AKKLQNYVPKLNASLLLTPSIY VTRITRSGPIPPARQ
21757	52125	A	21885	249	398	GYFDIFS YDTAIPGQSAEQDAR ED*AF*MPDRAYSQPCSSLVFP KGCKK
21758	52126	A	21886	309	845	CGAREERGRGCHHVHSQLRGP GPAPGQVQQQLVPAPVVPPLP GLRGLSQWQARRTRARHRQGV QDHQPDPTVHAQLRGVQLGEA PLQLHHGD*DHRA*GYFDIFS YDTAIPGQSAEQDARE*AF*M PDRAYSQPCSSLVFPKGCPVPG RGCAAGVQAAGAAHPPLDHPA LQPLQGR
21759	52127	A	21887	1236	2100	DLLCGRCGCGRRPRHLQPQTEL EAEVPAERPGRGPAVAARSDP RAQAEDVPGYNPLSGKPAKQQ VHEGHHGPAGHRRPAGGAAVP AGGPHRCLPAQPARPCGGAAEP RGGPAGAH*ARGSRAAGEGQP WWPSRLGAGPPAAPVHAAPG SHLLPGHHLTPQPSALAAQ*PL AEEPREQPGAGGPQGSPTLRG VEVVPLPHAAGGAGAVPVGGA ACPTAPHAASAPVLLSQLG TQHPPRRDPPHCSCAGIQDSGW AGPPALWSLLHVAKPAQARRP CALLHPGV
21760	52128	A	21888	1931	2185	AKAFSFFRYISRVRNRTCLRS SMRRSFDSSNADAAFGSTDA MFLLVPLSARKPASPRSS*TF HLATEPLPASIK*AAA
21761	52129	A	21889	1254	1760	
21762	52130	A	21890	1	2001	SIRRPKRARPIRIKKIPEQQG/PQ PAVLVPQTVATRDRELQMP/P VGPELTKRDPVVRAMTIPATAA VYKPYWGATPLPIA/KPSPAG*Q *SRFSKGYFGFD
21763	52131	A	21891	195	545	HSPGSFYRSDAQSPAPAIRAA V*AEVQ*TPLCHDRITHFPEW RGWQRS*F*PAACRVAGSLPVP VSPQIHFPYCRSSAQYLPAGAG LPLPGFDRLCPRSLFQGLAVTG GSCGPS

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21764	52132	A	21892	825	1299	YSCRTEHPRLATAEYRHHQRA ADAGR*RHAGVAFYPIKERYR QPEPAFSYQ/PRRWSASNRNRP R*RMRRFPANSSTPFPAPPLRR KRVASLIGGRMLRLTGAGIAEE RMIAQLPECILHELTERPHFPF LGIDLITCGERLLAIPRTTHVE
21765	52133	A	21893	1460	1810	RATHVLTWVRGTPKRAEMILG SSRSMSAAAVTVLISPATAQRW ITRAP*PPIRSPSVSLTATRPSS ITKARALSPMAAPALRSTVTP PRITVEKPLLMKIPRVKSRAL SAL
21766	52134	A	21894	231	704	QSQKPDTRGRLFAVAKPPCVQR HKVVRWRLVLVMTSAHYLPLRR *PAHPASGGCCPNRAKYTQRP E*ISYRPD*EAVR*SRAPAKVTQ SNPASRVALLRRPAPRAVHQATII PVDESTLLPAPLAVSARQKVRQ AIPLRDSVRRPTLDVHRHATG L
21767	52135	A	21895	1291	1925	RQLLRWSNR*IA*SLTQPARRF PAYHYAHPAAAPGDPGLGAD LQLCARHYHRQRHCVPRHAGY PRSDGLHPQPRGRWRIRCSACL RVPF
21768	52136	A	21896	1	445	MFISGLDDFFIDVVYVWRRIKR KLSVYRRYPRMSYRELYKPE KPL/DDYGSQVE*NGRHRQYGR AGGDHARLRKLSYLCVHLPQR PRYSA*C*RSVRSLECA*GSLR ASWP/HPAKPTV*TTCTWTPSPN LSVAPISLLLVLCMTPKM
21769	52137	A	21897	79	377	SRKSGISIGAVKRPTH*GS*KAR SIC*NAAYVSKKAESLSSFPKES ESTQRVKAVLSS**ASQCGDGT AQYVLLSFQGSQQA*QVCGR* KAY**DLSRE
21770	52138	A	21898	1282	1535	GSTYELASATSPSAKPSNRSPSP MSRPQSNPKPNLHSC*P*GNL RSTPESGK*ATPPPPAYTLVLF KLANPQLPEESPWAF
21771	52139	A	21899	3775	4031	CRRTAASRTPRKRTQTATPHAT NKPQKQPTSTDRGNRREPEKTE PS*HLRPNPQEPGRRGQTQQEP APRHQPPKQGEPTTPQKQ

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21772	52140	A	21900	1	2595	MESHTVTVDYNFGRLLNESFAN CETDRNYLGIFKCGFWLSGTRK SAFLTKSQVTLTRPVDHTLRNE VLGSTKYQVPGYRRKTNTNLE ESNVLIGYDVAPGGGQIDGKK AEGRELMVVPVAGRPLCRSSSM ELLLLLPLHIPREQMLLADAYW NLHQSCQSKTSPDTAKCPLDRC PRVFKSQSYKASTFDGLSMDTE VIKSNGKQGWQRRLANMKDI DKQTQAATFVLSQGMQRSGND RIILVTGASDGIGREAAAMTYAR YGATVILLGRNEEKLQVASHI NEETGRQPQWFILDLTCTSEN CQQLAQRIAVNYPRLDGVLHN AGLLGDVCPMSEQNPOVWQD VMQLFRAGIINADPGAFFVTGF RRYCCFTLCCRSFRFGFYRRRF RHRSCRQRAMRHS GTGQGQGN EQCFNSVFHTVFSLFVNSGITLT AVKTVNKKWCSEMEKAAKAT FSCYSCNAFFCEAAASGLLLFQRI ANFDRLFTQVTHQSFKDDLGI KMETTKPSFQDVLEFVRLFRRK NKLQREIQDVEKKIRDNQKRVL LLDNLSDYIKPGMSVEAIQGIIA SMKGDYEDRVDDYIIKNAELSK ERRDISKKLKAMGEMKNGEAN RKERSMFRDRPLKRMKSKRD DDSYDEDVEDDEGVGEVRVHR VNHAPANAQEHEAARPSQHQ YQPPYASAPRQPVQPPEAQV
21773	52141	A	21901	1	96	
21774	52142	A	21902	105	430	ASIFVMLVRGAEPMEKRQQRG LFTVPGLLAFCSHVLSCVNPLI PVDNPPYPLSELIPAPQPNDR AQRVSRGSGRAPNTQTASPR LADSLMQLARQVSRLESGQ

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21775	52143	A	21903	843	2055	HHRMAQNLSRYGNDKRPEESQ FRVNVNKPVTLYDVAEYAGVS YQTVSRVVNQASHVSAKTREK VEAAMAEALNYIPNRVAQQLAG KQSLIGVATSSLALHTAPSQIV AAIKSRADQLGASVVVSMVFAR SGLVACHTAPHNLL/ARKRGPA GLIINYPLDD/QDAIAVEA/ACT NVPALFLDVSQDTPINSIISHE DGTRLGVEHLVALGH/QQIAL LAGPLSSVSARLLAG/WHNFL TGN/QIQPIA/ER/EGDWSAMSGF QQTLQMLNEGIVPHWRLLVAQ RRSMALGAMRRHYSPESGLRV GA/DILRVGGNTTIPED/SSCYIP AL*PPIKQDFRLLGA/QTSVDRIL LQLSQGQAVKGNQLLPVSLIV KRKTTL/APNTQT/SPRALPRF H*MLA/RQVSRLESGQ
21776	52144	A	21904	1	1201	
21777	52145	A	21905	1	492	
21778	52146	A	21906	646	934	
21779	52147	A	21907	1	1713	MLCTKWDLGLEKNAGKNKN AYKWYGPANAPDEPHIEQLV GECRVMRQLKLRIAPSPSSV MVGESGTAIPVSHAEFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDFGYLEFEGGANFWSGEM YGFDDWENFYNGRHNKPGSEQ RYTFKNTKPYLSWVDTGFSLYL HAYGTYGSANRVNFLDDMFL AGFGQF*PAGGW/WGSNPFFA KRYTRSKPYTTGDNGYVAG WVAGYNFM LGSEKFTLNWN EYEFDRDATYAADFLPLYDVD CQDNGNLEYDITYSQPEWKHNL FDHYLAVLYRFKDESGKEQFSG AVVKTREATPGKEIEAITRML DFSRLKKLADCPSPRPVFEALC ICSMLDALLLCLPDYHASCND YSYALLDPQGFPLPHRRLWGPY IDVDVPMHLHLIQAHAQDALL SCLYSDLLYMSSFPYPAGTLTR LMGVTSYNHKNLTLLTYCITLMS TIRFAYDGDDEIAMKYTDFLKG ELSMNIRPLHDRVIVKRKEVET KSAGGIVLTGSASAKSTRGEVL AVNGRILENGEVKPLDVKIGD IVFNDGYRGEI
21780	52148	A	21908	2060	2404	
21781	52149	B	21909	1	1377	

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21782	52150	A	21910	52	1719	IGQVVDVDTCTRIHLVFNFD NDTGSIHVLNDTTTFSYRSYTG VNGNSTFHTSTNQRLISAQSRN GLTLHVRTHQCTVGIVVFQERD QGRTDGYHLLGGYVHVNLV AAEQAGFAFATASYQVFYEVA FFIQVGVR LGDNVVAFFDSRQV VNFVSYNTVGHFTIRSLKEAVF VSLCVHGRVDQTDVRTFRGF DWTDATVVS RVVYSNFEACTF TGQTAWAECGDTTFVRNLRQR VVLVHKLRLQAGTEELFHCCG SQDPQQPWGWNLRVNPLAQTT GHAHEAQRKQWHKGNEEADD PEPERAFTPGFVQFETERFRPPV GHPCEAAEDHAADDHVMEVR NQEQA VMQNEVRARYGQQHA SHPAHREGDDKTDGPQHRRME HDAALIHGEQPVEDLHPGRDG DNHCGDTKEGVYVRARTHRKE VVQPNDERQHGD TDGCPYQRG ITKQFTTREGCRNFGHE TENRQ DQDVNFRVAPGPNQVDVHHH VATHIVGKEMGAQIAIQGQHAT YRQNGKDL*SNRGV ASGNPQC RHRAHRRATDCQTVIKQPVFFG

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21783	52151	A	21911	608	2508	YITATSCSGWMIRWCAKAAKCA/CA/CSRGGGKLRRLRHKGAETL CGNTRVLIAPQLPAVIAITLSGS RSQGTGRREGPTTTVMIQDHTG SSTDDECSANVQRIFNRMILCSI VSRPTIPFHDLAQSFQFRNVK CLWCAFEQAQLMRIQPAIVMV KTIHRERLNSGQFRCHQEARNI PPHRQSRFLASRGLLAELMFML YGIGELPEIVTLPKEIRGNVDNS RHAVFLANSMPLELRFIRTHGS RFTSQDCTLFNWLAKIITPVLQS WLNDEEQQVALRLLEKDRDHH RVLVDITNAVLSHLDLDDLIAD VAREIHFFGLASVSMVLGDHR KNEKFSLWCSDLASHCACLPR CMPGESVLLTQTLQTRQPTLTH RADDLFLWQRDPLLLLLASNG CESALLIPLTFGNHTPGALLAH TSSTLFSEENCQLQHIADRIA AVGNADAWRSMTDLQESLQQ ENHQLSEQLLNLGIGDIYQSQ AMEDLLQQVDIVA KSDSTVLIC GETGTGKEVIARAIHQSPRRD KPLVKINCAIPASLLESELFHG DKGAFTGAINTHRGREFIADGG TLFLDEIGDLPLELPKLLRVLQ EREIERLGGSRITPVNVRVIAAT NRDLWQMVEDRGVI
21784	52152	A	21912	147	2699	MTIRAIACSCCLPDA*NVLM*ITY MSTFQASNGGQQLQIARIVIQNI TG
21785	52153	A	21913	432	1016	FCPSSCLAATAPAA*AGWSFLP SPAEQNRWRFLSRFCQIPAPL/ LGTLIISLVFCSILAAASAEIPG SVDGIYNKSPSLI/VVKIPRQLY *AAREPSAPKAPPAAWFSASA VLSATA/MINTNQKAIERVTAFR RNFA TDPVAHQDRDHYDRQQR RTRHRIRFGERQRAKQTPFLPFQ GEDRDKRQRDNQQTDK

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21786	52154	A	21914	1	1146	MTTSMNLNAKLLPSAPSAVVV VRVVVVVGNAPT SRKVGPEEK DWSMASSGTTSTRKRFTGAEFI VHFLEQ/PGH*DCDRHSG/S/CSI LPVYDALSQSTQIRHILARHEQ GAGFIAQGMARTDGKPAVCMA CSGPGATNLVTAIADARLDSIPL ICITGQVPASMIGTDAFQEVDT YGISIPITKHNYLVRHIEELPQV MSDAFRIAQSGRPGPVWIDIPK DEQTA VFEJETQPAMAEKAAAP AFSEESIRDAAMINAAKRPVL YLG GGVINANARVRELAEK AQ LPTTMTLMALGMLPKAHLPLSL GMLGMHGVIRSTNYILQEADLLI VLELAGVQTVDTDVNASKPAS ATRHIAFQTVTIGCDRNLDASV VFPHSVDDIGKVAA
21787	52155	A	21915	1001	1037	MVGMASSCMPAFTRL ELYSVIS QSTQIRH/LARHEQGAGFIAQG MA/RTDGKPAVCMACSGPG/AT NLVTAIADARLDSIP/LICITGQV PASMIGTDA/FQEVDTYGI/STM TLMALGMLPKAH/ALSLGMLG MHGVRSTNYFCQEADLSIVLG ALFDAGQIGKTSSFCPNAK/I/H VDIDRAE/REFPCPIPKACDLLS H/YGLINAVAACVDDNAIITTD VGQHQMWTAQAYPLNRPRQW LTSGGLGTMGFGLPAAIGAALA NPDRKVLCSFGDGS LMMNIQ* MIIAIP TGVKIFNWCSPICRPHR VPFCDAVAIGFIVTFSYDIQIASI YEIPCRDPTGVASTEYSSSCRR RRNTTLCDPGSPAQRQSPQAGQ NPSCPAHRRSATGVGD
21788	52156	A	21916	135	449	
21789	52157	A	21917	5	214	
21790	52158	A	21918	2	337	IGIAKHAQQLLLNVMTQTRAVG AEVQTVSATGSAVRQALANNL QPFAIFFQINA/W**RAGRYPDD HGISPETALYGWHTSATGTAG MR*SVRPWLQSGQGCSGWRRQ QPRWSP
21791	52159	A	21919	1	774	

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21792	52160	A	21920	2	914	RHRTPAHLERFIVDIALNVADG HRAKLIVQSAGTFAQTVLRA SANFRQGVGLVRQFRFKNTPL VGELQPVVDVVYRAFLAVW VAARQAAVSLRFGLAFGRRLV NFKLNFAQLRFLWRINAAQ LSCATTT/ADPAVLLHHWTSV* PAQI*WRIS*PVRQNLFTALRAG MLHMLGDKTTQMLFMDRQSV NA*DLQFRVNAFAEIAAFIEN VSETAGHARTEVNAGFTQNAD DTTRHIFTTVVANAIFYHGDSTG VTHAETFTRAACGIQITTTGRAI QAGVADNACFMAAEGGTNRRT TNGD
21793	52161	A	21921	204	371	PGPAGAQAALYRWSPGQAVS RADWFRFADC*IYPENRRNAGS AYRPLSPAYCG
21794	52162	A	21922	2664	2970	TPDTAPAGCRSAPDGPSPRQ MPRRRG*FHTARYCRTPRAITA *R*TE*STCPARTGEWYAHARY APGTSRQTATMPPTMPRRRASS YSSTQPDGRRQNC
21795	52163	A	21923	318	459	
21796	52164	A	21924	577	888	TNSSNQQLAEGNRRELIGRNTA GPERITAGRRL*LFSCQNRPCGW RFNKCHIGMPVVIWRIIVMGI QHDDLVPFGMRVNRVNMQF AKTLGQRALLRRNSLIA
21797	52165	A	21925	3	711	AGAHSGPSHPALATTAARQSV AGNRSGISGFSGHSRNPTRMSA RCL*SSVALERLMRRLNGEIQI SDVTTTTPSLSPQVYCSAMSRN LCTRATPRWQASAGHPYCRWTA SYCAIYSDRSIRGNYSRQSFAS GRRVPTGSGWQKTESEKDCSTC CANWANDRTPLPTSSANCST NVQTSVVPVLRRIWLTSLRV VLTSLKSVCAAGTSPQASCWCF VKRAASSATSPVVIITC
21798	52166	A	21926	244	535	TRYDDHGISPETALYGVWHTSA TGTAGMR*SVRPWLQSGQGCS GWRQQPRWSP**RSC**CSVY PATL*FCRLYNQTSQPGHSDLP AFPDSDRRKI

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21799	52167	A	21927	869	2923	PKKDLKIATSAMMEAAYSV*SR TLFW/SPVRDSQVTDLTQWQGL MSQLRLQGFDLVLQWTRYGD AFTQPEQRTLLFKRAAAQQA GLKLIVGLNADPEFFMHQKQSS AALESYLNRLAADLQQAQLW SAAPGITPDGWYISAEIDDLNW RSEAAQPLLTWLNNAQRLISD VSAKPVYISSFFAGNMSPDGYR QLLEHVKATGVNVVWQDGGG VDKLTAEQREYRLQASADCHD GAAPHGKIVFKLIIA*RARR
21800	52168	B	21928	72	690	
21801	52169	A	21929	1	2241	
21802	52170	A	21930	1607	1893	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLKTRPAFFQLLIK HVD/SMCHQRLSGSRKSKHNVI AVVFSYCSVSVFASCPHTQVL LQTQYF
21803	52171	A	21931	1	3960	
21804	52172	A	21932	1	1281	
21805	52173	A	21933	1	1491	
21806	52174	A	21934	1	1254	
21807	52175	A	21935	1	723	
21808	52176	A	21936	740	880	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLKTRPGFFPTVN
21809	52177	A	21937	1	1191	
21810	52178	A	21938	1033	1248	
21811	52179	A	21939	1	1425	
21812	52180	A	21940	1	2784	
21813	52181	A	21941	676	1467	
21814	52182	B	21942	1	3288	

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21815	52183	A	21943	145	1929	VSGVIEIADGSRRRKAAALTES DYRVVLVGLDDEQMAALSRIG NDYRPTSAAYERGQRYASRLQN EFAGNISALADAECNLTCTHT SHGSMVAETA VINHKKRKNSP RIVQSNDLTEAAAYSLRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEADAG DEKGYESFPWFVK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIERVQLPQS YQRMPPDFRRRLQGFCFRFNH IIQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVYAIK PTCWPLDIHPSCLALHRIETEL MGKFDEGKLPTDPLMLRLAIE TVAHDYDVVIDSAPNLGIGTIN VVCAADVLIPTPAELFDYTS LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSVMVLK NVVRETDEVGKGQIRMRVTVE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGSNSVLRK
21816	52184	A	21944	1790	2947	TDFSVRCKGCRIGPFLRLIFQDR IVGVELIAVF*NTGPRFSSCRLS WRRPFDKTCRMRWHQRLSGFP QEQNDGKQQPILC
21817	52185	A	21945	1	888	
21818	52186	A	21946	252	1863	RKNPFILH*LFR*TLRQTKPDSS AGKGVKI**HTQNQRSGRSQND F*RRLW
21819	52187	B	21947	1	1794	

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21820	52188	A	21948	138	341	PNPRLNLTITPEHFKSLHIPT TYRQSNGITASHYSYARN*RVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGLLELL KAAASLVFLEQHKPYEEIGTSF GSVLVSVVGEGPFVEEDLRKSF PGRWDKHKMFDAIEEPKKDS DKFDANDPILKQDTQEWSSGA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTFDGDGKTYQNVQQFID EGNYTSGDNHTRDPHYVEDK GHKYLVEANTGTENGYQGEE SLFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGHIELK YDYTLKKVMKAADHFQTPVTD EIERANVFKMNG
21821	52189	A	21949	761	916	NKRIFPSHVKVAEPDHSCV*SFR IGSLASNLSSLKTRPAFFQLSIE LSPT
21822	52190	A	21950	1	1437	
21823	52191	B	21951	50	1690	
21824	52192	B	21952	1	1032	
21825	52193	B	21953	1	1974	
21826	52194	A	21954	878	1202	SVYNKRIFPSDVKVAEPDHSCV *SFRIGSLASNLSSLKTRPAFFQ LSIEFRRPFDKTCRLMCHQRLS GFPHEQTQRDSTCIQLLFRQRF AAASCPTHQVLLQTQYF
21827	52195	B	21955	7	1702	
21828	52196	A	21956	527	665	NKRIFPSDVKVAEPDHSCV*SFR IGSLAFNLSSLKTPARVFTVD
21829	52197	A	21957	469	687	
21830	52198	A	21958	2	1018	EGSDSRAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWSKNAGRVFKDSD KFDANDPILKQDTQEWSSGATF TSDGKIRLFYTDYSGKHYGQS LTTAQVNVSKSDDTLKINGVED HKTFDGDGRKTYQNGQQFIDEG NIPPATPYAERPYYFEDKGLKY LGKPTVEPSVCGGRLESPWQTA GVSPVTQKLKSLKFDVGRQEES VWEKDEAALANWTVPNHCTD NLKTCHTLHGSVMAETA VFN KCLKNSPRIVQSNHLI
21831	52199	B	21959	7	1113	
21832	52200	B	21960	1	1188	

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21833	52201	B	21961	1	1414	
21834	52202	B	21962	1	1515	
21835	52203	A	21963	1652	1916	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQND F*RR
21836	52204	A	21964	1	1353	
21837	52205	A	21965	1	1507	MAAQDAMVTRISSQTDCKEPG LKWAGVVLMLLLCWLMPQVL WEACQOKTGEHKTMLQMILCN KSYQQLRLVITPMYMLGDL SKNCGQNSTPSLGDNPPEQTQ EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKITFDGDKTYQ NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQSAKKRDAELANG ALGIIHLNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDDLHIHAEDTL LPFYLGEKDDVITYAIKPTCWPG LDIIPSCALAHRIETELMGKFDE GKLPTDPLMLRLAIETVAH*P AEK*HQNHSSPF*PRFFAVSLRT GSSYHCILSSH
21838	52206	A	21966	729	843	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLINM
21839	52207	B	21967	1	1416	
21840	52208	A	21968	1	1794	
21841	52209	B	21969	1	1171	
21842	52210	A	21970	1108	1250	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLKTRPGGASRVP K
21843	52211	A	21971	1	2535	
21844	52212	A	21972	743	898	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLKTRPAFFQLSIE LSAT
21845	52213	B	21973	1	1605	
21846	52214	B	21974	1	1873	
21847	52215	B	21975	1	2946	
21848	52216	A	21976	1419	1498	
21849	52217	A	21977	1	2314	
21850	52218	A	21978	1	1215	

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21851	52219	A	21979	1	1851	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNRERTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGVSMAETA VINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGLTQEH D GICEIHVAKYVEIFGLPFAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAPSPS KGLYSVHINPYLIPFFIGLQNRL TQFRLSETKEIPNPYAM/RLYTN TLCQYRKPDGSGIVSLKIDWII E RYQLPQSYQRVWTPGINCPEPC PGVWTPGINCPGAWGIHGP HGS AENTGPHPGQTSQALETSLP SLRSARELELAQLSPRRKQNR S LQNGIVTPSLRVPWPKASNVQ Q FIDEGNYTSGDNHTLRDPHYVE DKGHKYLVEANTGTENGYQG EESLFNKAYYGGGTNFFRKESQ KLQSSAKKRDAELANGALGII E LNNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWYLF TDSR
21852	52220	A	21980	3197	5376	
21853	52221	A	21981	543	5690	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQND F*RRWRSY
21854	52222	A	21982	2241	2614	ETLTLTKTKAINTLYSKPTREQ KTDTKAKNLYLTKRTTAAART SSVKKAISFNALKNAMLS*RT APSVS*IRHRV*NLTMRSSSSA PSPWML*A*A*WLCRYCRASCGI SSIPTASPV TMACC
21855	52223	A	21983	31	892	
21856	52224	A	21984	548	855	
21857	52225	B	21985	1	1825	

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21858	52226	A	21986	1	3146	MEWGKFKRLVLPSQGKSKPEQ RCQYRHTVGDQATLPLRSRVE KRNGEAEGRIRKLDVVALLC CVQEINGEKPLRALTEVKS FRLREDSDKFDANDPILKDQTO EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQNQQFIDE GNVTSQDNHTLRDPHYVEDKG HKYLVFEANTGTENGYQGEES LFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGHIELN NDYTLKKVMKPLITSNTCDN
21859	52227	A	21987	1	3107	MNEMKREEKFREKRERNEQI LQEIRDYVKRSNHLIGVSKSD GENGTELENTLQDIQENFPNLA RQANIQIQEIQRMLQRYSSRRTT PRHIIVRFTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLSAET LQATKEWRPIFNILKEKNFQPRI SYPAKLSFISEGETKYFTDKQM LRDFVTTRPALKELLKEALNME RNNRLVKSLAWSQNGFRSPA LLPLSLMLCAPLQEADGTNLG WLAHCGLLCTGDH
21860	52228	B	21988	239	2825	
21861	52229	A	21989	7533	11119	
21862	52230	A	21990	1	3718	MEVIPEGYRLSELKKCSKWIVV MVARLYEYTKNQIIHLKWWN HMLGCLLDRNDPLRDVDEAAV PVLICCSADDPVCGPPDHTLTTE LFHSNPYFFLLLSRHGGHCGFL RQEPLPAWSHEVILESFALTEF FRTEERIKGLSRHRASFLGGRRR GGALQRREVSSSNLEIFNWK RSYTRLMAAAAGAAAAPGSRE PQDRPECGAGHPGPRYYRHPER WLLRPEAFGLPLRTRAPSADS QRERPAARSGPEM
21863	52231	A	21991	1	697	
21864	52232	A	21992	1	978	

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21865	52233	A	21993	145	1929	VSGVIEIADGSRRRKAAALTES DYRVI.VGELDDFQMAAISRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETA VINHKKRKNSP RIVQSNLDEAAAYSLSRDQKRM LYLPVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRLQGFCFRNII HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHFG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSLALHRIETEL MGKFDEGKLPTDPLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTS LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK

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21866	52234	A	21994	1184	2229	RSSVATVALLHAVINH/KRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPPDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THIFFDMLRDLKKNVDLKGFEF DVRILLTKYSNSNGSQSPWMEE QIRDAWGSVMVKNVRETDEV GKDTLSLTPAAPMVDSLIARVG VMARGNAITLPCGRDVKFTL EVLRGDSVEKTSRVWSGAVSQ GGESFIYMPLTGAAFLSEMP PERRNLKKQCGYSGFAACGYQ SQERKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHGICEIHVAKYAEIFGLT AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESFPWFIKRA HSPSRGLYSVHINPYLIPFFIGLQ NRFTQFRLSETKEITNPYAMRL YESLCQYRKPDGSGIVSLKIDWI IERYQLPQSYQRMPPDFRRRFLQ DHNSSPEREQNWMEFDELT EVGFRRWVITNSSELKEHVLTO CKEAKNLDKRLQELLTRISNLE NIDDLMEKNATAQELHETYTSI
21867	52235	A	21995	82	325	
21868	52236	B	21996	220	1173	
21869	52237	A	21997	1	1599	
21870	52238	A	21998	188	421	
21871	52239	A	21999	1	596	MGMTDMGSKSKKSQGPSFP GGAPPAIGAAGRERPPGTGD PFNRQPCNDLKTCHTSHGSVM AETAVINHHKKNNSPRIVQSN LTEAAYSLSRDQKRMLYLFVD QIRKSDGTLQEHDGICEIHVAK YAEIFGLTSAEASKDIRQALKSF AGKEVVFYRPGEDAGHEKGYE SFPW/FIKRSP*RRGKFPFTQM GQD
21872	52240	A	22000	1	1527	
21873	52241	A	22001	2	870	

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21874	52242	A	22002	1	4304	MAETAVINHKKRKNSPRIVQSN DLTEAAYLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPPDFRRRLQCINA GHEMTKAIQFNDDSPARK ITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPD
21875	52243	A	22003	740	1159	SLPNLDNSAICSSSSPTRTR*SL SVSAAALRRRLPSAISMTPDTL RPNAGVC*PVSRRKEGMRSSAS SVSSWSRSLPDHTREVFTLS RSTSRVNFTSRPHTGKVMALPR AITPIRAINESTIETAGEDNEVSS TG
21876	52244	A	22004	664	1844	SGNLKACHPSHGVSMAETA/VI NHKKRKNSPRIEQ*KDGYQQA YLSRDQKRMLYLFVDQIRKSD GTLQEHGIGI/QIHGAQYR*QIS D*PFAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWF FIKRAHSPSRGLFSGHIPP/YLIPF FIGVKNRLTQ/RLFETKEIPHPS AL/RYYESLGQDRK/PDGSSIGS LK/IDWIIERYQLPQSYQRMPPDF RRRLQHFLAHAGCPKGTQNF FRMKFIISIKKVLPPVDTLAHD PVIHTCHLRESFGSVSPSPKSN RLPCPEVILFHYGESWNLLRAD QRLIFAKSWPRASRYQQGHQD LFILRSDLPSQVFIIRDKLMERRN RRTGRTKARIWGSDDGQNGQE PGYVEAGCPPLLLTV
21877	52245	A	22005	3	272	
21878	52246	A	22006	1	528	
21879	52247	A	22007	461	831	LLNLATWRYLGLTRGTASIVA VAGILAAALRITNNKLSNHVVF QGAGEAAMGIAHLLVMAARRK K/GTERTTATRKIWMVDSK/GLI CQEGGSHLN/HHEKEMFAQDH PEVNSLEEVRLVKPTAM

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21880	52248	A	22008	3	1894	EGEDRGLPRTMGAAALGTGTRL APWPGRACGALPRWTPTAAPQ GCHSKPGPARPVPLKKRGYDV TRNPHLNKGMAFTLEERLQLGI HGLIPPCFLSQDVQLLRIMRYV ERQSDLDKYIILMTLQDRNEK LFYRVLTSDVEKFMPIVYPTV GLACQHYGLTFRPRGLFITIHD KGHLATMLNSWPEDNIKA VVV TDGERILGLDLGCYGMGIPVG KLALYTAGGVNPPQCLPVLL DVGNTNEELLRDPLIYGLKHQ RVHGKAYDDLDEFMQAVTD KFGINCLIQFEDFANANAFRL NKYRNKYCMFNDDIQGTASVA VAGILAAALRITNNKLSNHVVF QGAGEAAMGIAHLLVMALEK EGVPKA/EATRKIWMVDFKGL IVKGRSHLNHEKEMFAQD/HPE SNSLDEVVRLVKPTAIIGVAAIA EAFTEQILRNMAFRRAPIIFA LSNPPRKAECTAEKCYRVTEG PRGFFASGKSFRLSVDL/ESMGK TFIPGGRGNNAA*RVPRGWQLG VHSPGGDPGHIPDEIFLPDSRA KLPOEVSEQHL/SQGRLYP/PLS TNRDVSRLAIKVL DYAYKHNL VSYYPEPKDKEAFCKIPGSYTP DYDSFYTVDSYTWAGQKAMN
21881	52249	A	22009	322	567	
21882	52250	C	22010	338	603	
21883	52251	A	22011	127	417	
21884	52252	A	22012	253	424	
21885	52253	A	22013	124	1235	YLCLLPKQGQDRALSRTSQWP QMSQSACGGSEQIPGIDIQLN RKYHITRKLSTTKRFTACWR KKVGAFTKIIEAMGFTGPLKYS KWEDLRLRALRIVY*LCGRKLD FEGFFSKICSMPDTFNSWFLINP YFHVWMCLVRMKQEGRSGBK MCRITVHFMWEDVQQRGRVM GVNPPYLKKNMILMTNHEFYAA ILGYDEGILSDDHGLAAALWK NLLNARKCEDPRHLELLVEYVR KQIQYLD/S/MNGEDLLLTGEVS WRPLVEKNPQSILKPHSPTYND RGTFDGLGPPHGGPAGFRGTSR EEKCLVGRPTPARKWPEDLLN KHL SKYLAPICVEFPLSVPQESD LLGYRAWENPLALPGCPSSLRG

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21886	52254	A	22014	282	435	GGGASPAACSGSPDSS/HSATA GTGCRPPARPPAPPTPTPWRS RQQGSRAS
21887	52255	A	22015	3	399	IVALPFGHHHSQTSPLPNLLQTA ACLLHFLLLSGVETGRPGPWQ PRIRARPPAPPPGPARPAKPRRR /GCRGPAREACWYGCRRPARPP PAPPTPTHGAAGSREAERASEL/ C*GARPLRLGSAGTIMVSACVP
21888	52256	A	22016	279	872	KIPHISLSLKLQGAASSKIPTQNP HLSPGTKRDSSFQPWLSAFHIT GQCCSYIVRWGLWKPRILVV KKYAALSAEMLLVKEEPSA ACSGSPDSSSFCNCW*PAAAGR L/ASAAQRPPTPNAHKRSRQQG SRASERAS/CKGRGRYGLGALG GRGGRALGGSRWPPPLGETLF SGCKHRRRRRGSDAAPGEEAG
21889	52257	A	22017	106	398	NAAPFSRHAAFQGFSWAVCIFR LPAERALRLFASCLVLPGGPS GVAPHGWPLPTTAPLLQGVV RVEVGEHEMAEIFFSAKKEAAG ALQRPCIPVW

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21890	52258	A	22018	I	1806	MRGNTAGGPGDEKPDSTHPPV EGTLQEAQEMKKVVRFMWTS GGPDPQHWRGSLYGQLVAQ MLHIDVAQVYMDSWWPRCST LAWLRFIWTAGGPDAPHWLR GLGGQLVAWMLHVGAQVYYV DSWWPSCASMWLSFMEHKQ CLTLGYEVALFLQHFLSRAFLV VWVPRKEAQVLRQGLSLTFR ENPGVCVMSSYRPWLITAAAD MQPSKPGGTGSYCSYWSPTDN TPRLAAACTWNLGSSHGSAAG VRTFIEAGFSPFLAPKALALTL SDSDSRWGNPNVYAQPQ/PEP AWGNPNV*GQPQPRNRPG/PEP CVCSTPTAEPPWGNPVSTPTA EPAWGNPNVYA/PTPTAEPPWG PNPV*GQPQ/REPAWGNPNVY GQPQPRNRPGSPQGNLYCSA ALGATDPSQSWHQCSQNLLPA DKGAKREAPW/PRPPSGEVDHQ VWHLHGWLPTTAPLLQGVW RVEQTPASHHRQPRPRQSSPST KAPPVITVNQGPASHHRQPRPR QSSPSTKAPPVITVNQGPASHH RQPRPRQSSPST/TGPASHHRQPR RPRQSSPSTKAPPVITVNQGPAS HHRQPRPRQSSPSTKAPPVITVN QGPASHHRQPRPRQSSPSTKAP PVITVNQGPASHHRQPRPRQSSP STKAPPVITVNQGPASHHRQPR PRQSSLTAKAPPVITVNQGPASH

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21891	52259	A	22019	27	1367	R/LAGPARAEAGSASDRSTGHL FPRGVGMDLCHQPAELSSGET DELPR1*WHRKQLLEDIQKLKD EIADVFAQIDCFESAGDSRMAH KENELCIGRKKFNMDPRQGRW LWRARATGCCGCMGAPAWFL SGEGLNKTAIGTYLGER*ERVE P*RGRK*RCAGVYRCVDVQAL R*VVLGGQPGPGQWHSPSGWG CRDPRYCLCNPGVFQSTGARRG VGPRAPGLQHCQA*ISQTRPPF ERFVSMNRGINNGSDLPEDQLR VREAQPTQPGPGESRRDLSLDG WPFNFDPREGWLLKLGERPTD TRRRTHTHARAGTHRCMHITV SRVLLGLPLPPLPAQPTSQ/PPT SRC/LRLQDPE/CWSHWEIS*TE RGESRVVEGKHESYRISATSAE ERDQWIESIR*GVPRSGDGFSP SRRPCFFWVLRDSWRWHWGL VTLRVPSAAGDP
21892	52260	A	22020	140	356	
21893	52261	A	22021	2	1147	APARGPAVASGSPGPAEEPQ NTETAAMTTHVTLEDALSNVD LLEELPLPDQPCIEPPSSIMYQ ANFDTNFEDRNAFVTGIARYIE QATVHSSMNMEEGHEYAV MLYTWRSCSRAIPQVKCNEQP NRVEIYEKTVEVLEPEVTKLKMK FMYFQRKAIERFCSEVKRLCHA ERRKDFVSEAYLLTLGKFINMF AVLDELKNMKCSVKNDHSAY KRAAQFLRMADPQSIQESQNL SMFLANHNRTQCLHQCLEVIP GYEELLADIVNICVDYYENKM YLTPESEKHMLLKVMGFGLYLM DGNVSNIIYKLDKAKRINLSKID KFFK/HAAGGAPFRRHADRAGO IH*DQCSL*REQVQVDVHPEQH QPPVQYLADGSDPG

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21894	52262	A	22022	47	1581	ALVLMYLASSICMSPKRGTTCS CLERGSRCPTSEPPPPPEPPGRS SRCRPGLGPGGGGKEMADDP SAADRNVETWIKIKLIKSLAA RGNGTSMISLIIPPKDQISRVAK MLADEFGTASNISRVNRLSVL GAITSVQQRLKLYNKVPPNGLV VYCGTIVTEEGKEKKVNIDFEP FKPINTSLYLCDNKFHTEALTA LLSDDRQVWDFIVIGG/SVGALF GHTPKGNTRGGPWHKFTVGIFF K\KHG*EGGQ\A\RFARLRME KRHINYVRKVAETA\VLFISSGD KVN\AGLVLAGSADFKTELSQ SDMFDQRLQSKVLKLVDISYG GENGFNAIELSTEVL\SNVKFIQ EKKLIGRYFDEISQ/DLTGKYCF GVEDTLKALEMGAVEN\LVVYE NL\DIMRYVLHCQGT\KEEKILY LTPEQEK\DKSPFH\DKETGQ\EL ELIESMPLLEWFANNYKKGFA\ TLEMFTDKSQKGSVP**KDLGG IGG\ILRYQSRFPGEWNTKKET MNFLTLMITR
21895	52263	A	22023	1	296	VEDERVACGPAWERQAGQERP ARKVQKKAPEAGKHGCLLDI LVCTYLAELKGLSGCGLTEALV AFGESSSLGRKNCRDPWGSRL QEPHWSDP/WSGPPPERCKGKPK RRRGSTDAFWTWSWART*PRRG SLAAVG*QRHW\WPLGRAAV*E ERTAETPGAPSGRSLTGQTLGS LHV
21896	52264	A	22024	5	309	LPDADLFPCACGAAAGRARS GMRPVFAVSVARTPSR/PPPAE PQFPRLPCGSGSPFFRDIDTIQK FPDMLSSFFFRDIDTIQKFPDML VFNCCCLLNQSR
21897	52265	A	22025	1	258	RGRSRIARSASGPRPALVRPPAR PPAP*TPRSWSCWSSC*PRASAS TGSPSA*ATDAHADSSKAMLPE PTSSISKFS\TQTVPFRL
21898	52266	A	22026	119	692	PSSHVSRTATYSSLRQSAVSTR STTTTLAFMARAGGRAGGRAR VGGRTSPGQCGCPACGAAAGR ARSAGMRPVFAVSVARTPSR/ PPPAEPQFPRRPQR/GAPAPSGG GASLPAPRALASSIPAQLMKPG RAKGSAGNLHPG\EGRPGARRS DPAGAARSLACP*IWPKQTPSP LASSSSFFLSETECAH

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21899	52267	A	22027	2	246	
21900	52268	A	22028	1	927	
21901	52269	A	22029	251	1077	VTMGKVLAVSSLPAGPPPPVP ALVGLPPPP*HPGRLPLPGG LGARTSVGRGLERTPGAATASA AGGAEDGACRCLPNPCTFECH RKCKEL*MEGVKFTENKAL/SS KMAIQTQSKFVKWQVDGEYR GSDFTVDVTLWNPDVLMGSGI LVAHYLSITPCLALGSELVYH RRPGEEGTVMVAGKYTLNNW LATVDVEFEASTRMQDTNVSF GYQLDLPKANLLFKGSVDSNW IVGATLEKKLPPLPLTLALGAF LNRKNKLRSGFGLTIS
21902	52270	A	22030	1	1171	GGSGFGCAWRTGWERSPGRE QAPPPATMGNVLAASSPPAGPP PPAPALVGLPPPPSPPGFTLPP LGGSLGAGTSTSRSSERTPGA TASASGAEDGACGCLPNPGTF EECHRKCKELFPIQMEGVKLT V NKGLSNHFQVNHVTLVSTIGES NYHFGVTYVGTKQLSPTEAFPV LVGDMDNSGSLNAQVIHQLGP GLRSKMAIQTQSKFVNWQVD GEYRGSDFTAATLGNPDVLY GSGILVAHYLQSITPCLALGGEL VYHRRPGEEGTVMVSLAGKYTL NNWLATVTLGQAGMHATYYH KASDQLQVGVEFEASTRMQDT SVSGYQLDLPKANLLFKGSVD SNWIVGATLEKKLPPLPLTLAL GAFNLNRKNKFCQCGFGLTIG
21903	52271	A	22031	14	434	CYCQGILSPPPCPPFLGSAQTS AICSWVRGVPAESSTSSFPKAP* VALESRGAEPTLHLPVTSRFLQ CVSSEQECVPWK/HSSPRPRFL DISPSPTCVRL*APGPVPFDPHQ KTWRSPLGTRAQGVGPRDRDS CRIVPG

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21904	52272	A	22032	989	1859	VYGD SR W SL AS SP RL EC SGA VS AH*NLCLPGSSDSPASRITGISG ARHHAQLI/L/YVFLVEMRFHH VGQA GL KLLTSGNP/HHLGLPK CWDYSRKPPRPPRPII/FSFFFL RWSLALVAQAGMQWDDLSL QPLPPGFK*FSCLSLLSWDYVG CPPRLANFVCVCVCVLV/VDG GFTMLARLGLELLTSGDLPPFG LPKCLGFTGM SH CARPIFFFE MESCFATQAGVQWCDLSLQPL LP PR FK*FSCLSLLSWDYRHM PPCLANF/CFGIFSRDRVSSCW GRSQT PD LK
21905	52273	A	22033	157	376	SHQDFMRTAANLLQTGWCTGS NTGAGARWGLCRASLSRCRCA APSAPCSGSRCS*RSWKGTHPS LPPRCRGRS
21906	52274	A	22034	298	399	
21907	52275	A	22035	1	185	
21908	52276	A	22036	311	516	WKAERRTRHLLQTGWCTGSNT GAGARWGLCRASLSRCRCAAP SAPRS GS RC S *RLWK G THPSLP RCR
21909	52277	A	22037	1	1487	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGA KS QGC SR N ARHQA RS MPLQDQHLALAIL LELA VQR GTLSQMLSAILLLLQ LWDSRAQETD NER SAQGTSTL LLSL LQT FSIICS KD TPPSEGN MHLLSGPLSPSESFLRESFFTQV NCRNNEEVT LICK ADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEV TRES MHAF CV GQYLEVR LYALSDAEDGRGHPLMASV IHL LWRLQTSQIHYSYNEEKDEDH CSSQWAHL PAN RDCSHRWALG DHSQAFLQAIADNNIQDHN VKT HQE QGR SYKEVCTPVIERL RFL SNELRPAVGNLSIIEF KL SSL PRWRIAQKIIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIA IK SPKTITSEN LG/REPGEHPASPLPDDAQHA HPAAQRKQPRPPAQFRHAGPHS DGTAPDWPQL

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21910	52278	A	22038	263	375	AGPRRMRRISAWAVSTPLTDSPPGHHQA/GEVAGAGSF**HPP/PCPSRYCPQMTPPPPPPAPPALPPPPPPAPASPLPPAPSPPHAPQALPPPPALPPPPASPLPPALSPPLPAPP/PPSAPPASPPAPPPPAPPPSPPPAPPSPASPLPPAPASPPSPAPPPPAPPPAPHPPSPAPPCCPLPRPRGSPVQEKVHQV*IPVPAPAGEGGAPAGRIWPQGWRRAGKPPTWEEALAAFPWTALPPASA VPAQPPRAH*VAPAL*WALHRRSDSDSDSNLSPRIPGTGGRRQPR*DS*APACSEVAGAGSF
21911	52279	A	22039	1	2001	
21912	52280	A	22040	1846	7725	PEPFCHRAAHWSNQYCPFQFQDSDSPRQTLTVLIKDNGEPSLSTATLTVSVTEDSPEARAEFPSCGAPREQKKNLTFYLLSLILASVGFVVTAAGVHFKVYKWKQSRDLYRAPVSSLYRTPGSLHADAVRGGMLSPHLYHQVYLTDSRRSDPLKKPGAASPLSRQNTLRSCDPVFYRQVLGAESAPPQIRYPVPEESQEGTFVGNVAQDFLLDSDLSARRLQVAGEVNQRHFRVDLDSGALLIKNP
21913	52281	A	22041	108	340	PQPSQVMSFHGDSGSCRRWATAGT*ATSPPCSSIFLRRMHSGHWCSWPVRGTGCRDFTAQMAGPSRGSKINRSMW
21914	52282	A	22042	275	752	EKTHKTCRCGRGCGKRGT*HCWWECLLQPLWKMVVWKLKELVELLCDLAVPL/LGINPEEKSLYEKDTCT/R/LFMAAQLAIKKKWNQPKCPSINKWLQKLWYIYMMEYSAIKRNLTAFAATWMRLLETILSQGDPLESTCSRQANRQEITSVPKA
21915	52283	A	22043	25	202	DAEAWAMELADVGA*ASSQGAPQPEEPAASLGVNEKGAGGGRSGRRPLGRDRPPTRL

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21916	52284	A	22044	1	2290	MEKLGVEPEEEGGGDDEEDAE AWAMELADVGAASSQGAPQ PEEPAASLGVNEKGVHDQVLP PNASSRVIVHVDLDCFYAQVE MISNPELKDKPLGVQQKYL TCNYEARKLGVKKLMNVRDA KEKCPQLVLVNGEDLTRYREM SYKVTELLEEFSPVVERLGFDE NFVDLTEMVEKRLQQLQSD SAVTVSGHVYNNQNSINLLDVLH IRLLVGSQIAAEMREAMYNQL GLTGCAQVASNKLLAKLVSGV FKPNQQTVLLPESCQHLIHS HIKEIPGIGYKTAACLEALGINS VRDLQTFSPKILEKELGISVAQR IQKLSFGEDNSPVILSGPPQSFSE EDSFKKCSSEVEAKNKEIELLAS LLNRVCQDGRKPHTVRLIIRRY SSEKHVGRESQCCHIPSHVIQKL GTGNYDVMPPMVDILMKLFERN MVNVKMPFRLTLLSMCFCSLK AVNTATTRLIDYYLMPITISITSR SGKHSFKMKDTHMEDFPKDKE TNRDPLPSGRIESTRTRESPLDT TNFSKEKDINEFFCLSLPEGVDQ EVFKQLPVDIQEEILSGKSREKF QKGKGSVSCPLHASRGVLSFFSK KQMQDIPINPRDHLSSSKQVSS VSPCEPGTSGFNSSSSYMSSQK DYSYFLDNRLKDERISQGPKEP QGFHFTNSNPAVSAFHSIFPNL QSEQLFSRNNHTTDSHKQTVAT
21917	52285	A	22045	2	141	
21918	52286	C	22046	278	489	
21919	52287	A	22047	130	426	

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21920	52288	A	22048	357	1579	QRRPRFPSPQSGISMTECLPPTSS PSEHRRVEHSGSLTRTPSSEEIS PTKFPGLYRTGEPSPPHDILHEP S*SNGLMDEKDHGKKKGNFKK KEKRTEGYAAAFQEDSSGDEAE KLMPRFEEAYGRITTEKVVQEF QRLLKELPEGNYLLISLVVHM DHVITKELEAKMNIQNIYIVVSP TVQISNLVLYVFFTHVQELFGN VVLLKQVTKRRWSNVATMPTL PETQAGFKKEIRIQELLNCLHQ DLQGGIKDLSEERLWEEKIL TKQEELLGMEQFLRRQIASEKE EIECLRAETAIEIQSHQQQLSET EYSSSESESEDEELQIILEDLQR QNEELEIKNNHLNQAIHEESEA VIEPRMQPWWLLQLOPDRAKQQ AQEDEEPEWRGGAMQTPKNGI
21921	52289	A	22049	182	2212	VTEKTSLSLPSQSGISMTECLPPT SSPSEHRRIVEHG/SAGLTPGPPA SEEIQLPKFPGLYRTGEPHPHP P*HPSHESLM*CPDDEKDHGK KKGKFKKKKEKRTEGYAAAFQED SSGDEAESPSKMKRISKGIHVFK KPSFSKKVREKDFKIKEKPEEEK HKEEKHKEEKHKEKSKDLTA ADVVKQWKEKKKKKKPIQEP VPQIDVPNLKPFGIPLADAVR TMMYDGIPLPAVFRECIDYVEK YGMKCEGIYRVSGIKSKVDELK AAYDREESTNLEDYEPNTVASL LKQYLRDLFPENLLTKELMPRFE EACGRITTEKVVQEFQRLLKEL PECNYLLISWLIVHMDHVIAKE LETMKNIQNISIVLSPTVQISNR VLYVFFTHVQELFGNVVLLKQV MKPLRWSNMATMPTLPETQAG IKEEIRRQEFLLNCLHRDLQGGI KDLSKEERLWEVQRILTALKRK LREAKRQECETKIAQEIASLKE DVSKEEMNENEVINILLAQEN EILTEQEELLAMEQFLRRQIASE KEEIERLRAEIAEQSRQQHGRS ETEEYSSSESESEDEELQIILE DLQRQNEELEIKNNHLNQAIHE EREAIHELVRQLRLQMQRAKA EQQAQEDEEPEWRGGAVQPPR DGVLEPKAAKEQPKAGKEPAK
21922	52290	B	22050	34	322	

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21923	52291	A	22051	137	1546	QMLGRRPPRWLQAKARALA RRRPPPSLHLTLPTALSLSKSRTP VPKSIPISETNIPPVSVQPPASIG PPLGVPP/PEPSHGDDQPRPG/APL PIFMEQQIMQIQRPPFIRGPPVPM PPTPTAPCPTPCFPASGPRPVAP ETWAPLPACTGPGCY/PPHPPE/ PPPP/SPGNPPGLPPPPGAPLPS LPFPVSMMPNGMPVQMMN FGLPSLAPLVPPPTLLVPYVIV PLPVPIPIPIPSATPSPTGSP ATGRTSFRTLATPRRRAASQA DTPCPGTPSRARPSRTRPPAA RARP*AWRPPPSMAGARWWT *RGAPA/PPGPPGRGRPARLPRR AAGPAGRRHRPDRGPPSPAAQR DPPRAA/PRTSRRSASRAPRSAG PAAAAGTATAARPPATQARA PRRAPRRPRPATSS*TARAAPPP/ SGAKSAEPPPEQPPPPPPAPPK KLLSPEEPAVMRARVQGGE
21924	52292	A	22052	762	2049	RSSFMSGADLLACST/SGLGNM PYDLLRGMEPTLGCSFEDLAL A*PGGITQEQKINEMRVAPEQQ M/ADIHFMIAAGQDLWDIDAQ GATLLHIAGANGYLRAAEELLDD HGVVRVDKDWGWEPLHAAA FWGQMMAELLVSHGANLNA RTSMDEMPIDLCEEEEFKVLL ELK\HKHDVIMKSQLRHKSSLS RRTSRHRQAS/SVGKVVRRTQPV GTGPNLYRKEYE/GEEAILWQR SA/AEDQRTSTYNGDIRETRTD QENKDPNPRLEK/PVLLSEFPTK IPRGELDMPVENGLRAPVSAYQ YALANGDVWK/VHEVPDYSMA YGNPGVADATPPWSSYKEQSP QTLLELKRQRAAAKLLSHPFLS THLGSSMARTGESSEGGAPLI GGRTSPYSSNGTSVYYTVTSGD PPLLKFKAPIEEMEEKVHGCCR
21925	52293	A	22053	2	306	SKEAFAIGLGGGSASGKTIVAR MIIEALDVPVWVLLSMDSFYK/ NAFDFDLIIITLKKLKQKGSVK APIYDFTTLRKMWDWKTLYGA NVIIFEGIMAFADKTL
21926	52294	A	22054	2	379	

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21927	52295	A	22055	352	1227	GDVSPQLSPRQKSGPLCTSCCA WPVCSPHSDAQPSGEGGLWE KTPFLSVPHRFVPRAALASAHQ CHPLPRTLVLKSTPQVRGMHT IIRDKETSRDEFIFYSKRLMRLLI EHALSFLPFQDCVVQTPQQQDA *RITGVSIILRAGETMEPALRAVC KDVRIQTILIQTNQLTGEPELHY LRLPKDISDDHVLMDCTVSTG AAAMMAVRVLLDHDVPEDKIF LLSLLMAEMGVH/SVA YAFPR VKKSSPRRWKAGQLTFFRIIP GIGNFGDRYFGTDAVPDGSDEE EVAYTG
21928	52296	A	22056	72	2746	FLVETGLHHVGQAGLKLLTSN DPPASASQSTGITGMSHHAQPR QSSYVPPMSLPASAMPVEGVG GDALWAGHASGYLGGGQLWA TSEYIPLCSSNAESLDRLLPPVG TGRSPKRTRTRQCKSEPPLRTS KRTIYTAGRPPWYNEHGTQSKKE AFAIVPVEQKEAGQPQAAAA GWAPLGPICAGSLPVPHRGSPL PPAGLGGGSASGKTTVARMIE ALDVPWGGSSLSDMSFYKVLV EQQQEQAAHNNCNFDDHPDAFD FDLIISTLKKLKHGKSVKVPYID FTTHSRKKDWKTLYGANVIIFE GIMAFADKTLLEGPGAPCTGP EDSIIRHIAAPSLHKASSRANYC VLSMGTDPKLATSPIPQCVGAS YPKQRCPEVALARPTDQAAS VQGLVPVSPCLLASGHSCLARC LHQLLDMKIFVDTDSIRLVRR LRRDISERGRDIEGVIKQYNKFV KPSFDQYIQTMRADIVVPRG SGNTVGHRR*LLQHVHSQLEEV SGVPRPHGLAPSPSTHFSAAATP SWPVHLIPLRSLSPASSSQPAQ LCQQELGNCSSKLLGLGRGRIPL SLPKGRHAGGAALASAHQCHP LPRTLSVLKSTPQVRGMHTIIR DKETSRDEFIFYSKRLMRLLIIEH ALSFLPFQDCVVQTPQQQDYA GKCYAGKQITGVSIILRAGETME PALRAVCCKDVRIQTILIQTNQLT
21929	52297	A	22057	61	341	
21930	52298	A	22058	1	1086	
21931	52299	A	22059	1	498	
21932	52300	A	22060	104	3395	
21933	52301	A	22061	1	1653	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
21934	52302	A	22062	1	1717	
21935	52303	A	22063	172	13375	EDLFK CIMAHAAASQLKKNRDL EINAE EEPKRRKRRKSRDRK KKSDANASYLRAARAGHLEKA LDYKINGVDINICNQGLNALH LASKEGHVEVVSELLQREANV DAATKKGNTALHIASLAGQAE VVKVLVTNGANVNAQSQNGFT PLYMAAQENHLEVVKFLLDNG ASQSLATEDGFTPLAVALQQGH DQVVSLLLENDTKGKVRPAL HIAARKDDTKAAALLLQNDNN ADVESKSGFTPLHIAAHYGNL
21936	52304	A	22064	1	360	
21937	52305	A	22065	1	2577	
21938	52306	B	22066	323	3154	
21939	52307	A	22067	93	791	IRMSYAEKPDEITKDEWMEKL NNLHVQRADMNRLIMNYLVTE GFKAEAEKFRMESGIEPSVDLE TLDERIKIREIDT*KGQIQEAI RL *FNSLHPEL/LWD TNRYLYFHF ASNSILIPS*FRQ/GKTRGRRWG VAQTQLADRGEE SRECLTEME RTLALLAFDSP EESPFGDLLHT MQRQKVWSEVNQA VLDYENR ESTPKLAKLLKLLLWAQNELD QKKVKYPKMTDSLKGGD
21940	52308	A	22068	171	426	
21941	52309	A	22069	5	655	LLQPSVQLPNGTANTSLSFAAV SAVSPPPCRTSTATLPPMPSPF FCVFPSPSPSPSEFLSCIASVS RVHSLSSSSSGSSSTASSLNFSAI MGSSSATASWVLSTTTPPCPS ALPSSPAQES*SLAASSSAWLSE HPSFSSFTLSWASGAFCEVLSL FSGSKLSFLSSKGDCGIPPI* TSA CPSSLDSPCFSSSTKSSSYSEI GKSPQPI

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21942	52310	A	22070	87	1180	NQASLEVLPSVPDSDPSIPSP/SDNPNRNFSAAPVSCLPSPLPVAASWPSDPSSCSCSPSEVFRSRAPGVPTPASVYVYVTVISSAAGTSSPLRANSSTTTFPAAAVFPTNSSCWQVSSSATSEKEEALFAIVFSSAVSEPANTSLSSAAVSAVSPPPCRTSTATTLPMPSPFCVFPSPSPSPSPSEFLSCIASVSRVHLSLSSSSGSSSTASSLNFSAIMGSSSATASWVLTSTTPPCPSALPSSPAQES*SLAASSSAWPVAGISPSGACTFPAGSASGAAPSPSWRCPSFRALFSLLDSSLSLCSVSLASLSLSPPSFLRAVMFPATFKSRRCFKYGNHCLFSDLLWLEVCAL
21943	52311	A	22071	841	1052	IGEVLLDNVLKSVF*LGSLVLPITSLKLLP/SGSKRDPKAMSHSHAP*VTGAFPRCGRWRLQPAAPPPPS
21944	52312	A	22072	817	866	HANPVSPTSPWPKE*SWP*CSG**RTFQSVSFAGGRRGWSLKPPPATAWKSSSCHLP SGVRMAHF CRIPFGPRGRDFADFGTTIKQDF RLLGQTSVDRLLQLSQQAQVKGQQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRLES GQ
21945	52313	A	22073	2	3238	TTFPAAAVFPTNSSCWQVSSSATSEKEEALFAIVFSSAVSEPANTSLSSAAVSAVSPPPCRTSTATTLPMPSPFCVFPSPSPSPSPSEFLSCIASVSRVHLSLSSSSGSSSTASSLNFSAIMGSSSATASWVLTSTTPPCPSALPSSPAQES*SLAASSSAWPVAGISPSGACTFPAGSASGAAPSPSWRCPSFRALFSLLDSSLSLCSVSLASLSLSPPSFLRAVMFSSDFSNPGVASNMGTTVSF
21946	52314	C	22074	88	4374	
21947	52315	A	22075	73	616	VKESLTQKSKRFQNKLINRRGWERPRSGASWTQRRALGGRCVDRWLGI/WPHRIPGARLRGFPALNPTPQTAPSPSPDPRPRPP/CPSDPGPRTEAQCSL/PPPPSPRHLDPGPEPPTPLTQQGQKGTTRAPRPCRPSQK*ATSGPAVRRREA RGSASLRTRAPSRDSTHAGIQGNVALQP

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21948	52316	A	22076	1	421	GTVMGLPKYFISLSTKFFLSFS LSADELHIAFLWPRSKPFGVI QRSASQLNALPEVLKNPGDDP KMLRFAESPRNLPAVL/GDIW TDGKGSVSLQEQQVYHFLIRPT PGS*ARASFLSCG*EEFRRHGLT FSSTRE
21949	52317	B	22077	211	2041	
21950	52318	A	22078	200	1525	IMASAHLATSAFCIRSSSSGRSG SCKRGSWDSEQALIRAWTTLP SLHIAADGSGFAGGRGIPSKRWS WRAGQQSSLCIMQTSNCGNS FQLVSEGASWRGLPHCSCAELQ DSLNFYSYHPSGLSLVRPSSPGN SPKEQPFSSQLRPEPPDPEKL PPAPPSKRHCRSLSVVDLSRW QPVWRPAPSKLWTPIKHRGSGG GGGPQVPHQSPPKRVSSLRFLT SSQCLFSMCPSSQTLQPSFLQPG PGPSSSRPCAASPSQGSWESDA ESLSPCPPRRFSLSPSLGPQAS RFLPSARSSPASSPELPLAT*G/L SATFPESRSQPCDLARKTGVK RRHEEDPRRLRPSLDFDKMNQ KPYSGGLCLQETAREGSSISPP WFMACSPPLSASCSPGTGGSSQ VLSESEKEEGAVRWGRQALS KRTLQCRDFGDLNLNIEEN
21951	52319	A	22079	1	117	
21952	52320	A	22080	3	632	
21953	52321	A	22081	1	448	MQSETETVHLFIPALSVGAIIGK QQQHIKQLSRFAGASIKIAPAEA PDAKVRMVIITGPPEAQFKAQG RIYGKIKEENFVSPKEEVKLEA HIRVPSFAAGRVIGKGGKTAST *QNLCSGMMKGKALKAKPSTYN CVGCGWSPRPRCSLN

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21954	52322	A	22082	233	2096	RREDEGNKTSWIHPSPWVVLF RFFSLFFFKQPLFTMNKLYIGNL SENAAPS\DLKSIFKDAKIPVSG PFLVKTYGAFVDCP\DESWA\LR AIKAFSGKIELHGKPIVEHISVP KRQRIRKLQIRNIPHLQWEVL DSL\VQYGVVESCEQVNTDSET AVVNVTYSSKDQARQALDK/L LDKLNQFQLENFTLKVAIYIPDE MATQQNPFLQPRGRRGLGQRG SSRQGSPPGSSVSKQKPCDSPRL LVPTQFVGAIIGKEGATIRNITK QTQSKIDVHRKENAGAAEKSIT IPSTPEGTSAACKSILEIMHKEA QDIKFTEEIPLKILAHNNFVGRLI GKEGRNLKKIEQD\TDKITISPL QELTLNPERTITVKGNVETCA KAEIEIMKKIRESYENDIASMN LQAHLPGLNLNALGLFPPTSG MPPPTSGPPSAMTPPSQSEQSE SETVHLFIPALSVRALISKQGGH IKQLSRFAGASSKIAPVEAPDAK VRMVMIAGSPEARFKAQGRIY GKIKEENFVSPKEEVKLEAHIR VPSFAAGRVIKGGKTV\NELQ NLSSAEVVVPRDQTPDENDQV VVKITGHFYACQ\VAQRKI*EFL TQVRQHQQQKALQSGPPQSR

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21955	52323	A	22083	8	1675	TASCRLAMALHVPKAPGFAQM LKEGAKHFGLEEAVYRNQAC KELAQTTTAYGPKGMNKMVI NHLEKLFVTNDAATILRELEVQ HPAAKMIVMASHMQEQEVGD GTNFVLVFAGALLEAEELLRI GLSVSEVIEGYEACRKAHEILP NLVCCSAKNLRDIDEVSSLLRT SIMSKQYGNVFLAKLIAQAC\ YLFFLIIPAISMLITSEFVK/FLGS GISSSSVLHGMVFKKETEGDVT SVKDAKIAVYSCFPDGMITETK GTVLIKTAEELMNFSGKEENLM DAQVKAIDTGANVVVTGGKV ADMALHYANKYNIMLVRLNSK WDLRRLCKTVGATALPRLTPP VLEEMGHCDVYLSEVGDTQV VVFKEHEKEDGAISTIVLRGSTD NLMDDIERAVDDGVNTFKVLT RDKRLVPGGGATEIELAKQITS YGETCPGLEQYAIKKFAEAFEA IPRALAENSGVKANEVISKLYA VHQEGNKNVGLDIEAEVPAVK DMLEAGILDITYLGKYWAIKLA TNAAVTVLRVDQIIMAKPAGGP KPPSGK*NWLNIFYCR
21956	52324	A	22084	175	278	

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21957	52325	A	22085	208	1976	GPSPLKEHFSGLEETAYM/NILT CMELAQTRTAYGPNMNMK VINHLEKLLVTNDAAITLRE VQHPAAMIVMASHMQEVE GDGTNFWLVFAGSFPVNYLKN LWVRIGLSVSEVIEGYEACRKA HEILPNLVCCSAKNLRDIDEVS SLLRTSUMSKQYGLMKVFLAK PYLLQACRIYFSWIPASMLITSE FVK/FLGSGIRSS*VLAGMVFK KETEGDVTSVKDAKIAVYSIC PFDGHG*QET*GEQCLDKRTAL KDLDGIFR*GEQENLHG/AATSP KAIAADTGANVVVTGGKVADM ALHYANKYNIMLVRNLNSKM/W DLRRLCKTVGATAPRLTPSL SLKEMGHCD/SVYLSEVGDTQ VVVFKEHEKEDGAISTIVLRGST DN/L*LDIERAVDDG/VNTFQ GSLQRDKRLVPAGGGSNRNLN* PKQITSYGETCPGLEQYA/ILK KFA*GHLKAIPPAHWQKYSGE NSGVKAQWK*SPKLYAVHQEG INKNVGLDIEAEVP/SLVKDML EAGIPRYLTLGKYWAIPLATNA AVTVLRVDQHTLV*FFFMQIIM AKPAG/GGPKPKWGRKTWGD DQNGLKIGFNFCYR
21958	52326	A	22086	1	346	PF*CTPSCLWAF*TARSAQTWS APSTRSWCSEWPKSLPSTWLR *FRKVSSYSWSQSWSSPTASTD SSRPPHSLGASCHPGHQSLMP PSR*ATSTAYASLSSSHRPNTQ PSPS
21959	52327	A	22087	3	484	RSSQPRVGLCGKSLQP/SSEGSC HLQGWCSPFRVSSSIMAE*RT *PRVSSSMHGRGPTQNRATKK ASSSETSV/QVTAQEAQAEPGA AGVAG/SPASAPQDSAGACWPA QVL*GGSDRSCRGSHPGNTEPP SVLRTGTAPGA*G/SSPFSPTQS GSCCFPFSS
21960	52328	B	22088	181	339	

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21961	52329	A	22089	290	2014	STCTPLPTASSQSRPHPPPTPTTPP APWRSSNGQVPTLT*PGSTLPP G/SGKSP/VASGGPARAKPHRA VHVSPA/PSGGSPGDVAELPAAV AVRA*QAGSGQRLPAPVCVGE MGTLCGPADVHVQVCGLSE PRAPHRPGQPQARAHGVPSGQS LCPAQPG*DDS/AKVSSYSWSQ SWSSPTASTDSSRPHSLGASCH PGHQSLMPPSR*RA/TSTAWRA RTASTPRCLGPRPAPWSCASLSS SHRPNTQPSPTS/RRARLATP SSHWALAPWTMAPTQPTTW TRWGKTVSGRQMNTWRRPWS TCARYSGSAKRSSGSHSPWAP PRMRMEKSNSPTASWVRTDSS LRPWGGTRSSMGCEGLKLSR GTRCSPSGAMRSPAWSAHSLG CRLPSTTDLQDRWRLCVPGMT SSAASVATTSQNLGWPACTC*A LWGGGRWPA/TAA/QAQPALP GQLPTRWSRCCWPSSWPLCSAS GPSHARCCSPWAMSTPL*HC *PSGGSCTSPGVSCLSRLEGF ATQPHPAERTWEAPPGGNTV ILGLLERGSCSRGIWRKRNQE RKAGRAPAKE
21962	52330	A	22090	363	487	
21963	52331	A	22091	234	282	
21964	52332	A	22092	742	990	
21965	52333	A	22093	1	206	LFPAFSDSRECKLMKKLLEA/H EEQNVD/SYTEA/VKEYDSIFPG WTQWL/TTL/LR/KKTIQ/G/DEK DLR
21966	52334	A	22094	128	1062	KPFEEAMYN/SGKEAEAMALLA EAER/K/V/KNSQSFSG/LFGSS KIEEACEVYARAANMFKMAKN WSAAGNAFCQAQLHLQLQSK HDAATCFV/DAGNAP/KKADPQ GGPFNCFDCVAFIY/TDMGR/F TIAAKHHISIC*DLLRQKLVDIE KAIA/HYRALADYYYQGEESNS/S ANKCLLKVAGYA/ALLEQYQK/ AIDIYEQGWGPNAHWTSPPPSK YSAKDYFFKAALCHFCMDML QA/KLAF/QKYEELFPVFSDSRE CKLMKKLLKA/HGEQNV/D/SY TE/SVKGITDSISRL/DQWL/TTH CL/R/KKTI/RGD
21967	52335	A	22095	1	1038	

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21968	52336	A	22096	20	2482	RVCSSASTASQAVMADAWEE IRRLAADFQRAQFAEATQRLSE RNCIEIVNRLIAQKQLEVVHTL DGKEYITPAQISKEMRDELHVR GGRVNIIVDLQQVINVDLIHIE RIGDIKSEKHVQLVLGQLIDEN YLDRVQGQEVNDKLQESGQVTI SELCKTYDLPGNFLTQALTQRL AIIIGHIDLNRGVIFTEAFVAR HRARIRGLFSAITRPTAVNSLIS KYGFQEQLLYSVLDELVNSGRRL RGTVVGGRQDKAVFVVDIYSR TQSTWVDSFFRQNGYLEFDALS RLGIPDAVSYIKKRYKTTQLFL KAACVGQGLVDQVEASVEEAI SSGTWVDIAPLLPTSLSVEDAAI LLQQVMRAFASKASTVVFSDT VVVSEKFINDCTELFRELHQ KAEKEMKNPNVHLITEEDLKQI STLESVSTSKDKKDERRRKAT EGSGSMRGGGGNAREYKIKK VKKKGRKDDSDDESQSSHTG KKKPEISFMFQDEIEDFLRKHIQ DAPEEFISELAELYLIKPLNKTYL EVVRSVFMSTTSASGTGRKRT IKDLQEQEVSNLYNNIRLFGKRG WKFFADDTQGWLLPKHLELV QCVLISLNLAFNVLGFGILMDG Q*DDPGRPFTSELRKEILSKLS EETKVALTKLHNSLNEKSIEDFI FCILDSAAEACDIMVKRGDKKR ERQILFQHRQALAEQLKVTEDP
21969	52337	A	22097	1	711	VLSLFDGIATGYLVKLKELGIKV GKYVASEVCEESIAVGTVKHEG NIKYVNDVRNITKKNIEEWGPF DLVIGGSPCNDLSNVNPARKGL YEGTGRLLFFEFYHLLNYSRPKE GDDRPFWMFENVVAMKVG KRDISRFLCNPVIMDAIKVSAA HRARYFWGNLPGMNRPIASK NDKLELQDCLEYNRIARIFGFP VHYTDVSNMGRGARQKLLGRS WSVPVIRHLFAPLKDYFAC

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21970	52338	A	22098	406	2885	GRGILVNGACSDQSSDSPPILEA IRTPEIRGGWAVGTGVVSGADI VSGHCRQWSLLSLFQSGTLLSL AFITWAFRETRTRSESPAVSSHT SSQSTCGQHST*HT*HARGRQG RNHVDESPVEFPATRVGSPDAQ TPARSL*LGDMPHSLTIDLDDDT EDTHGTPQSSSTPYARLAQDSQ QGGMESPVQEADSGDGDSEY QADGRELLPRV/I*GP*TRGKTS YAMVVSWKATSKRQAMSGMR WVQWFGDGKGFSEVSPGKGKGF CRPEAVPACLPNKLVSRYKA MYHALEVTWDEGMRAP*EQ G*SKRPTELEDQLKPMLEWAH GGFKPTGIEGLKPNNTPGGNE SPWQHPLPLLPGPLLGRVRLKT NCYNNKGDRGDEDSRGDCW VPGIMGQMGGRCRSGIDVIPL TPWLGL*ACLVQCQTRVSPPTT ALDLPLASSNSPLLCEGRELL LCSNTSCCR*ALGPVGMWVVG PQGSYVPVAV*EPWSCYMCLPQ RCHGVLRRRKDWNVRLQAFFT SDTGLEYVSHRLPPLPPQIPGAQ GVGKLWFDGIATGEFGEHLET LSCHNRVARESEESIAVGTVKH EGNIKYVNDVRNITKKNVRAV CTLRASSLPVFFSPPHNPARK GLYGEHPSLWQSLESCHLTGT PGAGNK/RGLGWRWFQMPNALS SFLSTGVQQRDISRFLEVRESGD
21971	52339	A	22099	729	896	

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21972	52340	A	22100	1	2672	MAYKQGFLKVMVHFRKAEVT GKNHTSVHEGYTLISPAQVLT ISCKKSILLQEQVSKDVCVDFT QEEWYLLDPAQKILYRDVILEN YSNLVSVGYCITKPEVIFK/ES KGEEPWVLEKGIPQAQCPQK RKWKV/EMNVVREQPRKMKM TIFGEPPITNTKTVSVENGDRG SKTFNLGTDVPSLIKLSL*NM*L ISEMNLKNISGLIITKKNCSSRK PDEFNVCEKLLDIRHEKIPIGE KSYKYDQKRNAINYHQDLSQP SFGQSFEYSKNGQGFDAAFF TNKRSQIGETVCKYNECGRTFI ESLKLNISQRPHEMEPYGCSIC GKSFCMNLRFHQALTKDNP YEYNEYGEIFCDNSAFIHHQAGY TRKILREYKVSDDKTWEKSALLK HQIVHMGGSYDYNENGSNFS KKSHTLQLRRAHTGEKTFECGE CGKTFWEKSNLTQHQRTHTGE KPL*CTEC/GKAFCKQPHLTHN QRTHTGEKPYECKQCGKTFV KSNLTHEQRTHTGEKPYECNA CGKSFCRSALTVHQRTHTGE KPFICNECGKSFCVKSNIIVHQR THTGEKPYKCNCGKTFCEKSA LTKHQRTHTGEKPYECNACGK TFSQRSVLTKYQFIHTRVKAL* TS*MLEAFIHL/SKLVIQFQKRSS EKAKECQKFVE/KTSCCLNM*KL SRKIKTFF*KICKLTVKNKGKNK
21973	52341	A	22101	1	2817	

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21974	52342	A	22102	474	2766	NQTALYNQAQLLHGSRFANMS AEGYQYRALYDYKKEREEDID LHLGDILTVNKGSLVALGFS QEARPEEIGWLNQYNETTG DFPGTYVEYIGRKKISPTPKPR PPRPLPVAPGSSKTEADVEQQA LTLPDLAEQFAPPDIAPLLKIL VEAIEKKGLECSLTLYRTQSSNL AELRQLLDCDTPSVDELMIDVH VLADAFKRYLLDLNPNVIPAAV YSEMISLAPEVQSSEYIQLKK LIRSPSIPHQYWLTLQYLLKHFF KLSQTSSKNLLNARVLSEIFSPM LFRFSAASSDNTENLIKVIELIS TEWNERQPAPALPPKPPKPTTV ANNMNNMNSLQNAEWYWG DISREEVNEKLKRDSDGTF RDASTKMHGDYTLTRKGGNN KLKIFHRDGGYGFSDPLTFSSV VELINHYRNESLAQYNPKLDVK LLYPVSKYQQDQVVKEDNIEA VGKKLHEYNTQFQESREYDR LYEYTRTSQEIQMKRPAIEAF NETIKIFEQCQTQERYSKGNY HLEKFKP*RAKEKEIQRMHNY DKLKSRISEIHDRRRLEEDLKK QAAEYREIDKRMNSIKPDLIQL RKTRDQYLMWLTQKQVGRQKK LNEWLGNENTEDHYSLVEDD EDLPHHDEKTWECLGSS/RTRN QSLKNLFARGSRDGTFLVRESS KQGCYACSVVVDGEVHKCVI
21975	52343	A	22103	3	392	
21976	52344	A	22104	168	404	

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21977	52345	A	22105	49	1760	YQSPA WQSHWHQKLQVRKEN MAKRVAIVGAGVSGLASIKCCL EEGLEPTCFERSDDLGGIWRFT EHVEEGRASLYKSVVNSCKE MSCYSDFPFPEYPNYVPNSQF LEYLKMVYANHFDDLKHIFQKT KVCSVTKCSDSAVSQWEVVT MHEEKQESAIFDAVMVCTGFL TNPYLPDLSFPGINAFKGGYFHS RQYKHPDIFKDKRVLVIGMGNS GTDIAVEASHLAEKVFLLSTTGG GWVISRIFDSGYPWDMVFMTR FQNMRLRNSLPTIVTWLMERKI NNWLNHANYGLIPEDRTQLKE FVLNDELPGRIITGKVFIRPSIKE VKENS VIFNNTSKEEPIDIIVFAT GYTFAFPFLDES VVKVEDGQA SLYKYIFPAHLQKPTLAIIGLH/ IKPLGLP*LPTGETQVRWAVSG S*KVLTRLPPSVMIIEINARKE NKPSWFGLCYCKALQSDYITYI DELLTYINTKPNL/FSLWLLTDP TSGLWTVFFGPA/SPYQFRLTG PGKMKGGAQEIALHGPQWDP NISRVHSKVRSCYKFSIFPGK FFLKVFSFPGFGLWLFLLIFPYK
21978	52346	A	22106	262	969	EWSSVRRSLVEKRALRRPHQC LCFRMKTILSNQTVDIPEINVDI TLKGRGTGIREGPPETGLR/RDFN/ HINVELSLLWKEKKRGSRVDK/ WWGNQKRNWPTRSDFVSHV QNMIKGWLHWGFRLQG*GPV YAHFPHQPLL SRKNGVSWLKIR KFLWGEKYTRRVSG*RPGLL VSVSQGPRKDEINPLKANDIEL VSK/SSAGF*FQQA TTS*KTRNI RKFLADGIFCLLEKGLFRQA
21979	52347	B	22107	211	457	
21980	52348	A	22108	1	159	KEAENQCLDISSPGMSGHRQGH DSLEHDELREIFNDLSSSEDED ETQHQDEK*LDISSPGMSGHRQ GHDSLEHDELREIFNDLSSSEDED EDETQHQDEK
21981	52349	C	22109	167	367	

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21982	52350	A	22110	754	1950	VKGKDDAPHELGE/SQFILRLPP VEYASTVRRVQSGHVNLDRL TVELHPDGRHGIVRVDRVPLAS KLVDALPCVMEEPENLLKKPF SKTAHIGQMLVSTVDGDLFPV EESPCLALDPKAS\KKDKDKDE KKFIWNHGITLPLKNVRKRRF RKTAKKEIYVNLDPV*KKELKR VLEVPDA\EAVSTRWGIIKPKV ETKGAEANQGLDISSPGMSGH R\QGHVDSLEHDELREIFNDLSSS SEDEDETQHQQEEDINIITDEED LERQLQDKLNESEDEHQENEG TNQLVMGIQKQIDNMGKGLQ/E TQDRAKVRQEDLIMKVGNLGS PRTDFQAVLGMSFNQREDREK EQLUSSLQEELESLLREVKKNLN M FNFQSFRLVQHLGKFFGLLLL GYLRPCSS
21983	52351	B	22111	227	355	
21984	52352	A	22112	121	486	WGPALCIGGYLASFLASVHLM LP LR*GEMLSF*GLSFSFRFPGE KFE VRLVPGRHDI AFVEFDNEVQAG AARDALQGFKITLSPLKVSPP L GAFLEPCVSEWSPHSIVRVCQ Q TLHLALLGRN
21985	52353	B	22113	8	165	
21986	52354	A	22114	1	218	
21987	52355	A	22115	566	1412	TLHSMVVPETRPNHTIYN\NLN EKIKKDELKKSLLRPSFF/SSLG QILGYSWGIHGRP*RMEGARPF SIFKEVSSGTNALR\SMQGFPFY V DKPMRIPVLPRTRLQDIHLPRIE RAPFIGSRDPKAGERGRPKSQ G DPGPPKEGLCKGGGSHPRGGG LSRGPQPGHCPMT\KAPRIMH HMPGQ\PLTAAPLDMIPPG/L APGQIPGAMPP\QQLMPGQM P PAQVPLWRNPPNHLFLTNL P EETNELMLSHAFSNQVPPGKE E GPVVVPRAGNEHRPSVEV

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21988	52356	A	22116	2	1176	FGEISTFVAVRGPPRRCPDAD PRAPGLALPGRLLVSNRRTHS RESRAPPHLLGARAGMAPPQ VLA\FGLLLAAATATFAAAQEE CVCENYK\LA VNCFC E*INRQC QICTSVGAQNTVICS KLG CQMF W*MKAEMNGSKLGRRAKPEG GLQ\NNDGLYDPDCDESGLFKA KQCNG\TSTC\WCVNTAGVRRRT HKDTEVTCSEVRVRYWHIELKH KAREKPY\DSKS\LR T*LQKEITT RYTLGSKFLSRVFWYENN VITI\ DLFQNFSSKKLRNDVDIADVAY Y\FEKDVK\GESLFH\SKKMDLT VNGEQLDLDLLIPGQTL\IYNVD EKAP*/DFSMQGLK\AGVIAVIV VVVITSCCWKLLVLVISQKGRE WQKYEKA EIKGDGCRCHRELQ
21989	52357	A	22117	3	257	AKALQWPLGRGGGGT PRGSRP PGPH*SERGAVQPRSLPRQAA* RVPSGPADGQ*DGHG AADPGS RQRCKPWSEADLHSECYSS
21990	52358	A	22118	1467	1748	SEYNCC EIGCPQPSWGPWGRG\ TDVRQQQVGEEVHG/ECGGG SQG*RP G**AGSPAP*PGTWTGT AQQGPA AVL DPLRV*GGGIERH PLHSGVL
21991	52359	B	22119	1	1461	
21992	52360	A	22120	29	417	

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21993	52361	A	22121	616	1671	TATCKPWSMRTTISSSQPKLT NSVKLPSPSAKISVSRIGGFLVS LTSRMKLRTLLICKSKLLPSGGV RGLAGSGVKLQTFTVSVTALK AACLELFTSPGGFMVLLASEVK LQTFAGSDSDCLGQGRRAQRRP GPGVSAVGASGQQRAPESNERP AEEPTAPMPSSAPRGTEPALR RPSSADRPLAPGAGRAPGAMAS PSGSSKATGKPRGRDGRPRREE DDVTPEEKRLRLLEEESQAQPD DGEDAPRPGRKETGTQTGGDG RGAARAALLAVGGIRAPLPSLG VAPGC/PMKPPRRHPGATPR/P GQGGSDAAHGEEGCPCCSSAV ATCLGAGLLP/PGRGASSPSSGC ALPSSSNSRSLFSSGVTSSSSLLG RPSLPRGLPVALELPEGLAMAP GALPAPGASGLS AELGRLSAGS VGPRGA/G*ASGRAWAPPRAAR CSLAPSAG/PRAHRGHAGWPWA LSSP/GPGSSRCPLPRRSAASLL KPAR/AINPPGEVNNRHAALR AVLTVKVCSTPEPARPRTTPE GRSFEHIRRVRFILEVSETKNP PILDTLHLALGGSFTLFVNFCG WDELIVVLIDQGLHVAV
21994	52362	A	22122	892	1931	CTWNNENQRMIEIVWEVFLFLQA NFIVCISAQQNSPKIHEGWWAY KEVVQGWNVFVPSFWGLVNSA WNLCVSGKRQSPVNIETSHMIF DPFLTPLRINTGGRKVSGMTYN TGRHVLRLDKHLVNISSGGPM TYSHRLEEIRLHFGSEDSQGEH LLNGQAFSGEVQLIHYNHELVT NVTEAAKSPNGLVVVSIFIKVS DSSNPFLNRMUNRDFTTRN*H FKNDGIFYRGL*YRGELLFQG TSSFITYDGVDLFPPTPGY/SRT ASWIIIMNKPV*YNPGCKMHSRL LLSQEPAISRSFLMSDNFRPV QPLNNRCIRTNINFSLQKDKDCP NNRAQKLQYRVNWEWLK
21995	52363	A	22123	17	417	
21996	52364	A	22124	63	449	CHPALLGPTGHGAWPRHRAPD TLRASAGGRDP*GRRSAPA*ER QP*PPVYACAGSQYD*TALESSCL RRSVRTSTDTRSLLDKSNYSVF LCFLQLAGRRYFAMWTRPEFFL ARDPRSLSWGLEWRPLSL
21997	52365	B	22125	1	1131	

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21998	52366	A	22126	359	548	
21999	52367	A	22127	755	1031	TRGVLEHLMALGKGTLDKPSGP AP*NHPEVSHAASTQEAAGPP AGRPGHGSGCLALPASSTSLP GLRQDIDLLQLLWREQEVFH DVIQLL
22000	52368	A	22128	1	277	
22001	52369	A	22129	1	933	
22002	52370	A	22130	339	863	PSPVPARPVCPSSAPISMPPCP WREAADLRPEAPGHRDGED VGFLSSGQLSGCLKRKLPTR AALTLPASVANKIK/HFLKNNPE HVGKVGVRTRGCNGLSYTLE YTKTKGDSDEEVIQDGVRFIE K/KAKQLTLL*TEM DYVEDKLSK GVGVITPNIKGTCCGGSFNI
22003	52371	A	22131	16	419	QIQRHPWP/SRSYITNVLGRKVV YLPSTFTYAKYIVQVDGKIGLF RGLSPLMMSNALYTATRCFMK KDLPPDEIEQVSNKDDMTTSLN KVANDTSYEMMMHCVSRMLP HPLHVISMRCMDQIVGREAKYS GVLSSIG
22004	52372	A	22132	3	441	RSYTKFVMGIAVSMLTYPFLLV GDLMAVNNGCLQAGLPPYSPV FKSWIHCWKYLSVQ/GASTGRR RPFLFFATFS*NGFVDASLHAK GQLFRGSS/CFSGAGCHQDHALP WSNLNHLKNTVSTWPPWVRPD HLGTPARRLQPNNNQM
22005	52373	A	22133	1	1232	MAGAGAGAGARGGAAAGVEA RARDPPPAHRAHPRHPRPAAQP SARRMDGSGGLGSGDNAPTT EALFVALGAGVTALSHPLLYV KLLIQVGHEPMPPTLTGNTVLGR KVLTYLPSFTYAKYIGQRDGR GLVPRLSPLRLMSNALSTVTRGS MKKVFPPDEIEQVSNKDDYEDF P*RKLLKETS YEMMMQCVSRM LVAHPLHVISMRCMVQFVGREA KYSGLVSSIGKIFKEEGLGFFV GLIPHLLGDVVFLWGCNLLAHF INAYLVDDSVSDTPGGIGKRPE SRFPFSQALALRSYTKFVMGIA VSMLTYPFLLVGDLMAVNNGC LQAGVPPYSPVFKSWIHCWKY LSVQGOQLFRGSS/CFSGAGCHQD HALPWSNLNHLKNTVSTWPP WVRPDHLGTTARRFPQNNNQ

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22006	52374	A	22134	3	1156	PRHPRPAAQPSARRMDGGSGG LGSGDNAPTTEALFVALGAGV TALSHPLLYYKLLIQVGHEPMP PTLGTNVLGRKVLVLPSTFTYA KYIVQVDGKIGLFRGLSPRLMS NALSTVTRGSMKKVFPDEIEQ VSNKDDMKTSLLKKVVKETSYE MMMQCVRMLAHLHVISM CMVQFVGREAKYSGVLSSIGKI FKEEGLLGFFVGLIPIHLLGDV VFLWG/CNLLAHFANAYLVDD SFSQALAIRSYTKFVMGIAVS MLTYPELLVGDLMAVNCGAA SWGSPYPVPFKSWIHCWKYL SVQQLFRGSS/CFSAGC/HQDH GFALGVN*NHLKNTVSTWPPW VRPDHLGTARRLQPNNNQMC SSPAG/FQFHICHVS/VQMWG
22007	52375	A	22135	2	425	
22008	52376	A	22136	2	430	
22009	52377	A	22137	2	406	
22010	52378	A	22138	1	297	
22011	52379	A	22139	1	111	
22012	52380	A	22140	1	398	
22013	52381	A	22141	1	409	
22014	52382	A	22142	500	1234	GPNCRPSCSAVEGAWPRPQGA GARAALALSQKLELGGVGLVQ VQCPSLAPSTSSILFCLLPHPP PHRCLQENTTCLLGVGVLLQ SPFPLKTDHSSLPALAPTQSQA ALWGFADFGFMFESSPGGNLG WEPDIKLTDEMVMIMGGKMEA TPFKWFMEMCVRGYLAVRPY MDVVVSLVTIMLDTGLPCFRG/ QIKFLKHFSPNMTAREA*NFIM KVIQSCFLSNRSRTYNMIQVYQ NDIPY
22015	52383	A	22143	2	6378	SAGPAGPLQVQKLLCMCPVDF HGIFQLDERRRDAVIALGIFLIES DLQHKDCVGPYLLRLKGLPK VYVVEESTARKGRGALPVAES FSFCLVTLLSDVAYRDPRLDEI LEVLLQVLHVLLGMCQALEIQ DKEYLCKYAIPLIGISRAFGRY SNMEESLLSKLFPKIPPHSLRVL EELEGVRRRSFNDRSILPSNLL TVQCEGTLKRKTSSVSSISQVSP ERGMPPSPSGSAFHYFEASC LPDGTALEPE

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22016	52384	A	22144	3	398	IHKAAAGVPPQPDAGCPGTGEQ QGGQRCGQ*AGP/AQAPC*SRA GTR/PTCFV/LTSLRSWYRVDS NKLMLNPLVAGFFG/CHCGSGQC LRKCSSARDRAPDARPLDLAQ GRCHCHNKACLHASETGVGTT SVL
22017	52385	A	22145	344	498	
22018	52386	A	22146	344	406	FLADQEDPLDPRAGCR*ETTAP R/PSKGPSSTEPLHASTAVPPCQ GELGCSRASPASEK/IDLARGLIS PCNSDVTSPGLGGFMTCAQSLI SRRPGGPIGPPGWLQGPPLG
22019	52387	A	22147	3	2058	LSGSGAPPPGVGAQAAAAAEE EEREVVRVRVKYRLAVSRPSRR GKFRSFVDPQITSLDVLQHILI RAFDSLGS*VGRCWGLLRDRRL GQEVYLSLLSDWDLSTAFATAS KPYLQLRVDIRPSEDSEYSVPPG AISPQDVIGSDVLLAEKRSSLTT AALPFTQSLTQVFSGLTGTOQ VLSWSYGEDVKPFKPLSDAEF HTYLNHEGQLSRPEELRLRIYH GGVEPSLRKVSILSHLLVYPDG LTGRERMDYMKRKSREYEQLK SEWAQRANPEDELFIRSTVLKD VLRTDRAHPYYAGPEDGPHLR ALHDLTTAYVTHPQVSYCQG MSDLASPIAVMDHEGHAFVC FCGIMKRLAANFHPDGRAMAT KFAHLKLLLRHAIDPDFYQYLQ EAGADDLFFCYRWLLELKREF AFDDALRMLLEVTVSSLPDPPE HEVELVGPSPQVADTGFGDHR GWVPVRQRHMLRPAGGGGSTF EDAVDHLATASQGGPGGGGRLL RQASLDGLQQLRDNMGSRDDP LVQLPHPAALISSK*GLSEPLN YDPDLLSSFSHPDPSSSSSPPSTQ EASPTGDMAGVSPMLMQEVGSP KDPGKSLPPVPPMGLPPQEFQ RGNPFMLFLCLAILLEHRDHIM RNLGDYNELAMHFDRLVRKHH LGRVLRARRALFADYQLQSEVW
22020	52388	A	22148	130	387	
22021	52389	A	22149	1	279	

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22022	52390	A	22150	105	499	DMSDTSSESGAGLTRFQAEASEK DSSMMQTLTV/TPEAREAPA TQASSTQLTDTQVLA AENKSL AADTKKQADPQAVTMPATET KKVSHVADTKVNTKAQETAAA PSQAPADEPEPESAAAQSQENQ DTR
22023	52391	A	22151	285	984	TSLSCYFSRTKDSPLGLLMVL LSIIFMNGNRSSEAVIWEVLRKL GLRPGYDWALSALAVRVVLW QERTVLGLHQSGGLVERVGCW TG*RAQGSDLGG*WVNGPELS APSLVSWASMEIPSCAGNLF ILEMPLPTSGKCHSLE*YLFYIF SFSSRLIHHSFLGDDVKKLITDEF VKQKYL DYARVPNSNPPEYEFF WGLRSYYETSKMKVLKFGCKV QKDKPKEWAAQYRE
22024	52392	A	22152	259	578	
22025	52393	A	22153	296	2242	NMSDTSSESGAGLTRFQAEASE KDSSMMQTLTVTQNVVPE TPKASKAL/EVSEDVKVSKASG VSKATEVSKTPEAREAPATQAS SYLLSLTD/TQVLA AENKSLAA *HQGNRMVDPQAC*QLPATET KKVSHVADYGRFNYKGFRRRL LAPS/QAPADEPEPESAAAQFSG RFRVFGPKVKAKKARKVKHLD GEKDGSSDQSQASGTTGGRV SKALMASMARRASRGPIAFWA RRASRTLAA/WARRAFALPLEI TLKPRRAKGLRR/RVAKFQ/SSQ EPEAPPRG/LALLQGRANDLV KYLAKDQTKIPKRSMDMLKDII KEYTDVYPEINERAGYSLEKVF GIQLKEIDKNDHLYILLSTLEPT DAGILGTTKDSPLGLLMVLLS IIFMNGNRS/SEAVIWEVLRKL GLRP/GIHSLLGDVK/KLITDE F/VKQKYLGLCQKVPNSNPPEY EFLGACALY**EPAKMKSPQS FACK/VYQKEGSPRNWGSSVPP REGKGRMEADFECKLR/LTLE AKAKGPRLEAPNGPLGLSGGE MLAGP/CNWDEA/DIGNPWAK ARIPRREQKLKAKAPKRSASA/S TGA/STSTNNAS/ASA/STSGGF /SAAASL/TATLHIWGSSAGLWL ELGCQHQSARSAGC/GVSYK

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22026	52394	A	22154	1	487	EFRQPSFRRSIW/P/YLLTQA/VR TGNPAKFNQVLDDQGEKFAQD GTYTLIIRLRHNVIKTGVRMISL SYSRISLADIAQKLQDSDPEDAE FIVAKAIRDGVIEASINHEKGYV QSKEMIDIYSTREPQLAFHQEG KDSVYSFREWGTGTGMSWLVCFLKRL
22027	52395	A	22155	2	429	
22028	52396	A	22156	1	328	GTRFQADGTYTLIIRLRHNVIKT GV/RSSEGLLEEQKPGQKPS GYPWASEGSVSTLPTPSLLPLPG VRMISLSYSRISLADIAQKLQD SPEDADDFIVAKVGLVQEPQ
22029	52397	A	22157	138	2206	AVTPGAMKQEGSARRRGADK AKPPPGGGGEQPPAPAPQDVE MKEEAAATGGGSTGEADGKTA AAAA*SNFPAKSWDYSHLWKD IKEHRETS*RKAVSGKEPRFVLR ALRMLPSTSRRLNHYVLYKAV/ QGAFFTSNNATRDFFLPLERA HGTQEADLLFRPTGKAAGT/P LLPEVEAYLQLLVFIFMMNSKR YKEAQKISDDLQKISTQNRRA L/DLVAAKCYYYHARVVEFL/D KL/DVVRISLHGRLRTATLRHD ADGQATLLNLLLRNYLHYKL VPTSLRSLVSKSVFP/EEQAQQP NEWGQVTSYLHQGRKAIQLE YSEARRMTNLRKAPQHTAV GFKQTVHKLIVVELLLGEIPDR LQFRQPSLKRSLMPYLLTQAV RTGNLPRFTQVLDDQGEKFAQ DGTYTLIIRLRHNVIKTGVRMIS LSYSRISLADIAQKLQDSDPED AEFIVAKAIR/DGVIEASINHEK AYVQ/SKEMIDIYSTRDPLAL HQRISFCLDIHNMVWSRPMRV PSPKSYKQGSWSLQRNGRERR NKQDLEFPKEMA/EDDDSDPFL KLGWGGVGRKVGTRQLCPP WGYPLPQGTCPFFSPHTAHL AFRGRGWGCWEPATPDLPPGL LPSRVTLVQPGRRVGRQPPRG RVLASSVADRRGRISLCTPFRE WGTRTWDVYGLLCLFLKRL
22030	52398	A	22158	86	348	

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22031	52399	A	22159	3	356	LPLSMDVRAPPVMAAVDQAL KEFRGIDILINCSSSCGLPFCR AAGNFLCPAGALSFNAFKVTM DIDTSGETFNVSRLYEKFFRDH GGVIINITATLGNRGQALQVHA GSAKAAVD
22032	52400	A	22160	3	255	GPWSCHAGA*GPGATQVSEDQ GLREPHGSRDLCSLG*KH*GAPI CAWPMWWDGPPAAHKVPSVS APPVICINTLCYNLASAFS
22033	52401	A	22161	3	360	
22034	52402	A	22162	240	1356	AGNPSGIPGTRVHIRGQRGGFAS TWSGRGAGSTPLQNSPPRQPHR EKEFLRQVLEGGSHGTGFRPSA ARLVNPNHSLVSPDLL*LVSR TAPHFLAARKLAGATGRRCLPL SMDVRAPPVMAAVDQALKEF GRIDILINCESVLEVGGSQAP AAPAVSHSAGAAAGNFLCPAGA LSFNAFKTVMIDTSGTFNVSR VLYEKFFRDHGGVIVNITATLG NRGQALQVHAGSAKAAVDAM TRHLAVEWGPQNIRVNSLAPGP ISGTEGLRRLDASQGMWSWGRG EGAGSWGSRGLSLLPS/GGPQ ASLSTKVTASPLQRLGNKTEIA IISVLVLASPLASYVTGAVLVA DGGAWLTFPNGVKGLPDFASF
22035	52403	B	22163	214	1647	

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22036	52404	A	22164	1765	1910	LSHPHSRTTPNRTPRTRTRIPQRP AVMYSPLCLTQDEFHPFIEALLP HVRAFAFYTWFNLRARKRKYFK KHEKRMSKEEERAVKDELLSE KPEVKQKWASRLAKLRKDIR PEYREDFVLTVTGKKPPCCVLS NPDQKGMRRIDCLRQADKV WRLDLVMVILFKGIP\LESTDGE RLVKSPQCSNPGLCVQPHHIGV SVKELDLYLA/YFVHAGRISSQS ESP/SQPSDADIKQPENGTFGA SRDSFVTSGVF\SVT*A*LRVSQ TPIAAGTGPNFSLSDLESSYY SMSPGAMRRSLPSTSSSTSKRL KSVEDEMDSPGIEEPFYTGQAR SPGKWTVSPSGLSVSVSQGMPS PTTLKKSEKSGFQQPLPFRPPS LGNGFHTAFTDLFIYQGQPSKF HIATPSIL/HFPRHSPFFQQPGPY FSHPAIRYHPQETLKEFVQLVCP DAGQQAGQPNSSQGVHNPF LPTPMLPPPPPPMARPVLPVP DTKPPTTSTEGGAASPTSPITRS /PGRTRPQQPFL/SYGPP*PHFLR AGIHHL
22037	52405	A	22165	63	250	
22038	52406	A	22166	1	817	SRLGHPRKDMDDDTKATLISY MSLSFRHGYCFSEDPVHTELG IQSGRGGRRGDPDPGNALE*LA HLGP/SSHLGP*AQDGLVDAAG RASPLAGTEGAGRFSHLQPI/GP RGPPPE*GAAGERFPGVAG/GPR GAHGLPCPEQLQLQPPPPS*MP KTGSTFVAHFPSPLAQGHSPPG GGAGWCSCGSPDRPPLLGVS HGELLNPNSPA YEVGAG/RPAT GSSGTRAGPPSPSHAPGRTPSV SLCD/RHQCLRASPTGSIGSLPA HWREGLAGPLMD

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22039	52407	A	22167	240	1790	TAKNSYLESCPLHMENSIHQWP RQFPFVRRQGADAACGAGSQ ALVPSHSDTDGVLPGAELG GGPARVP/GAAGGRGAPTS*A GP*LSL*APLCF/SGLSGNGKQL LGAAGRSSSHAQMHELHPAQ* HE*ATDHTGGQGP/G*KQQNG PP/GPDNDLPAPESTPPTWNE LDAIPLAHVPVRQRRPTGPAGP PGQTGPAGPAGPPGSKGDRGQT GEKGAGPPGLLGPAGPRGLPG EMGRGPPGPPGAGNPGSPN SPQALYSLQPPTDKDNG/ITQG WPLPSWTQCW/SGVPGRGP PPGPPGPRGPPGPTGSGQLA GERGTGVPSP/AGGAAAEERGE DPGRASPHPGAHWDPRSPGLP RGRFWPGCCPESQDDEGWH PTRWGPCCPAWARPWTEERG/S RPAAGS/RGVSDISETPGRIY DKSQSAVSVCARSRLRAQLRP GAEQMNDCKGITGTRQDIHAV SFASEHNINQWVSKHLQLSPV TPATQAPLKVRVPQASTLVL
22040	52408	A	22168	104	271	PSCTNPYGGGRCDSSVVPNQCF TKHMQSRLLG*GEKALEGGGG RGVKS LVTKRDF
22041	52409	A	22169	494	1074	KGTTLCQKHWWGGGYLHWG\HF EMMRLTINRSMDPKNMFATWR VPSPFQ/PITRKS VGHM/GGGK\ GAI*HYLTP/VKAGRLV VEMG GRCEFARS AKVSLTQVALRSCP FASKRL*ACGTPREGCEQDQEE RERQQPRTPTWTH*AE*PTAQHG WAYGKVPPEHMTLT PQGEILG ARFYMPKTCVVSVGDILYIGY
22042	52410	A	22170	61	329	NQRS GKKSQPW*STITPPSLIWL SNSSTLSSSKMGQSYSSS*PSY NCSVSRMFGSNMVPAAATASGA SLTCPLLWLSMTHFRKRVGGW A
22043	52411	A	22171	21	444	STAQSISRSDLHYFLALLVYYW AADARFLGRIPLWLIHKELEKS HTEYCLVGSSQYTPLVQVFRSN TLVSVLSTKTI*NQRS GKKSQP W*STITPPSLIWL SNSSTLSSSK MGQSYSSS*PSYNCSSRAKSPTL TVFQS

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22044	52412	A	22172	163	1056	LEKSDHRISWSPGKTA\SPKSMPE RWHRR*WAQILKD\MGITNEYEP RVIN\QMLEFAFRYVTTIL\DD AKIYSSHA\KATVD\ADDVPIG QSRCRAGSSLFTSPPPKRF/L.LL RYLARQKKSNPFCPLIKPY\SGP RLPPDRYCLTAP\NYRLKSFTE KGHSTSAGKELTVP\RLSVGFRL LSRTKVLP\TLGAHPTPQ\TMSVF NLK*GTPHVPSPGQRFSTRCPT S\QSPAVKSFQFFGNLSQFQNV L\NPIH*IGSQKHSYYPLNMMS S\QNTA\NESSNALKRKREDDDD G\DDDDDDYDNL
22045	52413	A	22173	215	344	
22046	52414	A	22174	302	1330	ACEQKRGGEGGNKNRERRKGE KAGRRQGRTRQPCSRMRRTKQ VEKNDDDDQKIEQDGIKPEDKA HKAAATKIQASFRGHITRKKLKG EKKDDVQA\AEAEA\NKKDEAP \VFADGVEKKGEG\TTTARSSPQ PLAPKP\DEPGKAGET\SSEEKM GEG*LLATEQGSPPRLLAS\SEE KAGSAETESATKASTDNSSSK AEDAPAKVEEPKQADVPA/AFG VFPNPLGALLLAATTPAAEDAA AKATAQPPTETGESSQAEEINIE AVDEVTKPKESARQDEGKEEEP EA\DOEHAWNSGEMGFPHPHPP GCLACLSLPSSQLHSEVPSCPAH VCESVLSHPLALFLSVWANI

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22047	52415	A	22175	2	1577	HGFRLLPHPPALRRLLDQRRPK TEDRCGHWDQILDLIIKHLFS MSFIPVAEDSDFPIHNLPGVFS TRGDPRPRIGVAIGDQILDLIIK HLFTGPVLSKHQDVFNQPTLNS FMSLGHAAWKEARVFLQNLL/ SL*SQARLRDDTELKCAFIQA SATMHLPATIGDYTDFYSSRQH ATNVGIMFRDKENALMPNWLH LPVGIYHGRASSVVVSGTPIRRP MGQMKPDDSKPPVYGACKLLD MELEMAFFVGPGRNLGEPISK AHEHIFGMVLMNDWSARDIQK WEYVPLGPFLGEEFWGFLSLP WGGCPWDALMPFAVPPNPKAV PQAPCRYLCHDEPYTFDINLSV NLLKGEGMSQAATICKVQILK YMYWTMLQQAHSPTLSNGCN LRPGGPPGLSGTHQAGPEP/EKN FGSMVELSWKGTKPMDLGNQ QTRKFLLDIGDEVIITAMATRD FKWY/CQGGDGYRIGFGQ/CAGK VLPALLPIMRFSLLFWKQRAQS TTFQPCDWGSSPRAVGLVPPFQ
22048	52416	A	22176	3	623	DSRNSILPRRGALLKVNQELA GYTGGDVFSFIKEDFELQNLKQL IFDSVFSASFVGGMVPIGDKP SSIADRFYLGGPISIRGFSMHSI GPQSEG DYLGGEAYWAGGLHL YTPLPFRPGQGFGELFRTHFFL NAGNLCNLNYGEGPKAHYIVK LAECIRWSYGAGIVLR LGNIAR LVELNYCVPMGVQTGDRICDGV QFGAGIRFL

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22049	52417	A	22177	352	2397	GPMSEGIASQGARRRRGIMGLR GLWASRADGRRGETEPEAKQEI LENKDVSFLLKVLIELLVETFTS IHH*GDDVFKAKNLIIEVGVVST WCAFPVSSEELVNVPM*NIDTC QGTTCGVVSL*FPFCPSEKSCFY GQNNMTVGNNEGSMVCYRLF TFLYWNLELGTFTL*LHSEKTS YGLSFFKPRPGNFERK*EAQQII EYTGIEKLEK*VAYL*KSAEYS VSAFQSFPLGLGENRVAFSLIP KGSYLIQ*VSGNCWHLHCQPLL WGSYHRILAELRVLIESTWPF G*LNCNGTSQAFSCGCTPSRSSA RHGHSVCGQLLVADVPGVKG MLGENNHLFLKY*SMNG*FA/L YFPLDLFSCFL*ESFPLTAPSLEG SRLTLETMYLLCQGGFGLFRT HFFLNAGNLCNLNYGKTCIAIQE TIVVQLFSCLKAQYTKIRLGNI RLELNYCVPMGVQTDGRYVLG IIFHNHPLSSNIFLFWTWFASGD TAGAARLLRLPTDDRAFRDGG GCSHNRQLFPSTPLLSTQSPS WKGCSHAGCMHVCLGAQLPG LGAQLGHGSESQVERLLACGG RWGARRQGCCWHDLPKAPHA GCFLAGEKKVGGDQEPCTKTA AVREGESVGCTAEGGCLGLSG GCQGWLAPGLVELRSAARQE GSRRRRKRRRHLLRVHPQKV
22050	52418	A	22178	1	1017	
22051	52419	A	22179	1	435	
22052	52420	A	22180	1	1353	
22053	52421	A	22181	1	834	
22054	52422	A	22182	2	2675	

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22055	52423	A	22183	72	1339	AMRGANAWAPLCLLLAAATQ LSRQQSPERPVTCTCGGII.TGESG FIGSEGFPGVWPPESKCTWKIT VPEGKVVVLNFRFIDLESNLC RYDFVDVYNGHANGQRIGRFC GTFRPGALVSSGNKMMVQMIS DANTAGNGFAMFSAEPNER GDQYCGGLLDRPSGSFKTPN.W PDRDYPAGVTCVWHIVAPKNQ LIELKFEKFDVERDNYCRYDYV AVFNGGEVNDARRIGKYCGDS PPAPIVSERNELLIQFLSDLSLA DGFHGHYIFRPKKLPTTTEQPVA TTTTFPVTTGLKPTVALCQQKCR RTGTLEGNYCSSDFVLACTVIT TITRDGSLHATVSIINIKENL AIQQAGKNMSARLTVVCKQCP LLRIRGLNYIIMGPSRVKDGAR QNSWPNSFIMMFQTRNQKLLG CP*KISQC
22056	52424	A	22184	49	170	HTVGDGRLLRRP*REFGASFL* CFLEARFGLKNWGHGCWRH
22057	52425	B	22185	597	651	
22058	52426	A	22186	1	791	
22059	52427	A	22187	2	943	TGACAEPRVGLLFRLLKGRCRG GRNMELGSCLYGFREAAEEEG EPEVKKRRLLCVEFASVASCD AVAQCFLAENDWEMERALNS YFEPPEESALERRPETISEPKT YVDLTNEETDSTTSKISSEDIT QQENGSMFSLAITWEYLMGLAD LKQSVQRRARGVCSYLAL*VLS LLFNSNVSVYVYTERMNQLKMV LKKMQEAPESATVIFAGDTNLR DREVSDKVSMLFEDRLLLRLLI *VPFCQYTWDQTMNSNLGITA ACKLRDFDRIFRAAAEEGHIIPR SLDLLGIEKLDGCRFPSDHWGL LCNLDIIL
22060	52428	A	22188	277	534	

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22061	52429	A	22189	29	1305	VGVVLRVECLPCGPAPMSVPA FIDISEEDQAAELRAYLKSKGA\
						EISEENSEGGLHVDLAQIIEACD
						VCLKEDDKDAVESVMNSVGIPY
						SWILAEQDKQEAEDLKALCEKA
						GSKFPRR*TAPELTCFSLNLF
						HGMG*GILPVKIHVSICSLAIKV
						AASCGAIQYHPQLEPGIKFRK
						WDFLNWNLTGKKSTPLKTT
						FMKALVECKKSDAASKGMVE
						LLGSYPENASQARVDAHRIC
						IVRALKDPNAFLFDHLLTLKP
						VKFFGKASLFHCSFLTGFVSA*
						MGHHMSRFYPD*LRTFH*IPLG
						PVTMDPGIWPKMRLLF/TFMGN
						GQ*KNKEISF*PQCQEQPSRLGA
						DADVESHVIDAIVRN*KWVYC
						QNWSRPRRKVVVSHSTHR/TFG
						KVQQWQTTVLTHLNAWKQNL
						NKVKNLSLSLF
22062	52430	A	22190	194	413	
22063	52431	A	22191	3	160	EVKFWVVL.SLG*SFSLPKSSSF
						RCGAGGAVHWSTALFLLGAAS
						ASSYHQRPG
22064	52432	A	22192	268	473	
22065	52433	C	22193	93	500	
22066	52434	A	22194	2	398	FFLRRLSLSPRPDCGLQWRNL
						GSLQAPLPGFTPFSCSLPSSWD
						YRRPPRPANFLYF**RRGFLL
						ARMVSIS*PHDPPASASQAGIT
						GVSHRARPETYNFCSFIISLPV
						EPEARKMTKNSDIGEIW
22067	52435	A	22195	972	2180	PRHCCASASSAPAPSRPASSSSP
						PAACPW*GSLGPAATPATWR
						R
22068	52436	A	22196	2271	3074	RDPSTPTVVRSLGVPLLSRRRFK
						MAPSVAATKLAERNETMVQTC
						WTETQSSSDGSTPRRVRISLAL
						WRPSLFFSMADTSLVLNFRPVS
						SSGVIRPSNKRPSLAITRISRTS
						SPKYMPLTIFSNCFPLRDRPSI
						SLSNSVRMSSNDPSPKAPHIS/G
						IDTHPPLVSFHQINVPQFLHVAS
						IGASADDQADFTVLVVIATGHH
						GAHCVIHHSYDVGIIVPSLFDGF
						VKQFDHICSFHSARFKSLCPGD
						QDGLIYFGLLARKRKRESHR

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22069	52437	A	22197	1956	2747	FAFSPK*HSLRCPCP1*FSSGLLH EVL*LLPLCW*THGWDPGSRE ANKSPKLHAIRC VVWLEENL WLSNSQSLQTVKN*ESHIN*SC RSNLI/HH*FWNQVK*K*LLNIS GNCFFLRWL/DSVAQAGVY WRDLGSLQPPPGFKRFSCLSLP SSWDYWHLPCLAKFCIFSRDG /GFTIWARLVNLS*SCDLPASGS QSAGITGVSHHTW/LQVYFLK EMRSCYFSQVGFQTPGLKQC SHLKLSSWDYRHIMSPHLA/ISG
22070	52438	C	22198	85	228	
22071	52439	A	22199	2	434	
22072	52440	A	22200	1	1356	
22073	52441	A	22201	146	1909	ILHSLEISALLSLMMLTIGDVIK QLIEAHEQGKDIDLNKVKTKTA AKYGLSAQRLVDIIA/SVPPQY RKVLMPKLKAEPIKTA/SGIVV VAVMCKPHRCPHISFTGNICVY CP/GVGPDSDFEYSTQSYTG/EY PTSMRS/IFRARYDPFLQTKDRI EQ*RQLGHSVDKVEFIVMGGT MALPEEYRDYFIRNLHDALSGH TSNNIYEAVKYSERSLTKCIGITI ETRPDYCMKRHLSDMLTYGCT RLEIGVQSVYEDVARDTNRGH TVKAVCESFHAKDSGFKVVA HMMPDLPNVGLERDIEQ/TEFF ENPAF/RPDLGLKIYPTLVIRGTG LYELWKS/GRYKSYFS**PGLN WVARFLALVPPWTRVYRVQRD IPMPLVSSGVEHGNLRELALAR NEDLRIQCRDVRTREVGIQEI HKVRPYQVELVRRDYVANGG WETFLSYEDPDQDILIGLLR/LR KCSEETFRFELGGVSVIRELH VYGSVVPVSSRDPTKFQHQFGG MLL/MEEAERIS*RRNMGLGKI AVISGVGTR/NYY/GKIGYRLPR PRTMVKMLEIMGHTQSHSFC LPWHEHRRIRISLNTQQRGL
22074	52442	A	22202	1	457	
22075	52443	A	22203	2	297	CVMYRDYPLELFMAQCY/GNIS DLGKGRQMPVHYG/CKERHFV TISSPLATQ/IPQAARGPGYGIM/ SIRVDGNDVFVYNATK/EARR RAVAENQPFLEARPT

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22076	52444	A	22204	3	1446	DWLLAKMAEAIAAARIVWRLN RGLSHAALLLRQLGGSGD*AR SHPPRQQQCSALDDKPQFPG ASAGVIDKLEFIQ/PNVISGPIYR VMDPQGQIHQFQARDPHLAEG ERWLKLYKSMTLL*HPWDRIL **VFSGQGRILLT*TNVWLRR GTHVGSARRLGQTRTLVFGQY REAGVLMYRDYPLELFMAQC YGNISDLGGRQMPVNYGCKE RHFVTISSPLATQDPSGRWGAA YAATGGANANRVR/VICYFRAR GAAS*GGDAHA/GFNFRCHNL SCPIIFFCRNNGYAISTPTSEQYR GDGIAARGPGYGIMSIRVDGN DVFAVYNATKEARRRAVAENQ PFSHAHDRSRVQAPSPSDAS*T YRSVDEVNYYWENKGPPLPGF GHYLFSGQGWDEEQQKAWR KQSRRKDPGPVQPS/VMEAFEQ AERK\PKPNP/NLL/FSDVYQNM PAPVRQPPES/LARHFKTYGNH YPWDHFDK
22077	52445	A	22205	2	292	

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22078	52446	A	22206	1	1894	QSLADLLQSQPSITLTSQIWSP A*GFWSWGNSVTTPSK\PATP TRTIAATPIQTLPQSQTAPKRID TPSLEEPSDLEELEQFAKTFKQR RIILGFTQGDAGLAMVKLYGN DFSPTTIFRFEALNLSFKNMCKL KPLLEKWLNDALNLSDDSLSS PSALNSPGIEGLSRRRKKRTSIE TNIRVALEKSFLNQKPTSEEIT MIADQLNMEKEVIRVWFCNRR QKEKRINPPSSGGTSSSPIAIFP SPTSLVATTPLSVTSSAATTLTV SPVLPLTSAAVTNLSVTASTSEA SSASESTTTQTSTPLSSLGTSTQ VMVTASGLQTAAAAALQGAA QLPANASLAAMAAAAGLNPSL MAPSQFAAGGALLSLNPGTSLG ALSPALMSNSTLATIQALASGG SLPITSLDATGNLVFANAGGAP NIVTAPLFLNPQNLSLLTSNPPG GFTIEISNNNSTMVMTMGMRIQIG TQAIERAPSYYIEIFGRMTQNLNS RSRWDFPFRTREELQADKKLN LFTVRKFQNIHRLFCKENKNT FQQLLLEQDSSCGTGFCSMIT YPVMLLSSEQPVQSLSVRQCVI LLDAAVISGGMGAVCLLLTH LCPLCYAGLLSEITDPESFVKDL LYSVP

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22079	52447	A	22207	1	2417	MRVRTSSLPSTMLRVQNYARA KAGPEYAFVDSTECSPQWMVS PLKRGITQTNGLDFQKQPVVVG GAISTAQAQAFGLGHLHQVQLA GTSLQAAAQSLNVQSKSNEESG DSQQSPSPSPSVQAAIPQTQ LMLAGGQITGLTLTPAQQLLL QQAQAQAQLLAAAVQQHSAS QQHSAAGATISASAAATPMTQIP LSQPIQIAQDLQQLQQLQQNL NLQQFVLVHPTTNLQPA/QFIIS QTPQGQQLLQA/QNLLTQLPR QSQANLLQSQPR/TLTSQPATP TCTIAATPIQTLPSQSSTPKRIDT PSLEEPSDLEELQFAKTFKQR RIKLGFTQGDVGLAMGKLYGN DFSQTTISRFEALNLSFKNMCK LKPLLEKWLNDALNLSDDSL SPSALNSPGIEGLSRRRKKRTSI EAINIRVALEKSFLEN/QKPTSEE ITMIADQLNMEKGVIRV/WFCN RRQKEKRNPPSSGG/TSSSPIKA IFPSPSLVATTPSPVTSSATTL TVSPVLPLTSAAVTNLSVTGTS DTTSNNTATVISTAPPASSAVTS PSLSPSPSASASTSEASSASEVTS TTQ/TTSTPLSPLGTSQVMVTA SGLQTA/AQLLPFKGAAQLPAN/ ASLA/VAAAAAGLNPSLMAPS QFAAGGALLSLNPGTSLGALSP ALMSK/STLA/TIQTLASGGSL K*TSLECKLGT/LVCPMREEPPD
22080	52448	A	22208	3	114	
22081	52449	A	22209	1	505	NLGVDDLPGYQDPYSGRTLTK GEVGCFLSHYSIWEVVARGLA RVLVFEDDVRFESNFRGRLERL MEDVEAEKLSWYSYWTLAYA LRLAGARKLLASQPLRRMLPV DEFPLPMFDQHPNEQYKAHFWP RDLVAFSAQPLLAAPTHYAGD AEWLSDTETSSPWDDDSGR
22082	52450	A	22210	3	626	RAARAAPLLHLLLLGPWLEA AGVAESPLPAEVLAILARNAEH SLPHYLGALERLDYPRARMAL WCATDHNVDNTTEMLQEWLA AEGDDYAAVVWRPEGEPRFYP DEEGPKHWTKERHQFLMELKQ EALTFARNWGADY/LGATLGL WQDHSVNSLGGCSPGRAGACD VPSSKFADTDNLTNNQTLRL MGQGLPVVAPMLDSQTNV

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22083	52451	A	22211	1	2004	MRAARAAPLLQLLLLGPWLE AAGVAESPLPAVVLAILARNAE HSLPHYLGALERLDYPRARMA LCLQGPAPQPQWDLWLAGFEEE QTGTSEVHWGPTWQGSTTLEA SGHRCATDIHNVNTTEMLQE WLAAGVDDYAAA VWRPEGEP RFYPDEEGPKHWTKERHQLFM ELKQEALTFARNWGADYILFA DTDNILTNNQTLRLLMGQGLPE VAPMLDSQTYYSNFWCGITPQ GYRRTAEYFPTKNRQRRCGL RVPMVHSTFLASLRAEGADQL AFYPPHPNTWPFDDIIVFAYA CQAAGVSVHVCEHRYGYMN VPVKSHQGLEDERVNFHILILE ALVDGPRMQASAHVTRPSIKRP SKIGFDEVFVISLG/RRPDRRER MLASLWEMEISGRVVDVVG WMLQQQVPFRNLRP*DLLPGL/ YKDPYFGPHS*PRAEVGLSSD HYSIWEEVVSQGAWPRIVLVV *RNDVAPLRTNFGGGLERL/M EIDVEGKRNLSEWKPPFRILPLG RKQVEPLRRETAVEGLPGVLV VAG*LPNWTLA/YALRLAGGP ASLLALQPFAPHCCPVERISLPI HCFDQHPNEASTKAHFWRPD/ LVAFSAQPLLAAPTHYAGDAE WILLRHRHSPWDDDSGRLLISW SGSQKTLRSRPLDLTGSSGHSL
22084	52452	A	22212	1	468	ELSHNAKAKVMVASHNEDT/V LFALRRMEELGLHPADHQVYF GQLLGMDQISFPLGQAGYPIL TQIHLFSPHTCRAAGGEVRCPL ALPRVWALRCGNLIPAWDSH WKLLGTLLLELCAQGPHLCDPH VLGPRGLSTFCQGQPTQPEPLG EQWPGWG
22085	52453	A	22213	1	1893	

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22086	52454	A	22214	390	2005	INRDVETACTYILRNTEDVMLE FVMREWKKSRKLLGQRLFNKL MKMTFYGHFVAGEDQESIQL LRHYRAFGVSAILDYGVEEDLS PEEAHEKEMESCSAAERDGS TNKRDKQYQAHRAFGDRRNG VISARTYFYANEAKCDSHMETF LRCIEASGRVSDDGFIKLTAL GRPQFLQFSEVLAKWRCFFHQ MAVEQQQAGLAAMDTKLEVA VLQESVAKLGIASRAEIEDWFT AETLGVSGTMDLLDWSLSIDSR TKLSKH/V/*VPNAQTGQLEPLL SRFTEEEELQMTMLQRMMDVL AKKATEMGVRLMVDAAEQTYF QPAISRLTLEMQRKFNVEKPLIF NTYQCYLKDAHDNVTLDVDL SPREGWCFGAKPVRGAYLAQE RACAAEIGYEDPINPMYEATNT MYHRCLDYVLEELKHNAKAK VMVASHNEDTVRFALRRMEEL GLHPADHQVYFQQLGMCDQI SFPLGQAGYPVYKYVPYGPVM EVLPYLS'RRALENSSLMKGTH (RERQLLWLELLRRLRTGNLFH
22087	52455	A	22215	3	303	
22088	52456	A	22216	798	2250	VPRAPOGML*GPRKDAGTPER RAGPPGGRTADGGGCGALAG SGS/DDPRLCIWTLVTDQILLP TGPGRPRGSVAAAATGPGVGA LRAPARAQPRGAVDGRPLLQ VLPHRRLEVSLGKSPKECVLW/ RHLLSESEKRPVEEAERLRVQ HKKDHPDYKYQPRRRKSAKAG HSDSDSGAELGPHPGGGA VYK AEAGLDGHHHGDHTGQTHGP PTPLTPKTELQAGAKPELKL EGRRPVDSGRQNIDFSNVDISEL SSEVMGTMDAFDVHEFDQYLP LGGPAPPEPGQAYGGAYFHAG ASPVWAHKSAPASASPTETGP PRPHIKTEQPSGHHYGDQPRGSP DYGSCSGQSSATPAAPAGPFAG SQGDYQDLQASSYYGAYPGYA PGLYQYPCFHSRRPYASPLLN GLALPPAHSPTSHWDQPRRNGS TAQGPKEGVAGALQGAVRSKA GLGAEKPLHSRPHSLDNGCTGC PGSGVSVRRLG

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22089	52457	A	22217	299	1631	LLEPHCGGKCFKRHWFPSCSEA SC\PSAAPQRW*HTG/SPEVPAA PGAQGREPSM/RDGEAVRGGG CMEAGPMGLQCVDKKGQGVH N/RGEARVFLQSQVGAILPRPW PNPAPSEP/VQSPASSTGP*VFP SRPGQQAAGPA/RRHPGAEPGQ RGDVQQLPRPQTSHPGQDA ALSSAPHPWRQL/MASPLQEA PLHPFCGHRSPCPVPWQLSPTD PIQSRPPARGWAPANQGRPSHP RCRGGGAFCGHG/STYQPLT FRLASMVLSIHPKPPKETLFRFP NMVVAAEPGPVAMSQRPRGRC TRFSHTDKAPLDTCTDMNAYT CARRHSSTYSDHITLQGAFACT HTWAQSTCQPPPTPAAKCLDR GQSSGMLHAGCVGWGGGTHV RVDLSSQLNRRVRPHLCMLRC WSSCHRASVSCTHPSLHTTGPV LISARTGADHTWYTAGTY
22090	52458	A	22218	383	762	RHQGNQKRKELSLK/CQKSRQE SPRAENPKWREGKKETSESSV QKAGRAAAQAAGAAASRVPG LSGSNLAPCNKGRLSAREDVSN SKLKILSSGRKHTHEVIMLKAW GLGRQSLRCRLFDLIPSHKV
22091	52459	A	22219	325	945	QPSPLAPKADLSAREGRFQKLV RCRLQYQQQR/RKFAAAFLA FHFSLGSGGILAEAG/KKEKPE KK\VKKSDCGRIGSWVCVAPP SGDCGLGHHGRATRT*\AECKQ \TMKTQRCKIPCNWEGRQFGRG SAKLPSFQAWGECDLDTALKT KTGSLKRALHKSNAQKTVTIS/ KSPCGKLTQPNLQAES/KKKK KEGKKPEGRIRD

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22092	52460	A	22220	1	1908	MKYIQDFQREKQEERNLARFR EDHPDLIQNAKKSDEPEKPKTPQ QLWYTHEKKVYLKVRPDATTK EVKDSLKGQWSQLSDKKRLK WIHKALEQRKEYEIMRDYIQK HPELNISEEGITKSTLTKAERQL KDKFDGRPTKPPPNYSLYCAE LMANMKDVPSTERMVLCSQQ WKLLSQKEKDAYHKKCDQKK KDYEVELLRFLESLPEEEQQRV LGEEKMLNINKKQATSPASKKP AQEGGKGSEKPKRPVSAMFIF SEEKRRQLQEERPELSESELTRL LARMWNDLSEKKKAKYKARE AALKAQSERKPGGEREERGLP ESPKRAEIIWQSVIGDYLARF KNDRVKALKAMEMTWNNME KKEKLMWIKAAEDQKRYERE LSEMRAPPAATNSKKMKFQG EPKKPPMNGYQKFSQELLSNGE LNHLPLKERMVEIGSRWQRISQ SQKEHYKKLAEEQQQYKVHL DLVWKSLSQDRAAYKEYISN KRKSMTKLRGPNPKSSRTTLQS KSESEEDDEDEDEDEDEDEEEE DDENGDSSEDDGDSSESSEDE SEGD/EGGADRAQWEGRGVL PGGPPGDSTSLTPQNEEDED EDDEDEDEDEDENESEGSSESS SSSGDSSDSN
22093	52461	A	22221	129	2365	
22094	52462	A	22222	5	2730	PSLRFASIGFVWRLAAPASAAA ELRLDCSARRAPRCRPPALPSTR SAEAGVLCFRREEQQAATA AAAAAAATAAAAAAPPPRP EEELPPREGAAVPGRAGEGA ATQSQGSRWSGKPGGRAAPA RPRRWLDSWRMNGEADCPDL EMAAPKGQDRWSQEDMLTLE CMKNNLPSNDSSKFKTTESHM DWEKVAFKDFSGDMCKLKWV EISNEVRKFRTLTELILDAQ*HF KNPYKG/KKLLKKHPDFK
22095	52463	A	22223	1	446	RPSPTSSM/PGLWGYSRPCSSG VPASALQA*SPAFSPASQRPPTT SWWEVP*EEGRA/PVWEGRIRA VGPAPAS*PSDLPAWSCRSWRE TRGSPAEDAMLLRAVEPLEGC QRPLDSEPP/SPARTSAPAASA SPPAPGGPPCLARPLPR

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22096	52464	A	22224	582	1175	THTHVPAGTHPHTQTTSLSHLI GRALTVPESPKCPCLLPSAC*PR PGRAQAPAGPAWSKKEASNPGS E/PPQHSL*RRMAPPE/PVPARA VHTCRLSSAPPGARLPLDPER RAPQSPRSPPSAQPPPPPPPPPP PPPGRRGSPSQSWRPSPPPPRTR SRSPRRSRVRGPRAPALAAPPP GARPGCAAAACGSPGTGS
22097	52465	A	22225	609	5241	GPQTTWCGRPTMCQHCQPAVS SWKQPSHDPCCRGGENRRQPG TPARATQGRLLRRRPEGARVPSA RRGRPRARWRDKERNNTCVA ML*QVTNSTANAPQNNEPVD IMAEKVEAPASVDWQKRLT LETQLFRFRLQASKIRELLADK GHGTYISPFSLAKQMQELEQRL LEAEQRAENAETQVGVMEKV KLSNLKNVDSEGLHRKYQELL KAIGKDELISQLEAQLEKQKQ MRAEEAKTVQEKAQKKEW
22098	52466	A	22226	2	205	
22099	52467	A	22227	1	6186	
22100	52468	A	22228	96	1584	DLGSGITASPPRPEPEHPVFPPA PHTPSKMGKEKTHINIVVIGHV VDSGKSTTTGHLIYKCGIDKRT IEKFEKEAAEMGKGSFKYAWV LDLKLKAEREPGTTIDISLWKFE TTKYITIIDAPGHRDFIKNMIT GTSQADCAVLIVAAGVGEFEA GSKNQGTRHALLAYTLGVK QLIVGVNKMDSSTEPAYSEKRY DEIVKESVAYIKKIGYNPATVPF VPISGWHGANMLEPSPNMPWF KGWKVERKEGNASGVSLLEA LDTLPPTRTDKPLRLPLQD/V YKAGGIGTVPVGRVETGILRPG MVVTFAPVNITTEVKSVEMHH EALSEALPGDNVGFNVKNVSV KDIRRGNVCGDSKSDPPQEEAQ FTSQVHILNHPGQISAGYSPVIDC HTAHIACKFAELKEKIDRRSTK KLEDNPKSLKSGDAAIVEMVPG KPMCVESFSQ*PVIG/RTPVRD MRQTAA/VGVKINQKKSVA GKVTKSAQKAQKAGK
22101	52469	A	22229	1	1023	
22102	52470	A	22230	1	396	
22103	52471	A	22231	2	1259	
22104	52472	A	22232	1	2514	

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22105	52473	A	22233	3	2027	EESDCLTEYEEDAGPDCSRDEG GSPEGASPSASTASEMDVSLHFVL WGCLHVVQRMIDKAEDVCLFV AQPGELVGQLAVLTGEPLIFTL RAQRDCTFLRISKSDFYEDSP KLECGWIISED/PNPWTSPTSTGL NPLFLELCRHMVFQRLQGQDY VFRPGQPDASIYVVQDGLLELC LPGPDGKECVVKEVPGDSVN SLLSILDVITGHQHPQRTVSARA ARDSTVLRPLPVEAFSAVFTKSA RTITGCVWRYVRASASYCPYLP PLCDPKDGHLLVDGCYVNNVP GSLWRYVRASMT/RRATCPRCA TPRTGTYSWMAATSTICQASGR PHHPHTQAPPAPHTRTRRTSPA AWVPKRSSPLTWGARMRRTSA PTGTACPAGGCCGSG*IPGLTR* RFQTWLKSSPAWPTCPVCGS*R LSSAPTASTCARPSTASRPWTL GSSTRSILRTTRRMSTAVTTTAT PAPIITPST*GTNGTGCAQIRPA EPSPGARTSWNPSLSATFAPEEF VASP*LDVPICRMGQCCSLPGG ATLP*GPCGPQCMPGNVVPPER TAARYRQTTAYQTPACPTPPRG QRPT/CVPTVSSLQAGLQGGPRS DFDMAAYERGRISVSLQEEASGG SLAAPAREPREQPAGACEYSYC EDESATGGCPFGPYQGRQTSSIF EAAKQELAKLMRIE

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22106	52474	A	22234	281	1832	NDSGLPDRPSSWNQPM EAPLQ TGMVLGVMIGAGVAVVVTA V LILLVRRRLVPKTPADGPRY RFRKRDKVLFFYGRKIMRKVSQS TSSLVDTSVSATSRRPMRKKLK MLNIAKKILRIQKETPTLQRKEP PPAVLEADLTEGDLANSHLPSE VLYMLKNVRVLGHFEKPLFLE LCRHMVFQRLG/QGDYVFRPG QPDASIYVVQDGLLELCLPGPD GKECVVKEVVPGDVNSLLSIL DVITGHQHPQRTVSARAARDST VLRPLVEAFSAVFTKYPESLVR VVQGPSPGAPYAPPSYGHAP RALQIIMVRLQRVTFALHNYL GLTNELFSHEIQPLRFPSPGLPT RTSPVRGSKRMVSTSATDEPRE TPGRPPDPTGAPLPPTGLGGG PRSDFDMAYERGRISVSLQEEA SGGSLAAPAREPREQAGACEY SYCEDESATGGCPFGPYQGRQT SSIFEAAKQELAKLMRIEDPSLL NSRVLLHAKAGTIARQGDQ MEEVKVPAFAVIVD
22107	52475	A	22235	50	4287	PGRKSPGAEDRALWGPACRL TDSGLPDRPSSWNQPM EAPLQT GMVLGVMIGAGVAVVVTA VLI LLVRRRLVPKTPADGPRYRF RKRDKVLFFYGRKIMRKVSQSTS SLVDTSVSATSRRPMRKKLKM LNIKKILRIQKETPTLQRKEPP PAVLEADLTEGDLANSHLPSEV LYMLKNVRVLGHFEKPLFLELC RHMVFQRLGQGDYVFRPGQPD A/SIYVVQDGLLELCLPGPDGKE CVVKEVVPGD/VSNS
22108	52476	A	22236	283	403	TCLSLVSGCGHCEKMNSEENW *IPIQWASSNPGRRRKNIR
22109	52477	A	22237	33	222	NGPMICFVKQLEIPQYGRNNV PTTTPRSNLAKELEKYSKTSFEY TINDNHTYGGGLGCMRPLV
22110	52478	B	22238	1	1860	
22111	52479	A	22239	303	672	GITACVFFSMAEGRTRAERSCD SK*AIGAPAE*GGASPGKSP WQAGAGYPLGACGHKARLWIP WRRSWSGEKGARGCRGTGKK LGHQGWWRWETPGRPGGAGPA GFPDPVVMGCEKEASRV
22112	52480	A	22240	1	1377	

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22113	52481	A	22241	1	2232	MQDTEKDDNNNDEYDNYDEL VAKSLNLGKIAEDAAYRARTE SEMNSNTSNLEDDSDKNENLG RKSELSLDDSDVVRETVDLSK LLAQGHGVVLSNMNDRNYA DSMSQQDSRNMNYVMLGKPM NNGLEKMMVEESDEEVCSSL ECLRNQCFDLARKLSETPQER NPQQNMNIRQHVREEDFPGR PDRNYSMDMLNLMRLLEEQLSPRS RVFASCAKEDGCHERDDDTTS VNSDRSEEVFDMTKGNLTLE KAIALETERAKAMREKMAMEA GRRDNMRSYEDQSPRLPGED RKPSSSDSHVKKPPYKGDPSRT EKKESKCTPGCDGTGHVTGL YPHHRSLSGCPHKDRVPPEILA MHESVLKCTPGCTGRGHVNS NRNSHRRDIQVFNLQKQEMIDR LESLSGCPAAAAEKLAKAQEKH QSCDVSKSSQASDRVLRPMCFV KQLEIPQYGYRNNVPTTTPRSN LAKELEKYSKTSFEYNSYDNHT YGKRAIPKVVQTRDISPKGYDD ANGYCKDPSPSSSTSSYAPSSS SNLSCGGSSASSTCSKSSFDYT HDMEA AHMAATAILNLSTRCR EMPQNLSTKPDLCATRNPD EVDENGTLDSL MNKQRPDSC CPILTPLEPMSPQQAQVMNNRC FQLGEGDCWDL PVDYTKMKPR VRIDEDESKDITPEDLPFQEALE
22114	52482	A	22242	727	4372	LWACVLPGVTLPPFLGKETSCK MEVDTEEKRRHRTSKGVRVPV EPAIQELFSCPTPGCDGSGHVSG KYARHRSVYGCPLAKKRKTQD KQPQEPAPKRKPFVAKADSSV DECDDSDGTEDMDEKEEDEGE EYSEDNDEPGDEDEDEEGDRE EEEEIEEEDDEDGEDVEDE EEEEEEEEEEEEENEDHQMN CHNTRIMQDTDLDDNNNDEY DNYDELVAKSLNLGKIAEDA AYRARTESEMNSNTNS

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22115	52483	A	22243	34	1558	PASEEFNSLHGRTPRDLERN QQSTTEERRRHDCVQQAASEHN EGKWDFAFSAQSQPKP*KPFDV PC*DSRPACP*EHTAGTSGSTSS ETCFQSSSEWPYGELGAYNIPT GPKSTLSSLVTGVSNSSSLS*LP SPKNTITNWFHTRDHSSYSEIHS KACANP*APSQPSR*ASWIATG SFRRAGLAT*PCCTGSKLLPAW VLANHRWDRTRDGIQKQGNSE *PSSPGTAFEGNSSPAPAASIT SMLSPTSFTPTSIRKMYESKEKS KEEPASGKAALGDSKEDTQKA SEENLLSSSSVPSADRDYFSHY KFQTVRHYRGSSCS/PHLSQGQP FTPKEQDYSDLKGNWGRKNTH FGHSPVSLQHFFRPVPPSSPLSP MVPNG*GLLTKLHPGFGTEDA GPGSTSTASSKFAFNWCASSWD GLESFTGNIWPHPGSALLPFN*S LVHPLLNPRGNTSASNGGATA ANSAQSCILQALVSHGSSCSAF QDNPSETCPAGQACPHALP
22116	52484	A	22244	1502	2657	EGKVPLAFIVLTSLLNAVMSPSF FSCRLLVTKLVSSRCSAMKGV EFFTCWSTFKPFRPASTSSTEST TPECELSLSFSLFAERLERRGFK STLAFCSISKISTLFSAWSSNGIG AK*FPEFCPGDRMACSRPASLSS SSCG/S*PKTAGSAS*SARVREPP TEPTGRD*PFSQ/TSSIIEAKHGT LSRLKNSLKSKSPGDCSGKTAS LGTS*SAAGSCARMTSTSSSAT PPLHSTIPSTFEAVRRLVFLPL* SSSSILSSKPVSSMVSD*LVGPA ENHSGSSSV*ESFLLRSPKTRLL SPNSLLKRLSLKSLRSLSLKSR RSLSLSGDPSQQRSGRLSSHQ SYVHQADEAHYLSLMDFLSA GS*QRLSRGSPLOQSSVSEG
22117	52485	A	22245	324	391	
22118	52486	A	22246	42	274	

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22119	52487	A	22247	1	835	MCAGNLCSSWEERWAVDEKEA TDKKPHVGGFGGAPAPAAPA AAMSGRSVRAVTRSRF*DDIKK VMAAIEKVRKWEKKWVTVD TSLRIFKWWPVTDSKEKEKSKS NSSAAREPNGPPSDASANSLL LEFQDENSINQSVSDVYQLKV DSSTNSSPKPPKQSESLSPAHTS DFRTDIDSPPTLGGQDGRSPP LPSSSEVADEPPTLTGRTSFHL ETQVVVEEEDSGAPPLKRFCV DQPTVPQTGSEKLAPSRPSAFW ALPLFIWFVWPRRVCWG
22120	52488	A	22248	3	244	
22121	52489	B	22249	271	711	
22122	52490	B	22250	73	200	
22123	52491	A	22251	885	975	GSTWWPAD*AQL*LHLPTRCM AECWEIPA
22124	52492	A	22252	102	909	PGGRHGRQNDFAAPGGRLEARI HGTVSAPLYHRVLCRLGSRPA SAAGPAARGGDLAPGEHSFCE DGNVAVVESVDRSAINRAMQN PRKSTASVCWTFTASDLPAQGV VPTSSSTRTLREDPFPPSAEKWL RAVLHHFVNEKLQQIFIELTLKP SRRSMSGRHPLDSNPVLQQQGR CDLIENKLSPPGIMSVLDDVCP CTPRAGEQTRHCCRTAGGCGD PRAFQQLERRFVIHHYAGKTHR PLPGLTPTGNSTNARNIVMDTQ QRTGNN
22125	52493	A	22253	48	112	
22126	52494	A	22254	1243	1615	YSPSSWFSNLYQPSTGALSSSET PKDMAPMKSLREVRSQSHTSTL SRRSTSPGFRNLTKVSFHTGFSV AFTVRVFCVFRFRGSGMSFST* GSEPLGSGIRLIRASPTVTWISS AVGARISSC

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22127	52495	A	22255	468	1431	SVSTTRSFSDSSAKTAAAMPVT VTRTTHHNHPDVFIGA WGP* WGPLWALTQPLGLLRLLQLV STCVAFSLVASVGAWTGSMGN WSMFTWCFCFSVTLILIVELCG APGPPPPWSWR\NFPATFACYA ALFCLSAIIYPTTYVQFLSHGR\ SRDHAIAATFFSCIAACG\YATE VAWTRARPGEITGYMATVPGL LKVLETFFVACIIFAFISDPNLYQ HQPALWCVAVY AICFILAAIA ILLNLGECTNVLPIPFPSFLSALA VCLSSMPPLFSGPSTSSMRSM AASLGAREM*AAAAGMPTTW VPGTADWL RPS
22128	52496	A	22256	98	414	CTRVSVAEKTSVCLFGLYWESL SISSSESSAKWPFFSTIRASSTT RHLSCRRFLK**CFLINSHSRP GVATTISGRFSLCCFCVDIPPT KIAVLIPVNLAT
22129	52497	A	22257	2	224	
22130	52498	A	22258	2	115	
22131	52499	A	22259	2	118	
22132	52500	A	22260	472	648	GPGRSFVTWWNW*RRMAQC PPAEGVQRPECLGPHRAVPAP AHVGLHQEPSRLLPALH
22133	52501	A	22261	540	1893	GRCATPRPRWRGHQCDPPPGD VCVAWREMLRNKKRRR\DLG NLIKRFLTAPNSLPD/AVVLTTE EAVIFWCNVLAQQIFGL/PLEM MNEQPLEGAVREKALHTMREQ TQRMEGLVKQL/LTSLKIEAAPT HLLNEKVDVPM/MLRVVVEREA QTLVYNVNHTEPGTHITVRW QRVPHGAEFVVEE*SEGWPVPV PKPHRAVVGANAHISFCPPQEL SKRFTAIRKTKGDGNCFYRALG YSYLESLLPDAFQPLLPQAWV SPGESQGAGIRDPLWPVPVPKP HRAVVGANAHISFCPPQELSKR FTAIRKTKGDGNCFYRALGYSY LESLLPDAFQPLLPQAWVSPG ESQGAGTRDPLWLWLFRLWLL RLCLLLLLLIGETAQSRLALTW GRHKQGRRLARLSGILGLALRK QWLGGQVAQLLQNLHLLLLR WAGLGVIIVFQVSNQPAWERTG
22134	52502	A	22262	1	1772	
22135	52503	A	22263	107	294	LHLLSFGYLTHQLCLHLKWD HTLHSHSHHTIAR*AGCSEATWS PPRRLRAPRSRALCSCFR

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22136	52504	A	22264	1	474	
22137	52505	A	22265	1	148	VKYHEFTCSFKKQITVPEDARL LK*DVRGRPSRLFLADPPPHHT VNREY
22138	52506	A	22266	509	2755	YQSQSFEDEMNQVTDWVDP SFDFFLECSGVSTTIVATSLGVNN SSHRRKNGPSTLAESSRFPARKVR GNLSSLEQIYGLENSKEYLSENE PWVDKYKPIETQHLEAVHKKKI EVEVETWLKAQVLGRQPKQGG SILLITGPPGCGKTTTLKILSKEH GIQVQEWINPVLPDFQKDDFKG MFNTSSSFHMFYQSQIAVFKE FLLRATKYNKLQMLGDDLRTD KKIILVEDLPNQFYRDSHTLHE VLRYVYRIGRCPLFIISDSL.SGD NNQRLLVPKIEQEEWSISNIRFN PWAPTMMKFLNRIVTIEANKN GGKITVPDKTSLELLCQCGSGDI RSAINSLQFSSSKGNNLRPRKK GMSLKSDAVLSKSKRRKPKDR VFENQEVQAIGGKDVSLFLFRA LGKILYCKRASLTEDSPRLPSH LSEYERDTLLVEPEEVVEMSHM PGDLFNL.YLHQNYIDFFMEIDDI VRASEFLSFADILSGDWNTRSL LREYSTSIATRGVMHNSKARGY AHCQGGGSSFRPLHKPQWFLIN KKYRENCALAAKALFPDFCLPAL CRQTQLLPYALLTIPMRKSSFR FSFYSKDIGEGLPSGRRTLWGRI GKWEGLDRGTWDD*TPDSG DEAQLNG/GHSAEESLGEPTQA TVPETWSLPLSQNSASELPASQP QPFSAQGDMEENIIMEDYESDG DIEASLIRLLHSHFCHFHSGT
22139	52507	A	22267	2	161	
22140	52508	A	22268	1	599	VTRLFQPGYGTLPQQRLLMPK KNRVAIYEELLFK\EGVMVPPK\ DVPIPKHPELA\DRNVPNLHVM KPMQ\SLKS\RGYVK\EQFAW\R HFYWYLT\K*GYQGVSISSRDYL VHLP\AIVPCHPYGRSPSRRLAR PSG*KVLE\G*ANLRGLHKNGEA DKRLPTRRECLCHPGA\DKKAE AG/ALGSSNPNPQFRGGFGRGR GQPPQ

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22141	52509	A	22269	1	345	KHPELADKNVPNLHVMKAMQ SLKSRGYVKEDYLHLPPEIVPA TLRRSRPETG/RPRPKGLEGERP ARLTRGEADRDYRRSAVPPG ADKKAEEAGAGSATEFQFRGGF GRGRGQPPQ
22142	52510	A	22270	2	161	
22143	52511	A	22271	2	641	RRPQHRACSFFFSPGTGPCSRRR CLMPKKNRIAIYEILLFKEGIVM VAKKDVHMPKHPLELADKNG APTFFHVMKGHAGLSKSPRATV KGTSAWGDIFYWYLTN*GY QGVSISSRDYLSGPCREICCLAT ATARSPSKRLGKAFGLKRSWE GLRRPGEDFTRGGKFDRGYLT GRIAVATLVADKKAAG/ALGS SNPNFQFRGGFGRGRGQPPQ
22144	52512	A	22272	1	1693	MFNSVPVQNEGDSFNFEKVKA EFRPGTQTQEYIKGMEDSASEV TVNREVTDDNPYTISVTNKTL AIRIKMFMPRIA YELKVTVIKM AFELSTRCSKRLM/DGSFETVLT DVIEGKTMSGYDRSRVNLNPNF NNQVIFRVVRKTPDSNDSNVV DAIQVRSYAEVIDAKFRYPLTG LLFVEFDSKMFPNQLPTISIRKR WKIVNVPSNYDPESRTYNGNW DGTFFKAWTNPAWVLYDLM INQRYGLDQKELGISVDK WAL YEAAYQCDQMVLTA KAARNL ATFVT/CIIQSQTDAPREPAYIFT NDNVVNGDFSYSQARRACTR RAT*CLMMSKTCINRSLYSI/ V/EGHSTVRNNVTSITAIGAHV EA/KANRRGRWILKTNLRSTTV NFATGLEMIPTIGDVVAISDNF WSSNLTMLNSGRLLVSGSQIF LPFRVDARAGDFIIVNKPDKP VKRTISSVSADGKTIENIGFGFP VKPNTVFAIDRTDLALQYYVVT KIDKGDDDEFTSKSRRWSTIL ISTMKLITGLTSTTDRQASLSQI R/CPKPENVK/CPQSSRESSRG

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22145	52513	A	22273	1	1843	MEDNLSINKIKILLVSVDGEIDE TFSLKQLMFNSVPVQNEGDGSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPTYTISVT NKTLASIRIKMFMPRAAYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTVLLFVEFDSKMFPNQLPTIS IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKAWTNNPAWVLY DLMINQRYGLDQKELGISVDK WALYEAAYCDQMVLTAKA ARNLATFVT/CIQSQTDAYKV RDICSIFRGMSEFWNGPREPAYIF TNDNVVNGDFSYTSQARRACT RRAT*CLMMSKTCINRTLQYS I/V/EGHSTVR/NNVTSITAIG/AH VEA/KANRRGRWILKTNLRSTT VNFATGLEMIPTIGDVVAISD NFWSSNLTMLSGRLLEVSGSQ IFLPFRVDARAGDFIIVNKPDK PVKRTISSVSADGKTIEINIGFGF PVKPNTVFAIDRTDLALQQYVV TKIDKGDDDEFTSKSRRWSTI LISTMKLITGLTSTTDRQASLSQ IR/CPKPENVKICPQSSRRG
22146	52514	B	22274	1	1452	

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22147	52515	A	22275	1	1902	MIQKVISGSKGGSQKPHNPVEM EDNLISFNKIKILLAVSDGEIDET FSLKQLMFNSVPVQNEGDSFNF EGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRIKMFMPRIA YELKVT VIKMAFELSTRCSKRIM/DGSFE TVLTDVIEGKTMMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFNPQLPTIS IRKRWKNNVNA PSNYDPESRTY NGNWDGTFKKAWTNNPAWVL YDLMINQRYGLDQKELGFSVD KWALYEAQYCDQMVLTA AARNLATFVT/CIISQSDAPRE PAYIFTNDNVNGDFSYSQ RRACTRRAT*CLMMSKTCINRT LSQYSI/V/EGHSTVR/NNVTSIT AIG/AHVEA/KANRRGRWILKT NLRSTTVNFATGLEMIPTIGD VVAISDNFWSNLTMNLSGRLL EVSGSQIFLPFRVDARAGDFIIV NKPDKGPVKRTISSVSADGKTI EINIGFGFPVKPNTVFAIDRTDL ALQQYVVTIDKGDDDEEFTS KSRRWSTILISTMKLITGLTSTT DRQASEVKPVNFTSSRHQAQPE VGLIPPLWPQGGKIIAQTSKSS
22148	52516	A	22276	1	675	
22149	52517	A	22277	155	700	SGVLVGHALTARQPSSGRRLV VDHSANRRGRWILKTNLCSTT VN FATGLEMIPTIGD/GDFIIVN KPDGKPVKRTISSVSADGKTIEI NIGFGFPVKPNTVFAIDRTDLAL QQYVVTIDKGDDDEEFTSKS RRWSTILISTMKLITGLTSTTDR QASLSQIR/CPKPVNK/CPQSRE SSRG

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22150	52518	A	22278	1	1871	MEDNLSINKIKILLAVSDGEIDE TFSLKQLMFNSVPVQNEGDSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTNREVTTDNPYTISVT NKTLSAIRIKMFMPRIAYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDIAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS/ IRKRWKIVNVP SNYDPESRTYN GNWDGTFKKAWTNNPAWVLY DLMINQRYGLDQKELGISVDK WALYEEAAQYCDQMVL TAKA ARNLATFVT/CIHQSDTAYKVV RDICSIFRGM SFWNGESISVIID RPREPAYIFTNDNVVNGDFSYT/ SQARRACTRRAT*CLMMSKTCI NRTL SQYSI/V/EGHSTVR\NNVT SITAIGAHVEARPTDCGRWILK TNLRSTTVNFATGLEGM IPTIGD VVAISDNFWSNLT MNLSGR LQ EVSGSQIFLPFRVDARAGDFNIV NKPDAPVKRTISSVSADGKTI EINIGFGFPVKPNTVFAIDRTDL ALQQYVVT KIDKGDDDEEFT/S KSRRWSTILISTMKLITGLTSTT DRQASLSQIR/CPKPENVK/CPQS RESSRG

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22151	52519	A	22279	3307	5305	CRSSQNTQETSPDRALLVNLRP SQGPLLALWVPAEGVGGKGHC LPPRSFFRMDNQLVPAVSDGEI DETFSLKQLMFNSVPVQNEGDS FNFEVKAEFRPGTQTQEQYIKG MEDSSSEVTNVREVTDDNPTYI SVTNKTLASAIRKMFMPRIAYEL KVTVIKMAFELSTRCSKRLM/D GSFETVLTDVIEGKTMMSGYDRS RRVNLPNFNNQVIFRVVRKTPD SNDSNVVDIAQVRSYAEVIDAK FRYPLTGLLFVEFDSKMFPNQL PTISIRKRWKIVNVPSNYDPESR TYNGNWDGTFKKAWTNNPAW VLYDLMINQRYGLDQKELGISV DKWALYEAAYCDQMVLTA KAARNLATFVT/CIISQTDAYK VVRDICSIFRGMFSWNGESISVII DRPREPAYIFTNDNVNNGDFS TSQARRACTRRAT*CLMMSKT CINRTLSQYSI/V/EGHSTVR\NN VTSITAI\GAHVEA/KANRRGRW ILKTNLRSTTVNFATGLEMIPT IGDVVAISDNFVSSNLTMTNLG RLLEVSGSQIFLPFRVDARAGD FIIVNKPDKGPVKRTISSVSADG KTEINIGFGFPVKPNTVFAIDRT DLALQQYVVTKIDKGDDDEEF TSKSRRWSTILISTMKLITGLTS TTDRQASLSQIR/CPKPENVK/CP QSRESSRG
22152	52520	A	22280	3	412	PAAVA*VKTEPETPGPSCLSQE GQTA\VKTEESSELGNYVIKIDH LETIQQLTAVVKKIPLITAK\W QRAMTMRKVLQEILEKNPRFH HLTPLKTKHIAHWCRCHGYTPP DPESLRNDGDSIEDVLTQIDSEP
22153	52521	A	22281	2	513	IFACWGWKQAWPACCNLSRGQA VKGNQLLPVSLVKKRTTLAPNT QTASPRALADSLMQLARQVSR LE/QRAKREPENEEVDILSLE PVKINIKKEQEEKQEEVKFYLP TPGSEFIGDVTQKRLEEVDSFTG DDL VQGFSGGISRRYGEKPGVQ DLEVEPDSVTEMLQFYD

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22154	52522	A	22282	1	1197	MAWPCISRLCCLARRWNQLDR SDVAVPLTLHGYSOLDSEEPGT GGAASRRGQPPAGARDSDGRDV PLTQYQRDFGLWTTTAPGKDP PGRGPGAGRRGKSSAQSSAPP APGARGVYVLPIDADAAAAV TTSYRYGLGRDRNESPPCGGRT RRPGARGMGWAAERRRLEPGS HATSELPAASEVTPVWSVGTA GGAFAAPCPETVLEHPRAGSAP LPSQPPSWGQPSWPAFSRVGT GLPLTPTAGPSRARGARRPCPP ALPGHCLLDRTYTGLQTLGAET LLAVVNSAAMNVGVQVVDVE LHRHSLGEDCIYQSSSEDISDA PPSLPLTIPAPVKASSPIKQSHPEP VPDTSVEKGS/PGSCPFHL*GPL SHLGSSPGFLLWRPPGLLSSVA
22155	52523	A	22283	131	677	PSSLS/CDIFLRSPISTPSPSLPRT PTSTPVHVKKGTAGSVINNPVY IMDKQPGQVIGATTPTSGSPTN KISTASQISQGTGSPVKIHGSSF VTSTVKVIHQEPGEAPHVPAT GAASQSPLPQYVTVKGGHMA VSPQKQVITPGEGIAQSAKVQP SKVL/GQIG*CLPTLARADLLYS
22156	52524	A	22284	3	5128	LLKIHSSQSSPQAVLTTPSQLK PLSVNTSGGVQITLMPVNVVQ SFSTSKPPAILPVAAPTVPVPS APAAVAKGEDASCFSKSVQ YYGWNIGKRRAAEWQRAMTM RKVLQEILEKNPRFHHLTPLKT KHIAHWCRCHGYTPDPESLRN DGDSDIEDVLTQIDSEPDHGLG DGKSSSVGPTAVVTLACHLEC PSSFSSADNLCKRLLEDLQFQK REPENEEVDILSLSEPVKINIKK EQEEKQEEVKFY
22157	52525	A	22285	112	651	GGLCTMARTKADWPANRTGG KAPRKQLAYKKPASQECGPLT GGVKKPHRYR/PGTVGGSVKFR R/YQKSTVLLIRKLPFQ/RLVLR EIAQGL*NKILRFQSAAGALQE GKWRPNLVWPFLLKDTNLVC*S MAKRVTHIAKKTFLAPPHTVE NRALRIHWSWMGKHFSQKKKK NFSSSCYV
22158	52526	A	22286	1	339	

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22159	52527	A	22287	2	1369	EPAPPARRSLSAAAAASGTTVD TASHSLVFSQQQLNMQRIGFRV NCTVAM*DVYFKAHRAVLAAAF SNYFKMIFIHQTSECIQIPTDIQ PDIFS YLLHIMYTGKGPQIVD HSRLEEGIRFLHADYLSHIATE MNQVFSPTVQSSNLYGIQISTT QKT VVKQGLEVKEAPSSNSGN RAAVQGDLPQLQLSLAIGLDDG TADQQRACPATQALEEHQKPP VSIKQERC DPESVISQSHPSSE VTGPTFTENSVKIHLCHYCGER FDSRSNL RQHLH THVSGSLPFG VPASILESN DLGEVHPLNENSE ALECRRLSS FIVKENEQQPDHT NRGTTEPLQISQVSLISKDTEPV ELNCNFSFSRKRKMSCTICGHK FPRKSQ LLEHMYTHKGKSYRY NRCQRFGNALAQRFQPYCDSW SDVSLKSSRLSQEHLDLPALLES ELTQENVDTILVE
22160	52528	A	22288	363	947	STARRGKSRSPAVALQRQPSA ASRSPSSRRRRGVSKVSVPLA RTKQTARKSTNIGKAPRKQLA YKKPARKSA/PSTGGVKKPHRY RPGYCGRSVKFRR/YQKSH*DF* FRKLFPQAVVWRENLLKDF*K QILRLQSRSYRVALQGGQVEA LSGVGLF*KTTNLLC*SMPKRV NNYCQKDIPAKHARIPWRTVL
22161	52529	A	22289	1	92	
22162	52530	C	22290	10	198	
22163	52531	B	22291	74	205	

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22164	52532	A	22292	2	1914	RGHCEPSRAAPSRADRHPSAL ARDPGRRRGPAGQAAPQPMEP ENIVANTVLLKAREGGGNNRK GKSKKWRQMLQFPHISQCEEL RLSLERDYHSLCERQPIGR\LF* EFCATRPELSRCIAFQDGMAYE EATPDEKRRKACGRRLMQNFLS HTGPDLIPEVPARQLVTNCTQRL EQGPCKELSQELTRVTHEYLSV APFADYLDISIYFNRLFQGGGLE REAITKNTLRQYRVLGKGGFG EVCACQVRATGKMYACKKLE KKRIKKRKGEA\MSLNEKQILE KVN\SRFVVSLAYGYETKD\AL CLVLTLMNGGDI.KFHIYHMQ AGFPEARAVFYAAE\CCGL\EDL HREIRIVYRDLKPENILDDHGH RISDLG\LAHVHPEGQTIKGRVG \TVGYMAPECLKNERYTSPDW WALGCLLYEMIAGQSPFQQRK KKIKRE\EVERLVKEVPPEYSER FSPQARSLCSQLLCKDPAERLG CRGGSAREVKEHPLFKKLNFKR LGAGMLEPPFKPDPQAIYCKD VLDIEQFSTVKGVELEPTDQTF YQKFATGVSPIPGKNEQMVET ECFQELNVFGLDGSVPPDLDW KGQPPAPPKGLLQRLFSSPKD CCGNCSDEEELPYPLAPSPRP
22165	52533	A	22293	102	403	
22166	52534	A	22294	1086	1436	
22167	52535	A	22295	965	1231	
22168	52536	A	22296	1434	2215	TPFSLSLTGVNKEHVLLGFST EDGRWMFTRGGE\DTARIWD LRSRLQCQRIFQVNAPINCVC LHPN\QAEIVGDQSGAIIHWDL KTDHNEQLIPEPEVSITSAHIDP DASLHGQLFNSTGNCYVVD\LT GGUGDEVTOFIPKTKIPAHTRY ALQCRFSPDSTLLATCSA*LRR/ CKIWRTSNFSMLTEL\SIKSGNP GEVSSRG\WMWGCALIGGTPSNI VTASSNNLARLWCVKTGEEKRE YGGHQKAVVCLPFNDSVLG
22169	52537	B	22297	158	385	

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22170	52538	A	22298	145	1232	LPVRAEPTRAAAMSGDEMIFDP TMSK/NMKKKKKKPFMLDEEG DTQTEETQSETKEVEPEPTED KDLEADEEDTRKKDASDDLDD LNFFNQKKKKKK/TKKIFDIDEA \EKGVKDL\K*\SDVQEPTEPED DLDIMLGHHKKKKKNVFPDE DEILEKDEALEDEDNKKDDGIS FSNQTGPAWAGSERDYTYEEL LNRVFNIMREKNPGYWLPGG RKRKFGPWKPPQV\VRVGTGKT FFCPLLQDICKLLHRSQAISFA FLLG*IGVPSGSIDG**PNL*SKG RFQQKQIENVLRRYINKEYVTC\ HTC\RPDITLQKDTLLFPYS AETCHSRFCFWPFKTLGPQA VHGQSRGTAPVPKA
22171	52539	B	22299	50	319	
22172	52540	A	22300	3	235	LLLYPLRSLPENPLRLVQQIYSF LKGSSEK*NDLPRVPLLELGVG LLPPNQYSCSRAPCLTCGLTM SLDGAQQGFW
22173	52541	A	22301	3	2849	WAKPVARASPAAVPGRQCQIR GAWSWGEGRGQGPAPSPAGS PATSEESLAPMAWRCPRMGRV PLAWCLALCGWACMAPKGTQ\ AEESPFVGNP/GNITGARGLTGT LRQQLVQVQEPFVHWRDGG ILELADSTQTQVPLGEDEQDDW IVVSQLRITSLQSLDTGGYQCLV FLGHQTFVVSQPGYVGLEGLPYF LEEPEDRTVAANTPFNLSCQAQ GPPEPVDLLWQDAVPLATAP GHGQQRSLHVPGLNKTS
22174	52542	A	22302	3364	3899	LVFLFDDL GIVELVLPGNIVHGI MSVRPRVAAGLRVRLQPGRRW LRGPLQLGAPLGLDLLVDVPGS PRFVVGVELPLVV/EAPRPPTPP AAAQARS*GLECPGRGAAAP REVLHLQTAHIHGPGRGGPR ARPLPLGLCP**T/FSCQEAKGE RGGAHSGSGSKWPPPPPPPS

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22175	52543	A	22303	1660	4652	PNPNTCLCNHVESGPPCSTHT YTLTDLQPLFGVVRVPTPSGRG TQAEESPFVGNPGNITGARGLT GTLRCQLQVQGEPPVHWRD GQILELADSTQTQVPLGEDEQD DWIVVSQRLRITSLQLSDTGQYQ CLVFLGHQTFVSQPGYVVGLEGL PYFLEEPEDRTVAANTPFNLSC QAQGPPEPVDLLWLQDAVPLA TAPGHGPQKSLHVPAAVGA EGGSRLLWRAPEAGRRKRWGGE VPPVTHAGAGMLRSERD
22176	52544	A	22304	54	288	SEAGQAQPAAAVGVFWTGRRRA WETGEGYYSNLSMELQL*RQ CI*DCFFSSSWRCVPPVYFKEEK YKGNLVCLLFFK
22177	52545	B	22305	243	2641	
22178	52546	A	22306	35	204	
22179	52547	A	22307	244	424	PSLFKNIMTFYPNLHFLWCRGR LYLDVWRQ/VR*FVRNTNYQLP LVLHNLRSFNTFDELV
22180	52548	A	22308	1	477	
22181	52549	A	22309	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTMEEYAVTRRNKIVSFA ET*MELEVIIVSKLTQEQTCHKC MFSLTSGS
22182	52550	A	22310	30	199	
22183	52551	A	22311	547	682	LVFLTNQRLVSTHQGTWWE*K *CQPVPISL*FYFLRKFSVIVIW* *LLILP*HPMALK/C/CCQAACS GHFTAGTGEITRPCSISKVLKR LSRL*STSGS**LVFLTNQRLVS THQGTWMKLEAIIISKVTQEQQ TKHHMLSLRSGS
22184	52552	A	22312	2	194	CPSMIDWLKKMWHRYTMEYY AAIKKNEIMS/FAGTWMKLEAI ILSKLTQEQQN/KHCFMFLITGS
22185	52553	C	22313	1	1845	

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22186	52554	A	22314	I	1384	MRFQDRTWQVPYPSQCSWGSS RQGVVPOARGIVLDSQEAYPSP GGTTLCHMDPDKQAPG/PVRRP APGNPNRLVVSVALQFLTFHES GITSALRVRLPQSVVSFQGPCC TEA*RRASICRRRV*S*HSTKLDL GA VAAQQQAWVAG/PRSPQRR CHQYS*AGPAWLGLQGRGSH RPDTPSPWHWFALAGREEQVL PPESLL/RARTPGTHLAPGPGA* TRVQSGPGSWLTWAG*GTPQVI SS/PGAGAVGAPETTAVPTVSLA PRRSVEMWPETKEHLVAVARR KWVSAQEKLRLRGCGSEKMG VSPGETRVYFPALTSRCRRRCG RVSEPSPTASWAPAPSLGWAYQ LAGGRLVLRVGLSAGWRAACP QGGPISWLEGLSSGVLSAG WRAACPQGGPISWLEGLSSST MRQPRAPQSSLPAPAPWGAPDP LAMLAAWIEARPGVWPTQPGP WQVSWVCV
22187	52555	A	22315	II	431	RHLLAAPPAPAAAAAALSH CLRSSGRLAPHTSRRLPRVVKR RVNALKNLQVKCAQIEAKFYE EVHDLERKYAVLYQPLFDRKF EIINAIYEPTEECEWKPDDEDEI SEELKEKAKIVDEKK/DEEKEDP KGIPEFW
22188	52556	A	22316	64	467	PAAWLPIVLAARQLTVQMMQN PQILAALQERLDGLVETPTGYIE SLPRVVKKRVNALKNLQVKCA QIEAKFYEEVHDLQRKYAVLY QPLFDRKEIINAIYEPTEECE WKPDDEDEISEELKEKAKIEDE
22189	52557	A	22317	2	177	
22190	52558	B	22318	228	377	
22191	52559	A	22319	630	767	WRVKFKNTVKIQANF*KSRFIH LTVVPVTILSQVTLQLTMSPKT

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22192	52560	A	22320	80	1362	VTACAAPAAWLPILVADIWSSY NMADIDNKEQSELDQDLDDVE EVEEEEETGEETKLKARSA*LFR MMQNQPQILAVALQERLDG/LW VETPTNGYIESLP RVVKRR/VNA LKNLQVKCAQKETQFYEEVH DLERKYAVLYQPLFDKRFIIN AIYEPTEFECEWKPDDEEISEE LKVEKGQIEDEKKDEEKDPKGI P*IWLTVFKINVDLLSDMVQEH DEPILKHLKD KVKFSDAQQPM SFVLEHFHFPENYFTNIEVLTKT YRMRLEPEPDDSDHFSFDGQEI MGCTGCQIDWKKGNVTLKTI RK*/RRNHKGRGTVRTGH*NQ FPNDSFSNFFCPLLKSPESGDLD EDVAEAILAADFEIG/HFLRERII PRSVLYFTGEAIEDDDDDYDEE GEEADEEGEEEGDEENDPDY/D PKK/DQNPAECKQQ
22193	52561	A	22321	3	425	GCGCGGAAARGSPAPGRPAAS PPDCPLWLQGCYPPSCDALSA TEADGCD*IYPDTSRDGPHQA SLPGESSFFPGQPNDSYLPERGS ERSRQASYATPAETQDPDEGL PQPGPEALPGGLQVPKSAAPFC GAQHAAGQ
22194	52562	A	22322	2	285	SRFEPVRPTGGDRPHQASPPG DSSSFPGQPNDSRLPECGSECRG QASYATPAETQDPE*RSSPTRS *SPAGGFQVPKSAAPFCGAQHA AGQ
22195	52563	A	22323	85	473	FTMPAVALVPKELYLSSSLKDL NKKTEVKPEKISTK/QDYVHSIL GTANIKKAEAEERLSESLKRLRY KEAEVRK*LEEKDRQKEAQQL QQKRQETGRE/DGGTLAKVSLE NVLDYQDKTQKSNGEKSEKM

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22196	52564	A	22324	1	1449	MMRAHMFVYKELKQIYKKKT HPHQKVGKGYKQTLRGRHLR GQETYEKKLTHVYETIDFKQQ QYYFHSILGPANIKKATGETER LSESLKLRVEEVEIWKKLEEKD RQGEAQLQKQKQETGREDGS MLAKGSLEIVLDSKDKTKQSN GEKNEKCETKEKGAITAKELYT MMMDKNISLIIMDAQRMQDYQ DSCILHSLSVPEKAISPGVTASW IEAHLPPDSIDTWKGRGNVEY MVLDDWFSSAKDLQIGTTLWH LKDALFKWEKGGYKNWFLCY SQYTTNAKVTPPPQHQNELSI LDFTYPSLEESIPSKAAEMPPP PIKVDEDELISDQISDNDQNER TGPLNISIPVESVAASKSDVSPH QPVPISKNVPQIDHTKKLAVKL PEEHIKSESTNHEQQSPQNEKV IPDCSTKPVVSSPTLMLTDEEKA HIIHAETALLMEKNKQEKELQE RQQGKQ/K/EKLRRREEHQKAK
22197	52565	A	22325	185	2983	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECRDLDRDEERAYVLYM KYVTYVYNLIKRPDFKQQQAD CAYFLGQTVHILFOHRALLEKK YRAVGAITAKELYTMMTDKNI SLIIMDARRMQDYQDSCILHSL SVPEEAISPGVTASWIEAHLPDD SKDTWKKRGNVEYVVLDDWF SSAKDLQIGTTLRSLKDALFKW ESKTVLRNEPLVLEGGYENWL LCYPQYTTNAKVTPPPR
22198	52566	A	22326	313	3720	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHS/AP RKIFKTAEECRDLDRDEERAYVLYM YMKYVTYVYNLIKRPDFKQQQ DYFHSILGPGNIKKAVEEAERLS ESLKLRYEEAEVRKKLEEKDRQ EEAQLRQKQKQETGREDGGTL AKGSLENVLDSKDKTKQSNGE KNEKCETKEKGAITAKELYTM MTDKNISLIIMDARRMQDYQDS CILHSLSVPEEAISPGVTASWIE AHLPPDSKDTWKKR

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22199	52567	A	22327	46	562	LLQGPFGCGDMPVEARPSAA WRGGRAPGWTFPSPPDRETWK PQ/RASQGESGQRRFGPCPRSGG RPPGPGSAAHSSRSQRWKRASR AWPAAPRKGLLPPAQAWPTTP AAGL*GFLAACKR/PPVGGGRGP APAPCRPASSRCFLICDSGPPCL CSASRAAWMGSAASSRVLFIEG
22200	52568	B	22328	51	445	
22201	52569	A	22329	51	366	CQWNTQTQVCYKQDVQSITAL GSAAQCTCLSSPR*SGKFKLLFS PGLPGTLVPSTIPATSAPRA/SHR AGEAWVGEPRALALQNSSSP DWAGYQGLPCKPSIRAA
22202	52570	A	22330	257	916	SPSGSNLETHLRAPDLGGPCPP GPRWWA*TPQGHQPTRPSAA QPCPPFPQCQLIHCPC/SPAPGT VAAPPAPPTPASQCLLCPWTS PVCSPAPTFFCPMAPVMAFMLP SYSFP/PGTPNLPQAFPPSQPFP SHPTLTSEMASAQPGSPAGPR SPDSHVLVQPPGPPHHRPWVGP PHRSFSPAARPCSSSTCCSRWK PLRVALEPWGPGQGPQRQQL
22203	52571	A	22331	151	1232	GRLGDAARGPQGEAPGGEEAA RADSTRACRSCGLLLGRRGCR PSLKNAELLELTVRRVQCVRG RAREREQLQAEARRALRCRLHP VACTKVHTFVSTCQADATVA AELLNHLLESMPREGSSFQDL LGDALAGPPRAPGRSGWPAGG APGSPSPPGGDDCLSDLEEA PEAELSQA/PC*GARLGARSPGQ PDHSPNCPGVSGGLGDQCQFES CRGGARPSLGSPLLPGVQMWW WG*GPGSLPGSSLPPLMDGLQG QPLVTSPAQRPSVS*KNF*GPC SSGSWREGATGRRKNFVELP ALSQVSPSPAFAFNRLCGLWGQR WQKLVLGTSVPGSPGLNKS LN LPLQRGDERQVH
22204	52572	A	22332	1	1524	

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22205	52573	A	22333	3	8875	EDGSLLEQVGHICLARGPGCGPE TPLYSPATGLALQLQGPAAMG ALWSWWILWAGATLLWGKSG EDWISGPTIVFSQPGLTQEA DLKNTGREELTAFLQNYQLA YSKAYPRLLISSSPASVSILS QADNTSKKVTVRPGESVMVNI SAKAEMIGSKIFQHAVVIHSDY AISVQALNAKPDTAELTLRPIQ ALGTEYFVLTTPPGTSARNVKEF AVVAGAAAGASVSVTLKGSVTF NGKFYPAGDVLRT
22206	52574	A	22334	2	2214	ISATDGPLAPCHGLVPPAQYFQ GCLLDACQVQGHPPGLCPAVA TYVAACQAAAGALGEWRRPDF CPLQCPAHSHYELCGDSCPVS PSLSAPEGCECAREGCVCDAG FVLSGDTCPVPGQCGCLHDGR YYPLGEVFPYGPCECERRCECGP GGHVTCQEGAACGPHEECRL DGVQACHATGCGRCLANGGIH YITLDGRVYDLHGSCSYVLAQ VCHPKPGDEDFISIVLEKNAAGD LQRLVTVAGQVVSLAQGGQV TVDGEEVALPVAVGRVVRTAE GRNMVLQTTKGLRLLFDGDAH LLMSIPSPFRGLCGLCGNFNG NWSDDFVLNPGSAASSVETFG AAWRAPGSSKGCGECPQGC PVCLAETAPYESNEACGQLRN PQGPATCQAVLSPSEYFRQCV YDLCAQKGDKAFLCRSLAAYT AACQAAGVAVKPVWRTDSFCPL HCPAHSHYSICTRTCQGSAAAL SGLTGCTTRCFEGCECDRLFL SQGVCPVQDCGCTHNGRYLPV NSSLLTSDCSERCSCSSSGLTC QAAAGCPVGRVCEVKAEAR/N CWATRGLCVLSVGVANLITTF DGARGATTSPGVYELSSRCPL QNTIPWYRVVAEVQICHGKTE AVGQVHIFQDGMVTLTPNKG VWVNGLRVDLPAEKLASVSVS RTPDGSLLVRQKAGVQVWLGA

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22207	52575	A	22335	3	7639	ITCPENSHYEVCGPPCAPSCPSP APLTTPAVCEGPCVEGCQCD GFVLTSADRCVPLNNGCCGWAN GTYHEAGSEFWADGTCQWCR CGPGGGSGLVCTPASCGLGEVCG LLPSGQHGCPVSTAECQAWG DPHYVTLDGHRFDQGTCEYL LSAPCHGPPLGAENFTVTVANE HRGSQAVSYTRSVTLQIYNHSL TLSARWPRLQVDGVFVTLFP QLDSLHLAHLGADVVVTTS GLSLAFDGDGDFVRLRPAA
22208	52576	A	22336	2	224	HCYMVVQLWKPRSLRRKSDQL WSSWNQLNTESSSFAEMQT EAFDCGSMAGRM*QGGRYLLA ALWDSSVPLS*PQAEPWSGVGP AHLTE/LLSPSRFVSISDLLAPKD LGTESQVSMEV*KDMGRFHW DIPP*A*VFVIFVFQIFISRTYDA TTHFETTCDDIKNLL*R*QGRYL LAALWDSSVPLS
22209	52577	A	22337	2	206	LSSSYLDPQCYETINRIKLYSES LARYGKSPYLPLVGLGELPQG FAR*EPVFKTSVIQNLIFNIMCI
22210	52578	A	22338	2	457	
22211	52579	A	22339	2	1556	FVFPSEVAVGLALSPASIFLSFS PFLRAQERLPSLLWWARSPCAF SLLGSCVRACAMNEEYDVIV\I LGTGLTECILSGIMSVNGKKVL HM\DRNPYYGGESASITALEDL YKRFKIPGSPRVKVGEEERDW NVDLIPKFLKANG\QLVKMLL YTEVTRYLDFKVTGSEFVYKG GKIYKVPSTEAELASSLMGLF EK\RRFKEFLVYVANFDLEKDP TFEGIDPKKTTMRDVYKKFDL GQDVIDFTGHALA\LYRTDDYL\I DQPCYETINRIKLYSES LARYG KSPYLPLVGLGELPQGFARLR CYLWEGTYMLNKPIE\HIVQE WGKVIGCKI*REEIARCMQLIC DPSYVKDRVEKVGQVITVICIP QPPSKNTNDANSC\HIIPQNQ\I VNRKSDIYVC\MISFA\HNVAQ GKSIATVSTTVETKEPEKEIRPA LLELLEPIGTEILVSISDLL\VPKD LGVTESQIFISRTYDATTHFETTS DADIKNIYKR\MTGSEDFEEMK
22212	52580	A	22340	66	420	
22213	52581	A	22341	64	140	
22214	52582	A	22342	2	254	

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22215	52583	A	22343	82	3530	HLIVAMPEPTKKEENEVPAPAP PPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQANSQSLFIE KPQGGTVKVGEDITFIAKVKA DLSEKPTI/KWF/K/GKWMDLAS KAGKHLQLKETFERHSRVYTFE MQIIKAKDNFAGNYRCEVITYK DKFDSCSFDLEVHSTGTTPNID IRSAFKRSGEGQEDAGELDFSG LLKRREVKQEEEEPQVDVWEL LKNTKPSYEKIAFY/GITDLR GMLKRLKRSI
22216	52584	A	22344	66	358	TWVRGNPKPKITWMKNKVAIV DDPRYRMFSNQGVCTLEIRKPS PYDGGTYCKAVNDLGTVEIE CKLEVKVIYQGVNTPGQPVFL EGQQQSLHNKDF
22217	52585	A	22345	67	3515	HLIVAMPEPTKKEENEVPAPAP PPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQANSQSLFIE KPQGGTVKVGEDITFIAKVKA DLRLKPTIKWFGKWMDLASK AGKHLQLKETFERHSRVYTFE MQIIKAKDNFAGNYRCEVITYK DKFDSCSFDLEVHSTGTTPNID IRSAFKRSGEGQEDAGELDFSG LLKRREVKQEEEEPQVDVWEL LKNAPSEYEKIAFYGITDLR GMLKRLKRMREEK
22218	52586	A	22346	2	39	FQFCVSLFVYIQLNSDVLPE*PR HKKKPPTLSHWFLK*NLHL*N* NTKALKYRKL*V*LTQSKH*QM TYPFCNLYKT*V*TTNTKVK*T EGY*TAKTQKLYPDKVVMTN KPLKTRSPKPAKYGSPHDTAT WTGSGGLGLEAS*HSA
22219	52587	A	22347	1	113	
22220	52588	C	22348	47	337	
22221	52589	A	22349	1	2292	
22222	52590	A	22350	2	441	LRHAKWFPARANGLKSCVIVIR VLRLDIAVTRVPTWGPLRGWPLE LLECKSIGTANRPMGAGALRR VLECLASGIVMPQHALLRAAF GQLHKVLGMDPLPSKMPKKPK NENPVDYTVQIPPSTTYAITPM KRPMEEDGEKSPSKKK

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22223	52591	A	22351	45	402	HALAALEKLFDPDPLALDANK KKRAPVVPVRGGPKFAAKPHNP GFGMGGPMHNEVPPPPNLRGR GRGGSIRGRGRGRGFGGANHG GYMNAGAGYGSYGCGNSAT QGYK*LFHKTA YGYS
22224	52592	A	22352	243	3113	FPDITTEEVKMRPMRIFVNDHRH VMAKHSSVYPTQEELEAVQNM VSHTERALKAVSDWIDEQEK SSEQAESDNMDVPPEDDSKEG AGEQKTEHMTRTLGRVMR/VG LVAK/CLLLKGD/LDELVLLC/ KEKPTVAL/DK VADNLA/QL AAVTEDEKFEILQSVDDAAIVIK/ NTKEPPLS/LTIHLTSPVVREE/M EKVLAGE TLS/VNGPPGNVLD R SRIFAA FRGSLPETQRWFQAR ANGLK/SCV
22225	52593	A	22353	139	245	
22226	52594	A	22354	875	2019	NPNSQMPKMTTRSTKQLTNKSG QIDGCPGCRVVPVTCRLGHLSH YWA V WASILRFWEVWKYWL NMGRKSSEFPILKLNGR/TMGD *VLPFHMYV/QPVV/HPQLYPHS VTELTGDYFKPWWDGQPSLQQ VL/ERVDEWMAKEGLD/DPNV QVQFLFTLWEDWGLKKSVLPG/ QCQ*LGAWPVGGFTSKQWD*S *KKA YSFAMGCWPKNGLLDM NKGLSLQHIGRPHSGIDDCKNI ANIMKTAYGGFIFKQTSKPVLI GRGQDAGQGSLVGGPPQNPL PHQRGKRESGHKLCCPKVVP SLWGSMPGRGLCCPLQGALA TWPFLEARHFCAPSPTPQSQPS ISPSHCGPLRGTPGTHRLLPW YNRLWGHQDPRCAPSHP
22227	52595	A	22355	507	916	RKKNEKEGTPPRNMGICEKT KPTFDWCT*K*RGAWNQVGKY TSGYTGTGELPQSSKTGQHSNSG NTENTTKILLEKSNPKTHNW*I HQG*NEGKTVKGSQREK*GYP QREAHQTNSRSLCRNPTRQKRV GVNIKHS
22228	52596	B	22356	72	359	

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22229	52597	A	22357	1236	1987	GNSSPPGLPCKSSSSPPPPSLTG APARRAAAAAPRPASRRPPLA\ GGGVQQLFATRP/PGPTRARRP TWR*GPRGSPEETPRRRREWTR RPEPGCRAQGSRRPARPPSGSS AVRSASPASPAPAASAPLGPRS RWS*RPSPRRR/SPPPPPGRRS SDRER/GRRKEASPP/LTAAEAPA Y/RDQAPPPGSPHLGFQSAAG PSRTASSAP/RSIGGRCANTPA PAAIFPPSLRP/PRAGPVGD/LRAS GVDAAA
22230	52598	A	22358	287	2082	LKTETSEEKARRYKDRPSQLNA VFQEQKKMIQAQESITLEDVAV DFTWEEWQLLGAQKDL.YRD VMLENYSNLVAVGYQAKPD LFKLEQGEQLWTIEDGIHSGAC SDIWKVDHVLRLQSESLVNR KPCHEHDAFENIVHCSKSQFLL GQNHDFDLRGKSLKSNLTLVN QSKGYEIKNSVEFTGNGDSFLH ANHERLHTAIKFPASQKLSTKS QFISPKHQKTRKLEKHHVCS GKAFIKKSWLTDHQMVTGEK PHRCSLCEKAFSRKFMTEHQR THTGEKPYECECGKAFKKSR LNIHQKTHTEKPYICSECGKG FIQKGNLIVHQRIHTGEKPYICN ECGKGFIQKTCLIAHQRFHTGK TPFVCECGKSCSQKSLIKHQ RIHTGEKPFECSECGKAFSTKQ KLIVHQRTHTERPYGCNECGK AFAYMSCLVKHKRIHTREKQE/ CSQGGKSSCREAQLITHQ*CHA GEKLC*RGDYTSAFCGPSDIIKH QRP/HSQNRN/CSPOGTASGQM CSLRR*QWICTGQKPCCECEG CAFRDQLCLILCYRKPIGRK/PD LCGKGLSKNL*FIMWPKSIHCE
22231	52599	C	22359	90	344	
22232	52600	A	22360	2	543	
22233	52601	A	22361	373	490	
22234	52602	A	22362	111	396	GAPPGIWCLSLWACRALSPSS AAQHRKRPSALSPATPAGSRPL RRCAPGFAATKTQRVQRRPPRR *GAAAGAGGS*RPLCGVVIHSV LHNTPE

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22235	52603	A	22363	1902	3474	VPQRSTGSGRRASARRPLRAPD PCAAAPRVSPQPRPSECSGGR GGSKTWAKRNAGKELTDRNW DQDEAEAEVGTFSMAEEVLK NRAIKKAKRRNVGFESDTGGA FKGFKRFGGYPSEEEFSGFGVS GAGGKPLEGLSNGNNITSAAPP FASAKAAADPKVAFGK*LPSPS RLLVDKNVSNPKTNGDSQQPSS SGLASSKACVGNAYHKQLAAL DCSVRDWMVKHANTNSLCDL TPIFKDYEKYLANIETANTGN SGRNSSESSEKVAETQSPSLF GSTKLQQUESTFLFHGNKTEDTP DKKMEVASEKKTDPSSLGATS ASFNGKKVDSSVLGSLSSVPL TGFSFSPGNSSLFGKDTTQSKPV SSPFPKPLEGQAEQDSGECKG GDEEENDEPKVVVTEVKEED AFYSKKCKLFYKKNFKEKGI GTLHLKPTANQKTQLLVRAATL NLGNILLNVLPNMPCTRITGK NNVLIVCPNPPIDEKNA/TMP VTMLIRVKTSSEADELHKILLE
22236	52604	C	22364	65	283	
22237	52605	A	22365	3	419	
22238	52606	A	22366	1	512	CGRPPWKTGQSRQSPCPGSSG SGRGIPAAWHGEGPEAVLQ GHRAGRGDPACRGLCCLPSQL GGPTSPSTSAASRACGSRGAATL VVVKVWFYHP/CRRPSWARGS ATARMRCTSPA TRMRTTCRPSP TSASRWRASSMSRWGAASAR TGRSTTTGHLRPHHRA PGDG
22239	52607	A	22367	1	2940	MRRRRKVAIIHAGRPRAAAA SSEQRGRGPAARRAGGAEEA ASGVTGGGGGGAGQHAGGLG FSAGGRAPSRPLCGSMPARLF SKQEVGYCGLPAPASSLRSRG HRQRIYSLNQLLQEARLRTGRAR PGEGPGWLVTDKGGLGWGSSH SQAQGPDSQAAWGRAPPAHGS SPAFLQVLDVRPQSSRYLPPGT RVCAIYWSQKSRCLYPGNVVRA PPPCFGRLLGVPAASSGVPSTG ASGDEDEDLDSVVVEFDDGD
22240	52608	B	22368	215	356	
22241	52609	A	22369	282	499	YLLHCLPSDPPSFNTSPDGRGR RRRQRRRRSDPPGRGRTKSSSTR VPGSNRFV*FHQR*GRLKEWM ANQDTN

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22242	52610	A	22370	105	619	ACQASSHSGPVVWGPGERITTPG A*ASARREPSRNQHPLWVTE Q/I*IASPRTVANPLVPARTPTGP RTNKP KHLIKQGRGQPRQPLSG STGGAGESPASGCAGGQPAHR VWIAPAARGCGQHTPWKAPAG NGQSPRPASATRMIGPSPSLSP APPAVVGVVAALGSRNRCIL
22243	52611	A	22371	1	441	
22244	52612	A	22372	10	621	LRQLERGLAKGQSTPVDRLPG PDPSAPGTLAGAALPPLEPPAPC LCQDPQEDSVEDEEPPGSLGLP PPQAGVQAAAAVSGTTQPLG TGPRVSLSPHSPLLSPKVASMD AKDLALQILPPCQVPPPSGPQSP AGPQGLSAPEQQEDEDSEEDS PRALGSGQHSDSHGESSAELDE QDILAPQTVQCPAQAPAGGSEE T*LRQLERGLAKGQSTPVDRLP LGPDPSPAGTLAGAALPPLEPP APCLCQDPQEDSVEDEEPPGSL GLPPPQAGVQAAAAVSGTTQPL LGTGPRVSLSPHSPLLSPKVAS MDAKDLALQILPPCQVPPPSGP QSPAGPQGLSAPEQQEDEDSE EDSPRALGSGQHSDSHGESSAE LDEQDILAPQTVQCPAQAPAGG SEETIAKA

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22245	52613	A	22373	1	2271	MPGELLAPSCCCRGGPTRDRD LSCDAAAATITLGGDRREPCAL TPGPShLALTLFSPKPGARPQPE GASWDAGPGLSTEAPLPATLE PRIVMGEETCOALLSPRAARTA LRDQEGWGL/SPQGSMDEREL HPAGTPEPPSSSESL.SADSSSW GQEGHFDDLDFLANDPMIPAAL LPFQGLIFQVEAVEVTPLSPEE EEEEAVADPDPSASYAEADDE RLYSGEPHAQATLLQDSVQKTE EESGGLRYDTASAPTRHRSLSV PKACSCSHDCAP*AG*RGPHLTP GLRYDTASAPTRHRSLSPKAC GCSHDCVPAG*RGPHLTPGLRY DTASAPTRHRSLSVSPKACSCSH ACVPAG*RGPHLTPGLRYDSTS ASARHRPHLRSRSGCGHPSNL AGRSRLCPRDRACGHGSGS/ SAWTGSMGSA/RHR*WG*A*L TPKGDPPG*EPAGRRPEG/TGT GTWTQPGGLHGCRPGLADL AALPSASSLWAPEPSWPS/SALS PRAARG*QPGGRLASGPGLGP AFG*PRGVISRAGRAGHLGSSD RAVSSPGAQSRREGPSRRQ*GD HRQSQAESQ*EEGPKGNVKG LAADSGSHQDHHPEVQEHPCLC HRQA*CLQGDPAHAHLG/FWR GQ/T*GP/CPASASRS*EV*GAL R/DLSLGP*VST/QGPG*A*VQG KGKG/GGGGGPGGAGTA*HL
22246	52614	A	22374	2	211	
22247	52615	A	22375	43	241	
22248	52616	A	22376	184	332	
22249	52617	A	22377	1292	1923	KAGARGNQEGTMASSSG/TQK VLTIPRCYQ*K*SKETLP*CSG WPNDARIEAVVNC/CTEFNHLIS SEANEICNKSEKKTISPEHVQA LES/LGSGSYISEVKEVLQECKT VALK/RRKASSRFGKPLGPEEE/ LFGDQANKELFGKSLDQQQAE/ LAQQ/EWLQM/QQAA/HQA/Q/ AAASAKCI*SRRSFSGMEEDG GWISEIPPAEFLFL
22250	52618	B	22378	1	1701	
22251	52619	A	22379	1	147	

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22252	52620	A	22380	1	484	IRHEGRGQRGMELVQVLKRG LQQTGHGG/LFRGYLRVFFRT NDAKVGTLVGEDKYGNKYIE DNKQFFGRHRWVVTTEMNG KNTFDWDVDSMVPEWHRWL HSMTDDPPTTKPLTA/RKFHLG RNH*ISTWTGAPQEQYVPYSTT RK/KIQEWIPSTPYK
22253	52621	A	22381	3	258	DMAAQIAEGMAFIEERNYIHRD LRAANILVSDTLSCKIADFGLA RLIED/FTTKSDVWSFGILLTEIV THGRIPYPGMTNPEVIQN
22254	52622	A	22382	1	738	
22255	52623	A	22383	233	1898	GAGPTGYLRLPGWAGTGMGC GCSSHPEDDWMENIDVCENCH YPIVPLDGKGTLLIRNGSEVRDP LVITYEGSNPPASPLQDNLVIAL HSYEP SHDGLGFEKGQRLRL EQSVIEWWKAQSLTTGQEGFIP FNFVAKANSLEPEPWFFKNLSR KDAERQLLAPGNTHGSFLIRES ESTAGSFSLVSRDFDQNGQEVV KHYKIRNLNDNGGFYISPRITFP LHELASAITPIASDGLCTR/LSRP CQTQKPKQKPPWWEDEWEV PRETLKLVERLGAGQFG/RCGW GTTTGTTKVAVKSLKQGSMSA GR/LPAEANLMKQLQ/HQRL/VR LYAVVTQEPYIITEYMENGSL VDFLKTSPGKLTINKLLDMAA QIAEGMAFIEERNYIHRDLRAA NILVSDTLSCKIADFGLARLIED NEYTAREGAKPIKWTAPPAI*S RGNSPPRSDVWSFGDLLPEIFT HGRIP/YPPQGI/NPELIQKLERGY RMVRRPSNCEKLYQLMR/LCW KERPED/RPTFDYLRSLVEDFFK RHRRASNQPQALREPLRKLPLCF
22256	52624	A	22384	3	203	
22257	52625	A	22385	2	467	
22258	52626	A	22386	1	468	
22259	52627	A	22387	1	645	

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22260	52628	A	22388	821	2637	AAASAWRAHSTTAAGRRRTAL FRSPGPNTRDTRRRRRATAPD CCRPATSPRALDWTSLHTRRRHP VQNYLQWSYWQVLVSRWIAF AGLAMADYLSGGTGYVPEDG LTAQQLFASADDLTYNDFLILP GFIDFIADEVDLTSALTRKITLK TPLISSPMDTVTEADMAIAMAL MGGIGFIHNNCTPEFQANEVRK VKNFEQGFITDPVVLSPSHTVG\ DVLLEGKMRHGFSGIPITETGTM GSKLVGIVTSRDIDFLAEKDHT TLLSEVMTPRIELVVAPAGVTL KEANEILQRSKKGKLPVNDCCD ELVAIHARTDLKKSRYPLASK DSQPQLCGAAVDTREEDKYR LDLLTQAGVDVIVLDSSQGSNV YQYARVLYFKQYPHLQVVLG GNVVTAQAQKNLIDAGVDGLR VGMGCGSICITQEVMACGRPQ GTCCVTR*AEYARRFGVPIAD GGIQTGVGHVVKALALGASTVM MGSLLAATTEAPGEYFFSDGVR LKKYRGMGSLDAMEKSSSSQK RYFSEGDVKVIAQGVSGSIQDK GSIQKFVPYLIAGIQHGCQDIGA RSLSVLRSMMSYSELKFEKRT MSPQIEGGVHGLHSYEKRLY
22261	52629	A	22389	2	332	
22262	52630	A	22390	3	608	MTAVHAGHLNLKWDPKSLEIR TLAAERLVTVQVTLVNTNSKGP SDKKRGHSKKVHVLAASVEQA AENFLEKEDKIVKESQFL*E*LL AAVEYVRKQ/GKECLRPSLEEH LEGIISGAALMGDSSCKHDDHR ERIAAECNTVLQACRTCF/SEY MGNAAGCKERSNLSAIDKMT KKTRDLRRQLHKA VMDHVS DSE FLETNVPLL
22263	52631	A	22391	2	2864	

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22264	52632	A	22392	14	2897	PDWRETKQRPSASGLWNLALA QLAAEMTAVHAGHLNLKWD KSLEIRTLAVERLLEPLVTQVT TLVNTNSKGPSDKKRGHSKKV HVLAAASVEQAAENFLEKEDI KESQFL*E*LLAAVEDVRKQG DLMKAAARRRSHDDPCSSVEQ GNMVQAA*TLASVTCLLILA\ DMGNVYKLLVQLKVVEDGILK LRNAGNEQDLGIYKALKPEV DKLNIMAAKRQQLKDVGHRD QMAAARGILQKNVPILYAS
22265	52633	A	22393	1	1584	
22266	52634	A	22394	1	3519	
22267	52635	A	22395	3	673	
22268	52636	A	22396	1	1574	DVPRDLEVVAATPTSLISWDA PAVTVRYRYRITYGETGGNSPVQ EFTVPGSKSTATISGLKPGVDYT ITVYAVTGRGDSPASSKPSINY RTEIDKPSQMQVTDVQDNSISV KWLPSSSPVTYGRVTTTTPKNGP GPTKTKTAGPDQTEMTIEGLQP TVEYVVSVYAQNPSGESQPLV QVAVPTIPAPTDLKFQVTPTS LSAQWALPNVQLTGYRVRVTP KERTGPMKEINLAPDSSSVVS GLMVATKYEVSVYALKDTLTS GPAQGVVTTLENVSPRRARVT DATETTITISWRKTETITGFQV DAVPANGQTPIQRTIKPDVRSY TITGLQPGTDYKIYLYTLNDNA RSSPVVIDASTAIDAPSNLFLA TTPNSSLVSWQPPRARITGYIHK YEKPGSPPREVVPRPRPGVTEA TITGLEPGTEYTIYVIALKNNQK SEPLIGRKKTVQKTPFVTHPGY DTGNGIQLPGTSGGQPSVGQQ MIFEHGFRTTPTTATPIRHR PRPYPPNVGQEALS

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22269	52637	A	22397	3	2382	QTEMTEIQLQPTVEYVVSVAQ NPSGESQLPLVQTAVTNIDRPKG LAFTDV/DVDSIKIAWESPPQQV SRYRVITYSSPEDGIHELFPAPDG EEDTAEQLQLRPGSEYTVSVVA LHDDMESQLIGTQSTAIPAPTD LKFTQVTPISLSAQWTPPNVQL TGYRVRVTPKEKTGPMKEINLA PDSSVVVSGMLMVATKYEVS YALKDTLTSRPAQGVVTTLEN VSPRRARVTDATETITISWRT KTETITGFQVDAVPANGQTPIQ RTIKPDVRSYTITGLQPGTDYKI YLYTLNDNARSSPVVIDASTAI DAPSNLRLFLATTPNSLLVSWQP PRARITGYIIEKPGSPPREVV PRPRPGVTEATITGLEPGEYTI YVIALKNNQKSEPLIGRKKTD LPQLVTLPHPNLHGPEILDVPST VQKTPFVTHPGYDTGNGIQLPG TSQQQPSVGQQMIFEHGFRRRT TPPTTATPIRHRPRYPNNGEEI QIGHIPREDVDYHLYPHGGLN PNASTGQEALSQTTISWAFQD TSEYIISCHPVGTDDEPLQFRVP GTS/TSATLTGLTRGATYNIIVE ALKDQQRHKVREEVTVGNVS NEGLNQPTDDSCFDPTVTVSHYA VGDEWERMESGFKLLCQLG FGSGHFRCDSSRWCHDNGVNY KIGEKWDRQGENGQMSCTCL GNGKGEFKCDPHEATCYDDGK
22270	52638	A	22398	48	7500	GATMACCAAQGEERVTPCASG KRGPAAATSLVLWIPSVPPVPF PTLWPPSWRRQPPGGIRRDFS RRLRREANLVA TCLPVRA SLPH RLNMLKGGPGGLLLAVLCLG TAVPSTGASKSKRQAQQMVQP QSPVAVVSQSKPGCYDNGKHQ INQQWERTYLG NVLVCTCYGG SRGFNCESKPEAEETCFDKYTG NTYRVGDTYERPKDSMIWDCT CIGAGRGRISCTIANRCHEGGQS YKIGDTWRRPHETGGYM
22271	52639	A	22399	1	403	NSTNKRGRFCFITFKVEIEMKKY HNVLGSKCEIKVAMSKEQYQQ QQQWGSRRGFAGRARGRGGG PSQNWNQGYSNYWNQGYGNY GYNSQGYGGYGGYDYTGNN YYGYGDYSNQSGYGVVSRRG GHQNSYKPY

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22272	52640	C	22400	36	214	
22273	52641	A	22401	3	182	
22274	52642	A	22402	223	452	LESMTIFPYSDDKRAQYIFIQKD LLKKPVRRHYIMTLSHWAFNT RLALQYWKGHKTQIDSEA*Q LRNKTMKANFF
22275	52643	A	22403	1	1037	MSEEQFGGDGAAAAATAAVG GSAGEQEGAMVAATQGAAAA AGSGAGTGGGTASGGTEGGSA ESEGAIDASKNEDEGHSSNS PRHSEAATAQREEWKMFIGGLS WDTTKKDLKDYFSKFGEVVD TLKLDPTGRSRGFGFVLFKESE SVDKVMQDQKEHKLNGKVIDPK RAKAMKTKEPVKKIFVGLSP DTPEEKIREYFGGFGVEVSELP MDNKTNRKRGFCFITFKEEPPV KKIMEKKYHNVGLSKCELVVA MSKEQYQQ/QQQWDSRGGA GRAVRGRGGQAEQYGGKGIQA RWAIKNSYKPYLNYSICPPYP TAGTSLQALCRADFRFSQARSM
22276	52644	A	22404	299	1508	HYVGGSSSGDGAARAT/AR AVGGSAGEQFGAMVAATHG ARGGVWEADAATGGGTASGG TEGGSAE/SEGAKEYASKNEED EGHSNSSPRHSEAATAQGRM/ KMVIGGLSWDTITKKDLKDYFS KFGEVVDCTLKLDPTG/QSRGF GFVLFKESESVDKVMQDQKEH K/LNGKVNPKRAKAM/KTKE PVKKIFVGLSPDTP/EKIREYF GGFGEVSEIPLPMD/NKTN*RG RGFCFUTFKEEPPVKK/MEKK YHNVGLSKCEIKVLLNEQYQ QQQQW*SIGGFAGIALVIGGGP SQNWNQGYSNYWNQGYGNYG YSS/QGYG/GYGGYDYTGYN Y/YGYGDYSNQSGYGVKYS/RR GGHQ/NSYKPHTKFIPCNLFPN RWLKQYFPNKKIQFERGSCHELL
22277	52645	A	22405	3	189	ESEPERKARTDEVLP/EEAAP RRKMRTTRTTCPVSR/AA*QL LLQKLLQRRRKGSCSRG
22278	52646	B	22406	1	1356	
22279	52647	C	22407	135	260	
22280	52648	A	22408	1	1740	
22281	52649	B	22409	80	371	

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22282	52650	A	22410	257	1200	ISWCCMEQKKRLP\FSKREGVPY EFHCPSDESSPLLRC AFCIGGMS VKEQMETHRPLQTTRGPGPGP LFTDGPDPPEAFHGLLSIREM VSTKVKPVGQSESEPRVKPLEL DDASAGGVHMMVATPGRLMD LLQKKMVSLNICRYLALDEAD RMIDMGFEGDIRTIFSYFKHTSA AAIGLQALDGGTGSQKQKGC EEFPSSMSAVSTGLEASACCL VTMDPLETLSRMASSTSSMSL ARAWLSPEPGDSPGMVGGPLR ELPGMAPLECGEFQRPESLCAD RNELGSQSPFPQEEDEDED DEEDEDE
22283	52651	A	22411	107	2069	GGVSPWRACVQQRMESEPER KRARTDEVLP EEAAPRRKMRT TRTTCPMCRYGSAGSLLQKLL QR\RRKGAAEEEQDGSSEPRG DEDDIPLGPQSNVSLLDQHQL \KEAESAAKESQGRKQLEGK KEKILGRIVCRAELDVK*KAD WLKGITVLIDPIKTQLGLPPR/Y MFLSMSEERHERVRKKYHILVE GDGIPPPPIKSFKEMKFPAAILRG LKKKGIIHHPTPIQIQGIPTILSCR DMIGIAFTGSGKTLVFTLPVIMF CLEQEKRLPFSKREGPYGLIICP SRELARQTHGILEYYCRLLQED SSPLLRCALCIGGMSVK\EQ\ME TIRQGVHMMVATPG/RALMDL LQKKMVSLDICRYLALDEADR MIDMGFEGDIRTIFSYFKGQRQ TLLFSATMPKKIQNF\KSALVK PVTINVGAGASLDVIQVEVEY VKEEAKMVYLLCLQKTPPPV LIFAEEKADVDAIHEYLLKGV EAVAIHGGKDQEERTKA\IEAFR EGKKDVLVATDVASKGLVFPA IQHVINYDMP EEIENYVHRIGRT GR\SGNTGIATTFINKACDESFLI DLKALLVRKPKQKVPPVLI\QV L\HCGGWS PMLDIGRSSRGCAF CGGLGH\RTDCPKL\EA\MQTK QVSNIGRKDYLAHSSMDF
22284	52652	A	22412	435	1428	

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22285	52653	A	22413	3	597	HKMAPYSPLVTRLQKALGVRQ YHVASVLCQRAKAMAMSHFEPN EYIHYDLLEKNINIVCKRLNWP LTLLKIVYGHLDLDDPASQEIEQ GK/S/YLWLWPDHVAAMLQFISKI GATTSVFPYNHRMRRYLSK/TG RTDIANLADEFQDHLVPDPGCH YDQLIEINSELKPHINGPFTPD QAHFVAEVGKVAEKEGWPLDI RVGLT
22286	52654	A	22414	29	512	
22287	52655	A	22415	1	543	
22288	52656	B	22416	271	719	
22289	52657	A	22417	1	2438	SVIIKMAPYSLLVTRL*KALGV RQYHVGSVLCQRARVAMSHF EPNEYIHYDLLEKSINIVRKR LN RPLTLSEKIVYGHLDLDDPASQEIE RGKSYLRLRPDRVAMQDA/TA QMAMLCQFISSGLSKVA/VPSTIH CDHLIEAQVGGEE/DLARRAKDI NQEVYNFLATAGAKYGVGFV KPGSGIIHQILENYCVPWLSF*L GPDFHTPNGGGLGGI/CIGSGC WPNAWEWNGLGIPWELCKPK VIGVKLTGSLSGWSPKDVILK VAGILTVKGGTGAIVEYQGGPV DSISCTGMATICNMGAIEGATT SVFPYNHRMKKYLSKTGREDIA NLADEFKDHLVPDPGCHYDQLI EINSELKPHINGPFTPDLAHPV AEVGKVAEKEGWPLDIR/VGLAI GSCTNFKLWKI/WGRSAA VAKQ ALAHG/LKCKSQF/TITPGFPRQI RATFE/RDGYAQILRDLGGVVL ANACGPCIGQWDRKDIKKGEK NTIVTSYNRFNTRNDANPET HAFVTSPEIVTALAIAAGTLKFN PETDYL TGHGWARSFRLGGSR I AD*VFPKGEF*PRGRDTYQHPP K/DSSGAACWDLSPTSQRQLQL EPFDKWDGKDLEDLQILIKVKG KCTTDHISAAGPWLKFRGHLD NISNNLLIGAINIENGKANSVG NPVTQEFGPAPD/LARYYKKHG IRWVVGIDENYGE/SSREHAA
22290	52658	A	22418	14	260	RLCIGDAGVSPVCGP/CSAGGGP R*LNLEGGEESSVPRGG/CCSP VTATTAPGPCFPK*SDGSGCAE APDSGE/CS*ALGPHCGD

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22291	52659	A	22419	160	460	RLCIGDAGVSPVCGPLSAGGGP R*LNL*GGESSSVPRGG/CCSP VTATTAPGPCFPK*SDGSGCAE APDSGNGCAFCAIRSPHRHGP KPARERLLLTGL
22292	52660	A	22420	43	418	SLGCAEQN/FAIAIQPGMAQEE RLSRYQQKDFQRRILVATNLF GRGMDIERVNIIVFNNDMPEDS DTYLHRVARAGRFGTKGLAITF VSDENDAKILNDVQDRFEVNV AELPEEIDISTYIEQSR
22293	52661	A	22421	1	592	RFSKYMPSVKVSVFSGRLSIKK DEEVLKKNCPHVVRTRARILA LVRNRSFSLQNVKHFVLDCECD KMLEQLDMRRDVQEIFRLTPHE KQCMMF/ERLSRYQQFKDFQRR ILVATNLFGRGMDIERVNIIVFN YDMPEDSDTYLHRVARAGRFG TKGLAITFVSDENDAKILNDVQ DRFEVNV AELPEEIDISTYIEQS
22294	52662	A	22422	2	575	
22295	52663	B	22423	100	412	
22296	52664	A	22424	2	441	
22297	52665	A	22425	682	1032	
22298	52666	A	22426	1	1324	MAEQDVENDLLDYDEEEEPQA PQESTPAPPKKDIKGSYVSIHSS GFRDFLKPELLRAIVDCGFEHP SEVQHCEIPQAILGMDVLCQAK SGMGKTAVFVLATLQQIEPVN GQSGQVHIFGLHIGARALVISEH ILKDEGAVEGCGVVQCLMARV TVLVMCHTRELAFQISKEYERF SKYMPSVKVSVFSGRLSIKKDE EVLKKNCPHVVGTPGRILALV RNRFSFLKNVKNHFVLDCECDKM LEQLDMRRDVQEIFRLDTTPR KQCMMFSAITL/ISKDNRPVCRK FMQDPMEVFVDEETKLT/LHGA LQQYYVKLTSEKNRSLFDLLA DVLEFNQVJIFVKSVQRCMAL AQLL/VEQN/FAIAIHRGMAQE ERLSRYQQKDFQRRILVATNLF FGRGMDIERVNIIVFNNDMPEDS DTYLHRVARAGRFGTKGLAITF

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22299	52667	A	22427	9	1535	EAQQLVSRPAENRSWKLLA ARGEERGASIMAEQDVNDLL DYDEEEEPQAPQESTPAPAKKD IKGSYVSIHSSGFRDF/LCLKPE LLRAIGGLVAFEHPSEVQIH\CI PQGHPGAWDVLLPGQSPGMGK TAVFRCWPLQQL\EPVNGQVT VLVM\CHTRELAFQISKEYERFS KYMPSVKVSVFFGGLSIKKD\E EVMKKNCPHVVVGTPGRILAL VRNRSFSLKNVKHFVLD\EC DK MLEQLDMRRDVQE\FRLTPHEK QCMMF SATLSKDIRPVC RKFM QDPMEVFVDD\ETKLT\HGLQQ YYVKLKDSE\KTRKVFDLWD\V LEFNQVDILRQGQCKRCMAL\A QLL\VEQNFPQWPI\HRGNGPQ KERPVNAYQASSKDFPSGRDPL VATQILFG\RGMDIEAKSN\VFN YDMP*GLGTPYL\HRVARRGR FGTKRP*PFTFVSDG\NDA\KILN DVQDRF*S*MWAE\PEEIDIST YIEQSR\LNHQLARAGPPGAAPH AASPLSRRHC
22300	52668	A	22428	3	290	
22301	52669	A	22429	1	690	MNQTSEKEIISKEQGNVKAAGA SDVVL\YKIDVPANRYD\LLCLEG LVRGLQVFKERNFFLT\VEVEK SKTKVEQIQCLCSQED\ADKLG VDISATKAVHISNPKTAEFQVA RTTLLPGLLKTIAANRKMP\PL KLFEISDIVIKDSNTDVGAKNYR HLC\AVYYNKNPGFEI\IHLLDRI MQLLDVPPGEDKGGYV/IQSVG KLGVLHPDVI\TKFELTMPCSSL EINIGPFL

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22302	52670	A	22430	2	1834	GTRPTVSVKRDLFLQALGRYTY DEEFDEL.CFEGLLEIDETSKE IISKEQGNVKAAGASDVVLYKI DVLATRYDLLCLEGLVRGLQV FKERIKAPVYKRVMPDGKIQKL IITEETAKIRPFAGAAVLRNIKFT KDRIYDSFIELQEKHLQNICRKR ALVAIGTHDLDTLGGPFTYTAK RPSDIKFKPLNKTKEYTACELM NIYKTDNHLKHYLHIIENKPLYP VIYDSNGVVLSMPPIINGDHSRI TVNTRNFIECTGTDFTKAKIVL DIIVTMFSEYCNQFTVEAAEV VFPNGKSHTFPELAYRKEMVR ADLINKKVGIRETPENLAKLLT RMYLKSEVIGDGNQIEIIPPTR ADIIHACDIVEDAAIAYGYNNI IQMHSPENFTP*ANQPLNKULT ELLRHDMIAAGGFH*STLPLAL CSQGRYWLKDLGVGYLWQQR AVHISMPKTAEFQVARTTLLPG PP*RP*AANRKVPLPLKLFEL DIVIKDSNTDVGAKKTTTQSL VAGLLPTKNPGFEINSWGCDW RIMAVCSDVPPGGRQGGDM*F KASEGPAFFPGAMCRDSFARGQ SLGKGLVGLHPDVIHQIWS*PLP CSSLEINIGPFL
22303	52671	A	22431	1	304	
22304	52672	A	22432	1	642	
22305	52673	B	22433	1	423	
22306	52674	A	22434	1	525	LHEHPVTESPMNCSTVLQSLY MKSVA/GIGQTGKIEPVVPLLL WFAESGAMEGETLHTFYQLV LMPKVMHYAQVLLALGCVL LLVPVICQIRSQ/DRCWPEGSPG *QPFAPPPA*TDIILWTEPATLM AEVSACCAPELPPPHRVPIIG AQAEVNEPGGPAFRALLDPGA
22307	52675	A	22435	3	483	VRSGNSHGEVSKGRMCLAGA LPLPGACAAVLVLLVILPEPLRC PLHTLYGGRDPVDSIRLWROA GEFRHKSNTFNNDTVSFLEY RTFQFQPSKSHGESDYIVMPN ILVLNKRSTWISVCFVHGCI SRTGPRTESMHSKSLWKAWLA APGLPL

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22308	52676	A	22436	1	1623	RRRPRLPGAEPCEPRVGPARRA DMGCSAKARWAAGALGVAGL LCAVLGAVMIVMVP SLIKQQV LKNVRIDPSSL SFNMWKEIPIPF YLSVYFFDV MNPSEILKGEKPQ VRERGPYVYK/ESSRHKS NITFN NNDTVSFLEYRTFQFQPSKSHG SESDYIVMPN I LVGVAVMMME NKPMTLKLIMTLAFTLGERA FHGTALWGEVMMWGYKDPLVN LINKYFPGMFPFGGGFVFAEL NNSDSGLFTVFTGVQNSRIHLV DKWNGLSKVDFWHS DQC NMI NGTSGQMWP FMTPESSLEFYS PEACRSMLKMYK/ESGVFEGIP TYRFVAPKTLFANGSIYPPNEGF CPCLESGIQNVSTCRFSAPLFLS HPHFLNADPVLAEAVTGLHPN QEAHSLFLDIHPVTIIPMNC SVK LQLSLYMKSVAIGQGTGKIEPV VLP LLWFAESGAMEGETLHTF YTQLVLM PKVMHYA QYVPS WALGCVLLLV PV/LSCQIRSQE KCYLFWSSSKGSKDKEAIQA GSE*SLMTSAPKGSV LQEA KL
22309	52677	A	22437	198	1062	STC VEMPRNLLYSLLSSHLSPHF STSVTS AKVAVNGVQLHYQ/HF GEGDHA VLLLP GMLGSGETDF GPQLKNL NKKLFTVVAWD P/R GYGHSRPPDRDFADFFERDAK DAVDLMKALKFKKVSL LGWS DGGITALIAAAKYP SYIHKMVI WGANA YVTDERPAG*YEGHP RMVSQMGVEGKKESL*EALYG YDYFARTCEKWVDGIR/QFKHL PDGNICRHLLP/RVQ/CPPLIVH GAEKDPLVPRFHADFIHKHVKG SRLHLMPEGKHNLHLRF ADEF NKLA\EDFLQ
22310	52678	A	22438	223	393	AQASPPLLPP*ERSNVPCPIS

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22311	52679	A	22439	524	1516	FILEDITGYVMAPIDGLLCREPR RGLYLEGTKPMTLFIQJFLNSV GDLLDLIPSLSPTKNGSLKVFKR WDMGHCSALIKVLPGFENILFA HSSWYTYAAMLRIYKHWDNFII DKDTSSRLSFSSYPGFLESDD FYILSSGLILLQTTNSVFNKTL KQVIPETLLSWQVRVANMMA DSGKRWADIFSKYNSGTYYNNQ YMLVGPESKAEPQSLTKGT/P VTLWEQIPTV/VRNISGTNLMFL RGKGFWA/SYNVVPFEKIYNWS GLSHC*FRKGLGPTPYDFRPH EPKIFRRDPR/DK*LIRHPMKYI MRYNNYKE/DPYSRGDPPVNT
22312	52680	A	22440	1	306	
22313	52681	A	22441	698	1613	FQFFQIFPEYKKNDFYVTGESY AGKYVPAIAHLIHSNPNVREVKI NLNGIAIGDGYSDPESIIIGYAE FLYQIGLLDEKQKKVYFQKQCH ECIEHIRKQNWFEAFEILDKLLA DGDLTSDPFLTSQNVGTGCS/NY YNFLRCTEPEDQLYYVKFLSLP EVRPAHPTLGN/QTFNDGPIV* KVPCGEDTSTSPVKPW/LTEIM NNYRVLIYNGIQLGHPSVAAAP DQSAPLMGMDWKGSP/EYKK AEKK/VWKIFKSDSEVA/GYIR QVGDFHQVIRGGGHILPYDQP LRAFDMINRFIYKGKWDPPYVG
22314	52682	A	22442	1	258	
22315	52683	A	22443	366	848	
22316	52684	A	22444	1	585	ECLCVSTAVRIRHEKTMTEL LRGGSFEFKDMRVPSALVTLH MLLCSIPLSGRDSDQKIQNDI IDILLTFTQGVNEKLTISEETLA NNTWSLMLKEVLSSILKVPEGF FSGILISELLPLPMQTTQVS LPYNMHLINDCSNTF*KASDSV KKQKPSSPFLPKRHKITG*GGD KTETSWSLRKYGGKNFK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
22317	52685	A	22445	625	2700	YIRGHSTPRKLWSMHLHVQAK LLQEIVRSFSGTTCCQPIQHMLRR ICVQLCDLASPTALLIMRTVLD LIVEDLQSTSEDKEKQYTSQT RLALLDALASHKACKLAILHL INGTIKODERYAEIFQDLLALVR SPGDSVIRQQCQVEYVTSILQSLC DQDIALILPSSSEGSISELEQLSN SLPNKELMTSICDCLLATLANS ESSYNCLLTCVRTMMFLAEHD YGLFHLKSSLRKNSSALHKLK RVVSTFSKDTGELASSFLEFMR QILNSDTIGCCGDDNGALMGSR RGAHTSRTMSINAAELNQLQ TEESPEDLFLELEKLDLEHSD DDNLYSLD**RGLKQMLESSG DPLPLSDQDVEPVLSAPESLQN LFNNRTAYVLADVMDDQLKS MWFTPFQAEIGITDLDLVKVD LIELSEKCCSDFDLHSELERSFL SEPSSPGRTKTTKGFKLGKHHK ETFITSSGKSEYIEPAKKEFMLC PPPRGRGRGGFGQGIRPHDIFR QRKQNTSRPPSMHVDDFVAA EISKEVVPQDGI/PSHPNRPKVS QRISSRVGFSGNRGGRGAFHSQ NRFFTPPASKGNYSRREGTRGS SWSAQNTPRGNYNESRGGQSN FNRGPLQLRPLKFPTG*PAK SLGTRAS*MVRGG/UGTFPGLS AKLAASGGSRGKFVSGGSGRG
22318	52686	A	22446	2487	3161	TWWLHISIIIPGGKKSYSPRLGR GKRFAFVLLVGGELCLTYSAP PSIHPILRSEAECLNYSIFSFLA PAGEFALPRSFDCPRVRLRAL RLALLILITFILCWTPYYLLGM WYWFSPHMLTEVPPSLSHILFL LGLLNAPLDPSPSYGAFTLGCR RGHQELSIDSSKEGSGRMLQEEI HAFRQLEVQKTVTSRRAGETK GISITSI*S*QSM*EQNSKSLVP
22319	52687	A	22447	232	337	
22320	52688	A	22448	1	1449	
22321	52689	A	22449	1	2004	

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22322	52690	A	22450	3	1558	APARDRAGGGRRALPRLPAAS ARARGLTRALSAMACRQEPQ PQGPAAAGAVASYDYL VIGGG SGGLASARRAAELGARA AVVE SHKLGGTCTNVGCVPKVMW NTAVHSEFMHDHADYGFPSCE GKFNWRVKEKRDA YVSR LNA IYQNNLT KSHIIRGHAFITSD PKPTIEVSGKKYTA PHIL IATGG/ MVPSTPH*EPRSRGASL*ITSDG FFQLEIIVPAAASLVGARLP.LSV EMAGIL/SALGSKTSLMIRHDVK VLRSFDSMISTNCTEELNAGV EVLKFSQVKEVKAL/SGLEAS MVTAVPGRLPVMPMPD VDC LWAI GGVPNTKDL SLNKLGIQT DDKGHII VDEFQNTNVKGIYAV GDVCGKALLTPV AIAAGRKLA HRLFEYKEDSKLDYNNIPTVVF SHPPIGTVGLTEDEAIHKYGIEN VKTYSTSFPMYHAVTKRRTK CVMK MVCANKEEKVVG IHMQ GLGCDEMLQGF A VAVKMGAT KADFNTVAIHPT SSEELVTLR
22323	52691	A	22451	51	464	
22324	52692	B	22452	103	1184	
22325	52693	A	22453	52	148	
22326	52694	A	22454	1	3282	
22327	52695	A	22455	145	436	
22328	52696	A	22456	1	3622	MPGYRAGPFEEAFDREDERQIE CQGRGVDRKITGEHTTFSGRSG PDHEL TLDSGKGCTSRMVPASA ASEDRRKLPII VEDEGGPTSRSA CSSPARGSRPPPSAIGCSPVAQA SDSAAGPARRTALQSLSSWLG QIDRHSVPVYVFKSPLFSVIMAP KHKSSDAGNLD RPKRSRKVLPL SEKVKVLDLIRKDKKSYAEVA KIYKNESSIREIVKKEKEIRASF AVSPPTAKVTATVRDKCLVKM EQALHLWVEE
22329	52697	A	22457	3	422	VVELRCQDKEGNPAPEYTWFK DGIRLLENPRLGSQSTNSSYTM NTKTGTLQFNTVSKLDTGEYSC EARNVGY/PQVPGKRMQVDD LNISGIIAAVCGLGVCYAQRKG YFSKETSFKQSNSSSKATTMSE NDFKHTKSFI
22330	52698	A	22458	1	208	
22331	52699	A	22459	122	321	

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22332	52700	A	22460	2	1169	HTPKTEQTPIPLGEDPPLGSQLR RRPGEGETDIPSRVPLPPLPT LCSFPAPEVQPPASCAPAAGT LDLLRAAGCRPGKMARRSRHR LLLLLLRLYLVAALGYHKAYGF SAPKDQVVTAVEYQEAILAC KTPKKTSSRLLEWKLGSRVSF VYYQOTLQGDFFKNRAEMIDFNI RIKNVTRSDAGKYRCEVSAPSE QGQKPGVEDTIVTEVLGDVHVL APAVPSCVPSALSGTVVELR CQDKEGNPAPEYTWFKDGIRLL ENPRLGSQSTNSSYTMNTKTGT LQFNTVSKLDTGEYSCEAIRNS VG*SEGPCETNASR*SQHKVGII GSRSL*WALVDFPFVGLVYSYG SEKATFSKETSFKSNSSSKAT TMSENDFKHTKSFIH
22333	52701	B	22461	57	168	
22334	52702	A	22462	1	682	
22335	52703	A	22463	398	1465	GTFPPSGLITGKKRKALLGACD CTQIVKPSGVHLKLVLRFSDFG KAMFKPMRQQRDEETPVDFFY FIDFQRHNAEIAAFHLDRILDFR RVPPTVGRIVNVTKEILEVTKN EILQSVFFVSPASNVCFKCPY MCKTEYAVCGKPHLEGLSLA FLPSNLNAPRLSVPNPWIRSYTL AGKEEWEVNPVLYCDTVKQIYP YNNSQLRLNVIDMAIFDLIGN MDRHHYEMFTKFGDDGFLIHL DNAIRGFGGRHSHDEIPILSLLSQ CGMIKKNTLLHLQLLAQADYR LSIDVMRESLLEDQLSPVLTEP HLLALDRRLQTLRTVIEGCIV AHG/QQSVH*FDGPSGNSGPR
22336	52704	A	22464	2	424	GRVGSAVIVRAWITHKYSGR DWNVKWEENLLHAYAKNYTL LQTIPPFERPFKDQHVQCLEWNM GYIWNLRANRPQCPLEN/DFRE DFHYNDTAGYFIIGGSRYVAGI EGFFGPLKYRYRLSLHPAQIFNP LLEKQLAEQIS
22337	52705	A	22465	23	323	
22338	52706	A	22466	3	287	LSVQMYAQAALDGDSDQGFNL ALLIEEGTYERCWWSHNEESFS PCSLAWLYLHLRLWGAHLHSA LIYFLGTFLLSILIAWTVQYFQS VSGKDL
22339	52707	A	22467	1	348	
22340	52708	A	22468	1	738	

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22341	52709	A	22469	1	507	
22342	52710	A	22470	187	3682	SILCLLSPCVVQFGKPVVSILSS RSRHSPCTKKGWEGMRKHLHT RQGHK*VHVKFPISIMGLQGM DYFHPDISIFCNLAIVIRAWITH KYRGRDWNVKEENLLHAVA KINYTLQTIPPFERPFKDHQVC LEWNMGYIWNLRANRIPQCPL ENDVVALLGFPYASSGENTGIV KKFPRFRNRELEATRQRMDYP VFTVSLWLYLLHYCKANLCGIL YFVDSNEMYGTIPSVFLTEEGYL HIQMHLVKGEDLA
22343	52711	A	22471	3	153	
22344	52712	A	22472	1	408	TEPEFPGRRFRPRMAVMAPIRT LVLLLSGALALTQTWAGSHSM RYFSTSVSRPGRGEPFIAVGYV DDTQFVRFDSDAASQRMEPRA PWIEQEGPEYDEETGKVKAH SQTDRNLRIALRYYNQSEAGS HTLFPR
22345	52713	A	22473	1	823	MAVVAPRTLLLLSGALALTQT WAGSHSMRYFSTSVSRPGSGEP RFSVAGYVDDTQFVRFDSDAA SQRMEPRAPWMEQEEPEYWDR QTEISKTNQAIDLESRLALRY NQSED/GPPPKTHMTHHPISDHE ATLRWCWALSFP AEITLTWQRD GEDQTQDTEL VETRPAGDGT QKVASVVVPSGQEQR YTCHVQ HEGLPKPLTLR WEPSSQPTPIV GILAGLVLF GAVIAGAVVA MWRKSSDRKGGSYSAASSD SAQGS DVS LTACKV

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22346	52714	A	22474	1	1162	NSRVDDFVAVMAPRTLALLLS GALALTQTWAGSHSMRDFFTS VSRPGR*EPRFIAGVYDDTQF VRFADSDAASQRMPEPRAPWIEQ EGPEYWDQETRNMKA\HSQTD RENRLIALPLTYNQSEAGSIHTL QMMFGCERGGSDGALSFRGLP PVTAYVDGKGFTFALNEDLRS WTAADMMAAQITQRKWETPPM WRS/EQEEAYLEG/QCV/DGLRR YLAENGKEDAAARQTPPKTHMT HHPIIS*P*RPL*RCWAL\AFYPC GDHT*PWQRDGEDQTQIDTEL VETRPAGDGTFAHKWAAVVVP SGEESEITPANVQQ*RVLPKPLT LKM/WEPPSSPAHPSPIVGHLLLA LVL/LLGAFDHLKLWAAVVML KEGTAQVGKG*KIEKGGSYSSR LPSQ
22347	52715	A	22475	9	316	IPAMGLETEKADVQLFMDDDS YSHHSGLEYADPEKFADSDQD RDPHRLNSHLKILMPFVKTL MVLPSVQTIWKSVDVIIAPLCT SVGRCFSSVSLQLSQD
22348	52716	A	22476	3	606	RPRTKAAMGLETEKADVQLFM DDDSYSHHSGLEYADPEKFADS DQDRDPHRLNSHLKLGFE\DI AEPVTTHSFDKVW\ICSHALFEI \SKYRM\YRSLTVFLGHSPWAFI CGEFSFATL\SCLAHLGF*WPFV \KTCLM/VFLPSVQTIWEEC*QM V/ISLAPLCYTSVG\RCFLFLFSLA TEPRNGILGPQVWRLGYCNTSF VIIT
22349	52717	A	22477	101	432	ATRDQLKAKPENLLGISRDSG RTQEGIPARVPYPPPP/PTREPPQ ST*PGRNGLLGCLGGGAPRPG WLDSEAGGAPAFHCPCG*CPRRH RRGGTRLKQLPPPPPTTVHDQPL
22350	52718	A	22478	794	1209	VKVDDEVTVKHLGCRCQWSRC PPSCSGTCLCCGAEAPCAQAQA WPPPPAAAPPTPPAPPSPD\NSSCT Q*PTPRCGT*DKDKGIFTLPKGGH P*V*SLHGFLLKLGSCPPPPPHA LVRPPQVRFNTPHGAEPQRDQL PQST

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22351	52719	A	22479	3	1041	GSNCPLRQADPGPPRHTLFMDF VAGAIGGVCGVAVGYPLDTVK VRIQTEPKYGTIWHCVDRDTYHR ERVWGFYRGLSLPVCTVSLVSS VSFGTYRHCLAHICRLRYGNPD AKPTKADITLLGCGLRTRPRVP DVAH*GGQSPADADTGFLSSS GGFRLSALLAAPPMPVPPACP EPKYRGPLHCLATVAQEEGLC GLYKGSALVLRDGHFSFATYFL SYAVLCEWLSAPAGHFRPDVPG VLVAGGCAGVLAWAVATPMID GIKSRLEANGQGGQNGYRGLLI CMVTSVREEGPRVLFKGLVLN CCRAFVPMVMVVFVAYEAVLRL RPGSAHHSRSPTRGATHQQLV
22352	52720	A	22480	38	453	
22353	52721	A	22481	287	413	DMDYRRGGWTVIHRKIGGRID FORVR*DYLGHYADLLREFWL
22354	52722	A	22482	1	393	MPKLLKWNVEGGACWGNLW KLPNVERLCFSEATVFRSAAQC LVVGLGLLLVSRACSHEDIAEW RGDSSVNVNVEDGSNAKDESKS NDTVCKEDCEESCDVKTKITRE EKHFMCIFHNQSLGTVCGEK GIDVN*NYTRRKTFHVYLPQCS VTGNSLRGERH
22355	52723	A	22483	505	854	
22356	52724	A	22484	584	1009	FTQKDLFIPFEVMCDMDYRGG GWTVIQKRIDGIIDFORLWCDY LDGFGDLLGDAFLFI.*KEDNQ NAMPFSTSDVDNDGCRPACLV NGQSVKSCSHLHNKTGWWFN KCGLANLNGIHHFSGKLLATGI QWGTGNQKQLTWQE
22357	52725	A	22485	1	3123	MSHRARPCAPFLFWMLGVKT EPAGQDRRKARSRCIFRVHA SGLWGLRFPSVEWGKPSRDKA QLSESPPQSVYLFAETALSAIVP GDGVAGGGGTGDGGPGAPYPG AVADMEEELTIWEQHTATLSKD PRRGFGIAISGRDRPGGSMVV SDVVPGGPAEGRQLTGDHIVM VNGVSMENATSAFAIQILKTCT KMANITVKRPRRIHLPATKASP SSPGRQDSDEDDGQPRVEEVD QGRGYDGDSSSGSGRSWD
22358	52726	A	22486	191	267	

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22359	52727	A	22487	2	609	PPRRSDEDPAKMAEVEHEEGSG PFRKFTLPAAVDL\DQ\RLDISY DQLEQPMQAVPVARPAAGGLN PGACGRKQ\HSPA*KRLQGPGS KGGAAPCHKPEAGEDATLRD\ MIILPEMWGS\WGVVYHGKTF \NQVEDQGVCGRPCRLGWAGV A*CRRDQLTPSFLGALPQPEMI GHVLEGFSTYKPVKHGRPGIG ATHSSRFIPLK
22360	52728	A	22488	3	461	STISLYCGLKTCPKLTACFPVS PDSCCRVCRGDGLSWEHSDG DFFRQPATREASHCHRSYD PPSRQAGGLSRFPGARSHRGAL MDSQQA\SGTIVRFVNLNNKHH GQVCVSNGR\TYSHGSEWHPNL RAFGIVECVLCTPTID\WPQGD *GKCRHGCPTLHYVD*LPLEKQ VILATALTMILHQADRLEVC PLGPEVTGELLWIPSKHQEPLC DLSSITNTSMDKCVFPMEGPIL MASPGTQTSGLLALW\SVCYVL PPPSIVPQGD
22361	52729	A	22489	656	1495	TGDGELSWEHSDGDIFRQPANR EARHSYHRSYDPPPSRQAGGL SRFPGARSHRGALMDSQQA\SG TIVQIVNNKHHKGQVCVSNKG TYSHGSEWHPNLRAFGIVECVL CTCNVTKQECKKIHC\PNRYPC YPQKIDGKC*QNSTCFIPEELP GQSFNDKGVYFCGEETMPVYES VFMEDGETTRKIALETERPPQVI CSTFCLA/QGILQHFHIEKISK MFEELPHGHFAFVCLLGQWKIF TEGEAQISQMCSSRVCRTELED LVKVL\YLERSEKGHC
22362	52730	A	22490	1	477	
22363	52731	A	22491	1	294	
22364	52732	A	22492	56	4042	VFFTSMEHLQKLIPASPACLA* IPQACQP*PPTPAWQCRNLRL AASRHQEP\RGVGGPLGHGAE RILAVPVRTDAQRLVSHVVSA ATSRAGVRRRAAPV\RTSPFPG GNEEEPGSHLFYNVTVFG\DLH LRLRPNARLVAPGATMEWQGE KG\TRVEPLLSCLYVGDVAG LAEASSVALSNC\DLGALIRME EEEFIEPLEKGLAAQEAQGR VHVYRRPPTSPPLGGPQALDT GASLDSL\SLRAL

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22365	52733	A	22493	173	1148	QALGLPSLLAVLALSTTDRAF SAVISRSPQRTVSSTRKEQRP L V FAPSALRLGTNACKMDGFCSTF LGAPGIRLKLTPAGTHKSERD RTATPTRHHEKRLFCSSLSIGRQ AEEAWRADHPLPESRLFGLVPL GGAAWCRLAGSFCVCSLRLPRP IELVRAASGALLGAVRRRNHGP PHCFSTATLLCKAYRGGHLTIR LALGGAPNRPFFYRIVAAQNK C PRDGPFP*SKLGPPYPD/LLPNS HGEKTPCPLN/LDRIRHWIG/CG APLLSPMEKLLGLAGFFP/LHP MMITNAERLRRKRAREVLLAS QKTDAEATDEATET
22366	52734	A	22494	2	4985	AGATTALELPGQPSVTGVP ELP GLPSATRALELSGQPVATGALE LPGPLMAAGALEFSGQSGAAG ALELLGQPLATGVLELPGQPGA PELPGQPVATVALEISVQSVVT TSELSTMTVSQSLEVPSTTALES YN/DERSMMSSYERSMMSYER SMMSMPAERSMMSAYERSMM SAYERSMMSMPAERSMMSAYE RSMMSAYERSMMSPMADRSM MSGADRSMSSYSAADRSM MSSYSAADRSMSSYTADRSM
22367	52735	A	22495	18	174	ALIKKHFI*IAAAKPTPPKSQV TLTKFFPVSSGSHRKKHEADSV YGEWVL
22368	52736	A	22496	3	595	IKKHFI*IAAAKPTPPKSQVTLT KEFPVS/GPQHRKKEADSVYG EWVPVEKNGEENKDDDNVFS NLPSEVSRNRNIMYFSFIPESAH FIVMLCLIWDSVSLFLRAGVKR QGRV*DGQMKQPAASHLTVT RM/CNSLCG/TKATKWKRLRFA ENSVITSLPNIGPSLHLWEGSP WYSIPFSFPSLLLLKVGVEFEK

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22369	52737	A	22497	3	5618	SSELPGPSVTPVPQLSQELPGLP APSMGLEPPQEVPEPPVMAQEL PGLPLVTA AVELPEQPAVTVA MELTEQPVTTTELEQPVGMTTV EHPGHPVEVTTATGLLGQPEATM VLELPGQPVA TTALELPGQPSV TGVPELPGLP SATRALELSGQP VATGALELPGPLMAAGALEFS GQSGAAGALELLGQPLATGVL ELPGQPGAPELPGQPVA TVALE ISVQSVVTTSELSTMTVVSQSLEV PSTTALESYNTVAQ
22370	52738	A	22498	1	4685	MAPESHILASNTMETHILASNT MDSQMLASNTMDSQMLASNT MDSQMLASSTMDSQMLATSSM DSQMLASNTMDSQMLASNTM DSQMLASSTMDSQMLATSSMD SQMLATSSMDSQMLATSTMDS QMLATSSMDSQMLATSSMDSQ MLATSSMDSQMLATSSMDSQM LATSTMDSQMLATSTMDSQML ATSSMDSQMLASGMTMDSQMLA SGTMDAQMLASGMTMDAQMLA SSTQDSAMLGSKSPDPYRLAQD PYRL
22371	52739	A	22499	291	7655	KRAPEKVDAYLYKQILLMKLP TKKSKKHKHKHKKKKKKKKE KEKKYKRQPEESESKTSHDD GNIDLESDFLKFSEPSVALE LPTRAFGPSETNESPAVVLEPPV VSMEVSEPHILETLKPATKTAE LSVVSTSVISEQSEQSVAVMPEP SMTKILDSFAAAPVPTTLVLK SSEPVVVTMSVEYQMKSVLKS ESTSPEPSKIMLVEPPVAKVLEP SETLVVSSETPTVEVPEPSTSTT MDFPESSAIEALR

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22372	52740	A	22500	90	2166	SQHFGRLRRVDYLRTSKMQTSS SRSVHLSEWQKNYFAITSIGCT GPKADAYRAQILRIQYAWANS EISQVCATKLFKKYAEKYSALID SDNVESGLNNYAENILTLGASQ QTDSDKWQSGLSINNVFKMSS VQKMMQAGKFKFDSLLEPALA SVVIHKEATVFDLPKFSVCGSS QESDSLPSAHDRDRDQDFPES NRLKLLQNAQPPMVTNTARTC PTFSAVPGESATAKHFVITPLFG NVKKENHSSAKENIGLVNLSN QSCFPAACENPQRKSFYGGGTI DALSNPILNKACSKTEDNGPKE DSSLPTFKTAKEQLWVDQKKK YHQFQRASGSSYGGVKKSLGA SRSRGILGKFVPIPKQDGGEQN GGMQCKPYGAGPTEPAHPVDE RLKNLEPKMIELIMNEIMDHGP PVNWEDIAGVEFAKATIKEIVV WPMLRPDIPTGLRGPPKGILLFG PPGTGKTLIGKCIASQSGATFFSI SASSLTSKWVGEKEMVRALF AVARCQQPAVIFIDEISLSLQR GDGEHESSRIKTEFLVQLDGA TTSSDDRILVVGATNRPQEIDEA ARRRLVKRLYIPLPEASARKQI VINLMSKEQCCLSEEEIEQIVQQ SDAFSGADMTQLCREASLGPI AV/SQTADIAITIPDQVRPIAYID FENAFITVRPIVSPKDL*LYENW
22373	52741	A	22501	3	523	FFFFPAFKMSKRGRGWVSPG CRKFPDFPLGLPVGTL*SNWCL TNTGAQKTLTYIISREGGIKGTG LTRLPRLPVGIDMVMMAHSSRK ANPELQKKGYIPA\VVIRQRKVI TVGKRWRCCFFIFED\NAGVIGD\ NKG\EMKGFAITG\PRAKECAD LWPRDCIQMLGSIWFSQYIL

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22374	52742	A	22502	3	946	GPSASVSFWLWSQQHSPRIHP RPGERRRLHGIPHTAEKQPA PLRPERRGRRRRPAGRRGCA* /GGARPCSSRSS*PASTPAPRAA PPCRSPCSARPTGPRTGAGRPR AP/HDGPPCATPDPRDQAS/PLPP RGPRPRVAPGSP/PEGHPRELPS EGSPGPRAPGQRHVPRPRAVL R PRGLRGGGCGPAHPAPRLQRR RAPGEEAAPGPRWPGRPGRR AQALVPAARSRCFWKLWEAVF CLPVAAAPTRRFGARQRPQLW LHGHKGQGVGEVSSHSAEEH LVPAAAPKRAREPHRGSGSPGG IASSWQDGS
22375	52743	A	22503	34	823	
22376	52744	A	22504	424	2339	LLRGTLSQYAWTSVIPDIATELR DAPEKTLACMGLAIHQVTICLM HTFV*ITFLMFAHTCTPCLTMVN VPHIHAR*GI*CIKVLLRMGH*R PFKNENAHRTGVVVRVSNIKPLC TKMAFLCAAAGEIQSFPLPDGK YSLPTKVIRSLTASLILVKKAN QNTENISRQSIK*AIRLLHKRQA LDVTLLRKSIILLHDLDVDSVPG DTVTITGIVKVSNAEEGRVQLF SLFVSQ**FINVHLF*DAPPHILV VGDPGLGKSQMLQVDNQSFVS CSFACKMR**FTSEFSLKDS SGDFALEAGALVLGDQGERPK GIISDSGTF*KAFSFSVNFLSISL AKAGVVCSLPARTSIIAAANPV GGHYNAKTYSENLK*VSSNIY TFNVLNHFNSIRKRNSSHLSEH VIAIRAGKQRTISSATVARMNS QDSNTSVLEVSEKPLSERLKV *MFLLLIQFGSV*MSKFSVWLI DVYPRLSTEAARVLQDFYLELR KQSQRNLNSSIPTRQLESILRLTE VCFFLWSCFFWLKGEGCALTSL LKRY*DKNFKLF*MKYQLSSHL KLGNRPNRSTAKRFISALNNVA ERTYNNIFQFHQLRQIAKELNIQ VADFENFIGSLND/QGYLLKKG PKVYQLQTM
22377	52745	A	22505	73	214	
22378	52746	A	22506	1	503	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
22379	52747	A	22507	3	1000	ESKLEGKAAQDIKDEEPDGLGR PKPECEGYDPNALYCICRQPHN NRFMICCDRCEEWFHGDVCGIS EARGRLRLRNGEDYICPNCTIL QVQDETHSETADQQA*WRPG DADGTDCTSIGTIEQSSSEDQGI KGRIEKAANPSGKKKLKIFQPG PGPVPTQLPVLWQVLEIAVSRSI SAFTLLHCISCKVIEAPGASKCI GPGICCHVAQPDVSYVC\SNDCIL KHAAATMKFLSSGKEQKPKPK EKMCKMPEKPSLPKCGAQAGI KISSVHKRPAPEKKETTVKKAV VVPARSEALGKEAACESSTPIS WASIDHNYNAIVKPEKTAAPSP VTVV
22380	52748	A	22508	1	2330	MAAAEGERAGGRASGRGRSE PPRPGARASDAGPGLREVEGT GEHSVVAAGTVPRVGVGAAAR GEERRAGLGECGPGLGCGVAG LISGKSVQAFSVGAGRWP LLRV FGGNVTFCVSVWSLCA\YTLPL GMDDKGDPNSNEEAAPKAIKPTSK EFRKTWGFRRRTIAKREGAGD AEADPLEPPPPQQQLGLSLRRS GRQPKRTERVEQFLTIAARRGR RSMPSVLEDSGEPTSCPATDAE TASEGSVESASETRSGPQSASTA VKERPASSEKVKGGDDHDDTS DSDSDGLTLKELQNLRKREKQ EPTERPLKGIQSLRLKRRREEGP AETVGSEASDTEGVLP SKQEP ENDQGVVVSQAGKDDRESKLEG KAAQDIKDEEPGD\LRPKPEC EGYDPNALYCICRQPHNNRFMI CCDRCEEWFHGDVCGISEARG RLRLRNGEDYICPNCTILQVQD ETHSETADQQA*MGDLGDA\ID GTDFTSIGNIRSRSLRRPKGLK GRIEKAANPSGKKELKIFQPVLE EIAVSRISAFSTLLHCISCKVIEA PGASKCIGPGCCHVAQPDVSYVC SNDCILKHAAATMKFLSSGKEQ KPKPKCKMCKMPEKPSLPKCG AQPVQWLLLLSSWQLGTSSGL QVTLQPPFTEHKWLKFSVLHG ETAGPPRAHRIRKLNKYWGAC HHCMLRPLRPLCPGWPRSSPSL

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22381	52749	A	22509	149	2001	IQPPDPRNMTLAAAYKEKMKELP LVSLFCSCFLADPLNKKSSYKYE\ AGVGDSVGGRMKASGKTVLT GRERRAQADTV\DLNWCVID MEVIELNKCTSGQSFVILKPPS FDGVPEFNASLPRRRDPSLEEIQ KKLEAAEERRRKGPDV\YEIH SPASLPFHSSDASVLGDIPPTTY SNISNSNQELLLMGGSPEQEP HYEANILERSETTSYDNGSDAA QSFKVDGRCVFYINIPISNEGK VLWKAPEIATAKEPTWSPLGST GPRPCQILVVKSPV\HGKGPVL SGCGLDLLQPTFALCFVLVAGA VTITFLSCSGEEAREESAPKAMS ERQARRGGAEEKQGAEGRLQA VTPPEL PYRMGLGA AFLKERS GVLPGSFICEDFTAALKQDEEIG TMKGKIREAYFKSFVPTPAFS GGV\MLPTGTGLEMCNNFGGH KEQAGTVLPFAIALRVTPSAS LVLRPLNLDQAMLQGSGLQL ADGLFWDLASIMDW\TASRIQPS VSSSMKICQAFGRPLAILLAQC AYVYGTWMKLEA\ILT\KL\TQE QKTKHHLFSLPCCMPADISYRQ RCLGEPHCTV\WNRHLES\VM MSNSTTSPCELLIFEVPPVAPE
22382	52750	A	22510	373	990	IQPPDPRNMTLAAAYKEKMKELP LVSLFCSCFLADPLNKKSSYKYE ADTV\DLNWCVIFRHWKVIE\LN KCT/SGANSFEVILKPPSFDGVP EFNASLPRRARPIPWEIIPVRKL GRRLRERREVTREADP*KQLAE KRIEHEERGDSKRAFRET\TFIK MAK/EKNLAQK\MESNRENREA HLAAMLRLQEK\DKHAEVVR KNKELKEEASR
22383	52751	A	22511	524	1107	LCSPKVLGLNASCQKNFLKQK KSIKTLSTSQ/YVSGYSLARSE NAHPEFRMAMKDGELVIWDSV HPCYTVFHEQTETFSWLSEYH DDFRQFLHIYSQDVACYGENLA YFPKGFIENMFV\ANPWVSFT SFDLNVANMDNFFAPVFTMGK YYTQGDKVLMP\AIQVHHAVC DGFHVGRMLNELQQYCDIEWQ
22384	52752	A	22512	1	1413	
22385	52753	B	22513	1	2787	
22386	52754	A	22514	1	1638	

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22387	52755	A	22515	71	2421	YTVCYFLQAAEEDETQNQHDD SSSDSGTPSGPDFNYILNMSLW SLTKEKVEELIKQRDAKGREIV NDLKRK\SPSDLWKEDLAGIC WRDWDKV\ENSPRNEEDVLAG MSGKSNLKGKVGKPKVKKLQ LEETMPSPYGRRIIPEITAMKAD ASKKLLKKK\KGVLDLTA\VK\I VEFDEEFSGAP\VEGAGEEGIDS HQFPINK\GPKP\RRKEKKEPGSR VRKTP\SSGKPSAKKVKKRNP WSDDESSESLEETEPPVIPR DSLRLRAADIHRLGGEGFDAGL TVFAPLFA\SPFPGRAPYLKAA CQTPRSIGIGATAISGEALKGAV SSGVDPRWASHLRVKLLEKSFS LQEIQSTKVLSQQA\TSLSLG EPKLSKQLTGTCIYRKTNLALC RGPA\AAKSLFQGA\VRNDRNKK KKETSKOECTESYEMTAELDDL TEKIRKAHQETFP\SLCQLGKYT TSLQKGMQRQILDLSSVRPIV DVRPPELQDSKLVVQAACKA PLADHCSKPVLLEKGPEDQKD QHDVGDWCWNEPCQTLFDQNN AAKKEESETANKNDSSKKLSVE RVYHIKTQLEHILLRPDTYIGSV EPLSKVAEEGPA\VGWKGWF GTESRKDPKPTGTTEE\VERGVW LSGREGRLLSPSVTTMVLAEN SAIRFVGKPSDTPVKPKRAP KQKKVVEAVNSDSDSEFGIPKK
22388	52756	A	22516	1424	4860	GRDRYGVFPLRGKILNVREASH KQIMENAEINNIKIVGLQYKKS YDDAESLKTLYGKIMIMTDQ DQDGS\HIKGLLNF\IH\NWPSLL KHGFLEEFITPIVKASKNKQELS FYSIPEFDEWKHIENQKAWKI KYYKGLG\YSTAKEAKEYFA\ID MERHRILFRYAGPEDDAAITLA FSK\KKIDDRKEWLTNFMEDRR QRRLHGLPEQFLYGTATKHLTY NDFINKELILFNS\SDNERSIPSLV DGFKPGQRKV
22389	52757	A	22517	87	292	
22390	52758	A	22518	1	903	
22391	52759	A	22519	3	311	

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22392	52760	A	22520	1	1087	MPSAAWKRPVEGPATLRRPLGI AAASQCPSSPQPGCLIGAVNLK SSNRTPVQEFESVELSCIITDS QTSDPRIEWKKIQDEQTTVVFF DNKIQGDLAAGRAEILGKTSKLI WNVTRRDSALYRCEVVARNDR KEIDEIAIEVTVQVKPVPVCR VPKAVPVGKMATLHCQGE*GP PPAIHYSWYRNDVPLPTDSRAN PRFRNSSFHLNSETGTLVFTAV HKDDSGQYYCIASNDAGSARC EEQEMEVCHTDKRGGFPWSW AAPHLWFLQDTALLPAALTGW CSVSVAFPGAQCKLSVDLSFWG LEDGGPLLTAPLGSTPVGTLCR GSDPTFPFCTALADDLYESPTPA ANFCLDIQAFSYIL
22393	52761	A	22521	628	1117	FFISVINGQVSSVQRLSGVGPAC LSCGSANPGPPGTSPGAGAQR R*IPRADGSGSPQWPRGARVGG GRLGTGGGRGPGRVQVPRRLS PGFGR*GGTGPGPVGTSGKRGP SRRRAPANDKAAACWPRFPGQP AS*TGFRGERGVKGFSSWGSG WRAWEDGGTVH
22394	52762	A	22522	2	238	
22395	52763	A	22523	131	2891	
22396	52764	A	22524	131	3103	LVSFLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPGDPDPPIVASEE ASEVPLWDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTSTIIT TTVITTEQAP

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22397	52765	A	22525	474	2527	SASPLGPYLLPSGAPERGSPGKE HPEERVVTAAPPSSSQSAEVLGE LVLDGTAPSAHHDIPALSPLLPE EARPKHALPPKKKLPSLKQVNS ARKQLRPKATSAATVQRAGSQ PASQGLDLLSSSTEKPGPPGDDP PIVASEEASEVPLWDRKESAV PTTPAPLQISPFTSQPYVAHTLP QRPEPGEPPDPAQEAPOEDTS PMALMDKGENELTGSASEESQ ETTTSTHTTTVTITTEQAPGMQPP TPMGEPPIVKHTWILDKCNVA TLQST*ALGPNEGYIDSSDYPLL PLNNFLECTYNTVYTYGYGVE LQVTPGEYFDGELLIRGVGDP TLTVLANQTLLVEGQVIRSPTN TISVYFRITFQDDGLGTFQLHYQ GRVPRPLFPRRPSGDVTVMDL HSGGVAHFHCHLGELQGAK MLTCINASKPHWSSQEPICSGM LQPQPHNATIGRVLSPSPYENT NGSQFCIWTIEAPEGQKLHLHF ERLLLHDKDR*SSEGPTNKSA LLYDSLQTESVPFEGLLSEGNTI RIEFTSDQARAASTFNIRFEGEG PWELYEPYIQGNFTTSDPTYNI GTIVEFTCDPGHSLEQGPALIECI NVRDPYWNDTEPLCRGERIHN ASAVAGVVLSPNWPEPPYVEGE DCIWKIHHVGEKRIFLDIQ/FVS V*NGSVFSQEKVRPTPEWW
22398	52766	A	22526	131	3125	LVSFLFDQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLVDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDDPIVASEE ASEVPLWDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPOEDTSPMALMD KGENELTGSASEESQETTSTHTT TTVTITTEQAP
22399	52767	C	22527	161	352	
22400	52768	A	22528	2	368	LGSTHASVRINILSVDLVIFYFY RRDDNKDIDSEKAAAMEAEIKA ARERAIVPLEARMKQFKDMLL ERGVKQSLGEIFLCISINMS C*KVKS KVSASFWEKELHKIV FDPRYLLNLI

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22401	52769	A	22529	2	614	KDHRWESGSLEREKEKLFNE HIEALTKKKREHFRQLLDETSAI TLTSTWKEVKKIIEKEDPRCIKFS SSDRKKQREFEEYIRDKYITAK ADFRLLKKEFKFITYS*FSERCE SESL*KMLGLAAPQTEVLCSSST EVRSKKLIQESQHLKDKVEKILQ NDKRYLVLDVCPPEERRKLIVAY VDDLDRRGPPPPPTASEPTRRST
22402	52770	B	22530	201	296	
22403	52771	B	22531	1	1290	
22404	52772	A	22532	3	3369	SSSVMAERGGVGGESERFNPGE \LRMAQQQALRFRGPAPPNNNA AMRGGPPPLMRPPPPFMMRGPP PPPRPPFGRPPFDNMPMPMPPG GIPPPMGPPHLQRPPFMPPPMSS MPPPPGMMFPPGMPVPVTAAGTP ALPPTTEI\WVENKTPDGKVYYY NARTRESAWTKPDGVKVIQQS ELTPMLAAQAQVQAQAQAQA QAQAQAQAQAQAQAQAQAQA QAQAQAQAQAQAQAQAQAQA QAQAQAQAQAQAQAQAQAQA
22405	52773	A	22533	43	347	
22406	52774	A	22534	1	1776	
22407	52775	A	22535	3	433	PLAPNHLGGGAVVLGAESHAS KDVAIDMMDSRTSQQLQLIDE QDSYIQSRADTMQNIESTIVELG SIFQQLAHMVKEQEETIQR*DR VNSAHPWDPVHLLPSTQQVFIE HLFM
22408	52776	A	22536	304	1403	SRGNATGLRTRIRVSTWVSQRH RSCPLQLLA\AAATSSPLPPVPT LVPPPPDTMSCRDRTOEFLSAC KFAARPVKNGI\QTN*GQLLRW LVQRQSEIHPSLAKRHLGKDL NTFAKLEKLTILAKR\KPLFDDK AGEIEELTYIIKQDINSLIKQIAQ LQ\DFVRAKG\SQSGRHLQTHS NTIV\VSLQSKLA\ASMSNDFKSV L\EVDRDGT\KQ\QREPEERQFS RAPV\SALPLSPTHRAGGA\VV GAESHASKDVAIDMM\DSRTS QQLQLIDEQDSYIQSRADTMQNI ESTIVELGSIQQLAHMVKEQ/ ERETIQRIDENVLGAQLDVEIAA HSEILKYFQSVTSNRWLMKIF LILVFFIIFVFLA
22409	52777	B	22537	147	506	

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22410	52778	A	22538	2	1397	AAPGNGLSPSSWRSELACEFQH ECTAEVRFGAVVCRGARSHSFY LEREILQ/PPGMSL/PENPVTPL RHLMYKIKSTGPITVAEYMKEV LTNPAKGYVYRDMLGEKGDF ITSPEISQIFGELLGIWFISEWMA TGKSTAFQLVELGPGRGTLVGD ILRVFTQLGSVLKNCDSVHLVE VSQKLSEIQALTLTKEKVPLER NAGSPVYMKGVTKSGIPISW*S RICTDVPKGYSFYLAHEFLDV LPVHKFQKTPQGWREVFVDIDP QVSDKLRFLVLAAPSATPAEAFIQ HDETRDHVEVCPDAGVHIEELS QRIALTGGAALVADYGHGDTK TDFRFGCDHKLHDVLIAPGT ADLTADVDFSYLRRMAQGGKVA SLGPIKQHTFLKNMGIDVR/L*R FF*INQMRSVVRQQLLQGYDML MNPKKMGERFNFFALLPHQRL QGGRYQRNARQSKPFASVVAG FSELAWQ
22411	52779	A	22539	2	377	
22412	52780	A	22540	2	1427	
22413	52781	A	22541	2	568	CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVVNPYTL LSQIPEEAESFTVLDLKD AFFCIP LHSDSQFLFAFEDPTDHNSQUT WMVLPQGFRDSPHLFGQAQAQ DLVHFSSPGTLVVQYMDLL ATSSEASCQATLDLNLFLANQ GCKRVGIALGVLTQTGHTTPQP VAYLSKETDVAAK

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22414	52782	A	22542	1	1230	GPRGTGPGKARSEKGCSSLHG PQTNKPLVVQKGQKMEQANHP VGLVISVYKDKILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIHNMNMG KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKCCSSPCNTPLGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAWEF VLDLKDAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPPQ FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGILARTRTL GKERIQPILAYPHPKTLKQLWG FLQIT/GFCQLWIPR*SKI
22415	52783	A	22543	1	211	
22416	52784	A	22544	1	472	
22417	52785	A	22545	1	393	
22418	52786	A	22546	59	411	SWPSDKQTLVVQRGQKMEQA NHDPDTHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSEASCQ QATLALLNFLANQGYK/LSRSK AQLCLQQVKYLCL
22419	52787	A	22547	43	236	TSSLRKEDSAPSQGSVVFTL TSQG*VPLWRTLQQLGPFFTPSS RK*LELSSANSQQHLGCPV
22420	52788	A	22548	1	1446	
22421	52789	A	22549	1	1521	
22422	52790	A	22550	2	689	
22423	52791	A	22551	1	64	
22424	52792	A	22552	636	1586	SNDRTEDDCGKHPFMSSPPATEP WVCLIEGQEIDFLDGTGTFVS LIPCLGLRSSRVTIQGLGQPV RYFSHLLSCNWETLLFSAFLV MPESPPTLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPLG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPPEAEW FTVLDLKDFAFFCIPLHSDSQFL AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQALQDLGHFSSPG

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22425	52793	A	22553	292	1493	SNDRTEDDCGKHPPMSSPPTFP WVCLIEGQEIDFLD.TGTTFVS LIPCLGRLSSRSVTIQGILGQPV RYFSHLLSCNWETLLFSHAFLV MPESPITPLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPIIG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLSSQVPEEAEW FTVLDLKDFAFFCIPLHSDSQFLF AFEDPTDHTSQLMWMLPQRF RDSPLHFGQAQDLGHFSSPG TLVLQYSEIAKTLTLIKEMER ANTHLVEWEPEAETAFETLKQ ALVQAPALSPTGQNFALYVIE RAGIALGLTQTHTTPQPVAY
22426	52794	A	22554	2	307	
22427	52795	A	22555	3	400	
22428	52796	A	22556	2	78	
22429	52797	A	22557	395	1336	SNNRTEGASSCHPLTEPQVCLT IEGQEIDFLD.TGTAFSVLISCPA WGTGQDSVSKKNEKKRKEKA KGNHQANAEAKIAARWNPSLE IPTEGPLVWNNPLQEIKPQYSLT ETEWGLSQGHSFLPLGWLMT EVKVLPIEASQWKILKTLHQTF QMGIENTQMAKSLFTGPNLL WTIRHVVKACEVCQRNNPLVH HKAPLGEQRIGHYPGEDWQLD FTHMPKSKGFQYLLVCVDTFT NWIEAFPCKIEKAQEVNKLVIH ETIPRFGPLQSLQSDNDPAFKA MITQGIFQGAKTISPCLLEATI LREGREGN
22430	52798	A	22558	244	638	GPLNPTFLGPPCGLGGKLVFL LRQ*VQLFRSAGSRDRCGFLDR ERNKTNQNCQKQAKKSPKDHK NPRAVGYVPFNL*QEGNLAQP GYMSPSPSLI*SRSRQTWGSFQ MILIGTKRNRPKRKSEIRERLQP
22431	52799	A	22559	210	600	RGKRTWRERRNGWSRGFCPLP LTGWSLISRESPLACLGELG VPGM*DLPHAWPTTLMCPFLV GSWSH*LQE*SHGPSQ*VLQLL RWCVWSLFLMFGCVWSFFLL VSSWSRWLRSEATDLGCEYSS

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22432	52800	A	22560	2746	5211	ETSCPLVRVHYEAETGRCTAP EDEGLGQKPPARRSNRTEGA WGKRQLMSSP/STEPVCLTIEG QEIDFLDGTAAFSVLISCPGRL SSTSVTIQGILGQPVTRYFSHLL SCNWETLLFSHAFLLMPEPRTG LLGRDILAKAGAIYMNMGKNL PICCPALLVEGINPEVWALEGQF GRAKNARPLQIRLKDPTTFPVQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSCNTPIILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAEWSWAL TFKDAFFCIPLHSDSQFLAFED PTDHTSQLTGTVLPGGFRDSPH LFGQALAQDLGHFSNPGTLVLQ YVDDLLATSSSEASCEQATPDL LNFLTNGYKVSRLKAQLCLQ EVKYLGLILARGTRALSKE*IQP ILAYPHPKTLQLRGLEITGFC *LWIPGYSKIARPLYTIKETQR ANTHLVEWEPEAETTFKTLKQ ALVQAPALSLPTGQNFSLYVRE RARIALGVLTQTHGTTQPQVAY LSKEIDVVAKGWPHCLRVVAA VAVLASEAIKIIQGGDLTV*TTY DVNGILGAKGSLWLSNCLLR YQALLLEGPVLIQICTCMALNPA TFLPEDGEPKHDCQIIIVQTYA ARDDLLEVPLTNPDLNLYTDGS SFVENGIRKVSVDVTILESKPLPP GTSQAELVALTWALELGKG
22433	52801	A	22561	903	4440	DHPGHHSSPCHERPNNVSTLFF LPGEQHPIILLPRNCPGDKILEE NFRYNNYKRTMMSFKERLENT VERCAHINGNRPRQSRGFGELL STAKQDLVLEEQSPSSNSLENS LVKDYIHYNGDFNAKSVNGCV PSPSDAKSISSEDDLNRNPDSPSS NELIHYRPTFNVGDLVWGQIK GLTSWPGKLVRREDDVHNSCQQ SPEEGKVEPEKLTLEGLEAY SRVRKRNRNGIKVPPRSRSTIG SPRPSMPSSPS
22434	52802	A	22562	1	501	

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22435	52803	A	22563	1688	2038	SATHGLSDSCYWLVSRAIGRN NLPSPASPIIHVFLAEPQLF QPRILGLIDEESGHEGGRPAKT RKLSGPWSRPAAFMSTLLINQP QYAWLKELGLREENEGVYNGS WGRGEVITYTCPANNEPIARV RQAISVADYEETVKKAREAWKI WADIPAPKPKELVRQIGDAL REEDSKLLRKPWCPLDWGKIL LEGVGEVQEYVDICDYAVGLS RMIGGPILPSERSGHALIEQWNP VGLVGIITAFNFPVAVYGNW AIAMICGNVCLWKGAPTTSLIS VAVTKHIAKVL/DNK/LPGAICS LTCGGADIGTAMAKDERVNLL SFTGSTQVGKQVGLMVQERFG RHYQNWRSLLELGGNNAIAFE DADLSLVVPSALFACCGELGQ RCTT/SRGRLFYYMESIHDEVFK QTLKRAYGTRSRVGNPWDPN VLYGAISHQGRQLSMFLGAVEE AKKERLAQWVYGGKVMDFPG NYYVEPTNVTSLDHDASIAHTE TFAPILYVFK/FKNEEEVFAWE* WK*NRGLSS*HSLPKDLGAESF RW/LGP/KGTQTCG/IVKQPFPT KWGLRLGGA/FGGEKAHLVVA RESGQ*C/WGKQYMRKVYVL FNYS/KDLPSGPQGIKQFQ
22436	52804	B	22564	1	1434	
22437	52805	B	22565	1	1185	

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22438	52806	A	22566	1	2450	GQACHASSSPLKSGRSGPPNFEI LYGPIFEDSLAPD*PKVIAGQIT LRDAVTVGPSSPNEAGKIYQLKP NPAVLICRVRLHLPEKHVTW RGEAIPGSLDFALYFFHNYQA LLAKGSGPYFYLPKTSQWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDLHLALR DHIVGLNCGRWDYIFSYIKTLK NYPDRVLPRQAVTMDKPFLN AYSRLLIKTCCHKRGAFFAMGGM AAFIPSKDEEHNQVLNKKVA DKSLEANNHGDGTWIAHPGLA DTAMAVFNDILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKQSQNLWKFA VYSGLRHGLEAALAWEDVDLE KGIVNVRRLTILDMFGPPKTN AGIRTVTLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPPRCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFIA SQMGHETAQMVEIYGMWID DMSDEQIAMLNARVMVYDVA SGNALFISELGLPENVTWLSP GEFQKWNGTAWVKDTEAEKL FRIREAEETKNMLMQVASEHIA PLQDAADLEIATEEEISLLEAW KKYRSIPLCSKVVTMMFDDRP GCPVGFPMWGRGGFDRMPGP WGGRPMPPSRDMSPHRGPPPP
22439	52807	A	22567	1	941	MIPNVQGPMPRGLEGPNYIFIKIS KNRRYTMAVTSVGLASSLCRV VRPCRAPAGVVSRSPPDEWL FCPQARIQQQDID/NGTLPDFIS ETASIRDA/DWKIRGIPADLEDR RV/EITGPVERKMVINALNAIF MADFEDSLAPDW/NKVIDGQIN LRDAVNG/TISYTNEAGKIYQL KPN/PAVLICRVRLHLPEKH/V TWGEAIPGSLFDLA/LYFFHNY QALLAKGSGPYFYLPKTSQWQ EAAWWS/EVFSYAEDRFNLPRG T/KATLLD*TLAGGFQMVDP LGG*TGPDHRLRYIKVENIPKV GEGDAETTGTA V
22440	52808	A	22568	2	393	
22441	52809	A	22569	1066	1824	
22442	52810	A	22570	2	165	
22443	52811	A	22571	3	902	

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22444	52812	A	22572	1	2034	
22445	52813	A	22573	176	873	RLFGEMSKLN/HNLSEVMSKLE KQHSSKVVFVKRLSSSSRRSLVI SPPVRTSTVSSPLTSTPSLSS KSKSESVSATEDLAPDAAQGED NSEIKELLEDEEIGKEGSEASS EEEEPLLTCTNGPSQAQSPHIESA RSQEEVPPSSPALSPGGALSPSG HPLSSAAEVVLRTRTAVPQAKG NNVVITSYMTNRGFFEDKKATF APSFMLMNIKGKNTSVVKNSILE QGQLTVN
22446	52814	A	22574	1	1890	
22447	52815	A	22575	2	1279	LSVFPRVRNFTTQAECH/KLFK VLKNFLIAGGGVHESKRAS*T LQFIYYSEWYGHEELKATVWN NDLLWEDYEELADQAVRTM EIYVAQFSEIKERIAKGRKLV YDSARHHLEAVQNATKKDEAK TAKAEEEFNKAQTVFEDLNQEL LEELPILYNSRIGCYVTIFQNISN LRDVFYREMSKLNHNLYEVMS KLEKQHSNKVFVVKGLSSPSTL SLKSESESVSATEDLAPDAAQG EDNSEIKELLEEEIEKEGSEASS SEEDELPACNGPAQAQPSPTT ERAKSQEEVLPSTTIPSPGGALS PSGQPSSEATEVVLRTTASEGS EQPKKRASIQRSTAPPKPEKPV RTPEAKENENIHQNQPEELCTSP TLMTSQVASEPGEAKKMEDE KDNKLISANSSEKIYFQRPSVLI

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22448	52816	A	22576	1	1791	MPGARTSSSGASENHRARGQG GGPOGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEAL*KLQ KAVETKDERFEQASNSFYQQQ AEGHKLKLDLKNFLSAVKVMH ESSKRVSEITLQEIYSSEWDGHE ELKAIIVWNNDDLWEDYEKL ADQAVRTMEIYVAFSEIKERI AKRGRKLDVYDSARHHLEAVQ NAKKKDEAKTAKAEFEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMSKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPSTLTKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEDEPLPA CNGPAQAQSPPTTERAK\SQEE VLPSSTTPSPGGALSPGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPRRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSPRAS LGTGTASPRTSLEI*PNPE\PEK PVRTPEAKENENIHQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEQEEVSTSE
22449	52817	A	22577	2216	2568	RPSLGLGM/CTIWQ/TSLA/GKH RRTIETHDDYRISLEQGTGPLE PPLNALTAKSKIGCNGFFPFQIR PGKNETDGRMFSPAIGIVEDPV TGNANGPMGAWLVHHNVLP DGNVLRVKGH
22450	52818	A	22578	108	532	WGSKGNLLYSHQTHSVSHQFS LVACCLELEYSPPFYACLLSS LMRLEKHQELNLWPAHQRSRMR HPQDTLVVFS/HHGRVLL*DKT SRGTIRQQHSRFTKICCSAATAA VTQANRVWSGPLANSNRPAAE GPVLAAFMGWL
22451	52819	A	22579	1	1125	

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22452	52820	A	22580	1	985	MCARGSLWGCYSLERKCEAA LPDRVVSSKSACGAVSQDLLQ AQGRRAQPPSWLYADPVHTGT IECGHGWCLNAAALLDFQSPQRL LTYLHCGLQRPMESSDPPELAPM VHHQEGIYLNIRKAMYDKPTA NKLNWDKSNVSSLITGTRQEET TANGTTFAITHLQFFIQAIPVPR KTLNLRADYYFPEHNPSLTLVI NRRITKFSEPNWEAPPSRGLTP HTAGYSSETKIPEERSDSIRGS RKSAVLQPLLLDSQANRVWSG PLANSNRPAEAGPVC*LWVVT LHGPKATMQVCQQLPW
22453	52821	A	22581	294	934	YPPSPAELTVCLRLQQLRDVL YCIAYPSGPGVKPFRGNSA/G/V VFPADNLSEAQMQLIARELGH SETAFLHSD/DSVRI/RFTPTV EVP/CGHATVAAHYVRKVL/ GLGNCTIWQTSLAGKHR/VTIE KHNDYRISLNALTAIS/KKIGC NGFFPQIRP/KNETDGRMFSP AIGIVE/DPVTGNANGPMGAWL VH/HNVLPHDGNVLRVQ*GPR
22454	52822	B	22582	1163	5585	
22455	52823	A	22583	2	429	AACAAAMSLVIPEKFQHILRVL NTNIDGRRKIAFAITASSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSVNLLSNGLYL/VKG VGRRYAHVVLKADIDLTKRA GELTEDEVERVITMQNPRQYKI PDWFL
22456	52824	A	22584	84	424	GVHAASDKPCWITTSQTPDVQ HRW/WLLISSML*TAENRRSDK AFTPHPTNHAGSQLRKHPTCSI DGVIDIFHAVNTFVQHHMEETL KAFHVTGHHILIAHGLGVGKE NTEHAANVVNDQRNSGFFCRF QQTFCQTCQQLIQRFFVNARLRD FISC
22457	52825	A	22585	88	381	IQVLANGLDNKLRREDLERLKKI RAHRGLRHFWG*VGGLSLPTS TQHSSYSLFFFPNLLFLLCMTCD SSLFTCSLRVRGQHTKTGRRG RTVGVSKKK
22458	52826	A	22586	355	699	FIDTTEAGSHFLYALVRFAATIT TITDDGARRLRTLFRQQAQDLV SVSKSGFFTADCTHTNALIDVV RTIFNNAVF*NPGFVIARLKIEIA IIKATFGQLTEDREQVLMFQAV RR

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22459	52827	A	22587	1389	1532	SVLPGRPDARQYRQTRQSW*R WSLRRLRGSYVPVAGRSLRRHRQ TERF
22460	52828	A	22588	1	427	LVHQQWQIQTKKKSLIYPFCHSP SQRVVEVAALDQWLAMLYPR VEHQAVLAVVVVVVGLVLRP YHTRRDVRLRLQPAVFIVAV DIVRILRDVIRPHCECTVRVIR SGSGSRLPAGSVAYGMRMSRS GARVRTLSILPVAL
22461	52829	A	22589	1	915	
22462	52830	A	22590	1166	1321	
22463	52831	A	22591	813	977	
22464	52832	A	22592	3485	4237	
22465	52833	A	22593	1	499	ARAAACAAAMSLVIPEKFQHIL RVLNTNIDGRRKIAFAITAKG VGRRYAHVVLRKADIDLTKRA GELTEDEVERVITIMQNPTQYK IPDWFLNRQKDVKGK\FQPGS *ANGLSTTKLRENKLPKEDSG PIKGLRQLP/WGLRVRGQHTKT TGRRGRTVGVSKKK
22466	52834	A	22594	1	1197	
22467	52835	A	22595	1	1905	
22468	52836	A	22596	37	514	WTWWLRRCYENRRHCHLLQQ LPTSPHQHAVATPTTVAVPTAP AATPPVVVAVVAVPVVVVVVP VVPVVASVPFVEPGSDVIVCAE MDEQWGYVGAKSRQRWLFYA YDSLRTVVAVHVFGERTFDVI WMTDGWPLYESRPAFTGRDC VDDAFFAVAGV
22469	52837	A	22597	1	471	
22470	52838	A	22598	2	323	SRIQPGSDVIVCAEMDEQWGY VGAKSRQRWLFYAYDSLRTV VAHV/FGERTIRTLRLRFLCLR SSHDLVSSPVSHRRRRAGSRQR HRRARGENVEYQWGALRHG
22471	52839	A	22599	2033	2310	ARYVGNAGCTGGALFGRSQTI REAVG/ERRLAESRDVAALDTP CDPEIKMAEWMQTLKETGSTS GHIVTRRISVRISHVTPGASQD GPDVQQR
22472	52840	B	22600	1	4891	
22473	52841	B	22601	7	1233	
22474	52842	A	22602	193	492	
22475	52843	A	22603	1	486	

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22476	52844	A	22604	62	443	RSDRLLIHGFSFPAMGFRLRKT VVAHVFGERTMATLGRMLSL SPFDVVIWMTDGVPLYESRLK GKLVHISKRYTQRIERHNLNR QHLARLGRKSLSFSGGTACCG HCLTRDIPMLHHQGNQLF
22477	52845	A	22605	971	1444	SMGSGDMRSPSRAAALRQLPR PFRQLAVRMEMISFRSAKEQT KSLRKWRKAKSIF*SVAQTGFN VLVCTTHIETGIDSRQPTLLSLNA RITSVCAAAPVTRSRRTFASSGY AWLLTPHPKAMTTDAKNVLKQ LPRWKISGQVRAGTARSGDSRR W
22478	52846	A	22606	1	1047	
22479	52847	A	22607	318	598	LTGFRRLCDLRFGGGAVRSVLA RSREFILQH*FRIVTGSMSRSL VPSAPLR/PSIVLVFRKAW*L VKTQRKMHVVSIVQKKASCWYP LLGCL
22480	52848	A	22608	1	2652	
22481	52849	A	22609	1	852	
22482	52850	A	22610	1	807	
22483	52851	A	22611	1	1740	
22484	52852	A	22612	1	3144	

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22485	52853	A	22613	173	1983	PVQNGSSPLGALPGAPLIFGPSV PAISRPGSCSPWPTLDTSGYSA PR/WLFTAYAGSEAVFAHVF ALGDAGLLMSLLSPFDVVIWM TDGWPLYESRLKGKLVHISKRY TQRIERHNLNLRLQHLARLGRKS LSFSKSVEQHDKLESLPGQIDKS LDEASLSLRAGSLRTITHILLPLL RPAILSALIYSFVRAITTVSAIVF LVTPDTRVATAYILNRVEDGEY GVAIAYGSILIVVMLAIIFIDWL IGESLLSRFEKTVDDHSQSRLPA EGSILSQDISGVKLFSLTPARG YVPIRAPCPFLCASYRFFCVARQ QGLDAALIDAPLAVDALTPLE LLSHVGQAPCSVPVDEDDQY VGIISKGMLLRALDREGGVRVP VDYILNGFHPLLLGMPAPLAIIV FALIAACRFPGSGNRIRRSRRIRH LHKMPDATALSASYQAYVRHQT NVTALVLRSSHRFRKDRHCWG FVFLQQPILRATGQFEIQTFRYL SVFSVQRHKTNGKTALMSGNV ADKAVNRATGPTACVWLFSLR NSSMVTTRFCGLCEWADQQGA RPARISENGKRGYSYLYDVHM GAQSGETRGRQGEYASKPPSRE
22486	52854	B	22614	1	2149	
22487	52855	A	22615	1	1815	
22488	52856	A	22616	2014	3411	
22489	52857	A	22617	1	922	MVICQPINGGWQWPPSTGTDP APYFRIFNPITQGEKFDHEGEFI RQWLPELRDVPKVVVHEPWK WAQKAAAPPQTRLHSTPTTIPH RVPGHPTPNLKPIWEVDLPKFSH KATSHATDKPSDTTQNDQIVIA YMEPPEIVHETTTSTHPSLYIIL KRQTRELRPQSVTSRIQPGSDVI VCAEMDEQWGYVGAKSQRQW LFYAYDSLRLKTVVAHVFGERT MATLGRMLMSLLSPFDVVIWMT DGWPLYESRLKGKLVHISKRYT QRIERHNLNLRLQHLARLGRKSL SFSKSVELHDKVIGHVYLNKHY

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22490	52858	A	22618	1458	2185	YGHEWRWMPGNRPH\YGRWP QHDFFPKKLRPQSVTSRIQPGS DVIVCAEMDEQWGYVGAKSR QHWLFYAYDRLRKTVVAHV GERTMATLGRMLSLSPFDVVI WMTDGWPLYESRLKGLHVIS KRYTQRIERHNLNLRQHLARLG RKSLSFSKSVEKITSGPTTNA TP GTQKTATDKRGGKKLPQIPIGP ISRIASGAAINTISIGLRKFLVTA GVMLSTQRSIYDRHQVITSAGIT
22491	52859	A	22619	493	1518	
22492	52860	A	22620	963	1597	
22493	52861	A	22621	1	3052	MATDSVGLNCTPAPHARDVLL WRPSSLPVSTSCVFPGLGRIGDVS DESDDKTEAPTPHRLKAREEG QIPRSRELTSLILLVGVSVIWF GGVSLARRLSGMLSAGLHFDH SIINDPNLILGQIILLIREAMLAL LPLISGVVVLVALISPVMLGGLVF SGKSLQPKFSKLNPLPGIKRMFS AQTGAELLKAILKTILVGSVTG FFLWIIHWPQMMLMAESPITA MGNAMDLVGLCALLVVLGVIP MVGDFVFFQIF
22494	52862	A	22622	1	1233	MANDLPHSNSGDGQKPSPLDF TAPLLADPTVGFLPNDAEELFIF LTEITEITPCRVTDQPLVVTLHE KKGDVALPVYPYDHQGFSGIFE DRSYICKTTIGDREVDSDAYYV YRLQAVPPVQLLTGWCVTAKA PPDISAISALTAVKHGNCSSLTP LLNPPGSDVIVCAEMDEQWGY VGAKSRQRWLFYAY\DSLRLAR RVVAHVFG*RTMATLGRMLSL LSPFDVVIWMTDGWPLYESRL KGLHVISKRYTQRNERHNLNL RQHLARLGKSLSFSKSVELHD KPSQHQREGVKDVMRFNEPMY PLESRPRLYVCHLRNGAQASGR RCQLPMGCACHPVSQRNDRPN RRPERHATRKTTTRQORQNSRQ HKQTQKKAKPNKRRATERGKG PQQKAERPKRHTHCFCLKQ

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22495	52863	A	22623	3	1386	HEASSPLAMASLTVKAYLLGK EDAAAREIRRFSCSPPEAEAE AAAGPGPCERLLSRVAALFPAL RPGGFQAHYRDEDDGLVAFSS DEELTMAMSYVKDDIFRI*IKE KKECRDRHRPPCAQEAPRNMV HPNVICDGCNGPVVGGTRYKCS VCPYYDLCSVCEGKGLRHGHT KLAF\SPFGHL\SEGF\SHSRWL\ RKVKHGHFGWPGW\EMGPPG\ NWEPTFLPRAGEARPGP\TAES ASGPSDEPSVNF\K\NVGESVA\ AAFSPLANFEVD\IDVEHGGKRSR LTPVSPSSSTEES\SSQSPSSCC SDPSKPGGNVEGATQSLAEQM RKIALESEGRPEEQMESDNCSSG GDDDWTHLSSKEVDPSGTGELQ SLQMPSESGPSSLDPSQGGNPQ GWKEAALYPHLP\PEVEPAA*F ESLSQMVPVPGF*\LKGWVH QGSCRPRNYDIGAAL\DTIPVIQ
22496	52864	A	22624	1032	1127	FYAKAEAGDRTVA*PHKPKMF LSIHHRVAKI
22497	52865	A	22625	121	561	VFPGLGSLVDICGPSRVFPFWV VPAVLVPVQVQRLPRFFRCPPV LVTSVIRISITLIQALGSSPFARR YWGNLG*FLFLGVLCFSSSTGS PH*PMNSVNDVS\SKHT/EVTPF GNPGNNGSYHLTDAYRRLARP SSPLTPGHPPLYG
22498	52866	A	22626	243	454	ATAGCPCSCATEGVVRNGKST AGHQRYLCSPCRKTWQLQFTY TASQP/GARIMGVGLNTVLRHL KNSGRSR
22499	52867	A	22627	3	640	
22500	52868	A	22628	236	410	
22501	52869	A	22629	116	359	

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22502	52870	A	22630	276	1905	LFLYSSHGQYGCPCSATDGVV RNGKSTAGHQRYLCSHCRTW QLQFTYTASQPAGQ*RTAIATVI CCNNCQRRHTNSRCHTDNCRR ADSASSHATSGSSRGCAGSGR CGASSTRCLGPVCCFRGSKRS WRRQHEGHKDCRKLVFHNFSEI HRMDNTAVPPVQLLTGWCVTA KAPDISAISALTAVKHGNCSSL TPLLNPPGSDVIVCAEMDEQW GYVGAKSRQRWLFYAYDSLKK TVVAHVFGERTMATLGRMLSL LSPFDVVIWMTDGWPLYESRL KGKLVHISKRYTQRIERHNLNL RQHLARLGRKSLSFKSVELHD KQQGLDAALIDAPLAVDAQTP LSELLSHVGQAPCAVPVDEED QQYVGIISKGMLLRALDREGGV RVVPVIYPKFRFTTDCMPLSLG TCIREIEAEFPDPIFRRSVVYICE HNTNGAMGIIYNKPLENLKIEGI LEKLKITPEPRDESIRLDKPVML GGPLAEDRGFILHTPASNFASSI RISDNTVMTTSRDVLETGLTDK QPSDVLVALGYASWEKGQLEQ EILDNAWLTAADLNILFKTPIA DRWREAAKLIGVDILTMAQD GTPDWNIERLLKEWQPDIIIVG LPLNMDGTEQPLTARARKFAN RIHGRFGEVVKLHDERLSTVEA RSGLFEQGGYRALNKGKVDSA SAVILLESYFEQGY

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22503	52871	A	22631	399	2337	PEVQGLQQAGAAARRPGVGLA APRVVCEGRRLRSGGLQSRCLPG ASV*ATDGVVRNGKSTAGHQ YLCCHCRKKTWQLQFTYASQP AGQ*REKEKEKEVEEEEEKEK KRRREGEKEKEKEKEKEK FKKKKKKKKKKKKKKKKKKK KKKKKKKKQLSLVTVMSSQQQL WRNEARTTGACLPSTVSAAP PIVSTTVTAFAAATLAKGDLRS RASSKQVPLLVVLVWVWPHPG WFKAGSVALGSSPGCVLELL CKLLTGWCVTAKAPPDISAISA LTAVKHGNCSSLTPLLNPFGSD VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSLRTTVVAHVFE RTMATLGRMLSLSPFDVVIW MTDGWPLYESRLKGLHTQER KARSKQKQDADTAPPIQVGTQ TPQTVHAARDTRQASPRASKIS QHRQADGDKRQTRHAEAQAT RHTGRRKTIKETATQQAAYADE QTRRTARTHRRRTARHTAAHTH RTRVAARQTTEKDNEQSDTQPP TQKTPSATATAHTPRRTETTTNI VQARHTSARERNHTRQHQA RETTINAHTNTPHYHAEHTQSR SQQQTSTERTPTDSSTTINNN HTPRTVRDERMTQHKHPSRA STTTNRTTTTGAYQHTQDRDTRD TRRDTHEDTTTQPHTTTPTAN EAYTAHTTKTDHHRHTADDT
22504	52872	A	22632	103	313	ATAGCPCSCATGTVVRNGKST AGHQRYLCSPCRKTWQLQFTY TASQP/GARIMGVGLNTVLRHL KNSGRSR
22505	52873	A	22633	620	832	

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22506	52874	A	22634	453	1047	AADDRGHLRPTDGLLRNGKST AGHQRYLCSHCRKTWQLQFTY TASQPAQG*RVGTGTSERREQIIQ RLRQQGSVQVNDLSALYGVST VTIRNDLAFLEKQGIIVRAYGG ALICDSTTPSVEPSVEDKSALNT AMKRSVAKAAVELIQPGHRVIL DSGTTTFEIALRLMRKHTDVIAM TNGMNVANALLEAEGVELLMT AGICALLTGCCVTAKAPPDISAI SALTAVKHGNCSSLTPLLNPFG SDVPVCAEMDEQWGYVGAKS RQRWLFYAYDSLRTTVVAHV GERTMATLGRMLSLSPFDVVI WMTDGWPLYESRLKGLHVIS KRYTQRIERHNLRLRQHILARLG RKSLSFSKSVELHDKVIGHYLN GDFLQSTLREAPIPHREHP
22507	52875	A	22635	1089	1686	TSPGYWRANSTDPDGRYCRTG TSGGVCHALSSLRCPSCSATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQPAQG*RFLSK QEKTLINQLASEEQKQVTSRL SDALRNGRVWQLAIIYLTIQVA VYGLIFFLPTQVAALLGTVKGF TASVVTAIIPWVAALFETWLIPR YSDKTGERRNVAALTLAAGIG IGLSGLLSPVMAIVALCVAAGIF IAVQPVFWTMTPTQLLSGTALAA GIGFVNLFGAVGGFIAPILRVKA ETLFASDAAGLLTLAAVAVIDR RGTSNLRLNRTMIALLSNPFKE RLRKGEVQIGLWLSSTTAYMA EIAATSGYDWLLIDGEHAPNTI QDLYHQLQAVAPYASQPVIRPV EGSKPLIKQVLDIGAQTLLIPMV DTAEQARQVVSATRYPPYAVH PVQLLTGWCVTAKAPPDISAIS ALTAVKHGNCSSLTPLLNPFGS DVIVCAEMDEQWGYVGAKSR QRWLFYAYDSLRTTVVAHVFG ERTMATLGRMLSLSPFDVVIW MTDGWPLYESRLKGLHVISK RYTQRIERHNLRLRQHTGTGW DGSRCRSQKSGGAA
22508	52876	A	22636	91	200	SGIIAFQYLLMTLKVLPVASVSI SCPSCSATDG VVRNGKSTAGH QRYLCSHCRKTWQLQFTYTAS QPAGQ*RGGA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
22509	52877	A	22637	2649	3270	GAPVASVSISCPSCSATDGVVR NGKSTAGHQRYLCSHCRTWQ LQFTYTASQPAQ*RTIGRAML KNKHMTITEFVAQRMDDAQK GEISPDINTAMTSRLLLDLTYGV LADIEAEDLARKRRLRLTRDD WRYLNRILILSLFRAGDNCAR VSYQTPTREIKKLDGLWAFSLD RENCIDQRWWESALQESRAIA VPGSFNDQFADADIRNYAGNV WYQREVFIKQWAGQRIVLRF DAVTHYGKVVVNNQEV
22510	52878	A	22638	1	2470	MNADTDYSIAEAFNKGETAM TINGPWAWSNIDTSKVNNGVT VLPTFKGQSPKPFVGVLSAGIN AASPNKELAKEFLENYLLTDEG LEAVNKDKPLGAVALKSYYEE LAKDPRIAATMENAQKGEIMP NIPQMSAFWYAVRTAVINAAS GRQTVDALKDAQTRITNCCRI RRESLIRPGMRKNPMDVIKKKH WWQSDALKWSVLGLGLLVG YLVVLMYAQGEYLFATITLILS SAGLYIFANRKAAYAWRYVYPG MAGMGLFVLPLVCTIAIGFNN YRRTKQVAGMPAKSSSLRSSQ DREMRPGAKAERTYDPSGSY GVAGPGFLGSRGSPFGGPGKY NNTITKYALNIAPSAQNQSPHG PKLNRRQETQHALDWLDAGYT FTYSEDQALTPYFKLAYVYDD NNDNDVNGDSIDNGTEGSAVR VGLGTQFSFTKNFSAYTDANYL GGGDVDQDWSANDLTGITAKD AQMLSVVKPLQEFGLDKCLS RYGTRFEFNNEKQVIFSSDVNN EDTFVILEGVISLRREENVLGIT QAPYIMGLADGLMKNDIPYKLI SEGNGCTGYHLPKQTTITLIEQN QLWRDAFYWLAWHNRIELRD VQLIGHNSYEQFAHIFMIAAM QMGSVWGDDFSSGQHSVARKS QLHKPILRVKCHEGFTISANPNS SPRYPTHEQAEQPRIVDFSVRF
22511	52879	A	22639	1	852	

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22512	52880	A	22640	1	747	MIIDPRYTDGTGAGREDEWIPIR PGTDAALVNGLAYVMITENLV DQAFLDKYCVGYDEKTLPAS PKNGHYKAYILATD/GVVRTAK STAGHQRYLCSHCRTWQLQF TYTASQPAGQ*RYTDTGAGRE DEWIPIRPGTDAALVNGLAYV MITENLV DQAFLDKYCVGYDE KTLPASAPKNGHYKAYILATDG WCVPPKAPPDISAISALTAVKH GNCSSLTPLNPPGSDVIVCAE MDEQWGYVGAKSRQRWLFYA YDSLRTTVVAHVFGERTMATL GRMLSLSPFDVVIWMTDGGWP LYESRLKGLHVISKRYTQRJE RHNLNLRQHLARLGRKLSFSK SVELHDKVIGHYLNKHYQ
22513	52881	A	22641	1722	2463	NPRLAGSEGCSPCSATDGVVR NGKSTAGHQRYLCSHCRTWQ LQFTYTASQPAGQ*RKLTGCL FVALKGERFDAHDFADQAKAG GAGALLVSRPLDIDLPLIVKD TRLAFGELAAWVRQVPARVV ALTGSSGKTSVKEMTAAILSQ GNTLYTAGNLNNDIGVPMITLL RLTPEYDYAVIELGANHQGEIA WTVTHPPRFVTKWQLCLPDG LLLFAEARFVIWQMOPAVMAV DVAAFAHLFNQQYQRFTRGP PDSSKLPWKITCNGECVTFHW WLLGVAVRISRLLPVRVMTAL EGNYNGTEGIALPFGIILAH NESEWVTRNNKNNEAFLDRV YIVKVPYCLRISSEIKIYEKLL HIFECWQHFLNPESLQCYIWA ANADFREARQVIFKTFVTGVGE EELGIRQTRTNDLFTGDNLLRI FRFDVGNEDKVRQQA VVRIH REVFLVTFHGVNQRFSRHREEF LFECVSVTANLTRCFGIGFNL RLTFFVIGDDFPTLTQNFRLIGV IDGFEFLAHKAVAAANHAIGLNA QNGCRNDFVAHAAGSRALAAD GRSLEHAPTVETVVAGPLCESG DVFTQEQEGGNVETRALPEVKA AVPPVQLLTGWCVTAKALPDIS AISALTAVKHGNCSSLTPLNPP GSDVIVCAEMDEQWGYVGAKS RQRWLFYAYDRLRKT VVAHRL

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22514	52882	A	22642	90	1254	KGLCSHSEMVVPSYSATDGVV RNGKSTAGHQRYLCSHCRKTW QLQFTYTASQPAQG*RDIVLTK LMMVWHSQSGYEKAYAHQIR WWYRAILLTGWCVTAKALPD ISASALTAVKHGNCSLTPLLN PPGSDVIVCAEMDEQWGVYGA KSRQRWLFYAYDRLRKTVAHV VFGERTMATLGRMLSLSPFDV VIWMTDGWPLYESRLKGKLVH ISKRYTQRIERHNLNLSSTSLVL LNGATQFQDLGDLNKELEETY TDSKNHISCVGNDGFGNDIFSR YVEAVGREGDVLLGISTSGNSA NVIKAIAAAREKGKMTLTLTK DGGKMAGTADIEIRVPFHGYA DRIQEIHIKVIHILQIEKEMVN FTGLVQGGGTGPHKDGWGIT FYEVAFEDVAVNFTQEEWALL DPWOKKLYRDVMLETYRNLAS VGDDDNIPSLREQVAHQRYFKT WHVEREYFSK
22515	52883	A	22643	690	1233	RLQSLHYQGRGKPVPMRSYLS FLFTISNSAGVFRCPSCSATDGV VRNGKSTAGHQRYLCSHCRKT WQLQFTYTASQPAQG*RLLGP KNRPREQNWLLWCERGVMRL QALYLREQGFNNVKVDNFQTK VDSCTRPLAGQFYPCIPDDAL VQPLFGGNFVFORREAGHITNR EDIVRHQHGGRGANSRDDTP GTVELFNGFNQSAIAKTLRAF NATRQHDHVIFAISHFDQRIR QQLHAARAGNRQVTIAGDAGS GDFDTAANQQIDS GDGFSLFTT RGEANQCRCACAHHSPPFLPFQT VRVFSAPVPVQLLTGWCVTAK APPDISAISALTAVKHGNCSLTP LLNPPGSDVIVCAEMDEQWGV YVGA KSRQRWLFYAYDSL RKT VVAHVFAVKPYWDTGGGFHC RWIYMQQEKELLQLSLQQGY NQKRAAELLGLTYHQFRALLK

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22516	52884	A	22644	1314	1483	RIQRYCGKTCGPCSATDGVVR NGKSTAGHQRYLCSHCRTWQ LQFTYITASQAGQ*RMFNADG SEVAQCGNGARCFARFVRLKG LTNKRDIRVSTANGRMVLTVT DDDLVRVNMGEPNFEPSAVPF RANKAEKTYIMRAAEQTLGCV VSMGNPHCVIQVDDVDTAAVE TLGPVLESHERFPERANIGFMQ VVKREHRLRVYERAGAGETQA CGSGACAAVAVGIQQGLLAE VRVELPGGRDLIAWKGEELQET LTELDRAVVDYLIKNEFFIRN ARAVEAIRVPHVRGTVSLVE WHMARARNHIHVLEENMALL MEQAIANEGLFYRLLYLQSLT AASSLDDMLRMFRHWARDLG LAVAMPVTINKGNQIENQLDT ETITISYEFILCQHIANTEFSYL ALPENYNRLCLPNSKNQTNRF KTLNSKAIGRLLAAGVYNGNI EGFRDTAEKLAVPPVQLLTGW CVTAKALPDISAISALTAVKHG NCSSLYTASQAGQ

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22517	52885	A	22645	1479	1793	TRYRSCPCSATDGVVRNGKST AGHQRYLCSHRKRTWQLQFTY TASQPAQG*RRNACQYRTPAV VASRQKRWHGDLGMIGSRDV MLFISDSVGAKELDLIIPLEDK SIALLAMITGKPTISPLGAAKAV LDISVEREACPMHLAPTSSTVN TLMMGDALAMAVMQARGFNE EDFARSHPAGALGARLLNKVH HLMRRDDAIPQVALTASVMDA MLELSRTGLGLVAVCDAQQQV QGVFTDGDRLRRWLVGCGALT PVNEAMTVGGTTLQSQSRAIDA KEILMKRKITAAPVVDENGKLT GAIKLQDFYQGRGLFNPSIPRVS TADAGLANRARNWVGSSWK QVGQIILQGGPQNAEKSGQRYT VSHDRHRDAERQVRKSGLPY AECSTYPCPVALDLAFASHGI HMHAPGEALRMLVTAMDKAA DARTKLARLLATKGITHEIQIPD ISTKEKAQQPIGLNMEQIKPEKQ DFIKPVIPQAGKHNGVNMVLR SLLTAGVLASGLLWSLNGITAT PAAQASDDRYEVTQQRNPDAA CLDCHKPDTEAVPPVQLLTGW CVTAKAPPDISAISALTAVKHG NCSSLTPLLNPPGSDVIVCAELD EQWGYVGAKSRQRWLFYAYA QSPRTTRCCARIRLHALWRRW

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22518	52886	A	22646	807	1350	NRGCPSCSATDGVVRNGKSTAGHQRVLC SHCRK TWQLQFTYT ASQPAGQ*RLNRLIEPTRGQV LIDGV DIAKISDAELREVRKKI AMVFQSFALMPHMTVLDNTAF GMELAGINAEERREKALDALR QVGLENYAHSYPDELSSGGMQR RVGLARAINPDILLMEAFSAL DPLIRTEMQDELVKLQAKHQR TIVFISHDLDEAMRIGDRIAMQ NGEVVQVGTPEILNNPANDY VRTFFRGVDISQVFSAKDIARRT PNGLIRKTPGFGPRSAKLLQD EDREYGYVIERGNKFVGAVID SLKTAAPPVQLLTGWCVTAK APPDISAISALTA VKHGNCSSLT PLLNPPGSDVIVCAEMDEQWG YVGAKSRRQWLFYAYDSL RKT VVAHVFGERTMATLGRMLSL SPFDVVIWMTDGPWLYESRLK GKLVHISKRYTQRIERHNLNLR QHLARLGRKSLSFSSVELHDK VIGHYLNKHYQ
22519	52887	A	22647	1	1270	MTAATEQLNASRGLSTREMER QAEAKITTDYINSGGSEGDEK LQNMKAQNDYYAAEDAKRA DWLAGAESAFADYGD SAMDM YGNVNEIASSALNGMTMMV QFLTGTGKAFADF AKNIISMIK MIAQMVIFNTSLRNDGRSVSSG GAAVSLAAAAGSVATSGFNAS NSAPKVVITIREVERSDVSGME ASSTSWITIRSFATETSTFGPTM TASMTFLPTYCSIIASLLSSFKLA AATDGVVRNGKSTAGHQRVLC SHCRK TWQLQFTYTASQPALA RNPNRDITIYWGGREEQHLYDL CELEALSLKHPLQVVPVVEQP EAGWRGRTGTVLTAVLQDHAT DGVVRNGKSTAGHQRVLC SHC RKTWQLQFTYTASQPGTHQKII DMAMNGVGCRTARIMGVGL NTIFRHLKNSGRSR

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22520	52888	A	22648	381	945	GAPVASVSI SCPSCATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAQ*RTENQTPH VLTHKWELNYENPWTQGGHLL TMGLVVGWRGLQEGDPARTN LSYYQANVGSGQHRENGKPIN LGNVGKSNGERGGKSLYRCKIF LESSVTMKDRELPPVYDGVFEV LQWLLFLSAVPPVQLLTGWCV TAKAPPDISAISALTAVKHGNC SSLTPLNPPGSDVIVCAEMDE QWGYVGAKSRQRLFYAYDS LRKTVVAHVFGERTMATLGRLL MSLLSPFDVVIWMTDGWPLYE SRLKGKLVHISKRYTQRIERHN LNLRLQHLARLGRKSLFSKSVL LHDKVIGHYLNKHYQ
22521	52889	A	22649	354	1119	RRWRRGAHEAATGGTGRGPAE EAAPEGAAGRAAPKSGGKRL GGVLGRG GVGRRSGSPDRSGA HSAAPRRRCRLPGRCPSCATD GVVRNGKSTAGHQRYLCSHCR KTWQLQFTYTASQPAQ*RSK GAIGEGPPDRGIVEQNLGGDIS IPCYNRP RRRSAQKTTGLPLN QPRIPSAQCAGAFPRVAAAGAG GGGGGGSGSGFCLGWRLRRR RQRRRRWRRGEGEGDGDAGH MRPRPAGRAEARRRRLRGPN PPGARLPNREGNSGVSWAEE VSGDGRGARTEAARTRRRPGG ADNYPGA VPPVQLLTGWCVTA KAPPDISAISALTA VKHGNCSSL TPLNPPGSDVIVCAEMDEQW GYVGAKSRQRLFYAYDSLRLK TVVAHVFGERTMATLGRLLMSL LSPFDVVIWMTDGWPLYESRL KGKLVHISKRYTQRIERHNLL RQHLARLGRKSLFSKSVLHLD KVIGHYLNKHYQ
22522	52890	A	22650	23	658	VISRFSGSIQVRGLLSRHGLAL GSAPDLWKLPPWNLVQGMGQ QSQSSCREGCSRPQCPSAAPC GAAPAHFCSAATFWESEVQSIP R/CRATDGVVRNGKS/TAGHQ RYLCSHCRKTWQ/LQFTYTASQ EVISSPTAPRSDGKTVPPLM GISP*SAHHRLATSDPSLCSLES LCSREPA AVPRASNQQPQGVK DVHHQFTARTSRYPSC
22523	52891	A	22651	926	1093	

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22524	52892	A	22652	343	817	GGARSRQNPRCGPCMVVVPGQ SGRSVSADSSTEFREQGGVAIS FPKSINRAGPELFRFMENPFNSV *YRKNVRELTPAIVAVLPVEFR TRLAPQNDTMSLIASAMKECSE AKQAVLLNAPEHQMKKEVSEG IASLFRLMPEQVGPLMTMVT MLGVI
22525	52893	A	22653	115	425	
22526	52894	A	22654	747	1173	
22527	52895	A	22655	1	2709	
22528	52896	A	22656	1	2583	
22529	52897	A	22657	636	1029	APSDQKRDFLVPHGADSAMAK SG*CESGNDLSSSHMNQLR/A/ ESIPEDVIAGASALVLTFIKFI AENPQWWQFLKDHVSILAMN EDEAEALTGESDPLASDKALD WVDLVLTCTAGPIGLYMAGGGD VN
22530	52898	A	22658	1611	3300	QSAWANRHLRVDCRPGNGSD AGVAARSGRNDGTGRCLCHS CSRYGDHHRQSDRIYRHYDAG RSPSGAVDYGTRQGNRFSRAV YPVGA/RRWR*GLPLV/QQFQPE NETSAAWVVGINQPLVDIEAK VDDEFIERYGLSAGHSLVIEDD VAEALYQDVQQKNLITHQSAG GTIGNTMHNSVLAADDRSVLL GVMCSNIEIGSYAYRYLCNTSS RTDLNLYQGVDGPIGRCTFLIG ESGERTFAISPGHMNQLRAESIP EDVIAGASALVLTSLVRCKPG EPMPEATMKAIEYAKKYNVPV VLTGTGKFVIAKNPQWWQFL KDHVSILAMNEDEAEALTGESD PLASDKALDWVDLVLTCTAGPI GLYMAGFTEDEAKRKTQHPLL PGAIAEFNQYEFSSRAMRHKDC QNPLRVYSHIAPYMGGPEKCN LGRSGWLLYGRGLDKQRLTQY QSKLGAAMVIVAACWVEDYQ VIRLAGSLTARATRLAHEAQLD VAPLGKIPHLRTPGLLVMDMDS TAIQICIDEIAKLGTGEMVAE VTRTGDARRTRFYRQPAQPCG
22531	52899	A	22659	430	586	
22532	52900	A	22660	1	131	

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22533	52901	A	22661	1	1282	MLPAHLDACVTTLQKIRWTL VVDPPTLALRVPLPALSRDDPPL RAYLPGRGALKVIRFDDMDFA TIDGINRMLVDIDTNYLFLPRVT SSTIRCLSVPTRTVPAVTSAGR SVKYYPPDFDPSKIPKLLPKD RQYVVRLLMAPFNMCRKTCGEY IYKGGKFNARKETVQNEVYLG \LPI\RFYIK\CTRCLGRDSPFKT DP\ENTDYTM/ESLGATRNFGQ* EASWEEEEKRVQK\EREDE/ES LNNPMKVLENRTKDSKLEMEV LENLQELKDLNQRQAHVDFEGV MLRQHRLSEEEERRSQQEEFEQ KTAALLEEARKRRLLEDSDSED EAAPSPLQPALRPNTATLDEA PKPKRKEVEVWEQSVGSLGSRPP LSRLVVVKKAKADPDSCNGQP QAAPHPRSPAEGEGGPYTPDA WRVLPPTGCPGQ
22534	52902	A	22662	1	412	
22535	52903	A	22663	298	532	MGSWSLPGRTLWKEKVRFLKS KERTNPGSNFFSPGQHTREER SQECLSLPVLPSYLATRLSLPDS CPLKGRKAH*QRHSEI*LMGFE PGWPGKL*GWIELAFLGCLHL TLPLPCPTPLPPKSTKSGCFLSI ALCFNKQFAVTK
22536	52904	A	22664	1	193	
22537	52905	B	22665	55	281	
22538	52906	A	22666	86	159	
22539	52907	A	22667	63	1036	VRGGLAAGRGRGSAGAAPVVV AAMLGA WAVEGTAVALLRL LLLLPPAIRGPGLVAGVAGAA GAGLPESVIWAVNAGGEAHVD VHGIHFRKCIPL*GRVGRALYY GMKLPILRSNPEDQSCYQTE\RS N\ETFGYESPIQREGGLTCWSL KFAEVYFAQSQQKVFDVRLNG HVVVKDL\IFDRVGHSTAHDEI IPMSIRKGLSVQGEV\ST\FTQG KLLPLSFSKGYL*PIPKVCALYI MAG\TVDDVPKASAFNPGLEK KEEEEEEEYDEGSNLKKQTNK NRVQS\GPRTPNPYALDNSSL MFPILVAFGVFIPTFLCLRL
22540	52908	A	22668	1570	1773	

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22541	52909	A	22669	62	454	NKQLNKKRRRTMIALIQRVTRA S/VTVEGEVTEIGAGLLV/LLG VEKDDDEQKAN/RDAEQGM/N LNVQQAGGSVLVVSQF/TLAAD TERGMRPSPFSQGHHRRAQAFY DYFVES/CRQR*YAQGGLSAE FRLLNS
22542	52910	A	22670	1	1930	MAGKPEYDKTISTIVL.NALNA LGVSAEASGRNDLVVKTVEGD RKVSGSAYRETKDRGFHHGTL LLNADLSRLANYLNPKKKLA AKGITSVRSRVNTLLELLPGITH EQVCEAITEAFFAHYGERVEAE IISPNTDPLNFAETFAQQSSW EWNFGQAPAFSHLLDERFTWG GVELHFDVEKGHITRAQVFTDS LNPAPLEALAGRLQGCLFSLYN SDLNTVIDNVLRIFFLLSWISF WLLYSIVPTIRVFNDAIVGAFV AALLFEAGKKGFALYITMFPST QLIYGVLAIVIPILFVWVYWTCV TVEGEVTEIGAGLLVLLGVKE DDDEQKANRLCERVLGYRIFSD AEGIKMNLNVQQAGGSVLVVS QFTLAADTERGMRPSPFSKGVID DIGFNTEISQTRFHQASHLFKRR GIYRLHFARRCQIQRRQRRR RFMQRTAVAITHQORMKQGIL RLWRNWLLWLLILLRRNRLL RLILLLLWRNRLLRLILWLR NRLLWLLILRLRRNWLLRLIL LLRCNRLLRLLYRFNNWRKQR FVWTIIQQRFWRKFKIIQRERI RPSRLFAGITLLLSRLKTSQFS LCRSICIFCVYGHIMILFAJALL LCLGELTCQFILLHRIDFIIIVLI
22543	52911	A	22671	377	463	QTISQTTVQSN*NSGLRISPKTA QLHGD
22544	52912	A	22672	129	615	KARQKSCQPVTTDTQCRHTSSS IGKRLAFQNLQIHTESTMKP WILLVVMFISGVVMLLPVLGSGF WNKDPFLDMIRETEQCWVQPP YKYCEKRCTKIMTCVRPNHTC CWTYCGNICLD/IRRA*/HQC* TPRFYWPITTVG*RMTIWSKKS AAFYLLGTPTWL
22545	52913	A	22673	3	412	
22546	52914	A	22674	2	390	

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22547	52915	A	22675	180	507	CCGGRARSELCLLNLCIKGAD*I QAW*KFCQWPCERADGRGCRK AERICPCPKGAYSL/YCRESVCC LPSFVNKNSSSLCVAHNWGRH CYLWTAADVQFISSHMFPVE HL
22548	52916	A	22676	3	227	GGGRARSELCLLNLCIKGAD*I QAW*KFCQWPCERADGRGS*F DRGAEVNQTDWQSIRSSQGG RDQRFFTERA
22549	52917	A	22677	567	842	
22550	52918	A	22678	1	1400	MGWGQGPDPVQLMNGHERSPS HSPREAKKSGSPLPTDIHCFSPQ SQPAMVITGVPTAPAGASAKM GLCATPITGACPLWLRGFRGWR CEDRCEQGTGNDCHQRCQCQ NGATCDHVTGECRCPPGYTGA FCEDLCPGKHGPQCEQRCPCQ NGGVCHHVTGECSCPSGWMLS FPGWRPI*FSKSL*MQGTVCQG PCPEGRFGKNCSQECQCHNGGT CDAATGQCHCSPGYTGERRAAV PDVRKICQDECPVGTGYVLCAE TCQCVNNGKCYHVSAGLCEA GFAGERCEARLCEPEGLYGICD KRCPCHELENTHRGDDREKA EF GHLLIALEVQYTEISNCIEKSQE ASCYDIRMLKQPYGETNTEEL AVNYVYSIYASKEQIRYKHGRS FANGHVKELMEGFSRRRIGSGG EKYKRDEEKNLTLRGQNRGGR GKNPKKTKAWVKIQGQNKIEIS GVGADRKRFFREK

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22551	52919	A	22679	1	2210	MEQKGFEKNDTLIYEFFHIVAK PHPLIKSSTYTTTFSARVTRFF LDAEKECRCEGQVEAALIAM GGTCQGTQRLSTAGESESATH MREPAVQCRRDSQCVSVLAGR RRFFQGAASPLHPASVALTQLH VRWASTATIGQVSGFPGKIRVS PTTNLGDSDYIFTASHWGLGHY GPAVHVHSQGGIDERGSNDSG RLYVTNPGGNVPSWTPNIDRLA EDGVKLTQHISAASLCTPSRAA FLTGRYPVRSGMVSSIGYRVLQ WTGASGGLPTNETTFAKILKEK GYATGLIGKWHLGLNCESASD HCHHPLHHGFDHFGMPFSLM GDCARWELSEKRVNLEQKLNf LFQVLALVALTLVAGKLTHLIP VSWMPVIWSALSAVLLASSYF VGALIVHADCFLMRNHTITEQP MCFORTTPLLQEVASFLLKRNK HGPFLLFVSFLHVHPLITMENF LGKSLHGLYGDNVEEMDWMV GRILDTLDVEGLNSNTLIYFTSD HGGSLNQLGNTQYGGWNGIY KGGKGMGGWEGGIRVPGIFRW PGVLPAGRVIGEPTSLMDVFPT VVRLAGEVPPQDRVIDGQDLL PLLLGTAQHSDEFLMHYCER VLHAARWHQRDRGTMWKVHF VTPVFQPEGAGACYGRKVCPCF GEKVVHHDPPLLFDLSRDPSET HILTPASEPVFYQVMERVQQAV

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22552	52920	A	22680	185	2091	GSTERDNMLHLHHSCVCFRSW LPAMLA VLLSLAPSASSDISASR PNILLMAIDDHGVGDIGCYGN NTMRTPNIDRLAEDGVKLTQHI SAASLCTPSRAAFLTGRYPVRS GMVSSIGYRVLQWTGASAGFT TNETTFAKILKEGYATGLIGK WHLGLNCESADHCHPLHHG FEHFYGMFSLMGDCARWELS EKRVNLEQKLNFLQVLALVA LTLVAGKLTLPVSWMPVWS ALSAVLLASSYFVGALIVHAD CFLMRNHTITEQPMCFORTTPLI LQEVASFLLRNKIHGPFLLFVSF LHVHPLITMENFLGKSLHGLY GDNVEEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLNQ GNTQYGGWNGIYKGGKMG WEGGIRVPGIFRWPGLPAGRV IGEPTSLMDVFPTVVRLAGGEV PQDRVIDGQDLLPLLLGTAQHS DHEFLMHYCEFLAARWHQ RDRGTMWESPTL*PPCVSSQEG AGACIVGRKVCPCFGEKVVVHH DPPLLA FDLSRDPSEHTILTPASE PVFYQVMERIVQQA VWEHQR TLSPVPMQLDRLGNWRPVMQ PCCGPFLCWCLEDDPQINVC SEKLEPRFLNFVTQIETNQLAM
22553	52921	A	22681	209	392	
22554	52922	A	22682	1	513	
22555	52923	A	22683	3	613	
22556	52924	A	22684	1	2115	

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22557	52925	A	22685	53	1966	VGQPRGLRRTLEKLTASVAGGA ANFFGDIERDLGPRDTSRGIRG GNLGDRCSSAEMAYASWQR WSPVEWARWMWTAVTSSGDS SLLVLQGDSDGKRSSDSEAFET PESTTPVKAPPAPPPPPPEVIPEP EVSTQPPPEPGWGSETVPVPD GPRSDSVEGSPFRTQAHFSGVF DEDQPIASTGTDILDFDNIELVD TFQTLEPRASDAKNQEGKVNT RRKSTDSVPISKSTLSRSLSLQA SDFDGAASSGNPEAVALAPDAY STESAKRVVPPASGGGRVQNSP PVGRKTLPLTTAPEAGEVTPSD SGGQEDSPAKGLSVRLFYSE DKSSWDNQENPPPTKKIGKKP VAKMPLRRPKMKKTPEKLDNT PASPPRSPAEPNDIPIAKGTYTF DIDKWDDPNFNPFSSSKMQES PKLPQQSYNFDPTCDESVDPF KTSSKTPSSPSKSPASFEIPASA MEANA V DGDGLNKPAKKKKKT PLKTMVEDVMSVCSLFDTRFV KKSPKRSPLSDPPSQDPTPAATP ETPPVISA V VHATDEEKLAVTN QK WTCMTVDLEADKQDYQPQS DLSTFVNETKFSSPTEELDYNRF YEIEYMEKIGSSLPQDDDAKK QALYLMFDTSQSFVKSSTVR

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22558	52926	A	22686	662	2927	HLRRKRNLPRREGLSPALLEET PLEPAVGPKAACPLDSESAEGV VPPASGGKRCLFTTAPAEAGEVT PSDSGGQEDSPAKGLSVRLEFD YSEDKSSWDNQENPPPTKKIG KKPVAKMPLRRPKMKKTPEKL DNTAPSPRSPAEPNDIPAKGT YTFIDIKWDDPNFNFPSSTSKM QESPKLPQQSYNFDPTCDESV DPFKTSSKTPSSPSKSPASFEIPA SAMEANGVDGDLNKPAAKKK KTPLKTDTRFRVKKSPKRSPLSD PPSQDPTPAATPETPPVISAUVVH ATDEEKLAVTNQKWTCMTVD LEADKQDYPQPSDLSTFVNETK FSSPTELDYRNSYEIYMEKIG SSLPQDDAPKKQALYLMFDT SQESPVKSSPVRMSEPTPCSGS SFEETGSLRNTAAKNQ\HPVP TRDWAP*PRSHLAGCQRKSSQ E/VELGGPWGLGHFPQEGDLKF TASPRGSFASADALLSRLAHPV FSL/CGALDYL\EPNFRQKRNP LFAQKLQREA\VHPTDVS\SKT ALYSRIRTTVEKPAGLLFQQP DL\DSALQIARAEL\TKEREVSE WKDKYEESS\REVMEMRKNLA EYEKTIAQMIEDQREKSVSHQ TVQQLVLEKEQA\ADLNSVEK SLADLFRRYKMKEVLESFRK NEEVLRKCAQEYLSRVKKEEQ RYQA\LVHA\EEKLDRANAEL
22559	52927	A	22687	374	1268	AETNMVWYDWMRPSHAQLHS DYMQLTEAKAKSKNKVRGV QQLIQRRLRIKSPAIEIEMQIAG KLTSQAFIETMFTSKAPVEEAFL YAKFEFECCRARGADILAYPPVV AGGNRSNTLHYVKNQLIKDG EMVLLDGGCESSCYVSDITRTW PVNGRFTAPQAELYEA\LEIQR DCLALCFPGTSLENIYSMMLTLI GQKLKDLGIMKNTQKG*CL/RR LLE/QYCPHHVGHYLGMDVHD TPDMPRSLPLQPGMVITIEPGIYI PEDDKDAPEKFRGLGVRIEDDV VVTQDSLILSADCP

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22560	52928	A	22688	329	1389	RIWKTQMMRRMKMMMMMM MMMRITTLFFQESQEAIFFFD LFPMCPFGCCQCYSRVVHCSDLG LTSVPTNIPFDRMLDLQNNKI KEIKENDFKGLTSLYGLILNNN KLTKIHPKAFLLTKLRLRLYS HNQLSEIPLNLPKSLAELRIHEN KVKKIQKDTFKGMNALHVLEM SANPL**/SMGIEPGAF*RG*RC S/YIRIAEAKLTSVPKGL/PPTLLE LHLDYNNKISTVELEDFKRYKEL QRLGLGNKKITDIENGLANIPR VREIHLGNIKLKKIPSGLPKLY LQIIFLHNSIARVGVNDFCPTV PKMKKSLYSAILFNPNPVKYWE MQPATFRCVLSRMSVQLGNFG
22561	52929	A	22689	1	4608	
22562	52930	A	22690	1	465	
22563	52931	A	22691	1	1542	
22564	52932	A	22692	1	4226	EAVLCSSRRGRPDSSMPDCCRNA ALEARSCQSMSTLSFNTVSPTQ DGTSSLPRRQSSFAKPLRALY DLLIAPMEGGVVESTEPLGTSR SGFASGTALFWLGDNGKAASP PGVSVSSLENNEDNTQCNRLQ GYREAAVPDWTQDLALCLLPT LQSLKARTAPHLCVPSSCYKA WYTLAVSKVSGMVEGKAWIIL LLAASTHALLQRPEGDITPL AGSRAAAVSCQARPFTFSGLM HSSGPVGRHRQLILVLE
22565	52933	A	22693	2	4197	ALDFPGRFRPTASFIWASVLFE TIRHEAEVSTDYKLSLFDLTSS YQALQVRVLSLGHHDALAVA ERGRTRAFADLLVERQTGQQD SDPYSPVTIDQILEMVNGQRGL VLYYSLAAGLYSWLLAPGAG IVKFHEHYLGENTVENSDFQA SSSVTLPTATGSALEQHIASVRE ALGVESHYSRACASSETESEAG DIMDQQFEEMNNKLSVTDPT GFLRMVRRNNLFNRSCQSMST LFSNTVSPTQDGTSS
22566	52934	A	22694	1	618	
22567	52935	A	22695	1	3528	

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22568	52936	A	22696	85	1193	RPIEGQLGTCHPGSEPRTIRWRA PGKGLRLYTHPPTSDIAGRTGA AASFAPLHLPREPRAGVDGTD AERILYPRRAAPAAASGVGSRPA GEAVRADEAGAAAGLGGFQSER NRSWGGESLGSRQPKMPAFN RLFPLASLVLIY*VSVCFVWGE VPLENGGRARANPMKLRICSI MKREEVEATTVVEWFYRPEGG KDFLIYEYRNHGHQEVESPFQGR LQWNGSKDLQDVSITVLNVT NDSGLYTCNVSRFEFEFAHRPF VKTTRLIPLRVTEEAGEDFTSV VSEIMMYILLVFLTLWLLIEMIY CYRQVSKAEAAQENAPGNSL EGGSQGLQINSTQDGLVTGQQ DVGSHRAREHMPDFEPPSAK
22569	52937	A	22697	277	527	VRVSWEYFCAPGAPGSPAGPG RGEKQRLGLLIRDARSPAPPG PPVGSVRG/PKPAPAGRVRKAG RRA*GAACSLAAGAWVEPGI

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22570	52938	A	22698	226	2268	SVKNTYKCHVRNEQICNKLTSCKSCSLNLCQWDQRQCEQCALPAHLCEGEGWSHIGDACLRNVSSRENYDNAKLYCYNLSGNLASLTTSKEVEFVLDEIQKYTQKQVSPWVGLRKINISYWGWEWMSPTNTTLQWLPGEPNDSGFCAYLERAAVAGLKANPCTSMANGLVCEKPVSPNQNARPCCKPCSLRTSCSNCSTSNMGECMCWCSSTKRCVDSNAYIISFPYGGCLEWQTATCSPQNCGLRTCGGCLEQPGCGWCNDPSNTGRGHCEGSSRGPMKLIGHMHNEMVLDTNLCPKEKNYEWFSIQCPACQCNHSTCINNVCCEQCKNLTGKGQCQDCMPPGYGDPNTNGGQCTACTCSGHA NICH LHTGKCFCTTKGIKGDQCQLCDSENRYVGNPLRGTCYYKTLIDYQFTFSLQEDDRHHTAIYFIVNPKQSNKNLHISINASNNFNLNITWPC*STAGTISGEETYIVSKNNILEYRDSFSYEKFNFRSNPNITFYVVSFNFSWPIKQIAFSQHNTIMDLVQFFVTFSCFLSLLL EAAVVWKIKQTCWASRRREQLLRERQQMASRPFASVDVALEVGAQEFTFLRPLEGAPKPIAIEPCAGNRAAVLTVFLCLPRGSSGAPPPGQSGLAIASALIDISQQKASDSKDKTSGVRNRKHLSTRQGT
22571	52939	B	22699	252	360	
22572	52940	A	22700	1	84	
22573	52941	A	22701	1	404	
22574	52942	A	22702	86	292	NPEMRCREFCLPSCRPELALE*G*SVRDVA*AQMCSVVWAGRPLGFAA*S*GSGHSCGRCSIWGE CWG
22575	52943	A	22703	82	379	HTLQPFISMGS LTKMFKVISEGPM D*RPHPKVRPMT*HSTPAPANFMGHHFFWKIMICTDRTEVATLVAGVVS GASVGGKSPPYRKWNSPEPDVKGPRLV
22576	52944	A	22704	2	382	

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22577	52945	A	22705	1	479	HMPSGETAPLRIVDTGTGTGTV VAYAPTEVGLHEMHKYMASHI LESPLRFYVTTPTVPSVAYGPG LVYGVAN/NTATFTIVTEDAGE GGDLAIEGPSKAEPRPRLSRA PGVDGAGASPLGEDTGPQAP GLQVLTERIPGPSAPTEFLSVG VSAVC
22578	52946	A	22706	1	590	
22579	52947	A	22707	171	406	
22580	52948	A	22708	269	2477	
22581	52949	B	22709	167	7472	
22582	52950	A	22710	1	520	
22583	52951	A	22711	2218	2472	
22584	52952	A	22712	722	1555	SRNWYEALNNTWGREDICVVD GWQSFRRQDYAFQERGSGGD LWSSTLAQAMTLVESRPHRHQ ALSTQLLDAIMPYCGNTRLRLGV TGTPGAGKSTFLEAFGMILLIRE GLKVAVIAVDPSSPVTGGSILG DKTRMNDLARAEEAFIRPVPSS GHLGGASQRARELMMLCEAAG YDVVIVETVGVGQ/SETEVARM VDCFISLQIAGGADDLQGIKKG LMEVADLVINKDDGDNHTNV AIARHM/YESALHILRRPPMHR VPRNPKNLLPGTAMANLLS
22585	52953	B	22713	381	425	
22586	52954	A	22714	1	1185	
22587	52955	A	22715	1	3009	
22588	52956	A	22716	22	527	YEGIVMKPLIIVNPADCIGCART CEIVACVVAHPSEQLNADVFL PRLKVQRLDSAPVMCHQCEN APCVGACPVGALTMGEQVVQT NSARCIGCQSCVSACPFMITIQ SLPGDTRQIVKCDLCEQR*EG PACVESCPTQALQLLIERELRRV RQQRIVVTGENPL
22589	52957	A	22717	187	325	

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22590	52958	A	22718	1	2240	MRSDPDTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRV TLEMKYGRIMLDTAKIIDQDV PTHILSKLTFTLRNHPEGVVVK NFEVLQPLQNSLSGLPLVWSE ILQQINQLTHYEPVIGIMGKTGA GKSSLCNALFAGEVSPVSDVAA CTRDPLRFRLQIGHEFMTIVDLP GVGESGVRDTEYAALYREQLP RLDLILWLKADDRALATDEHF YRQVIGEAYRHKMLFVISQSDK AEPTSGGNILSTEQKQNSRKIC LLHELFPQVHPVCAVSVRLHPV VALLQQFRTDDETRHYHYDS QHRLVDYTRTQYEEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPOVTWYGWDGDR TTIQNDRSRJQTIYQGSFTPLIR VETATGELAKTQRRSLADALQ QSGGEDGGSVVFPPVLVQMLD RLESEILADRVSEESRRWLASC GLTVEQMOMQMDPTEGTTAW Y/AEYDEWGNLLNEENPHQLQ QLIRLPQQYDEESGLYYNRHR YYDPLQGRYITQDPIGLKGGW NFYQYPLNPISDIDPLGLSMWE VARQMNAIASKLPEGFHIGINFS ASHIISPTFVDECLNFRDSFTRR DLNLVLEVTERDLLNVDES LVQ RLNILHENGFIALLDDFGTGY GLSYLHDLHIDYIKIDHSFVGRV NADPESTRILDCVLDLARKLSIS

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22591	52959	A	22719	1	2301	MALTSGVHTGEKPYKCAQCEE AFSRKSELIHIIHTGEKPYECT ECGKTFSRKSQLIHHRTHTGEK PYCKTKCGKSFQQSHLIGHQR IHTGEQPYLGLSVAERPKEYED DRALKMAAPCGNSSREQPCCFL NKASEDAERAKPPS*EPGRLRT P*VAQPH*VPHFMATWVRKHP VHDRQFRLHGQIRELNWDVVR PEQFTGVA TNCSGITYPQGGWL CPAELTRNVLELAQQQLQIYY QYQLQNL SRKDDCWLLN FAGD QQATHSVVVLANGHQISRFSQT STLPVYSVAGQVSHIPTPELAE LKQVLCYDGYLTPQNPANQHH CIGASYHRGSED TAYSEDDQQQ NRQLIDCFPQAQWAKEVDVS DKEARCGVRCA TRDHLPMVGN VPDYEATLVEYASLAEQKDEA VSAPVFDDLFMFAALGSRGLCS APLCAEILAAQMSDEPIPM DAS TLAALNPNRLWVRKLLK GKAV KAG
22592	52960	A	22720	1021	1734	
22593	52961	A	22721	1247	2412	RRSHHAANLDIRIMPQTRQVT LPDPELHPDSTLSMWPDRRIAR DAHLYLYRDRHGRLTEKTDLIP EGVIRTDDETHRYHYDSQHRL VHYTRTQYEEPLVESRYLYDPL GRRVAKRVRRERDLTGWMS LSRKQVTVWYGWDGDRLLTIQ NDRTRIQTIIYPQGSFTPLIRVET ATGELAKTORRSLADALQQSG GEDGGSVVFPPVLVQMLDRLE SEILADRVSEESRWLASCGLT VEQM QNQMDPVYTPARKIHL HCDHRGLPLALISKEGTTEWCA EYDEWGNLLNEENPHQLQQLI RLPGQQYDEESGLYYNRHRY DPLQGRYITQDPIGLKGGWNFY QYPLNPVTNDPLGLEVFPRFP LPWPWKSPAQQQWYPTFCC
22594	52962	A	22722	1	4767	

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22595	52963	A	22723	668	1922	YPHADSPECWLSSSSERGKSSV TADLSRPRRLRPIPTCHGKPIAC TTTKAKNAFRPIAGASATGRLA NSPIIILPNAAIRQEFGITLDPEEV FTFQGVKLYEYRYPDCVRSRN EAGILVEQILSTLFSVGEHFLK RAPFFKVPSLSFYAFGGLTTG VVRNRNGNIIGVNTTPARKIHLHYH CDHRGLPLALISKEGTTEWCAE YDEWGNLLNEENPHLQQLIR LPGQQYDEESGLYYNRHRYD PLQGRYITQDPIGLK/GGWNFY QYPLNPVQYIDSMGLASKYGH LNNGGYGARPNKPPTDPSPKLP DIAKQLRLPYPIDQASSAHNVF KTFFRALSPYDYTL YCRKWWK PNLTCTPQDDSQYPGMDTKTA SDYLPQTN/WVPSSIVSCTTGV VP*VVCQWVFA WPPDISHRRTG
22596	52964	A	22724	25	510	RITDFGVKKIIRVSGCGAVLPHV KL RDVVI/GMGAC/TDSKYNRI RFKGQAFGGIADFAMGRATAVD PGKALGINARVGNLVSADLFYS PDGEMFDVMEKYGILGVEMEA AGIYGVAAEFGAKALTICTVSD HIRTHEQTAAERQTTFNDMIKI ALESVLLGDKE
22597	52965	A	22725	415	759	HRRRIVDDTGIFRPRNTAQQLR QRPIAMSASGVVQIILEGHWRT HSLRNGFHRGRL*SSPKVGMQ HGSROVDHRTQRALRFFRQPGI DFLRPVFTPRRQRLAATNHFSR FVEH

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22598	52966	A	22726	2	2329	GTLPGCGAMHTCPSGPATHLV RRRRVRLPACVVTRANVPTPSR PVNATIGAFHSG*MASQGRRLS AQYPWSPFQY A\ARPVPTVPGR LVFTGTSKAPKISVMGPGMGIP SCSISAKELITDFGVKKIIRVGSC GAVLPHVKLRDVIIGMGACTD SKVTRIRFKDIIAFAAIADFDMV RNAVDAAKALGIDARVGNLFS ADLFYSPDGEMFDVMEKYGIL GVEMEAAGIYGVAAEFGAKAL TICTVSDHIRTHEQTAAESQTT FNDMIKIALESVLLGDKEEDRVI RFGKARATRYALLRPYRGIERIP VWRVDDTGKAHKFADIRLCWP QGSCLDVAKAREVIRGSQPLPA WCENWAQEVDARLTKEAQA LRPVINLTGTVLHTNLGRALQA EAAVEAVAQAMRSPVTLEYDL DDAGRGRHRRALAQLLCRITG AEDACIVNNNAAVLLMLAAT ASGKEVVVSRGELVEIGGAFFRI PDVMRQAGCTLHEVGTNNRTH ANDYRQADFQDDFVMAFTQN INGPTQNTRALHGGHKRPDFLP LLGAFHGAIDILAPGGLHGYSL PSSFFHALALSAAFPGRCKLS VHLPFWGLKDGGPLLTAPLGG ALVGIVGGVGGSNLTFPFHTNF LNVRFVIRRIHRIHHIFYRIAKL LMNGAQGSNMLIAAVAGVPHQ NGHFPFTVADRFAIVLSEGSIRV
22599	52967	A	22727	1	702	
22600	52968	A	22728	876	1318	RCHLANASPAAGSHAPSPDSLS/ KIR/QEVG/PPLP/PLLA/PLIATPP RTSQPLSLISSSSPSPASPVGQ VSPFRETPVPPAMSPWPEDPRR ASPPDPSPSAASASERVVPSP LQFCAATPKHALPVPGRLLPPCA SGHAMPCWRACKIK

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22601	52969	A	22729	485	1455	PVVQRARNASSCQPFSTSVWAI PSISATSVPMCGATHSILSPKKS TVSDRIGSMQISFFPLSRSAEK* ESPCSSDAFHAIFSVLSGLALHS TTTSLCSSTSGQLVCC* TSLPPT TYGMIACAAPVE*SPRCPV*PPA SAI*RCNNVEALCSTPFERQP*E PAKISMPDHPHECVVVG*E PAPHPNSREQIHPAHECLAGFP VTQESLFAPLEIVPAYCCEPGRE PRSARSFPFAPREL T*VQLELGT GL*RETLDLVVSAGWA*ARRIS GAVTATPETGTLCQLDSGAECH YRETGVLP*RSRPVGHGSSR IISRRWRT
22602	52970	A	22730	814	5001	PENSSHRPKPIIPMIASTLINANQ NSVSPYKRTFTRLTALMIKKKA AAQIHVGTSGNQYWRKLD FNS PGGSSPVENS DCS TNSRLSFSPE NILIQNQDIVREA VQGDGQKQ RQPQATDLDSSTHGSEMLPAT EVTVSGGFSVEETSCGDTGRSG GEALAVANDSTSTPQNANGLW KLKSTTPGGALPECFGTDTDTFS SAFCRKHGETQDTSQSSLPGLT HCYTGIREGGDDTEVESEAFSC SEGSEQQDAPD
22603	52971	A	22731	34	102	
22604	52972	A	22732	584	893	QKLLPNRMGHPVFKSSQDPV LLSRIAWKDASTVTWVIEQDPV LRRRRRTTRRRRTMRRRRGR* */SKRRRMR/GRRRGR*CRRRR RSSRSRPTRRQRNRNQV
22605	52973	A	22733	2	269	IGKLYWFMPPSANLALREL GIV LFLSVVGLKSGLSWIGYGALIT AVPLITVGILARMLAKMNYLT MCGMLAGSMTDPPA*PRFQTN DREEQHDPQLPQREVGA WRHK PVQLAD

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22606	52974	A	22734	3	958	RCYSLLSRAPHPGIYISIAERV*IRLNSANFTLNSLLPAEKKLAEEFAVSRMTIRKAIDLLVAWGLVVRRHGSGTYLVRKDVHLHQTASLTGLGEVLKRQKTVTSQVLIFEIMPAPPAIASQLRIQINEQIYFSRRRVFVIEGIPLMLEDSYMPVKLFRNLSQLHLEGSKFYIEQECGILIGGNYESLTPVLADRLARQMKVAEHTPLLRLITSLSYSESGEFLNYSVMFRNATQIQGWRSHFRRLHPKKSLTVPERAPPVFGGLIMRKNHSQRIDSGVRERRRTAGWMKHSKRQRRRIGHGTCQHPAHGQVIHFG
22607	52975	A	22735	2	285	GDEMTTSTLQKAIDLVTKATEEDKAKNYEEALRLYQHPVEYFLHAIKYEAHSDKAKESIRAKCVQYLDRAEKLDYLRSEKHEHGKLCCLKDRVT
22608	52976	A	22736	545	791	NHKAIDLVTKATEEDKAKNYEEALRLYQHAVEYFLHAIKYEAHSDKAKESIRAKCVQYLRYAEKLDYLRSEKHEHGKPKPVKENQSEGKGSDDSDSEGDNPEKKLQEQLMGAVVMEKPNIRWNDVAGLEGAKEALKEAVILPIKFPHLFTGKRTPWGRNLLFRPPGTGNSNRPKAGAPKATNSTFFSVSSDVKSKRLGETEKL*NLFLRLARQHKVPSIIFIDEVDSLCSGRNENESQAARRIQNGSSLVQIAGGLGINNDGDSGFFGATNIPWVLD/SAIRKRV*KTGFYIPLPEKACPRPDVSRHLHGSTPHNLRVATFHKLARKTEGYSGADISIIVRDSLMMQPVKRVQSATHFKKVCGPSRTNPSMMIDDLTPCSPGDPRAMEMTWMDVPGDKLLEPVVCMSDMLRSLATTRPTVNADDLKVKKFSEDFGQES
22609	52977	A	22737	249	1574	
22610	52978	A	22738	52	567	
22611	52979	B	22739	1	1293	
22612	52980	A	22740	443	1027	
22613	52981	A	22741	2077	2430	
22614	52982	A	22742	1	504	

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22615	52983	A	22743	3244	3947	RNEITPFRAMMIIRMAHRFQT EEIKRISFIKRRVGNKDEINPGA RWRRFHDDGITFLRLLDAGLTI PSGKTIVHPLARQRRGLVKIQFL R*LLAKLTRQPLPLQPVTA CLNPRLRRQRKIRMPAGTKWQ RLCPLIGDR*RHRQRSVAVYALS VRHNPVHHILRKNGDMYSFPIT IGNNVWIESHVVINPGVTIGDNS VIGAGSIVTKDIPPVVAAGVP CRVILEINDRDK
22616	52984	A	22744	742	1158	
22617	52985	A	22745	439	2882	PDWQAFQSPPEFASLIHPKPAK LPGWLQVQWSSLAITRTPTPV RWAQQTETVGLVVGVDSDPF FGAMVKAVEQVAYHTGNFLLI GNGYHNEQKERQAEQLIRHRC AALV VHAKMIPDADLASLMKQ MPADKQCESIPDQNNQTGTQY PRGKEPKLLRRLMHMNRKVGP RGPRRMLLRYLDVEFLSVALA VVHLGPQGTCSRFLVARALV VAVSEMDKSLSAQAQYFASN GPVPDLAYQVDFPRLEIGL*F/E YVDTGAETTLVPGDVLYVPAG GWNFPQWQAPATTFSVLFGKQ QLGF/SAVVQWDGKQYQNLAK QHVARRGPRIGSFLLQTLNEMQ MQPQEQQTARLIVASLLNHCR DLLGSQIQTASRSQALFEAIRDY IDERYASALTRESVAQAFYISPN YLSHLFQKTGAIGFENENLSHTR LGHA*TLKGVDLKVKEVAHA CGFVDSNYFCRLFRKNTERSPS EYRRHRRLHDNRICQFKTPTDN PENPDRLYTLFRIDKETSSLPKK VAPSCKRLSVSRSSPKPSISIRRC MRLMLIEGRSSFIHPDKDVDG FHPYNVGRLCQRAPRLRPCTPR GIVTLLERYNIDTFLNNAVVIGA SNIVGRPMSMELLAGCTTTVT HRFTKNLRHHVENADLLIVAV GKPGFIPGDWIKEGAIVMMSGI NRGVATDASCFLVPFANRVSG
22618	52986	A	22746	2	126	
22619	52987	A	22747	1	465	
22620	52988	C	22748	78	308	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
22621	52989	A	22749	1	2797	MEHPPVLAVQRVALPSRSSEPE LFLNPPTDEETEAHRGMYLDQ GPRTKDWIPVAPGVREPSPLGP GPSSLWLLVVGTVVEEGSRKH RPTCKKDFTKSKTVDAQPTLCA RHQMLNIQFLISDRDPQCNLHC SRTQPKPICASDGRSYESMCEY QRAKCRDPTLGVVHRGRCKDA GQSKRLERAQALEQAKKPQE AVFVPECGEDGSFTQNTSCIHSS VYQIGENSSLTFLEKREESGHL QRDWFLWFRKARVI
22622	52990	A	22750	1	5295	MNLNQEEIPDLPEKEFRRLVIKL IREGLEKGAQCKEIQKMIQEV KREIFQIEISLKKKPPKIQTLDI LLKMQNALESLSDRTEQAEEIN SELEDKVFKLTQSNKDKEKTR KYEQSLQEVWSYVKRPNLRIIG VPEEEENTKLENILGGIIEENFP SFARDLDIQIPEAQR TTGKLIK RSLLRHIVFRLSKVKMERILR AVRQKHQATVSQKNKAGGITL PDFKLYYKATVSQKNKAGGITL PDFKLYYK
22623	52991	A	22751	1	891	GSPFEVMPRDDVFFIVDKI*DI GVYSCTAQNSAGSISANALTIV LETSPFLRPLLDRTVTKGETAV LQCIAGGSPPKLNLWTKDDSP VVTERRHFFAAGNQLLIIGDSDV SDAGKYTCEMSNTLGTERRGNV RLSVIPTPTCDSPOMTVL/HLLD DDGWGHGCLYVILA VVCCVVG TSLVWVVIIYHTRRRNEDCSITN TDETNLPAIDIPSYLSSQGT LADR QDGYVSSSESGSHHQFVTSSGAG FFLPQHDSSGTCHIDNSSADVE AATDLFLCPFLGSTGPYVFEGK CVWAQNPF
22624	52992	A	22752	1	2947	MSAPSLRARAAGLGLLLCAVL GRAGRSDSGRGELGQPSGVA AERPCPTTCRCLGDLLDCSRKR LARLPEPLPSWVARLDLSHNL SFIKASSMSHLQSLREVAGNRIV EILPEHLKEFQSLETLDLSSNNIS ELQTAFFALQLKYLELNRNKIK NVDGLTFQGLGALKSLKMQRN GVTKLMGDAFWGLSNMEILQL DHNNLTETKGWLYGLMLQE LHLSQNAINRISPD AWEFCQKL SELDLTFNHLRLDD
22625	52993	A	22753	2	417	

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22626	52994	A	22754	1	262	VLDIGS/SLTVPDEFKQE/RADGMWWKQLVAGAVAGAVS/RTGTAPLDRLKVF MQIKRAILGQQETLMCRSASWLAPWLVPQPNHHLPGY
22627	52995	A	22755	1	762	
22628	52996	A	22756	1	1527	RLAAGADPAGSRGGRGSREA PTEAACRCASPPPRAGAMRGSP GDAERRQRWGRLFEELEDSNKD GRVDVHELRLQGLARLGGGNPD PGAQQGISSEGADPNPGLDLE EFSRYLQEREQRLLLMFHSLDR NQDGHIDVSEIQSFRLGISIL LEQAEKNFAQA/VDRDGTMTID WQEWDRDHFLLHSLNVEDVLY FWKHSTVLDIGECLTVPDEFK QEKLTMWWKQLAAGAVAG AVSRTGTVPDLRLKVF MQVHA SKTNRLNILGGL*SMVLEGGIRS LWRNGINVLKIAPESAIKFMA YEQIKRAIPG/E*ETLPVLERFVA GSLAGATAQTIIYPMEVLKTRL TLRRTGQYKGLAGLRGGILER EGPRAFYRGYLPNVLGIIIPYAGI DLAVYETLKNWWLQQYSHDS ADPGILVLLACGTISSTCGQIAS YPLALVTRMQAQASIEGGPKL SMLGLLRHILSQEGMRGLYRGI APNFMKVIPAVSISYVVYENMK

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22629	52997	A	22757	1	2127	MDQSGLLALRAAVGAVVGSTL AVDIGLVKDWHPRLGGKHC QLLGAFRCRQHRRGKEERRGE TKEKKGERENERGKRRRIEGER DKYVKENEKQTCVQKERHSCT GNSPNHMATVQAERGALDSHG GWHPWDYCAVQGGRYHQLLL TKEEIEVQSRKKMCLLQAFLIC CQKSHFLGPGCTRSMVPASASG ESLKLPLMVEDEGEPPVTERER KREGERERGERERRRRRKRK RRRKRKRKRKRKRKRKR*EFLS LG*NERGKRRRIEGERDKYVKE NEKQTCVQKERHSCTGNSPNH MATVQAERGALDSHGGWHPW DYCAVQGGRYHQLLLTKEEIE VQSRKKMCLLQAFLICQKSHF LGPCTRSMVPASASGESLKL PLMVEDEGEPPVTEREQEGGGE RERERERKKEKEKEKEKEKEE EKEKEKEEERIVPLPRVELRLT NIAAKQVGNLTLDVAAADPHS ESSCVYVRFVIKIPVAAAFRKK SYVTNNVESCEDGIHYFWKSH MHSENSCCKLPCPPHLPAAER LGDALEPLPTMRRQRQCQNT GDCDGRRIQIGTEREMHRDTS LVAVKTVQDTSREGMGEVPEPNS CFWRDTHMASGVGAFAELPH DGTCDCEPDEAPGAEEVCREC GFCYCRRHAEHRQKFLSHHL AEYVHGSQAWTPPADGEGAGK
22630	52998	A	22758	348	881	WRQPRWPHHQACLWQRAGSS YSQHKDPHFTSFSTPRAVQNFD GFPCFFLRETTTLVLIPSVPLTDP GSFYRAWFSQCGPRSPRLGR TLSQKFLRLRGRPRPYMSTL TPF*STRIFERAFQVMGAESGG RIEKTTLCKRSLGPLMEPRV
22631	52999	A	22759	1	347	MVPASASGESLKLPLMVDER EPVTERE/REKGRGREGERERE KEREGERERERGERKGERER RRG*QPPFHNRFSEGGGRSFLCS RRPRVSRRGHTSRGPARKAAE RRGLG
22632	53000	A	22760	145	258	PENGLIGLS*KIVLSLNPVNEN DMKVDEVLVEDSSTA

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22633	53001	A	22761	1	1479	MALKEIFCPVRETETCTINCGTR ISPSILHVGLPYPSTPNVPERE GCGGGVSGNSKQPGALETAEI GKKEGRREESRPESASSLSLLL SLAYDVKSAQICTRIHSSVPLE AVYPGYIHQSINQADLSALAPY DPCVCQIHKYHGAYNCLQYSV QNTLYSPTTEQYKRCQAPWVL PAIFTIPASGAASAVPVRAQA QGGQAAGQRRRLATAPLTGEG EPDHGDRTRAGSQGPEARPRIH LGAARGGDRTRGRPRRRGRDW TRLGREMAAAVSSAKRSLRG ELKQRLRAMSAEERLRQSRVLS QKVIAHSEYQKSKRISIFLSMQ DEIETEIIKDIQCRGKVCFPVP RFSRAITMDMVRIGSPENGFN FPKTSWEYSLRLGEGDVREEG LVPPGGI/EILILPCPQALGLDQ NHGQPRLLGRQGAYL*CLS*K RLFCSHSGKLPPTPPGGWLFK EQICPPRSPVNENDMKVDEVL
22634	53002	A	22762	1	813	
22635	53003	A	22763	1	368	
22636	53004	A	22764	327	4281	SASASRCDPGSGSRREEREELQ WRRRRRRRRRRRRRRRQQRRA AAPAAPAGGIEAVNMASASYHI SNLEKMTSSDKDFRFMATND LMTLEQKDSIKLDDDSERKVV KMILKLLLEDKNGEVQNLAVKC LGPLVSKVKEYQVETIVDTLCT NMLSDKEQLRDISSIGLKTIVIGE LPPASSGSALAANVCKKITGRL TSAIAKQEDVSVQLEALDIMAD MLSRQGGLLVNFHPSILTCLLP QLTSPLAVRKRTHIA
22637	53005	A	22765	2	271	
22638	53006	A	22766	299	451	IVALFRSLVRHIRGTMAMESTA TAAVAALVSADKIEDAPAPST SADKVES

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22639	53007	A	22767	1	1122	MA TESTATAAIAAELVSANKIE DVPAPSTSADKVERIENGVLGN TLDGVHVEEEEGEKTEDESLVE NNDSIDEAEARKELREQVYDSM GEKEEAKKTEDKSFAPETDKE QDCEMEKGGRDMDISAEAEPP QEKVDLTGLGWLTEISEGAKGG GAPEGPNEAEVTSKGPEQEVDP VEEEKSVSETDVQKECKEKG WEKHREVIIVSIEEKPKEVSEEQP VVILEKQGTAVEVAEESLDPTV KPVVDVGGDEPEEK/GTVPGLR PSPCRDPLPAGLGLWVQLSV** GSGTVQQIY*SH*EENGCTKRA GEGG*RIVC*IQERN*GTGTAT RNYRKDRCKGVSDYWECS*T GSESYSGGELVYFRFHS*WRRLF
22640	53008	A	22768	223	339	
22641	53009	B	22769	341	496	
22642	53010	A	22770	12	1099	VSGVPNCLFFSQALFRSLVRHL RGTMAESTATAAVALVSA DKIEDVPAPSTSADKVESLDV DSEAKKLLGLGQKHLV/MGDIP AAVNAFQEAASLLGKKYGETA NECGEAFFFYG/KSLELARM NGVLGNALGVHVEEEEGEKT EDESLENNDNI/D*N*RLGRG* *RK**D*RNAK*FSP*KQVSSRK *GGGDWEPRACLGAGFSKDH F*KARNKRSTALCCPGTS*TRRS *C*I*KLCASC/GGVPLP*PTGP VPGSPRPSPCRDPLPAGLGLWV QLSV**GSGTVQQIY*SH*EQNG CTKRAGEGG*RIVC*IQERN*GT KGTATRN*REDRRCKGVSA*W ECS*TGSESYS

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22643	53011	A	22771	11	2485	VSGVPNCLFFSQALFRSLVRHL RGTMAVESTATAVAADVVS ADKIEDVPAPSTSADKVESLDV DSEAKLLGLGQKHLVMGGIP AAV\NAFQGAASLLGKKYGET ANE\CGEAFFYG\KSLLLEARM ENGVLGNALGVHVEEEGEEK TEDESLVENNDNIDEEAREELR EQVYDAMGEKEEAKKTEDKSL AKPETDKQDSEMEKGGREDM DISKSAAEPQEKVDLTLDWLTE TSEEAAGGAAPGPNAAEVTSG KPGQ\EVPDAAEEKSVSGTDVQ EECREKGGQEKQGEVIVSIEEK PKEVSEEQPVVTLKQGTAVEV EAESLDPTVKPVDVGGDEPEEK VVTSENEAGKAVLEQLVGQEV PPAESPEVQTEAAEASAVEAG SEVSEKPGQEAAPVLKPDGAVN GPSVVGDTPIEPQTSIERLTET KDGSGLEEKVRAKLVPSQEETK LSVEESEAAGDGVDTKVAQGA TEKSPEDKVQIAANEETQEREE QMKEGETEGSEEDDKENDKT EEMPNDSVLENKSLQENEEEL GNLELAWDMLDLAKIIFKRQET KEAQLYAAQAHLKLGEVSVES ENYVQAVEEFQSCNLQEQYL EAHDRLLAETHYQLGLAYGYN SQYDEAVAQFSKSIEVIENRMA VLNEQVKEAEGSSAEYKKEIEE LKELLPEIREKIENAKE\SR\SG
22644	53012	A	22772	52	161	FQNPGLY/CDTEYNRLQKQK TEKTKQKKTQFHPICN
22645	53013	A	22773	3	115	FFQNPGLY/CDTEYNRLQKQK TEKTKQKKTQFHPICN
22646	53014	A	22774	229	358	
22647	53015	A	22775	257	386	
22648	53016	A	22776	259	294	
22649	53017	A	22777	217	398	KAWWNLLRKSEPKSCGS*GGL STSRLRVCCSSPLGLGYCG**L CHLQEPHYGSLHRMSS
22650	53018	A	22778	1	3386	

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22651	53019	A	22779	391	2100	SRRTAGVRLDILCKDPIMWVSA DGHSYQPQYPKAKRATEFHFF NFKALLARAAVGAARGIHHRC GLTKRPDARRRRVAGA QGREP AISLPGDRAAGARATRTRGPGP APKMPAIAVLA AAAA WCF L QVESRHLDALAGGAGPNHG/NF L/DNDQ/WLSTVSQYDRDKY/W NRRFDEVEDDYFRNW/NPNKPF DQAL/DPSKDPCLKVKCSPHKV CVTQ/DYQTAL/CVSRKHLLPR QKEWGTWQKHWGLDL*ILV KICKPCSRGRSSAMGLAGSDGP LLTAFQVANLEFHACSTGQK/S FATLCDG/PCPCSSQSLEPPKHK GRKGVPCTDKELRNLASRLKD WFGALHEDANRVIKPTSSNTAQ GRFDTSLPICKDSLGMFNKL DMNYDLLLPSEINAIYLDKYE PCIKPLFNSCDSFKDGKPLNNE WCLLPSONPGGLP/CAQNEMNR IQ/KLSKGKSLLAGFIPRNEEG YYKATQCHGSTGQCWCVDKY GNELAGSRKQGA VSCEEEQETS GDFGSGGSVLLDDLEYERELG PKDKEGKLRVHTRAVTEDDED EDDDKEDVGYIW
22652	53020	A	22780	2	441	HGVQGAGCGEVA AVSIELGAG GPVWRAAPRACSRLLRLRGFG LEGQWFGESCRRGAS*EGSTR *PPRRQPWPEWVMSWVPET REPARISPAPAKQN*PPAPKSP AAPA/QAAVAATPSPPGEISEA WDSLESFSKPAFFSQ
22653	53021	A	22781	3	121	

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22654	53022	A	22782	2	1488	FVNNMADGEEPEFKRRRIEELL AEKMAVDGGCGDTEWTKDR WNHVKK/FLERSGPFTHPDFEP STESLQFLLDTC/VLVIGAGG LGCELLKNLALS/GFRQIHVID MDTIDVSNS*IRQFLFRPKDIGR PKAEVAAEFNDRV/PNCINVV PHFANKIQDFN/DTFYRQFHIV CGTGTLSGARRWINGMLISLNLN YERMVS*DPSSIVPLIDGGTEGF KENARVILPGMTACIECTLEL YPPQVNFPMCTIASMPRLPEHCI EYVGMQLQWPKEQPFGEVPL DGDDEPHIQWIFKSLERASQY NIRGVTYRLTGQVVKRIIPAVA STNAVIAAVCAT*/EVFKIATSA YIPL*ITWVFNDV/DGLTYTYTTE GRKGK/ENCPACISQLPQNISVF LHQAKLQ/EVLGIILTNASLQN EILPAITATLGGEKIGTLYLQSV TSNEERNRANFFQTIERNWGLL DGPKTGRLLDVTTPTQTVLFQTS ILLKKGKSPT
22655	53023	A	22783	1	1719	
22656	53024	B	22784	199	460	
22657	53025	A	22785	226	1620	NGSGLALATGNRDPLCLP SCPWR*KSAGASTQQA YSSQSQ/HPAYHRITPTLT NFALRLYKELAADAPGNI FFSPVIS/TTCLLC LGAQANNSALILEGLGF NLTETPEADIHQGF RSLLH/LVLPSPKL ELKVGNSLFLDKRLKPR QHYFDSEKELYRAFA SAHFTDSVTTGR QINDYL*RRTYWPGV DLPFRS/LARDTFM VLA/NFILFSKAKVKA TLSSRVDPKSRPVFL VDERTSFQVPMMHQ KEMHRLYDQDLA CTVLQIEYRGNALAL LVLPPGKMKQVEA ALQPQTLRKWGQL LLPSLLDLHLPRFS ISGTYNLEDI LSPNWFSPITYLNK ITLSQSVG G*LNKSISKVSHKSM VDMNEKGDQRPGL LQASSPSPHL*/YTMS DPHAHFNRPFL LLLWEVTTQSL LFLGKVVNPVV WVTMVGQGE LSYLILDQTD RPEPACILGLLCG
22658	53026	A	22786	64	288	
22659	53027	A	22787	1	1923	

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22660	53028	A	22788	309	2286	CAVCHISFQDTPVLVSSNVTMQ FGSKPLFENISVKFGGGNRYGL IGANGSGKSTFMKILGGDLEPT LGNGSLDPNER\IGKLRQ\QDFA FEFTVLDTVIMGHKEL\WKVK QERDRIYALPEMSEEDGYKVA DLEVYKYGEMAGYSAEARAGEL LLGVGIPVEQHYGPMSEVAPG WKLRLVLLAQLFADPDILLDE PTNNLDIDTIRWLEQVLNENNS TMIHSHDRHFLNMVCTHMA LDYGLRVYPGNYDEYMTAAT QARERLLADNAKKKAQIAELQ SFIDKIKLEEVCASSRQNPFI QDKKLFRLNALEVEGLTKGFDN GPLFKNLNLLEVEGEKLAVLGT NGVGKSTL\KLT\VGNLQPD TVKWSENARIGYYAQDHEYEF ENDLPVFEWMSQCKQ*GDDEQ AVRSIFGRLLFSQDVIKKPAKVL SAPFCKDSILEAIDAGIKLIITTE GIPTLDMLTVKVLDEAGVRMI GPNCPGVITPGECKIGIQPGHIH KPGTGELNITTGIVKARDTQIA LNDKSKGDVRVDQNSLLET NMYVGTSGTGTLTLTNGTLN VEGGEVYLVGFEPVGTNLNIGA AHGEAAADAGFITNATKVEFG LGEGVFVFNHTNSDAGYQVD MLITGDDKDGKVIHDARHTVF
22661	53029	A	22789	1	553	
22662	53030	A	22790	1633	2207	ILFFDKGMPAQTPSLQKRWEK M*LVLW*GDREGIKAI/SEESW GARAPIFLLR/MMEDQGLYSIR MGGARGLPKGSAL*GAGRGP YSGERTWTLSLPSGNCAPYQR GGWWYHACA\HSNLNGVWHH GGHYRSRYQDGVYWAEFRGG AYSRLKAAMPHLAPEAVTLCSP GPLGRGHWSAGAPSCSGHTFF
22663	53031	A	22791	34	210	AAADPLRLHRRGAFIKAGRHA G/PSLPVCLQATAH*MDLARLA LVLVVRTSASTKSSTRE

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22664	53032	A	22792	397	1168	LLSRISKVSSKLPVRGGAGSLCT GDQRKVRKFLVETVELQISLKN YDPQEQQSFAFGHPSRL*VVPSP PLSSLVCVLGGPSKHL*RRLRP VGYPTMDIEGA*KKLNQELKN LVKKAGPRKYDCVFWPQESLD SSKIPPNPSGPGFK*RAKGVFPF CLTHNGKHGLAQSGIEVEVPT/ LSFQMKKGVYVWVAVAVWSRE R*QTNELVYNIHLACQLSWVSL LKEKNWQ/NVPGPYIKSTMGO SPSSHILRHIRINSITS
22665	53033	A	22793	1	377	SVSRVPTRSLRTSTWRLAQDQT QDTQLITVDEKLDITLTGVPEE HIKTRKVRJFVPARNNMQSGVN NTKKWKMEFDTREWRWENPLM GWASTWSYDIEERKVPKPKSK SYGANFSWNKRTRVSTK
22666	53034	A	22794	183	368	
22667	53035	A	22795	3	623	ILAFACSKMAAVMSVVLRTQ LWRRRAVAVAAALSVSRVPT/R RSLRTSTWRLAHVDTQDTQLI TS*KIGISLTFNWPFPPEHIKNL EKSQIFVPCSPITCQSGVNNTK/ KWKIMEFDTREWRWENPLMG/ WASTGLIPLSNMVLNLPVLKE DAVSFAEKNGWELWTLEERK/ VPKPKSQVFMGANFSWNKRTR VSTKIGLALTSPA
22668	53036	A	22796	1	798	MNKVNPTQDQKEDHPELIITSIG DKRQLTLEASGVCHRGQTQR VKEESKKFLISMFRGGKPVHK VVERACVCTCLHHTSVPAATHN TQRRHTTPTTRKNRGRKRGKK EREKRRKDREHNTGRRTKRKKT RNIGGQRTQKQKQSEDKARR EPGGGRKQGRGREDGTRQRRG GRTRNREEGAQRGRNGR/RGEG RRTEETHMA*APDITATQQT EQGHGTRQRDITLRRHTAEDA QPSEHASADQAHTKKTE*SVSR TNGQYLLT
22669	53037	B	22797	85	322	

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22670	53038	A	22798	165	4733	AATALLTHGQEEGQVEGQDED IPPITCVQNGRLRYHDRVWKPE PCRICVCNKGVLCDDEVICDET KNCPGAEVPEGECCPVCPCDGS VTHRPKKPPGVGEPKGDTPPPR PKGTGPPPPGRDGPQGPGPLPGP PGPPGPPGPPGLGGKLLPKLSY GYDEKSTGGISVPGPMGSPGPR GLPGPPGAPVSIQDVIFCLGLW SFGGKTGMRAEMLRDGLGPQ GFGQPPGEPGEPGASGPMGPRG PPGPPGKNGDDG
22671	53039	C	22799	88	392	
22672	53040	A	22800	37	293	
22673	53041	A	22801	55	1917	GGGGVRRRRGTRRSEPGDSRSA MAPIGLKAVVGEKIMHVDVKK VKKKGWVKLVVDQLSMRML SSCKMTDIMTEGTTIVEDINKR REPLPSLEAVYLITPSEKSVHSLI SDFKDPPTAKYRAAHVFTDSC PDALFNELVKSRAAKVIKTLTEI NIALFPYESQVSLDSADSFQSF YSPHKAQMKNPILERLAEQIAT LCATLKEYPAVRYRGEYKDN ALLAQLIQDKLDAYKADPTM GEGPDKARSQLLILDRGDPSSP VLP* *LFQGMSY*SCLP ENDV YKYETSGIGGGHGVKGGASGT EDDDLWIALRHKHIAEV/SQE VTRSLKDFSSSKRMNTGEKTT MRDLSQMLKKMPQYQKELSK YSTHLHLAEDCMKHYQGTVDK LCRVEQDLAMGTDAEGEKIKD PMRAIVPILLDANVSTYDKIRJIL LYIFLKNGITEENLNKLIQHAQI PPEDSEHTNMAHLGVPIVTDST LRRRSKPERKERISEQTYQLSR WTPIIKDIMEDTIEDKLDNKH PYISTRSSASFSTTAV/SARYGH WP*GTRPPGEYRSGP/RVFIIFHP LGGVSLNEMRCALRR*PRANG KWGGA**GSTHILQPHRNLPGH

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22674	53042	A	22802	46	1931	GGGGVRMLCGTRRSEPGDSRS AMAPIGLIAVVGEKIMHDMIL NDLNMGEWKALLVDQLSMRM LSYCCLMTDIMTEGIVEDINK RR*PLPSLEAVYLITPSEKSVHS LISDFKDPPTAKYRAAHVFETD SCPDALFNELVKSRAAKVIKTL TEINIAFLPYESRVYSLDSADSF QSFYSPHKAQMKNPILERLAEQ IATLCATLKEYPAVRYRGEYKD NALLAQLIQDKLDAYKADDP MGEKDPKARSQLLILDRGDFPS SPVLHELTFQAMSYDLLPIEND VYKYETSGIGEARVKEVLLDED DDLWIALRHKHIAEVSQEVTRS LKDFSSSKRMNTGEKTTMRDL SQMLKKMPQYQKELSKYSTHL APCLRTCMKHYYQGTVDKL/CR V/EQDLAMG/TDAEG/EKIKDP MRAIVPILLDANVQTY*QIRIILL YIFLKNKGITEENLNKLIQHAQIP PEDSEIITNMAHLGVPIVTDSTL RRRSKPERKERISEQTYQLSRW TPIIKDIMEDTIEDKLDTKHYPI STRSSASFSTTAVSARYGHWHK NKAPGEYRSGPRLIIFILGGVSL NEMRCA YEVQTANGKWEVLIG STHILTPTKFLMDLRHPDFRESS RVSFEDQAPTME
22675	53043	A	22803	2	51	
22676	53044	A	22804	236	451	LHLPLFLGAIRSGQYGLWNLFR VLGWTCSLGIYLGWRVS*NFG RGTKALKVLSTIS/E*RNNHCHP *NNIFVY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
22677	53045	A	22805	3	1173	GAGAPAAGQAGLTSTSAVRAR PVSPARQSDPAASLSLHLSLPP APGAGCARWRRRGPAQMAAA GAGAGSAPRWLRALSEPLSAA QLRRLEEHRYSAAAGVSLLEPPL QLYWTWLLQWIPLWMAPIISIT LLGLAVNVVTTLVLSISCLTAT EEAPYWTYLLCALGLFIYQPLD AIDGKQARRTNSCSPLGELFDH GCDSLSTVFMAVGASIAARLGT YPDWFSSRFFYLGLCLVFYCAH WQTYVVS/GMLRFKGVDVTEIQI ALVIVFVL/SAFG/GATM/WGD YTIPILEIKLKILPVLGFLGGVIFS CSNYSHVILHGGVGKNGISTIA GTSVLSPGTPH/MGLIILAIIMY *KVRQLMVF*KSIPCL*YPQCLG CVFAKVVSQKISGSSHDQK
22678	53046	A	22806	2	1091	CPGRRRRRRPGRSRARATALPT PGPRKRGGPAGRKRRPERCASS SSGSSSSGDEDEGLDGLDGA GKRAAQPVAAAGKVGGA AEPEHTKKHVKLETLITTEGK LWSWGRNEKAQLGHGDTKRV EAPRLTEGLSHEVIVCVTCARNH TLALTEGVSFAFGENKMGQL GLGN*TDVPSPVQIMYNSLPIT KMA/CGYGLWGYTEQKDEMV PRLVKLFDFFPGHGASQIYAGYT CSFAVSEVGGFFWGATNTSHE STMYPKAVQDLCWRIWLSLAC GKSSIIVADESTISWGSPSTFG ELGYRDHKKSSSTAAQEVKTL HGIFSEPVAMGYSHSLVIARDE SETEKEKIKLPEYSPQTL

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22679	53047	A	22807	1	1409	MSLGLASERLWAGLGLPALPLADEGGEGCETLFVWRSQKLEFGSKCKGQLLIFGATNWDLIGRKEVPKQQAAYRNLGQNLWGPHRYGCLAGVVRVTVVSGSCAAHSLITTEGKLWSWGRNEKGQLGHGDTKRVEAPRLIEGLSHEVIVSAACGRNHTLALTETGSVFAGFENKMGQLGLGNQTDVAFSPAQIMYNGQPITKMACGAEFSMIMGLQKRLPLFLWALNMGQLGTQLRMGKFHSPGAQRIEYDCELVPRRVAIFIEKTKDGGQLPVPNVVVRDVACGANHTLVLDQSKRVFSWGFGGYGRGLGHAEQKDEMVPRLVKLDFDFPGRGASQ/SCWL/HTCLCCQ*NGWSVFLGGHQLP*IYHVPQKQCRSTAAAGESGTLACGKSSIIVADESTISWGPSPITFELGYGDHKKPSSAAQEVKTLDGIFSEQVAMGYSHSLVIARDESETEKEKIKKLPEYNRTL
22680	53048	C	22808	277	518	
22681	53049	A	22809	2	192	
22682	53050	A	22810	1	2946	MAEAGLRGWLLWALLRLAQSEPYTTIHQPGYCAFYDECGKNPELSGSLMTLSNVSCLSNTPARKITGDHLLILQKICPRLYTGPNTQACCSAKQLVSLASLSITKALLTRCPACSDNFVNLHCHNTCSPNQSLFINVTRVAQLGAGQLPAVVAYEAFYQHSFAEQSYDSCSRVRVPAATLAVGTMCGVYGSALENAQRWLNFGQDGTGNGLAPLDITFHLLPEGQAVGSGIQPLNEGVARCNESQGGDDVATCS
22683	53051	A	22811	258	362	
22684	53052	A	22812	1	4038	MAEAGLRGWLLWALLRLAQSEPYTTIHQPGYCAFYDECGKNPELSGSLMTLSNVSCLSNTPARKITGDHLLILQKICPRLYTGPNTQACCSAKQLVSLASLSITKALLTRCPACSDNFVNLHCHNTCSPNQSLFINVTRVAQLGAGQLPAVVAYEAFYQHSFAEQSYDSCSRVRVPAATLAVGTMCGVYGSALENAQRWLNFGQDGTGNGLAPLDITFHLLPEGQAVGSGIQPLNEGVARCNESQGGDDVATCS

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22685	53053	A	22813	198	380	ASSESDSTPCR*MAYSWPPNSN SSHCIKELPLFMGKIPAA* DGG PQGLAIFPPGVIVGI
22686	53054	A	22814	1	154	
22687	53055	A	22815	35	486	PARRGRDEC*VLAPFRATRPPS RRIR*SKATYPIPSNDQTRTI SRERASMPRSAEPKRPTIPRLHP SPRGIVTVSS/RPRSHALPVSHIH SCHSRITAISDNQVPAFLQVYGE EVRKRAGEVTQAITGFPRYRLF FKMLRCHRSIQVTAST
22688	53056	A	22816	212	365	RCRSGPAPRSAPGARPASPSPPA AGTCR*RPAGHCAGAAAGLLSL CPRCST
22689	53057	A	22817	293	618	QQNPTNCLPPASR*SKT* RARST AGPTRPHLHHPAAPAGSPACA GEGRLQR/HSPNPI.YFNWKKQR FAAKPHFRPQSSLNPQQWLLA GLLQEESSSLGTDAPLHSLG
22690	53058	A	22818	3	1129	FCLDDLSSAINEHLSARGRRRS IVKVS LHPAIVGLKSKFLKKPD QLRKLFIAGLSFETDESLSHF EQWGTLDTCVVMRDPNTKRS RGVGFVTVATVEEVDAAMNA RPHKVDIGRVVIEPKRAVSREDS QRPGA/HLTVKKIFVGGIKEDT EEHHLRDYFEEIILNSMGKLEV VEIH*LDRIQGWPRKRGFAFVT FDGHDSVDKIVIQKYHTVNG/H NCEVRKALSKQEMASASS/SQR G/RVGSGNFWCGRT/NGFGGND NFGIRGGNFSWSVAVFGG/SRG GVWIVWAVGDGYNGFG/NDGS HFG/GGGSY/NDFGDFH/NQSSK FWTP*RGGNLGGQKLWPPMGG GGQYFAKPTPKVAYGRFPAA ASSYGKWPEDFN
22691	53059	A	22819	1	568	MGKMSPGHVRDFHSGSCHHNR P GGPGGKSGFMGQALGPG/GCV QPRDLVLCVSATPAMAERGQC GAQAVASEGGSPRPWQLPCGV EPADFRRYMETPGCPGRNL/PA GAGPL*RTSAGAVWKGNVRS E SP/PQSLYWGATASGAVRRGPPSS RNQNGRSTDSLHCMPGKDTQ/P NP*KQPGGRLHPAKPQGRSCP
22692	53060	A	22820	232	389	

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22693	53061	A	22821	3	401	VGVCEKRGAPGPPAPGPARG PVAAAAPP/GPGASRAR* DAA AAAGGRGPPGQ* T*KAWGLHP GTGSL/RGHPAPM* PLLRAFP PLHPLPPHPLPRRAA/SNPGTS KCRTAAGTRQWGGRQS QLQRC QCLR
22694	53062	A	22822	1	410	MGKMSPGHVRDFHGRPSHHRP RGPGGKSGFVGKVQGP HAVCS LGTWCLVSQPLHP/G* KGP MYS SGVASEGGSPKPWLPRG VEP MGAQKSRTEVWEPLPRFQ KIY GNTWMPRI PMCCARDPGGAKG GCSNPSQRR
22695	53063	A	22823	264	979	GPRHADPANFSARNLSRP* DAP GRVQDPRPQAPQLPPGL GAPSR VRRPPRRPVDRTLPGG RPPA AAA/GPTGGRGS/PRAGGT AAA TGPRAGPGARGAAGSAPFL TDP NM/GRPPPPATTTPPGAAT APGP REEAPGKFRVSPGPGSAGG PPP TRASPTPTAAGGGGGDSEGE GP ILLVADAG/PDSARSPPLG PCV LSAAPRSRRDPDAVGG LAASA AARLNTTWKLPQLGASTL
22696	53064	A	22824	271	426	
22697	53065	A	22825	546	1296	KMVDCLANSEANTRRISIVENC FGAAGQPLTIPGRVLIGEGVLT KL/CRKKPKARQFFLRNDIVV* GNIVIQQKKYIKQHIIPL ENVTD SIKDEGDLRNGWVIKTPTKSFA VYAATATEKSEWMNHINKCVT DLLSKSGKTSPNEHA AVVPD SEATVCMRCQAKFTPVNRRH HCRKCGFVVCGPCSEKRFLLPS QSSKPVRI CDFCYDLLSAGDMA TCQPARSDSYSQSLKSP LNDMS DDDDDDMDQ
22698	53066	A	22826	1219	2370	
22699	53067	A	22827	164	601	DRTNIMVGYHQTNQKTDGKT PTRRPVLVDHNRLPEGSRGRL AVAVAGDHPAAVQVTMTLVN DTGFDPVFSGSIAESWGQHS GT PSYC*DWEAATMLRAFLAKK GETKDLRQFPNIDNAYMELGT NRADAVLHDTPNILYFMQF
22700	53068	A	22828	2	91	

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22701	53069	A	22829	1	1188	MGAEPSSLTSLGTLWSGERFQC MRAKIWERSRKGRFFSTDVISP TKDSFAGPFQPIDTLVQHQRIV GLKVCVLPDPCKIRILKPNPQC VGKWEVEVAENIEIQVFGGERF DINKYSKSPPPPTPQPLYLTAGF ASCRNHRKSEELREGKGESPGK SKPFHLQANFTVALVTTLQGDK HSQEAIRPVAKAKTTCTYLSN VCEMKDFKRINCPDPFHKMAP KAKKEA\PAAPKAEAKAGFK GPRRQVLK\GVHNHKKRKRKK ERSRTFTHLSRRPGRPLR\RRQP KYPSGRAAPRRNKLD\HYAIHK FPLT\TESA\MKKIEDNNTL\VF\I VELLKATTKNQIKQGC*RSLYD IDVGQGSTPWISAWMGEKKGI CSDQLAPDLPIAFGMFANKIWGFI
22702	53070	A	22830	1413	2197	RVEWRWYNVLPCLDVHSGPVD RRSHVMTAAEKPPFCPAWQQA VSQQSCALEPRTGEEGKGIGQ PASGLFPTGEEISVVPNRWLDA SLSPVILGVQG\GSQCLSCGVQG EPTLTLEVRIGASSLGTPQMML SLLKPGSPQPWCCGTP*QDSVD GSFASSLRILAKALLCGPGFCPS LTLPSFCRKPVTIME\LYLGAK SKSFTFYRRDMG\LTSSFESAA\ YPGWFLCTEPEADQPVRLTQL PENGWWNAPITDFYFQ\CD
22703	53071	A	22831	100	177	KRDHF*SRLQQVSRSVRWSSA TDSR
22704	53072	A	22832	610	1080	
22705	53073	A	22833	1169	1308	

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22706	53074	A	22834	1	1889	ACRRRAGTWTPRPRGSGSRA MAGNCGARGALSAHTLLFDLP PALIGELCAVLDSCDGALGWR GLAERLSSSWLDVRHIEKYVDQ GKSGTRELLWSWAQKNKTIGD LLQVLQEMGHRAIHLITNYGA VLSPEKSYQEGGFNLFKETA NVTVDNVLIPHEHNEKGVLKSS ISFQNIIEGTRNFHKDFLIGERG E/IFGGYQEGKIQTLYAVKLFK QEKMKQCKKHWRFLSELEVL LLFHHPNILELAAYFTETEKFC LIYPYMRNGTLFDRLQCVGDT APLPWHIRIGILIGISKTHYLHN VQPCSVICGSSANILLDDQFH PKLTDFSMAHFRSPLEHQSCCI NMPSSSRKHLWY\MPPEYIRQ GKLSIKTDVYSFGIVIMEVLTGC RVVLDLDPKHIQLRDLRELMEK RGLDSCLSFLDKKVPPCPRNFS AKLFCLAGRCAATRAKL RPSM DEV*RALESTQASLYFAGDPP TSLKALRGPSPLFLEKVT\SIPV VEDDEKPNNNLLPS**KALRMK RWPQK\TPFECSP\EVWFLSLE QKAREARENEEACNMPSS\CE ESWFPKY\IVPSQDLRPL*GK*K ILSSQA\SGHSC\RTKPVSSSCSS KFSWDEYEQYKKE

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22707	53075	A	22835	1	1560	RWERGGKRFRAADPMSALRRS GYGSPDGSYGRYYGPGGGDV PVHPPPLYPPLRPEPPQPPISWR VRGGGPAETTWLGGGGGDDG YYPSGGAWPEPRAGGSHQEQ PPYPSYNSNYWNSTARSRAPYP STYPVRPELQGGSLNSYTNGA YGPTYPPGPAGANTASYSGAYY APGYTQTSYSTEVPSYRSGN SPTPVSRGIYPQQDCQTEAPPLR GQVPGYPPSQNPGMTLPHYPY GDGNSVVPQSGPTVRPQEDAW ASPGAYGMGGRYWPSSAPSA PPGNLYMTESTSPWPSSGSPQSP PSPPVQPKDSSYPYSQSDQSM NRHNFP/CASVHQYESLGDQ*T MDDSRILLDSPSPSIVPEPSACM GNAHPVTHPNNQDQSSSLPEE CVPSDESTPPSIKKIHHVLEK VQ YLEQVEVEEFVGKKTDKAYWLL EEMLTKELELDSVETGGQDSV RQARKEAVCKIQAILKLEKKR IMKGFTWKVPVTLTKHELIW LITLFLKCLMLTRSNTFQLFL
22708	53076	A	22836	8	207	TPVPRALRSPAGLEGSHLSSIST MMPAVMSVGKVTENGSGSPQGI KSPSKPPGPNRIG*RNQVSVHT
22709	53077	A	22837	459	5520	RQVRPAGLESDLSINTMMSA VMSVGKVTENGSGSPQGIKSPSK PPGPNRIGRRNQETKEEKSSYN CPLCEKICTTQHQLTMHROHN TDTGGADHSCSCIGKSLSSASSL DRHMLVHSGERPYPKCTVCGQS FTTNGNMHRHMKIHEKDPTSA TATAPGRGDFASAKSSKRKLSH DAESEREDPAPAKKMVEDGQS GDLEKKADEVFHCPVCFKEFV CKYGLETHMETHSDNPLRCDIC CVTFRTHRGLLRHNL
22710	53078	A	22838	164	434	
22711	53079	A	22839	23	242	
22712	53080	A	22840	187	325	
22713	53081	A	22841	1	130	NCPMCWPGQSPRVFST*GRRNP PPKRRSVSAES*RHWPQSPSP
22714	53082	A	22842	614	774	QEPMRMCTMLANSSPSSQATP PGL*SWNQPSLPARTLSRHEWT SCLGSSANL
22715	53083	A	22843	396	560	LFPHDGIKHKKENP/PKGP PPP THPQTTPPRPADAPLVATKSTLD QAWALLAVATS
22716	53084	B	22844	124	205	

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22717	53085	A	22845	1	2355	MVGSRISGVIPLPFTTRAGIFS DPRANMQPLWAPVPPATFVPTS LPPVPTARPPTSASCHCQQVPC AGLEVALPGNRTICWLSLWPS WQLDEDAQSPALESSEIRQFPT APRSGYPTLCPSEFLGPRPRTC EYHSPVLCPASSRASPSAATL STRTLWGPAGSHPGVHNTR LSPDLCPGKIVLRALKESGAGM PEQHKDPRVQENPDDQRTVPE VTGDARSAFWPLRDNGGSPFV PRPGPLQTDLHAQSSEIRYNHTS QTSWTSSTKRNAISSSYSSSTGG LPGLKQRRGPASSRCQLTLSYS KTVSEDRPQAVSLGHTRCEKG ADTAPGQTIAPTASRPHINTSLH VEDKAISDCRPSRPSHTLSSLAT GASGGPPVSKAPTMDAQQDRP KSQDCLGLVAPLASAAEVPAT APVSGKKHRPPGPLFSSDPLPA NSSHSRDSAQVTSMPAPFTAA SRDAGMRRTSAPAAAAAAPP PSTLNPTSGSLLNEWMEAPHIS WPQQLQHVPGRQ/NVRYNQR SQTSTRTS/CPQTKCQLQLPQLY GRPPGSKAEEG/PASSHCQLALS SSNTVSEDGPQA/VSSGHRCEK AGTAPGQTLAPRGGSPPRSQASR PHIINTALHVEDKAISDCRPSRPS HTLSSLATGASGGPPVSKAPTM DAQQDRPKSQDSLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS
22718	53086	A	22846	1	1200	MPEQDKDPRVQENPDDQRRVP EVTGDARSAFRPLRDNGGLS/PP FVPGPGLQTDLHTQR/LGYRV TVEDLDREKAAAFQRINSALQV EDKAISDCRLSRPSHTLSSLATG TSGLPVSKAPSMDAQQERHK SQDCLGLLAPLASAAEVPSTAP MSGKKHRPPGPLFSSDPLPAT SHSQDSAQVTLIPAFFPAAASM DAGMRRTSPGTSAPAAAAAAPP STLNPITLGLLEWIEALHISGPQ PQLQQVPRGQNRQSQTSRTSSC PKRK/CHLQLQLYGRPPGTKA EEG/PASSHCQLTSSNTVSED GPQA/VSSGHTHCEKTADTAPG QTLAPRGGFPRSQASRPCRHKF PLLPRRRGEPLMLPPPELGYR VTAEDLDREKEVAFQRIKSALQ VEDKAI

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22719	53087	A	22847	2	1762	YHSKPVLCAPSSRASPSASATTLSTRTLWGPGAGSHPFVGHNTRLSPDLCPGKIVLRALKESGAGMPEQHKDPRVQENPDDQRTVPEVTGDARSAFWPLRDNGGPPSFVVRPGPLQTDLHAQSSEIRYNHTSQTSWTSSTKRNAISSSYSTGGLPGLKQRRGPASSRCQLTLSYSKTVSEDRPQAVSLGHTRCEKGADTAPGQTIAPTASRPHTSLHVEDKAIISDCRPSRPSHTLSSLATGASGGPPVSKAPTMDAQQDRPKSQDCLGLVAPLASAAEVPATAPVSGKKHRPPGPLFSSSDPLPANSSHRSDAQVTSMIPAPFTAA SRDAGMRRTSAPAAAAAAPP PSTLNPTSGSLNIEWMEAPHISWPQPQLQHVPRGQ/NVRYNQRSQTSRTRS/CPQTKCQLQLPQLYGRPPGSKAEEG/PASSHCQLALS SSNTVSEDPQAVSSGHRCEKAGTAPGQTLAPRGGSPPRSQSRPHINTALHVEDKAIISDCRPSRPSHTLSSLATGASGGPPVSKAPTMDAQQDRPKSQDSLGLLAPLASAEVPSTAPVSGKKHRPPGPLFSSSDPLPATSYHSRDTAQ

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22720	53088	A	22848	292	2053	GSVAWSFPSPSSSLCLWDLPV APTLWGPAGSHPFVHNTRL SPDLCPGKIVLRALKESGAGMP EQDKDLRVQENPDDQRRVPEV TGDARSA/FLAPAGQWSPLSLC AQSRASADIPPCPEVRNQI*PDIP DHLDELHQPKCHLQLLQLCG RLAGAKVEEGASGAKEQGRDA *AGQGTPEQQNPDDQRTVPEV TGDARSTVRPLRDSGGLSPFVP RPGPLQTDLHAQSSEIRYNQTS QTSWTSSSTKRNAISSSYSTGG LLGLKQRRGPASSRCQLTLSYS KTVSEDRPQAVSSGHTRCEKA ADTAPGQTLAPRGSPRSQGS PRRRKIALLPHR*GELQVEDKAI LDCRPSWPSHTLSSLATGASGE PPVSKAPTMDAQDRPKSQDC LGLVAPLASAAEIPSTAPVSGK KHRPPGPLFSSSDPLPATSSHSR DSAQVTSLLIPAAFTAASMDVG MRRTRPGTSAPAAAAAAPPST LNPTSGSLN/EWMEALHISGPQ PQLQQVPRGQ/NVRYNQRSQTS RTRS/CPQTKCQLELPQLYGRPP GTKGCRHEKNVLC SKLFEGFGF IFVGFFFFAYMGILQLLI

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22721	53089	A	22849	146	1789	RQPSTSGSSRSCPCARRSWWAR TARSGWWWELLGARRSPQTLH CPQATLITLPCRPSTSTSGSAM T*RGPWRSFGCTTSFCPTSR/PV ERNIDQTDLHAQRSEIRYNQTS QISWTSSCTNRNAISSYSSTGG LPGLKRRRGPASSHCQLTLSSS KTVNSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTFIDGGDKTYQN VQQFIDEGNYTSGDNHTRLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITR GSSRPSIREDENGRSQKPVHPEG DMTMNIKIVNQATVLTFTTAL LAGGATQAFAKENNQKAYKET YGVSHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKGLDV WDSWPLQNAADGTVAEYNGYH VVFALAGSPKDAADTSIYMFY QKVGDNSIDSWKNAGRVEFKDS DKFDANDPILKDQTQEWRGEA
22722	53090	A	22850	500	1034	

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22723	53091	A	22851	1	2396	MDKYLLHGPPRPPIASRCLA RVPGCAVSSIMVALSLVPLCAH MPTPSGLEVALPGNRTICWLSL WPSWQLDEDAQSPALESSSIQ FPTAPRSGISPLCAPHSCLGQGR GPASHPTSTQTLDISGVKTTTPRR FSVILQDLC SILGDSC LQFHLHR VPQQVSAVLLRVSGASPSATT LSTRTLWGPGAGSHPFVGHNT RLSPDLC PGKIVLRALKESRAG MPEQDKDPRVQENPDDQRTVP EVTGDARSAFWPLRDNGGSPSF VPRPGPLQTDLHAQSSEIRYNH ISQTSWTSSNTKRNAISSSYST GGLPGLKQRRGPASSRCQLTSL YSKTVSEDRPQAVSSGHTRCEK GADTSPGQTIAPTGGS PRSQDS RPRRRKIPLPRRRGEPLMLPPP LELGYRVTAEDLHLEKETAFQR INSALHVEDKAIPDCRPSQPSHT LSSLATGASGGPPVSKAHTMD AQQHRPKSQDCLGLLAPLASA AEVPTAPVSGKKHRRPPGLFSS SDPLPATSYHSRDSAQVTS LIPA PFTAASSDAGMRRTRPGTSA AAAAAPPSTLNPSTGSLNNEW MEAPHISWPQQLQHVSRGQ/N VRYNQRSQTSRTRS/CPPRKCQL QLPQLYGRPPATKAEEGPASSH CQLAHSSNTVSEDPQAVSSG HTRCEKKAGAS/RWASRF*STH YGCTAGQTQVPRLPGTGPSSI
22724	53092	A	22852	1	3392	MDKYLLHDP RPPIASRCLA RVPGCAVSSIMVALSLVPLCAH MPTPSGLEVALPGNRTICWLSL WPSWQLDEDAQSPALESSSIQ FPTAPRSGYPGTLCPSFLGPRP RTCEYHSKPVL CAPSSRASPSA TTLSTRTLWGPGAGSHPFVGHNT TRLSPDLC PGKIVLRALKESGA GMPEQDKDPRVQENPDDQRTVP PEVTGDARSAFWPLRDNGGSPSF FVPRPGPLQTDLHAQSSEIRYN HTSQTSWTSSST
22725	53093	A	22853	40	409	WKMRHETRYNVLVSRGVGCH RLFFLNGVFEHLGRAFVQRKV DTEHQLLRAAVPANQEHRLT QSQHVVDGHSLLLLTLNPSFLCQI QEPSLGSGSGALSGNVRI RPQA QEAPPEPSVLTLLW
22726	53094	A	22857	3	220	

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22727	53095	A	22858	1	356	MAGPVKDREAFQRLNFVYQVS LRQGPBGDGAARRPRVTAPLPQ AAHCVLAQDPENQALARFYLIH TERTIAKRLVLRDPSPVKEELL CRGCSSLLVPGLTCTPAPRDR RGQRWGTGTDLP
22728	53096	A	22859	2	270	
22729	53097	A	22860	2	364	IFSALPARRKVLNLAPVTEPR DQPWAMIIDVF/SRYSGSRGQPR QTLTKGELKVLMEKELPGIFL QSGKDKDAVDKL/KDGPGRPM GDAQGGTFSEVHPCSVAAITSA CHKVYFE/KAGLK
22730	53098	A	22861	282	469	DCGSELQAPPPSLPGPLCPSIM PA/PPYASPPMMPMMGPPFRGM MPVGLAPGPMLLQYNTCS
22731	53099	A	22862	7	522	SVVWNSNGLQSNMPKFYCDY CDTY/LTHDPSVRKTHCSGRK HKENVKDYQKWMEEQAQSLI DKTTAAFGQGGKIPPTPFSAPPPA GAMIPPPSLPGPPRPGMMPAP HMGGPPMPPMMPGPPPGMMP VGAPAGMRPPMGGHMPMMPG PPMMRPPARPMMPVTRPGMTR PDR
22732	53100	A	22863	3	455	WFLIHDRTHTEKPKYKNCNV KAFHRSTCLHAHKRTHTEKPK YECNQ*GKAFNSSHSFQIHRT HTGEKPYECKECGKAFKGPSSV RRHERTHSTKKPYECKHCGKA LSYLTSTFHNHLMHTGEISHTC KICGKAFYSPSVIQTHE*TH
22733	53101	A	22864	1	1665	
22734	53102	A	22865	1	2650	

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22735	53103	A	22866	107	2384	MFGVHGTFLGIESRPLLSLSPS LLYTCEMFQDPVACEDVAVNF TQEEWALLDISQRKLYREVMI ETFRNLTSIGKKWSDQNIYEY QNPRRSFRSLIEKKVNEIKDDSH CGETFTQVPDDRNLNFQEKKASP EVKSCDSFVCAEVGIGNSSFN SIRGDTGHKAYEYQYEGPKPY KCQPKNKKAFRYRPSIRTQER DHTGEKPYACEGKTFISHSG IRRHVMVMHSGDGPYKCKFCGK AVHCLRLYLHERHTHTGEKPYE CKQCGKSFTYSATHRIHERHT GEKPYEQCGKAFHSSSSFQA HKRTHTGKGPYECQCGKSFS WCHSFQIHERHTHTGEKPCECK CNKAFRSYRSYLHRKRSHTGEK PYQCKEKRKAFTYPSLLRRHER THSAKKPYE/CSFYHERHTHT EKPYECKQCGKAFCAPHLRR HGRTH/SAEKPYECKECGKA SASHLQIHERTQTHIRIHSGERP YKCKTCGKGFYSPKSFQRHEKT HTAEKPYECKQCGKAFSSSSSF PYHERHTHTGEKPYECKQCGKA FRSASILQMHAAGTHPEEKPYEC KQCGKAFRSAPHLRIHGRHTHT EKPYECKECGKAFRSAKNLRIH ERTQTHVRMHsverpyKCKIC GKGFYSKSFQIHEKSYTGKGP YECGLQLPRTAAESVDSEKLQG PGKQETHVQLLSLYCLRRVLD
22736	53104	A	22867	1	391	MKEHIERNPVTIKNVKPSINT VPLEDMKAHTGEKPYERQKCE LNQRLRDYAFQYHESNSGVVS ADSETKSGHSGCLIKEMKNATK THNGITGGIIFNANHWRNTNTIY TRIH/GEKSCDYKKCGKAFNQ YSSLRRHESHTGEKPYERQKC ELNQRLRDYAFQYHESNSGVV SADSETKSGHSGCLIKEMKNAT KTHNGITGGIIFNANHWRNTNTI YTRIHINKQEKYQATHVSYAAN
22737	53105	C	22868	179	289	
22738	53106	A	22869	3	206	

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22739	53107	A	22870	1	855	MPRAEPRATLGEQEKAAGLPLG AWRLYLLRHFRKQTELRRSGSR DVTGALLVAAAVASEAVGSLR VAEGGPNTLLQVLRIW/PWC NKEKLTMEERKVKRRSPKSFSA HCTQVVNVQKMSIPVSK/STG FSNPASQVNTSRPKVKKEVM KAEKTKPQGLEEQRHSSQLPIQ HSFLTVDVSRCSRKMERGLLSL LNDHFSWKTFKHFGNECSIEQ MEHVSSELQEKLARLNLLEYG ELEELPEDKRKTASDNLDRLL SDLEELNSSIQKLHLA/DAQDVP
22740	53108	A	22871	67	598	SIRRHCGQRCLVRIRIWLKLPP RLAVREGLRCGTLRDVMPSPM SGVVVGPPGPPGPGCDTTS GP APGTFGQASAPVSPRRGHGEY LCSSPTPVFFPGLWQPPRAGFTA PERSWSRGPRWQLRAA WAGR LSSSPVSALLTFKVILSTGLLFG PLGGWKILSSLPEIFANLAT
22741	53109	A	22872	1	372	
22742	53110	A	22873	1	3961	FALAPEAGFYSLGQQPSTRISGS GCVHPVRVWPFSEIPIAGTLNV GESMQLEVEFEPQSVGDHSGRL IVCYDTGEKVFSVLYGAAIDMN IRLDKNSLTIEKTYISLANQRTIT IHNRNSIIAHFLWKVFATQEE DREKYSKVTAVFSIAASSNSRF ALYESSYNSQRSPEWACDDLI KEEKDETFEFEECITDPLLREH LSVLSRTFANQRRVLVQGD SKLF FNNVFTVEPLGWSEKEMAEIR DVQKDKTKV
22743	53111	A	22874	1248	1716	WYAEQSAHEATAQLSTPMAIR RAVVMPEQQRNRTKKEY/SLRI PFGLPGDRMCFTHRNDD/PTG NEVTPPSLAADLGQOFGGDAT DROPMIHMQLIHQGEQLCF VEHGINMLRLGEILHLAATRHE AHFLAFRQFFNHQRSFCALNLA RQDRITDF
22744	53112	A	22875	478	663	
22745	53113	A	22876	508	884	RQRHPDQRPGRSLFHGHGMCP TTPQQQVDSQINGDNNSESA P*QRRADSIHRSSLHIKRRPPE DVSRCFLCIDAFRQGFTEFNKK GIRVRIPFGLPGDRMCFTHRN DDRPMAMKLLPFAGNKV

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22746	53114	A	22877	1	506	AFCRFSILVGSFISETDMCLLC PFPIGKAISVRLQYFKHETKQSI CLGNQKSPLVCPFFGEQGLDSS SSLDLPSNPAPTLCPVQPPR GPVSVSPVSVVMGSRAPLLSA *LFVSVILGRMVILKNPGVLGQ RQAGSPGAPGLPSPSVRAPLG HKCSERSPSAT
22747	53115	A	22878	621	877	RRRRRRKQRRKQPWSSPARGA *GPRRRSLRAAGTRRRRKRRA SWTRCSNTCPGRCTRCSRSNQA SCPSLLHLLLLFGSFFSFY
22748	53116	A	22879	1	1339	MPSYKGGCETQRHATNGTAAP PRRSSCRGDAIKLPHAEKKEGR PPASTSYPLRLGTRSRSSSHC WCTSWEDPPEATAGEEKRIHPK SPAVCCGEGTVLTASTVTWRA EPARGEIWARLCPDRPGSRAA AVIWERPCCDRLIADRTGPPNS EPHCRAATIPLTWLPEGQTLT LKALAKMAAPALLLALLLPV GAWPGLPRRPCVHCCRPAPW/L WTLCPGKEGEAGVRGRAGRS KEGAA\GCPGAPQASARRGSV GPPGAACRRAYAAFSVGRREG LHSSDHFQAVPFDTEL\NLDGA FDLAAGRFLCTVPGVYFLSNV HTWNYKETYLHIMLNR/QAA/V VLYAQPSERSVMQAQSLMLLL RRATPVVSVPEELPAVLPGQDE LGSLLQHAHHPLADGLVRHEL QPGLAGSSRTGHLVFRTDHGLR QHASHGCPVGPLHVP
22749	53117	A	22880	532	783	VGSTRGIVEGLIFLGEGGECYY PRSLFTVANFTVGKRVKTLNC PSTDKWINKMCHIHTVEYYSDI KRNEIPMRATCRQTLKA
22750	53118	A	22881	275	720	TPIHNCFKENKIPRNPTYKEHEG PLQGEQTTSQGNKRGYKQME EHSMLMGGRINIMKMAILPKVI YRFTIPIKLPMTFFTELEKTTSKF IWNQKRARIAKSILSRKNKAG/ AHHAT*LQTLQGYSNQNSMVL VPKQRYRPMEQSPQK

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22751	53119	A	22882	1	609	MGRNQSRKAENSKNQASSTP KDHASPA TEQSWMGND FDEL TELGFRKSVMTNFSQLKEDVRT HHKEAKNLKRLDKWLTRINSI EETLNDLMELKTMARELRDTC TSFSSRFQVEEGEIQTIREYY EHLYANKLENLEEMDKFLDITY TLPLRNQEEVESLRNPITGSEIE AIINSLPTKKIPGPDRTA*RRP* MT*WS*KPWHEHYVTHAQASV ADSIKWKKGKYKHHQRIL*TP LRK*TRKSRNRNG*IPGHIHSPKT KPGRS*IPETNNR*F*N*GNN**P TNQKNSRARQIHSQILPEVQRG
22752	53120	A	22883	191	564	PNARKLRLTKKDHSPD**RRKL RKIK*MQ*KMIKGISQ/RSRHRNT NYHQRTL*TPLHK*TGKSRNRNG *IPGHIHPPKSKPGRSQIPEYTN KI*N*GSN**PINQKKSRTGRIHS QILPEVQRGA
22753	53121	A	22884	337	589	TRRSRRNG*IPGHIHPPKTKPGR SRIPE*TNRL*N*GSS**PTNQK KPKRTRETDRLPEVQRGAGTIP SETIPNNRKRGTTP
22754	53122	A	22885	162	539	TRKSRNRNG*IPGHIHPSKTKPGR S*IPETNNKF*N*GSN**PTNQK KPRTRQVHSRLPEPISHGMGKS WKQSL*KPAQDKAVPSLIAPIQ HIISSGQGNQARERNKGYSNR KRGQSIVSVCR
22755	53123	A	22886	329	459	NDDTFRKPHRLSPKSP*AADKQ LQQSLRIQNQCAKLRSIPIHH
22756	53124	A	22887	58	440	GLSRQFSPHSVNVKAAGEVPTGR GPPQLSKANVARLPLSIPPLWA GHLWKKGSPSQGIIDKTLISLG QST*GKGQLWVQLQRT*AFLPA GSEESSGSPSTA/PNSAKGQTPS SSGSLTRASSSSLYLW
22757	53125	A	22888	219	332	NEGKNLKGSRERNNTNYHQRT Q*TPLHK*TRKSRNRNG
22758	53126	A	22889	1295	1435	QNQRQKPHDYLNRCRK/W/HFD KIQQPSMLKTLNLGNDGTYL RIIRDI

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22759	53127	A	22890	2	648	YRFSGPTIRSIQNHTHTNQGRK WIKKGIKKPRAQRYESLKGPE V*PSGQGVTCLLRADWLSPLL SGTYVGPFLRNTRFAKKHNK KGLKKMQANNAKAMSARAE AIKALVKPEVKPKIPKCS/RR KLRFDAFYIAHPKLWGRRCFVA RFCQGASGCSGPKGAKVPKA KVKVS/PKAKAKAKADQTKA QAAAPALVPAQAPKRTQAPTK ASE
22760	53128	A	22891	3	370	QMYCVFNERNEDACRY/GS/AIG VLAFLASAFFLVVDAYFPQISN ATDRKYLIGDLLFSGVLA SLAYQRYKAGVDDFIQNYVDPTD PNTAYASYPGASVDNYQPPFT QNAETTEGYQPPVY
22761	53129	A	22892	1	297	
22762	53130	A	22893	3	713	GGSGGDDGMESGAYGA AKAGGSFNLRRLTQPOVVARAV VLVFAVLFVSCFYGEGYSNAHES KQMYCVFNERNEDACRYGSAIG VLAFLASAFFLVVDAYFPQISN ATDRKYLIGDLLF/SALWTF LWFR/VGFCFLTNQWAVTK/PKT VLVGADSVRAAITFSFISFSG VLA SLGAYQRYKAGVDDFIQNY VDPTDPNTAYASYPGASVDN YQPPFTQNAETTEGYQPPV
22763	53131	A	22894	3	219	
22764	53132	A	22895	1445	1777	PVHLGSTCHQCRQKTIDTKNC RNPRLGA/CRGQFCGCLQNR YGEEVRDALLDPNWHCP/HCR GICNCSFCRQRDRGCATGLVY LAKYHGFNGNVHAYLKSQEF EMQA
22765	53133	A	22896	3	337	
22766	53134	A	22897	425	1209	TMSSTQFNKGPSYQLFAEIKNQ LLFKCDPQKQAALCSWIEGLTR LSFSPDFQKSLKEGIVLCTLMN KLGSPVKI/NRLMQNWHQLENL SNFIKAMVGYDMNPMDFEAN DLFESRNMNTQNRILP/PLDHSTI SLQMGANKRSSQ/VGMTAPGTP QHITYNTKLGAHKCDNSSMSLH MGDTQSANHSVQGFGLGQQIY YPKYCPQ/GPAASGAPLDAGNC PGPGAEAPDPPCSQEETTEAPE HAGSLHHRPVVWVGIFLYRLL SFFFL

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22767	53135	A	22898	156	559	QHIRETPGAQVHSCGKWNPPQALWRTAWQLLT/DTKHTLGKPPS/MPHLVIYPLEISC\HTKTCTRMILIASFFIITKTWKRPRCPSPVDKWKNKPWCIHTGLLSSTVPPGEPGCPPELSGLLMGLQTTSRSCSVRQVW
22768	53136	A	22899	161	359	
22769	53137	A	22900	151	383	
22770	53138	A	22901	238	546	PQEHIMEHLEGVINKPRGRRCRPQELQLHYLQKCMDYDGNLNDGFRITLPQPSTHV\HKKEEGSEQAPLMSEDEL\NIIDGVLRDDDKNNDGYIDYAEFAKSLQ
22771	53139	A	22902	1	819	MAAEDKLLLPQLPELFETSKQLDDVEVVTEPAGSRIVQKKVFKGLDLLEKAAEMLSQL/DLVAELPLPKTKNSAEINHTANFSMAYPSLIAMASQRQAKRERHKQKEL\EHRLSAIKSAVETGQADDERVR EYYLLHLQSLLEEIESIDQEIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQVKVFGAGYPSLATMTVSDWYKQHWKYGALPDQGIAKATPEEFRKAAQQQEGQEEK EEEDEQTLYRVREWDWKGIPHPRDYGSSQSMG
22772	53140	B	22903	238	410	
22773	53141	A	22904	1	638	VAEELPKTKNSAEINHTANFSMAYPSLIAMASQRQAKRERHKQKELEHRLSAIKSAVETGQADDERVREYYLLHLQSLLEEIESIDQEIKILRERDSSREASTSNSSRQERP VKPFILTRNMAQVKVFGAGYPSLATMTVSDWYKQHWKYGALPDQGIKATPEEFRKAAQQQEGQEEKEEEDQTLYRVREWDWKGIPHPRDYGSSQSMG

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22774	53142	A	22905	3	1083	RGNSRLRYSHEDLQLPRLPEL FETGRQLLDEVEVATDPAGFR IVQEKIVFKGLDLLERAAEML ISQSTLFGRECRFWKDLSPTHLI TFWGPAPQGAALPLKQVNP SKR LRILQRAREHFTNYLTQCHC YHVGQSFELPKTMNNSAENH TANSSMAYPMLGAMASQRQA KIQRKQKKELEHRLSAMKSA VESGQADDERVREYLLHLQR WVDISLEIESIDQEIKILRERDS SREASTSNSSRQERPPAKPFILT RNMAQAKVFGAGYPSLP/TLW TVSDWYEQHRKYGSIPTGFRGIA KSAPEGISGKAAQQEEQEEKE EEDDEPNFHRAREW\DDWKD TPSLGAYGNRQNMG
22775	53143	A	22906	30	457	
22776	53144	A	22907	401	1509	MWKMNCSSLQSKQMCNQLPP GSTRDGSWKFRQDPRGLGKNA/C DCDSCIASEFGVRGYPTIKLLKG DLAYNYRGPRTKDDIIEFAHRV SGALIRPLPSQQMFEHMQKRHR VFFVYVGGESPLKYVTLKEMP AVLVFKDETYFVYDEYEDGDL SSWINRERFQNYLAMDGFLLYE LGDIDLNASSLRERKLILPEDIP LYVGKLVALAVIDEKNTSVEHT SELTVPVTVVVLTNSNQYFLLD RQIKNVEDMVQFINNILDGTVE AQGGDSILQRLKRIVDAKSTIV SIFKSSPLMGCFLGLPLGVISIM CYGIYATDTDGGYIEERYVSK SENENQEQIEESKEQEPSSGGS VVPVTVQEPKDVLEKKKD
22777	53145	A	22908	53	543	LPISSLRTQTLFSSPLFPQHFEHY LALVSVLPFQLGRORTAPAKKG GEK/RKGHSAINEVVIQYETINI HKRIHGVRFKKRAPRALREIPK FAIKEVETLSVRIDSRFNKALCA KGIRNVPPYRIRVQLSRKRNEDE DSPNKRYTLVTYVPVSTFKNVQ TVHVHEN
22778	53146	A	22909	106	491	IGKGTNLMYGEK/RKGHSAINE EVVIQYETINIHKRIHGVRFKKR APRALREIPKFAIKEVETLSVRI DSRFNKAALCAKGIRNVPPYRIRV QLSRKRNEDESPNKRYTLVTY VPYSTFKNVQTVHVHEN
22779	53147	A	22910	1	321	

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22780	53148	A	22911	313	402	R*GGEKKKGRSAINVVTRYET INIHKRIHGVGFKKRAPRALKEI RKFAKMEKMGTPDVRIDTRLNK AVWAKGIRNVPIRYIRVRLSRKR NEDESPNKLYTLVTVVPVTTT KNLQTVNVN
22781	53149	A	22912	1	3801	
22782	53150	A	22913	2	535	GGGMADTVLFEFLHTEMVAEL WAHDPDPGPGVSAGLRGEEAG ATKGQKMSLSVLEGMGRVVGQ ALGERLPRETLAFREELDLKLF LCKDLWVAVFQKQMDSLRTN HQGTYYLQDNSFPLLLPMGSG LQV/YLEEAPKFLAFTCGLLRSA LYTLGIESVVTASVAALPVCKF QVVIPKS
22783	53151	A	22914	1	201	GDLPEINPLSSCSLLHEKDPPT TSGPQT/DQPKKHHTNFKSGP/T GNRTVQLTWQPLPEPLELWPK AL
22784	53152	B	22915	226	522	
22785	53153	C	22916	1	705	
22786	53154	C	22917	1	462	
22787	53155	C	22918	1	505	
22788	53156	B	22919	1	1059	
22789	53157	C	22920	1	411	
22790	53158	A	22921	1	212	LTSFLHCLSHHYHGAQIHPRH FLHLICRCHQYCHHAYLDPC PQDSHHLHWCWQPLPEPLELRP /RLSD
22791	53159	B	22922	1	864	
22792	53160	B	22923	1	635	
22793	53161	B	22924	1	874	
22794	53162	A	22925	1	566	MPSVRTGDPILHAHTLNPAVW LA WAVEGESLT LNIWICPWQI EPLRHLYATPGSDATSLTVPTR VISPLCVDSWLFDPMLKTHAP ERTFLSFPAAKRQAHLCVLAS NCDKPMYVVLVKAHCAEHQIN LIKDDNKKLGEWEGPCTIDRE GKPKCVVGCSA VVKDY/GKE SQAKDVIEQYFKCKK
22795	53163	A	22926	59	602	PTAMVEEGIAAGGVMDVNTAV QEVLTALIHDLARGIREAAK ALDKYVYQSYCGFLQPEQNC HPREEGMEFMVLAQKF*MASV LPET*EK/RQAHLCVLASNCDEP MYVKLVLEALCAEHQINLIKVD DNKKLGEWVGLCKIDREGKPR KVVGCSCVVVKDYGKESQAK DVIEEYFKCKK

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22796	53164	C	22927	135	293	
22797	53165	B	22928	20	325	
22798	53166	A	22929	677	1031	TPTMCLRSHPLPLALVSVILSFP QPSFSSSLINSSWSSPRSSLSSSS RSFSSGRVNLHPPTPSSH*SHL SSRSCCSAPLLTYHSSLLLVCS VPFPFPFPFPGENPLFVLSGSAP
22799	53167	A	22930	1	1011	MCLRVIFTIGAVSVILSFLSFFII LDQLQLVIPQSSLSSSSNLEDPY SESYAAARRPDSASTEPPPPAG KSSAEYRAHFLAVSTEAERIRA DLVLRARPLGPAHPRTLWPTTP AGPFCRMVAHNQVA\ADNAV TAAEPRRRPEP/SPSSSSSSPAAT ARPRPCPAV/PAPAPGDTHTFTF RSHADYRRITRASALLDA\LG YWGPLSVHGAHEPLRAEPVGT FPVRDS/RQRNCFALSVKMAS GPTSIRVHFQAGRFLDGSRES FDCLFELLEHYRGGSRADLLGA TLRQRRVRPLQELCRQRIRRPP VGREN/LARIPLNPVLRDYLSS FPFQI
22800	53168	B	22931	180	1466	
22801	53169	A	22932	1	207	
22802	53170	A	22933	408	3758	CLQQGPGGNQHCCHREEAPAV AACQEPGGHSEPVLPPLGAPP SEEDGRQQVGSSRLRHMAEMI ATEREYIRCLGYVIDNYFPME RMDLPQGLRGKHHVIFGNLEK LHDFHQHFLRELERCQHCPLA VGRSFLRHILGQKQFPESPSGER PGLTSSHAPCPWMPHYLPEGPA CPVLRIPCEAFNWKHVECTDPV VSPPKQSPLLFQEEQFGMYVIY SKNKPKQSDALLSSHGNAFFKVI PLGPPTACPAL
22803	53171	A	22934	3	355	EAAELDAMCTATRQWSRAGQ GVTGRPCQGRPLRCGLRSTITP KPIPGGHRKKPLLGA/GKHTLS YVERWHWEGHSGI*TRDRQNF ERRLTVPPSRQPFAPTDETRCG DDRISFCNNY

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22804	53172	A	22935	1928	5312	CLQQQPGGNQHCCHREEAPAV AACQEPGGHSEPEVLPLGAPP SEEDGRQQVGSSRLRHMAEMI ATEREYIRCLGYVIDNYFPME RMDLPQGLRGKHHVIFGNLEK LHDFHQHFLRELCRQHCPLA VGRSFLRHLLIGKQFPESPGER PGLTSSHAPCPWMPHYLPEGA CPVLRIPCEAFNW/KHVECTDPV VSPPKQSPLLFQEEQFGMYVIY SKNKPQSDALLSSHGNAFFKDK QRELGDKMDLASY
22805	53173	A	22936	3	306	
22806	53174	A	22937	3	460	LQRQRHPAAAPVVRCTFC FTDIVIMPKRKSPEITEGDKGS KVTKEPTRRSARLSAKPAPPK PEPKRKTSAKKEPGAKISRG KGGKEEKQEGAGKEGTAPSENG ETKAEIHHISRTVNVSTSRGTP PSTLSVKQGIETVRVKGTE
22807	53175	A	22938	3	285	SSCPAREQLQRQRHPAAAPV PVRCTFCFTDIVIMPKRKSPE TEGDKGSKVTKEPTRRSARLS /AVFV*FKLSLQKPAPPKPEPKP RKTS
22808	53176	A	22939	1	413	
22809	53177	A	22940	2	454	AEVQVEEAGLRRLRVSSCSGR GSIQRRFYAVPVRCTFCFTDIV IMPKRKSPEITEGDKGS/KVTKE EPTRRSARLSAKPAPPNPEQPR KTSAKKEPGAKISRGAKGKKE EKQEGAKIEGTAPAEENDETAE EAQKTESVDNEGRMNC
22810	53178	B	22941	55	186	
22811	53179	A	22942	2	397	
22812	53180	B	22943	339	470	
22813	53181	A	22944	1	139	
22814	53182	A	22945	1	416	MPLLYHLRCAVYVQQCNFANP VVSALCTCLVKPVVEKCTPYA VLLLEALALRNVRQLEDLVIEAV YADVLRGSMQDRNQRLVEDYS IGRDIQRQDLASAIARTLQEWG/C HQHLLSLRASAASRQRCQGYHK LHDKQRLRLG
22815	53183	A	22946	315	570	

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22816	53184	A	22947	933	1841	RPAEPDPGSGHPEPKSPTLSAV MSAEVKVTGRNQEQFLLLAKS AKGAVLATLIHQVLEAPGVY VFGELLDPMPNVRELAESDFAST FRLLTVFAYGTYADYLAERN LPPLTEAQKNKLSDTFSVVTL AAKVKCIPYAVLLEALALRNV RQLEDLVIEAVYADVLRGSLDQ RNKRUEVADYSIGRDIQRQDLS AIARTLQEWCVGCEVVLGIEE QVSRANQHKEQQLGLKKHIES EVANLKKTIKVTAAA\AAATS QDPEQHLTELREPAPGTNQRQ PSKKASKGKGLRGSAKIWSKS
22817	53185	A	22948	1	1319	
22818	53186	A	22949	365	1331	RAGGGAPWRFRTGTATVAPET AADLSLHRHLLSRTTSAWGTA CITVPIEPPTWPTWAVPIQWGG SATCIEQEDKLRQGLYGYSSQV NQAMDSGLRPVVDVSNAIRVP QDYVTQSVPLREMNGSLGVLA QQLQNAKLQADAHAHSALKQSD DLKPVPDQAFTKVVTTPADAL QPLIPAAQTFTQQLVMVGDYIA QQGTQECGKTFSRASYLVQHS RIHIGKKPYECKECGKAFSSGS YLVQHQRHITGEKPYECNCKG KAFTVYQQLIGHQSVHTGEKPF ECKECGKAFRLNSFLTEHQRVH TGEKPFCKCKCGKTFRYSSAP
22819	53187	A	22950	2	206	GGGQGATSFGRPESGFIRHQPPP PCRRSSPTRSKLYTL\SAPE*RS VPTSAPGPQDRPPGSVSKKSW
22820	53188	A	22951	571	1102	MGSVSLGNPQGPFPQFTRLPLAN VIHPTFFWETGPRGADSLGAKG RKWQPTFTSRCNKLKVVYLRAG SQAA TGGPSPSLPNLHVKKLRP RKAEA WPGRRNTGKVSGR/LA ALRAPYGESFARAAGPRDAPS/ QQPRPQPEHAPTILISLGSNFGG MVEESWCRMNPDSSGRPKEVAP WPPPS TK
22821	53189	A	22952	1	591	MGPHWKDFKEIDVKKYIDALSI HTYTHTHTHTHADITGDHGG GALLELEINSHLKVVQFRELNITA AKETEDGGGGKAIIFVFPFQIK SFQKIQVWLRRLPKPTRKSCVT QNMHWPPRSRTLKAMRDSIPE DLVFPSEIMCMRIHVKLGDGRL IKAHLDKAQQYHVERNAETFS GVYMKLTGKDINVEFPEFQL

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22822	53190	A	22953	2	508	APPFELPRAAGIRHEGKFSQEK AMFSSSAKIVKPNGEKPDEFES GISQALLELEMNSDLKAQLREL NITAAKEIEVGGGRKAIHIVVPV QLKSFQKIQVRLVRELEKFKFSG KHVVVIAHRRRLPKPTRKSRTK NKQKRP RSRTLTA VHDAIPEDL VFPSEIVGKRNR
22823	53191	A	22954	145	395	
22824	53192	A	22955	536	717	
22825	53193	A	22956	1	729	
22826	53194	A	22957	1	1158	
22827	53195	A	22958	1	2869	MAHLRSCSSLYQPGHLLPPHN PIQDHPLTAPSLTHLTRRAYFTD EKTGGQSAYAVSLLRECVKL RPSDPTVPLMAAKVCIGSLRW MAAKHLAGVLLHLSLEECYWS PLSHPLPEFMGKEESSFATQAL RKPHLYEGDNLYCPKDNIEEAL LLLLISESMLANKLLEEMERV QSPGVESGVDRQLSPSYSDTNVN AQNAQIVPVAAKSAQNEVPGY PEETESRVQSNLLTQFQDLRL LLAAPECLPPRMSPPS
22828	53196	B	22959	28	139	
22829	53197	A	22960	60	812	LASPPFVPLHRCSAGSQPPGPVP EGLIRIYSMRFCPSHRTLVLK AKDIRHEVVNINLRNKPWYY TKHPFGHIPVLKTSKCQLIYES VIACEYLLDDAYPGRKLPYDP YERVROQMMLLELFGKVPPLPK EPPGSVEDVGENAPNLKAALR QEFNSLEEILEYQNTTFFG/GTCI SMIDYLLP/WPWFER/UECMGY WNCVSHTPALRLWISAMKWD PTVCALLMDKEHFQGLFNPFY QNNPNAFDGLC
22830	53198	A	22961	2	251	ILLDFKPWDDTDMAQLEACV CSIQLEELV*GASKLVPMGYGI RKQLQCVVEDDKVGTDLLEEI TKFEEHVQSDVIAAFNKI

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22831	53199	A	22962	353	1071	APLWPRERKFKYQMNGPVAS ASRQSSAPG/NDHSELVLQIASL EVENQSLRGVVQELQAVSNL EAWLNIRRRREKSSPGH/RSTVP QTQHVSMPRQVERPSRPPYYD PGQEAEDNEDDDIDLDNKEED KEARRLREERLRLYAKKAKNP SLVAKSSILLDIKPWDNKTDMT QLEACVRSIQLDGLVSGASKLA SVGYGIRKMQICQVVEDDKVG TDLLEEITKFEHVQSVDI AAL
22832	53200	A	22963	3	482	PWANEAPAKK/PATPAEG/DAR DDIDLFGSDNEEEDKQAGHS CGEER/LRHYAGEEGPRKPA/ VWPKSLPSLLDV/KPWDDDDGP WPSLEACVRSIQLDGLVWGGF PSLVPVGYGIRK/LQICQVVED DKVGTDFPWRREIT/KFEARA RSVDIASFSTRS
22833	53201	A	22964	1	2835	
22834	53202	B	22965	571	1337	
22835	53203	A	22966	1	489	
22836	53204	A	22967	1	618	
22837	53205	A	22968	3	5227	SWSRVRPRTRPEGLRQLKMRT GWA TP RRPA GLLM L LF W FFDL AEP SGRA V NDPLTIFHGNTGKC IKPGYGWIVADHCD ETD EDKLW KWVPQHRLFHLHSQKCLGLDIT KSVNELRMFSCDSSAMLWWKC EHHSLYGAARYRLALKDGHGT AISNASDVWKKGGSEELCDQP YHEIYTRDGSNSYGRPCFFFLID GTWHHD CILDEDHNGPWCATT LNYEYDRKWGICLKPENGCE NWEKNEQFGRCYQFN TQT
22838	53206	A	22969	3	453	GQSPILVIYHETKRPSGISERFSG STSGNTATLTITGTQAMDEADY YCQAGRDFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKAHSN PVKAGVETTPSKQSNKYYAA SSYLSLTPEQ*KSHRSYSC
22839	53207	A	22970	2	354	
22840	53208	A	22971	1	315	

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22841	53209	A	22972	1	712	MAWTLFLTLTQTGTGWSWAQS ALTQPASVSGSPGQSITISIGTS SDIGAYYFVSWYQQYPGKAPK LLIFDVSGRPSGSSRFSGSKSGN TASLTISGLQAEDEADYYCASY ARSTTVFGGGTSVTVLGQPKA APSVTLAFPPSSEELQANKATLV CLISDFYPGAVKVAWKADGSP VNAGVETTTPSKQSNKYYAAS SYVYLSLTPEQWKSRSYSCQV THEGSTVEKTVAPTECS
22842	53210	A	22973	1	1779	
22843	53211	A	22975	1	2001	
22844	53212	A	22976	292	1497	TGQLNGFHEAFIEEGTFLFTSES VGEHPDKICDQISDAVLDA HLQQDPDAKVA/CETVAKTGM LL\AGEITSRAAV\DLPRKVVRE SCLNTLEYDDSSKGF*LQRLVN VLVALEQQSPDIAQGVHLDRNE EDIGAGDQGLMFGYATDETE CMPLTIVLAHKLNAKLAELRRN GTLPWLRPDSKTQVTQVYMQD RGAVLPIRVHTIVISVQHDEEVC LDEMRDALKEKVIKAVVPAKY LDEDTIYHLQPSG/RTFVIGGPQ GDAGLTGRKII\VDTYGGWGA HGG\GAFSGKDYTKVDRSAAY AARWVAKSLVKGGLCRRVLV QVSYAIGVSHPLSISIFHYGTSQ KSERELL*IVKKNFDLRPGVIVR DLDLKKPIYQRTAAYGHFGRDS FPWEVPKKLIY

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22845	53213	A	22977	67	1579	FFVRSLSHTDTNMGQLNGFHEALIEEGTFLFTSKADGEGHPDKICDQISEAVLD AHLHQDPDAKVACETVAKTGMILLAGEITSRAAVDYQKVVR EAVKHIGYDDSSKGF DYKTCNVLVALEQQSPDI AQGVHLD RNEEDIGAGDQGLMFGYATDETEECMPLTIVLAHKLNAKLAE LRRNGTL P WLRPDSKTQVT VQYMQDRGAVLP IRVHTIVISVQHDEE VCLDEM RDALKEKVIAKAVVP AKYLD EDTIYHLQPSGRV FVIGGPQGDAGLTGR IIVDPYD GWAHEEGAFSGKDYTKVSRSAAYGARWVARSLVKGGLCRRVLVQVGP PPKPD E DLYLECEPD PVLAL TQTLSFQVLMPSGPLPRTSVVPREQQMLPLKDSDLTQ P WYSGNCDRYAVESALLHLQKDGAYTVRPSSGPHGSQPFTLAVLLRGRVFNPIRRLDGGRHYALGREGRNREELFSSVAA MVQHFMWHPLPLVDRHSGSRELT
22846	53214	A	22978	3	325	
22847	53215	A	22979	15	1014	
22848	53216	A	22980	7	592	LLCSGRHSLQGVMGILSFLPVLATESDWADCKSPQPWGHMLLWTA VLSLAPVAGTPAAPPKAVLKLEPQWNV LQEDSVLTLCRGTHSPESDSIQWFHNGNLIPHTHTQPSYRFKANNND SG EYTCQTGTQTSLSDPVHLTVLSGQWRKAPGWTWEGQDG*NL LSGRGLQERGVACLLGSIASVCLSTYQWLF L P
22849	53217	A	22981	32	1150	EKA VTA V L WAPARLQGVMGILSFLPVLATESDWADCKSPQPWGHMLLWTA V L FLAPVAGTPAAPPKAVLKLEPQWINGGSR EDSVLTLCRGTHSP EDSIQWFHNGNLIPHTHTQPSLQVSRANNND SG EYTCQTGTSLSDPVHLTVLSEWLVLQTPHLEFQEGETIVLRCHS WRDKPLVKVTFPHNGKSKKFSRSDPNFSIPQANHSHSGDYHCTGWNIGYTLFIPRLLTITVQAPSSSPMGIIVAVVTGTAVA AIVAAVVALIYCRKKRISANPTNPDEADKVG A ENTITYFTSQWHPGWLWEEPDDQNRLVSI VLA LGIWRRNSEREDLVFPGLKFPLGEDTGRCCQFPKEKVLPGVIL

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22850	53218	A	22982	1	471	MKSSFQGHNKEKREKKGPSLFS AAYGGGSCLLLSIMAAALRPLVK PKIVKKRTKEFIWHQSDQHVKI KCNWRKPRGQILMPNTGHGSN /KKT K H M L P S G F R K F L V P S V K E L E V L M C N K S P C A E I A H S V S S K I N K T I V E R A A Q / L A V R V T N P N A R L R S E E N E
22851	53219	A	22983	103	564	GIFRGIMAAALRPLVKPKIVKKR TKKFIHQSDRYVVKIKRNWRKP RGIDNRVRRRFKGGQILMPNIGY G/SNKKTKHMLPKWLSGKFLG SHQRSREL/EKLLA*CCNKFFTC CPRFVSHCFSGFTGKGLRGER SLPNWAFRVTNPARNLRSEENE
22852	53220	A	22984	3	177	
22853	53221	A	22985	74	735	RFAGAGAIPEARARPPDVQAAE EEKEMDLPDSASRVF/CGDASS NMGEHRMNVNAIIL/AQKNML D/RFEKTNEMLLNFNNLSSARL ASRLSERFLHHTRTLVEMKRDL /DSIFRRIRTLKGKLARQHPEAF SHIPEASFLEED/EDPIPTQAPT TTIATSE/QSTG/SCDTSPTDV/S PSLEPLASEDSLHVQALASPAI NGPQPDQIDEEMTGRIALPARC
22854	53222	A	22986	3	275	MRTVAEKVDVAVRIVHIHVSNTL RRSDKRKDRVEISPEQLSAAST EAERLAELTGRPMRVVGVYHVS HPHITVWPSHVGVYHGVAMFI VFRN
22855	53223	A	22987	1	886	AKMAVQVVQAVQAVHLESDA FLVCLNHALSTEKEEVMGLCIG ELNDDTRSDSKFAYTGTEMRT VAEKVDVAVRIVHIHVSILRRSD KRKDRVEISPEQLSAASTEAE LAELTGRPMRVVGVYHSHPHI TVWPSHVDVRTQAMYQMMDQ GFVGLIFSCFIEDKNTKTGRVLY TCFQSIQAQKSSEYERIEIP/IHIV PHVTIGKVCLES/AVELPKILCP/ QEEQDAYRRHSLTHLDSVTKI HNGSVFTKNLCSQMSAVSGPLL QWLEDRLEQNQQHILQEL/HQE KEELMQELSSLE

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22856	53224	A	22988	10	988	LKAMSWAKMAVQVVQVAVQA VHLESDAFVLCLNHAI STEKEE VMGLCIGELNDDTSRSDSKFAY TGTEMRTVAEKVDAVRVHIHS VILARRSDKRKQVEISPGQLSA ASTEAEKLAELTGHPMRVVGW YHSHPHITVWPSHVDVRTQAM YQMMDQGFVGLFISCFIEDKNT RAGRVLVYTCFQSIQAQKSSSEL HGPQDFWSSSQHISIEGQKEEER YERIEIPIHVPHVTIGKACLES VELPKILCQEEQDAYWRIHSLT HLDVSVTKIHNGSVFTKNLCSQM SAVSGPLLQWLEDRLEQNQQH LQELQKEEELMQLSSLE
22857	53225	A	22989	1	1362	
22858	53226	A	22990	284	542	KLFQKKNKKSSCISDNFFFLAI MVNLLQIVRDHWVHVVLVPM GFVIGCYLDRKSDERLTAFRNK SMLFSFPHRELQPSSEVTWK
22859	53227	A	22991	272	1241	FPGGAACDICVWKEENGSLMS MKMGWKA KSCLPVTVHPRCL TPYSARLSSTFPL*NSITG*QS PACKRPF*LTTC*GGSRRNSNR KAA*GPCSPPPSPPPSPATLPR GPAGLQPPGPVLPPLRPKHY APGGLPAPPASLLEDDDDTFCTS QAMQPTAPTKLSPPALLPEKDS FSSALDEIEELCPTSTSTEATA ATDSVKGTSSAEGTQKLDGPQE SRADDSKLMDSLPGNFETTST GFLTDLTLDLIFADIDTSMYDF DPCTSSSGTASMAPVSA DDL KTALPYSSQPVTPSQPFKMDLT ELDHIMEVLVGS
22860	53228	A	22992	1	3234	MELKCVCLKNRSPSAEEQPSLL PEPSAQESHGGHPRSALYGRER LTGQPPSSPHNPAPWASCPAVI DPVPIYSSVAEAYDSGTGEGTPT PGLRIHVESGSLRATAQRLPPER RV/QQRTTAPPPRQPPRRPLRAS LSAAPPEPREPVVAAGPEPGSL QRPARTALPNRPEPQAASPGTL VEKYAAPVATQDLLDENPCTS RLGVVDLQAVLTLRKLENLRS GAQTPLEGGQSGRVPHALRW NRGEEEGERLLC
22861	53229	A	22993	307	1906	
22862	53230	A	22994	1	1752	
22863	53231	A	22995	588	704	

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22864	53232	A	22996	3219	3407	DQVVVTKRIQDAILVLV*EFL HSPALRLCVMKQVGMSSQGELE WGQFLKLSSRNKRKRSGERI
22865	53233	A	22997	1	588	
22866	53234	A	22998	1	917	
22867	53235	A	22999	1	1692	
22868	53236	A	23000	1	2266	MKRIRDYYERSHANNLDNLEE MDELLEETHNL.PGLNHEETENLN KPTITLSPLAGVSSTKKNTKNE LSIVLPFTGSILPVGFATRPRGL ASSNPILLHMFVFLFANGTEEL PVPLMTPTROKKVIPLIPLMVG LGVSASTIALGTGITGISTSVTTF RSLSNDFSASITDISQTLVLAQ LVDSSAAVVLQQLRGLDLLT AEKGGLCIFLNEECFYLNQSG LVYDNIKKLKDRAQKLANQAR QNLDMLHGTGMKSDSDQKKS ENGVTLAPEDTLPLKCYCSGH CPDDAINNTCITNGHCAIIEED DQGETTLASGCMKYEGSDFQC KDSPKAHVRRTEICCRTNLNCQ YLQPTLPPVIGVFPFDGSIRWL LLISMAVCIIAMIISSSCFCYKH YCKSISSRRRYNRDLEQDEAFIP VGESLKDLDQSSSGSGSGLPL LVQRTIAKQIQMVROVGKGRY GEVWMGKWRGEKVAVKVFFT TEEASWFRETEIYQTVLMRHN ILGFIAADIKGTGSWTQLYLITD YHENGSLYDFLKCATLDTRALL KLAYSAAACGLCHLHTEIYGTQG KPAIAHRDLKSKNILKKNGSCC IADLGLAVKFNISDTNEVDVPL NTRVGTKRYMAPEVLDLSLNK NHFPYIMADIYSFGLIHWEMA RRCITGGIVEEYQLPYYNMVPS DPSYEDMREVVCVKLRPIVSN
22869	53237	A	23001	68	636	GVTSNPKALLGALIAPAFASLPE GRGKRIQALNMFPRKNSWRLG LKYPSSSKEKTQVPKTLISGLPE RKSTTRVGEKLQSAHKMPLSPG LLLLLFSGATATA/APLPLEGGP TGRDSEHMQEAGIRKSSLLTF LAWWWFWTSQASAGPLIGKEA REVARREQEGAPPQOSARRDRM PCRNFFWKTSSCK
22870	53238	A	23002	1	144	GIRLPSSADWQKTEAQKRREQL LLDELVALVNRKDALVRDLDA QEQQ

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22871	53239	A	23003	2	667	RWNSSDPDADRTTLNHADHSS KIVQHRLLSRQEELKERARVLL EQARRDAALKAGNKHNTNTAT PFCNRQLSDQQDEERRRQLRER ARQLIAEARSQVGMSELPPYVG EMAAEKLKERSKASGEQNSKL VDLKLKLLLEVQPQVANSPPSSA AQKAVTESSEQDMKSGTEDLR TERLQKTTERFRNPVVFSKDST VRKTQLQSFQSYIENRPEMKRQ RSIQED
22872	53240	A	23004	1	1437	
22873	53241	A	23005	1	2009	MAKPPLYKKGYNQQGVAAIPD VPAAWEAEPSPIPSVPLGRKPN ASQSLLVWCKEVTKNYRGVKI TNFTTSWRNGLSFCAILHHFRP DLIDYKSLNPQDIKENNKKAYD GFASIGISRLLEPSDMVLLAIPD KLTVMTYLYQIRAHFSGQELN VVQIEENSSKSTYKVGNYETDT NSSVDQEKFYAELSDLKREPEL QQPISGAVDFLSQDDSVFVND GVGESESEHQTDDHLSPTAS PYCRRRTKSDTEPQKSQSSGRT SGSDDPGICSNSTDSTAQVLLG KKRLLKAETLELSDLYVSDKK KDMSPPFICEETDEQKLQTLDIG SNLEKEKLENSRSLCRRSDPESP IKKTSLSPTSKLGYSYSRDLDA KKKHASLRQTESDPDADRTTL NHADHSSKIVQQDEERRRQLR ERARQLIAEARSQVGMSELPSY GEMAAEKLKERSKASGDENDN IEIDTNEEIPGFFVVGGDDELTN LENDLDTPEQNSKLVDLKLKLL LEVQPQVANSPPSSAAQKAVTES SEQDMKSGTEDLRTERLQKTTE RFRNPVVFSKDSTVRKTQLQSF SQYIENRPEMKRQRSIQEDTKK GNEEKAAITETQRKPSEDEKGF KDTSQYVVGELAALENEQKQI DTRAAALVEKRLRYLMDTGQNL

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22874	53242	A	23006	145	3217	LDEYEARLTLANLDDFEEDNED DDENRVNQEEKAAKITEINKL NFLDEAEKDLATVNSNPFDDPD AAELNPFGDDPDEEPITETASPR KTEDSFYNNSYNPFKEVQTQ YLNPFDEPEAFVTIKDSPPQSTK RKNIRPVDMSKYL YADSSKTEE EELDESNNPFYEPKSTPPNNLVN PVQLETERRVKRRKAPPVLS PKTGVLNENTVSAGKDLSTSPK PSPIPSVLRKPNASQSLLVWC KEVTKNYR
22875	53243	A	23007	1	165	RPAAPRHERRPAADHGHHRPEP GRGTGQKACSELPSDEACS/GIA IG*SLACSACSVRSRRKQW
22876	53244	B	23008	26	625	
22877	53245	A	23009	325	526	
22878	53246	A	23010	1946	2224	LLQWRHGLNPNINSYNSPILPV QKPKDPYRLVQHLCLIQIVLPI HPMVNPNPYTLSSIPFTTHYSVL DLKHAFFTIPLYPSSQPLFAFTW TDPDTHQAQITLAVLPQCFIDS PHYFSQAQISSSVTYLGILMK THIGLGAVEQGVVLVGEARAA QEPMEWVGSGSMVGCRRALP RGKAAKARREIERSAVTIVPVL DFNPAFHIIPTTDPDHDCISLIH LFTTFPHISFFVPVPHLEHTWFD GSSTR
22879	53247	A	23011	1	1479	MEENFIRVFFTTTTMLLLIALIK QGELCESFDGKSLDGRDENVVI CFDAAAGLHRACSRGEQQNL GTHYFTWQRLFAEVIKLGGLM KPKARNASSLWKEKTKNGFFS LETPEERQTSDLHKYQLAFRLF FIKYKNPAQFMAHLATTLRHFT ALDPESHNFQNLFSSSHLMHIL SAPRLRLYSRFEVSTVITVPG PDFNPASNIPDTTPDPHDCISLI HLAFTPFYISFFVPVPHDHTWF IDGSSTRPNCHTPAKAGYAIYSS TSIEATALPPSTTSRQAEIALT QALTLAKGLRINIYTD/SHILHH HAYLWA/E/RGFLTMQGSSINA SLIKTLLQAALLPKEAEVIHCKG HQKASDPITQGNAYADKVPSL AHAPTLLAPVLQCPRLREVAGT EDDNGKAVLEIPSNIRKSAHVP VQTWKGWDPNTLLGGWFSNL GGFKTLVGTVIFIGFLFLPCVI PRIKAIKLTVETTVSRQIIQTILL

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22880	53248	A	23012	854	1777	
22881	53249	A	23013	27	496	
22882	53250	A	23014	117	210	
22883	53251	A	23015	124	414	
22884	53252	A	23016	3	627	
22885	53253	A	23017	1	567	
22886	53254	A	23018	44	551	GGGRRSAPLQLGFMSRQAKDD FLRHYTVSDPRTHPKGYTEYKV TAQFISKDPEDVKEVVVWKR YSD\FRK\HGD\LAYTHRNLF\RL RLEEFPAFPRAQ\VFGR\VEASV DSRER\KGAEDLLRFTVHIPAL NNSPQLKEFFRGGEVTRPLEVS RDLHLPPPLIPTPPPG
22887	53255	A	23019	25	488	
22888	53256	C	23020	9	119	
22889	53257	A	23021	52	241	
22890	53258	B	23022	4	402	
22891	53259	A	23023	249	984	GSTMYKMNICNKPNSNKAPEK SVWTAPAQSPGSPSELQGGQRSR RNGWSWPPHPLQIVAWLLYLF FAVIGFGLVPLPHHVVVPAGY AVSLGKRRAGPWNPFVSVAET ILPQCMGAIFAGHLVVHLTAVS IDPADANVRDKSYAGPLPIFNK SQHAHVIEDLHCNLCNVDVSA RSKHCSACNKCVCDFDHHCKW LNNCVGERNYRLFHSVASALL GVLLV/LGGHICLRGVLCQPH ASAHQPTL
22892	53260	A	23024	2	224	
22893	53261	A	23025	111	1368	QQPSGSGALARGSGLPPRGRL PARSPVQKRKGWPVKKKRNP PRDLAVRVPTTGVMIFLNEQRS QLRATHPDLPTFTEIMKMLAVQ WAQLSQDKKGRKYAGKALGV TPPPSALTVPYALIEPKQLDIQSL PFQPIDLRLKIKDKRQLVPSYLG GMHTVTEGLAGRVLLQQVQ GGAWESAFLTCPWAMAAAAP GPTLTMQLQPSISAVGFSQMAMG PHVQGRASKLSIYVNPRLQLST TTAMGDELNDLYCGTSRQLFSS LCNKKEPAAKAAAPLSSPGP PALGHAGHGRQLLERSLTLFH LYELLYKPRASPLWPPRVWM PHSLTCGTFVWPMIMMRFAH VASGLLRPPFNQVFAHLSPAQG RHPGENGIIVLTSRAAVRIRCSS CSRSLTGNLKKILPRTQSTWSL WRKRRDK

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22894	53262	A	23026	2	405	
22895	53263	A	23027	1	391	
22896	53264	A	23028	3	463	
22897	53265	A	23029	74	466	FAFNMPEPAKSAPAPKKGSKK AVTKAQKKDGGKKRRSRKESY SVYVYKVLKQVHPDTGISSKA MGIMNSFVNDIFERIAGEASRL AHYNKRSTITSREIQTAVRLLP G\ELAKHAVSEGT\AVTKYHQ
22898	53266	A	23030	168	597	KEETDFLWFCHYCFIMPELAK SAPAPKKGSKKAVTKAQKKDG KKRRSRKESYSVYVYKVLKQ VHPDTGISSKAMGIMNSFVTT F\ERIAGEASRLAHYNKRSTITS REIQTAVRLLPGELAKHA\VSE GTNA\VTKYTSSK
22899	53267	A	23031	18	321	FTATWLNQEVGIVGKYRTRYG VSLQKMVKKIEISQYAKYICF LWQNSKMKRRAVGIWCCG/SCM KTVKSSSRNHIVWTYNTTSAV TVKSTIRLKLKQDQ
22900	53268	A	23032	12	445	FTCRSHVSEVEERCVEAPLLG SRSITGFSLHKSQA\KRTKKVGIV V\GKYGNPLWGP\SLR\K\MKVK\IE ISQHAQVHFALFCGKTKMKRR AVGIWHCGSCMKTV\AGGAWT V\YNTTSAVTVKSAIRRLKEFERP SRTLLYSRLTSLGL
22901	53269	A	23033	3	175	
22902	53270	C	23034	378	434	
22903	53271	A	23035	1	578	MVRCVRLVEAGSVVRYLSTIC RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAVVRARELHLEVTGLET VAQSKAHIVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALT TLEVVGRRLGASL/HTSASKHTM VRALTYCSSREETFTAI
22904	53272	C	23037	236	379	
22905	53273	A	23038	178	534	VVQKTEPLRCFAVSPFSCSLPL PSLFPHSPLLGRPKRQAKPAAD EGFWDCSVCTFRNSAEAFKCSI CDVRKGTSTRYLKICVTWVVV VI*QVFIEHTAICALGVQWYKD RPGPCSYGA

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22906	53274	A	23039	44	1012	VGGGGVQPSMTMGDKKSPTRP KRQAKPAADGFWDCSVCTFR NSAEAFKCSICD\VRKGTSTRKP RINSQLVAQQVAQQYA T P P P P K KEKKEKVEKAGQKRKPEKRPR KFSP/SVVTKKNTNKKTKPKSD\ ILKDPSP\EANSIQSANATTKTSE TNHT\SRPRLEKRG TG G I A Q Q F G QLTVGNVTVITDFK\EKTRSS\ TSSSTVTS\SAGS\EQQNQRQLR GFRGATDKGSLPVP P P N K G R P C QAVNDESFLKLAHGNCGKLWN SGVWKFNLPAAHACLHPWEN LSCGTSTSLVDCQDNFLLCHG HSWPPRDFRHPDDYSGHF
22907	53275	A	23040	1	626	MAGCRNPCKAESHRSKSLSEA ESLFREAESQHDGSGKNAGHR DESVEVWLSLSSSQTRAEIER QSRGKQWL RHLLRDT EGPKET VRPELATRAAMDVAEVEFLAE KELVTIIPNFSLDKSYLIGVDNIP KADEIRTLVKDIWDTRI AKLRV SADSFVRQGEAHAKPDNLTL M EINPSGTFLTQALNHITYK/LRTN LQPESTQSQDF
22908	53276	A	23041	1	951	MDAAEVEFLAEKELVTIIPNFSL DKIYLGITWELKYREIRWLSQG PHGKPHADPGSSILQNSSGPGS VRTNGKSKPWEPFVAEEFAHQ FHESVLQSTQKALQKHGGSVA VLSAEQNHKVDTSVHYNIPELQ SSSRAPPQHNGQEPPTARKG PPTQELDRDSEQE Q E E D D E D G E DEEEVPKRKWQGEAVFEAYQ EHIEERTLERNRSSTAADKAQL LAANRQGHGQPTDPASDNIPKA DEIRTLVKDMWDTRI AKLRV ADSFVRQGEAHAKPDNLTL M EIHTSGITFLTQALNHMYKLRT NLQPLESTQSQDF
22909	53277	A	23042	1	626	MAGCRNPCKAESHRSKSLSEA ESLFREAESQHDGSGKNAGHR DESVEVWLSLSSSQTRAEIER QSRGKQWL RHLLRDT EGPKET VRPELATRAAMDVAEVEFLAE KELVTIIPNFSLDKSYLIGVDNIP KADEIRTLVKDIWDTRI AKLRV SADSFVRQGEAHAKPDNLTL M EINPSGTFLTQALNHITYK/LRTN LQPESTQSQDF

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22910	53278	A	23043	2	642	RPRRLRLDAEGPEETVRLWPAA RAAMDAAEVEFLAEKELVTIIP NFSLDKIY\IGGDLGPFNPGLPV EVPLWLAINLKQRQKCRLLPPE WMDVEKLEKMRDHE\RKKEET TPMPKPF\TTLELT\KLLLNHASD NIPKQDEIRTLVKDMWDTRIAK LRVSADSFVRQQEAHAK\DN LTVLMEIHTSG\TFLTQALNHMY KLRLTNLQPLESTQSQDF
22911	53279	A	23044	3	1038	TSSMAAGCSEAPRPAAG\SDGS LVGQAGVLPCELEPTYAAACA LVNSRYSCLVAGPHQRHIALSP RYLNRKRTGIREQLDAELLRYS ESLLGVPIAYDN\IKVVGELGDIY DDQGH\IHLNIEADVF\FCPEPGQ KLMGIVN\KVSSSHIGCLVHGCF NASIPKPE\QLSAEQWQTMEIN MGDELEFEVFR\LDSDAAGVFCI RGKLNITS\QFKRSEVSEEVTE GTEEA\AKPKKKKKKKDPETY EVDSGTTKLAD\DDTPMEES ALQNTN\NANGIWEEEPKKKKK KKKH\QEVSR\TQDPCFSQQQLT S\SGYQSDHKKKKKKRKHSEEA EFTPPLK\CSPKRKGKSNFL
22912	53280	B	23045	82	323	

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22913	53281	A	23046	3	1624	QLEIRAPTADEIHVTVGAEARNLI PMDPNGLSDPYVKLKLIPDRN LTKQKTRTVKATLNPVWNETF VFNLKPGDVERRLSVEVWDWD RTSRNDFMGAMSGVSELLKA PVDGWYKLLNQEEGEYYNPV ADADNCSLLQKFACNYPLEL YERVRMGPSPPSPSPPTDPK RCFFGASPGRLHISDFSLMVLG KGSFGKVMLEARRGSDLEYAI KILKKDVIVQDDVDCTLVEKR VLALGGRGPGGRPHFLTQLHST FQTPDRLYFVMEYVTGGDLMY HIQQLGKFKEPHAAFYAAEIAI GLFFLHNQGHYRDLKLDNVML DAEGHIKITDFGMCKENVFPGT TTRTFCGTPDYIAPEIIAYQPYG KSDVWWSFGVLLYEMLAGQPP FDGEDEEELFQAIMEQTVTPK SLSREA VAICKGFLT KHPGEAP GASGP*WGNLTIRAHGFFPLGF DWERLERLEIPASFSPRPPCGRS GENFDKFFTRAAPALTPPDRLV LASIDQADFQGFITYVNPDFVHP DARSPTSPVPVPM
22914	53282	A	23047	1	1522	MLRAPRQATRDRHHFAHIDIVQV TCFRYLRRSALAPAPAMPSPVR VDRGSFPVPAGGNHTRRRGGT QEGVTREALAFFDVVATTGAE MMWSNFFLQEENRRRGAAGR RAHGQGRSGLTPEREKVKLA LLLAAWAPRWRCPPWAPSSG WTQHLQGRQRRVRSQPTWG CGRRAPSGCGRRTCPWTGTPA APRSCPEASERNSEHPALICTLP QPHMLKRRARRAPGSMAPPLP RPPQAASVPVFPDPWEPLSRA RSKSPLHSQHRPAQETGRHSRP RTSTRKQKQKSTEKATHTPER APKPQTRENNPKGRAQGSAPR DHNPA SRHQKTSNDKRSTHDT HKTRKDSQTRKKKTRNNEKQ PDR/IGPQIIAYQP/YGKSDVW SFGVLLYE/MLAGQPP/FDGEDE EELFQAIMEQ/TVTPKSLSREA VAIC/KGCGRSGENFDK/FFTRA APALTPPDRLV/LASIDQADFQ FTYVNP/DFVHPDARSPTSPVP PASSPTRPQLLENKFGC

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22915	53283	A	23048	505	2345	SIWGMVMMNPTSSITLRRMM SLFPASLTTKYGGFYINSGTLQF RQASESEDDFIKEKKKKSPKRR KLKEGGKIKKKKKDDTYDKE KKSCKSKFSKAGFTALNASKEK KKKKYSGALSVKEMLKKFQKE KEAQKKREEEHKPVAVPSAEA QGLRELEGASDPLLSLFGSTSD NDLLQAATAMDSLTDLDLEHL LSESPGSPFRDMDGSDSLGV GLDQEFRRQPSLPEGLPAPLEKR VKELAQAAARAAGESRQKFFT QDINGILLDIEAQRELSSQVRS GVYAYLASFLPCSKDALLKRA RKLHL.YEQGRLKEPLQKLKE AIGRAMPEQMAKYQDECQAHT QAKVAKMLEEEKDKEQRDRIC SDEEEDKEGGRRIMGPRKKFQ WNDEIRELLCQVVKIKLESQDL ERNKKAQAWEDCVKGLDAE VKPLWPRGWMQARTLFKESRR GHGHLTILAKKKVMAPSKIKV KESSTKPKKKVSVPSQIGGPIA LPSDHQTGGLSIGASSRELPSQA SGGLANPPPVLNLESDLEDLIR NPASSVEAVSKELAAALNSRAAG NSEFTLPAPSKAPAEKVGGLVC TEEKRNFAKPSAPPPASSLQS
22916	53284	A	23049	1	379	AYRNFTSASDVWSYGIVMWVEV MSYGERPYWDMSNQDIPNTAL LDPASPEFSAVVSVDWLQAIK MDRYKDNFTAAGYTTLEAVVH VNQEDLARIGITAITHQNKLSS VQAMRTQMQQMHGRMPV
22917	53285	A	23050	1	123	
22918	53286	A	23051	3	221	
22919	53287	C	23052	80	379	
22920	53288	A	23053	71	924	AFSVNSSNSWEKA*SQKCLQV NYLSLSSASYLP/CMTCPPSAPL NLISNVNETSVNLEWSSPQNTG GRQDISYVNVCKKCGAGDPSK CRPCGSGVHYTPQQNGLKTTK VSITDLLAHTNYTFEIIWAVNGV SKYNPNPDQSVSVTTTNQAAP SSIALVQAKEVTRYSVALAWLE PDRPNGVILEYEVKYYEKDQNE RSYRIVRTAARNIDIKGLNPLTS YVFHVRARTAAGYGDFSEPLE VTTNTGNKDHDPSTSEAFIIQ LNPIVTKSKELSVIFGSADILLQ

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22921	53289	A	23054	1	1102	MRWLKKWERKYTYLYSSGVLK HKNLLESLLGQFLGPPAQRFD AGGVRPKNDGRFTVIQLVGM RGIGSGMKYLSDMSYVHRDLA ARNILVNSNLVCKVSDFGMSR VLEDDPEAAAYTTRGGKIPRW APEAIA YRKFTSA/SDVWSYG V MWE/VMSYGERPYWDMSNQD VKAIEEGYRLPPPMDCPIALHQ LMLDCWQKERSDRPKFGQIVN MLDKLIRNPNSLKRTGTESSRP NTALLDPSSPEFSAVVSVGDWL QAIKMDRYKDNFTAAGYTTL E AVVHVNQ/EVSTQRCNTKGDL ARIGITAITHQNKILSVQAMR TQMQQ/MHGRMVPRLSTVLNK LKTLEISLPHPCTLIEELHFFNFV
22922	53290	A	23055	148	3229	NAFRFHLLNPAGESHDLQDLL SAVRSPTKRQEQRWHRRTMAG IFYFALFSCFLGICDAVTGSRVY PANEVTLDSRSVQGELGWIAS PLEGGWEEVSIMDEKNTPIRTY QVCNVMEPSQNNWLRTDWITR EGAQRVYIEIKFTLRDCNSLPG VMGTCKETFNLYYESDNDKE RFIRENQFVKIDTIAADESFTQV DIGDRIMKLNTEIRDVGPLSKK GFYLAQDVGACIALVSVRVFY KKCPLTVRNLAQFP
22923	53291	A	23056	57	450	VGDCLTSRGMWSVQATLLAR/ ALCRAWGGT/CRGALTGTISIQ VPR LAPRGLHCSA/ASVSSEQS LVPSPEPRQR/PPGGERDKASF LQTVQKFADTSVVD SGHIDFIY LALRKMREYGVVERDLAVYNQL LNIFP

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22924	53292	A	23057	89	1502	VGDCLTSRGMSVWQATLLARG LCRAWGGTCTGAAL/SQEPPLSR SLASLPRGLHCSAAHSSEQVL VPSPPPEPRQEGPPRLVPFEGPV LGQGAGLGERGQGRAFL/LDGC RNLRTTSVRKRGPII/VDLFYLA LRKMREYGVVERG/DLAVYNQL LNIFPKVFPRNIIQRFVHYPR QQECGLAVLEQMHGVMMPNK ETEFLLIQIFGRKSYPMCLKVRL KLWFPFRMNVNPFVPRDLPQD PVELAMFGLRHMEPDLASARVTI YQVPLPKDSTGASKIPPKPHIVG HRACMSPHQESKKSRSKAA/\n ARHNPSIRPVFVEGPFSLWLRN K\CVYYHILRA\DLLPPEEGK WKRTPEEWELYYPRQLDLEY VRSWWDNYEFDINEVEEGPVF AMCMAGAHDDQATM/VKWNQ GPAGDQFQTLAQNPWSPFRLRR VQPGELPDILLQGWSP/HPAR GPPRKKTTTCKRQQQGPPELV
22925	53293	A	23058	1	2517	
22926	53294	A	23059	1	927	IIVVEFVSRLGARAPSGPAVFSH LAMARLPLRGVVRWGCLLTAVH PEPPTACREKQYLINSQCCSLCQ PGQKLVSDDCTEFTETECPCGE SEFLDTWNRETHCHQHKYCDP NLGLRVQQKGTSETDTICTCEE GWHCTSEACESCVLHRSCSPGF GVKQIATGVSDTICEPCPVGFSS NVSSAFEKCHPWTSCETKDL/V VQQAGTNKTDVVCGPQDRLLA L/VVPIIFGILFAIL/VLVIKKV AKKPTNKAPHPK/Q/EPQEIFP DDLPG/SSNTAAPVAGRIFTWG GQPV/TQEDGQRESHFSCRERQ
22927	53295	B	23060	24	439	
22928	53296	A	23061	1	582	
22929	53297	C	23062	1	2607	
22930	53298	A	23063	248	430	ATNYTREQDSMWNVCVR*GRIT ATTHSVTQRTDERQRRADTAL TLADYRNTSVTGVFAGLF
22931	53299	A	23064	776	1426	
22932	53300	A	23065	284	598	VFRLLRGQKSEPGKSRPKAL*N KPANTPVQSHISLYAAGIINSDS KVR*SCRQSSARQSGSYL*TSPP SPONRQQTGEITATVIAFGRTTR TAPDITPHPASAR
22933	53301	A	23066	3139	3792	

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22934	53302	A	23067	2	830	GVPNMAAPQDVHVRICNQEI KFDLEVKALIQDIRDCSGPLSAL TELNTKVKEKFQQLRHRIQPVL YQRAFIWTASTFFFKLTYSLTDF SSTQHDFFNSPTTPVTFSDL EQL AKEQDKESENQLLLQEVENHK KQMLSNQASWRKANLTCKIAI DNLEKAEALLQGGDLLRQRKTT KESLAQTSSITTESLMGSRMM AQVQVQSEAMQSLVTSSRTIL DANEEFKSMGSIQLGRKLITK YNRRELTDKLLIFLALRLFLAT VLYIVKKRLFPFL
22935	53303	A	23068	1231	1458	
22936	53304	B	23069	1	2133	
22937	53305	A	23070	722	957	VFRLLRGQKSEPGQKQAKSTLE QTSEYPSNRGIPIRQSECSIRTP PFVRLRD*VRGCGCAPLSSVD SFFCCTEAL
22938	53306	A	23071	2	1137	VPNMAAPQDVHVRICNQEI KFDLEVKAPIQDIRDCSGPLSAL TELNPVKVEKFQQLRHRTGP/ VEQLAKEQDKSEKQLLLQEV ENHKKQMLQQFRPSWEGKLN SSPGKICNSDNLEKAEALLQGGD LLRQRKTTKESLAQTSSITTES LMG/ISGRMMAQVQVQSEAM QSLVTSSRTILDANEEFKSMGSI QLGRKLITKYNRRELTDKLLIF LALALFLATVLYIVKKRLFPFI VRFPKVPVLAPFNSLFGICPWF PEAPRLPKAEHTPLRFAPQLP CRLGWEHQCPPLFLQSSWL VKGQSPWEEGPGIGMPPLGT YEP PPSHHCALWEAAAAWSTLKSE PPRTRMPLSPAPIVPLNARSGG GKREER
22939	53307	A	23072	64	665	RVRGGAEALMAAAEEESGAP NVPNRRGGAGRPKTPFECNIC LETAREAVSVCGHLYCWPCL HQWLETRPERQECPCVCKAGIS REKVVPLYGRGSQEA PRPELK TPPPPPRGQR/PAPESRGGFQPF GDTGGFHF/SFGVGAFFP/GFFT TVFNAHEPFRRGTGVDLG/QG HPSLQLGKEFPLPGSAIFLFW

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22940	53308	A	23073	1	416	MQRRRRRL.L.L.PRRQTDRAL PPPPSPGSMPPPLPPP/PPARGG GLRPGDGLYPK/PSPARRGSGA RTSWCTMCAPPSTAPRASRRP RPSSCATRPPTSKPPPA/GHAPH PPPRDLGGGLDSGVQSDGVQLQ HLQRPGH
22941	53309	A	23074	1	1713	
22942	53310	A	23075	1305	1538	LKVKRNTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAAAYRKRKKGHKSSLSLV KINKTAAANK
22943	53311	A	23076	49	355	
22944	53312	B	23077	253	471	
22945	53313	A	23078	1267	1497	LKVKRNTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAAAYRKRKKGHKSSLSLV KINKTAAANK
22946	53314	A	23079	3	1237	HEVAGAVPGAIMDEYYGSAA EWGDEADGGQEDDSGEED DAEVQQECLHKFSTRDYIMEPS IFNTLKRYFQAGGSPENVQLLS ENYTAVAQAVNLLAEWLIQT GVEPVQVQDTVEYHLKSLLIK FDPRIADSMFTEEGETPAWLEQ MIAHTTWRDLFYKLAEAHPDC LMLNFTVKLISDAGYQGEITSV STACQCLEVFSRVLRTSLATILD GGEENLEKNLPEFAKMOVCHGE HTYLFAQAMMSVLAQEEQGGG AVRRIDQEVQRFQAEKTVLTQE AIITVKGVSLSYLEGLMASTIS SNASKTIVAAMSNLVPPELAN PENQFRVDYILSVMNVPDFDFP PEFYEHAKALWEDEGVACYE RSNEYQLIDCAQYIFVLEMQVP CEEAAQSHPGQHGGVQVGRN
22947	53315	A	23080	1358	1589	LKVKRNTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAAAYRKRKKGHKSSLSLV KINKTAAANK
22948	53316	A	23081	33	458	GITGSDASGVTMKFNPFVSD RRKNRKRHVNPASHVRRKIMS SPLSKELRQKYNVRSMPIRKDD EVQVVRGHYKGGQIGKVVHV YRKKYVIYIERVQREKANG/DK DRKILERKAKSRQVGKEGK YKEELIGKMQEYIEP
22949	53317	A	23082	1	576	
22950	53318	B	23083	37	276	

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22951	53319	A	23084	124	549	NNSLSSPVQADVFFRLIVPFCG HIKGGMRPGKKVGVGMGIVDLN PKSFAINLTCGDSPPADGAIE LKAVFTDRQLLRNSCISGERGE EQVSNPLL SIHSTTMPFRVEILC EHMCFRIVFVDGHLDFYIIPH SNRYLAI
22952	53320	A	23085	1	215	QGFIKPLKEENFTLPPGKFGP PKGSLNSPPS/PSSP*SPGGGILL VYYLYRALFQKGCKEAAWLEY PLT
22953	53321	A	23086	533	983	PWGPGCNKRWPCLAKDPPTP QSSGVGQPFGAEPAGAYIRTG PHLGPPPPPPDSSNLHSPNPS DDGADTPLAQSDDEEERGDGG AEP/GVAASSGPLAYRDPAGY SPTSRPPGPSPEPLG/AEDPDSLL ASRAPRGNGWWDGCTLS
22954	53322	A	23087	1422	1670	NRVIDKTGWAWWLTPIRHF RPRWVDCLRLGVREQPGHSKI KSLQKNAKISQAWWHAPVDP ATWKADAGGSLEPGSLRLQ
22955	53323	A	23088	2	663	VLI.DERSAALDGAKRDGTAL AAGALCREARAAQVFFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEHGYQYKSLCGMTTHKA DISSWFNEAIDFISIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFV SIPDHSTNSALSYLQSLITSSHC
22956	53324	A	23089	3	206	

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22957	53325	A	23090	982	2252	LFLEKRRPALGPENRQRAPOGR STLGALRPAMVMEVGTLDAG GLRALDLGERAAQLPACLDQRS FFAFNAGHIAGSVNVRFTIVR RRAKGAIGALEHIVPNAELRG RLLAGAYHAVVLLDERSAGLD GAKRDGTLALAAGRA/LCREA RAAQVFF/LSKGGYEA/FSASCP ELCSKQSTPMGLSVLSLSTSVPD SAESGCSSCSTPLDYQGGPVE ILPFLYLGSAYHASRKD/MLDA LGHRLPWINVLSQIVPNHFEGH YQYKSIPIVEDNHKADISFWFN EAIDFIDSINKAGGRV/FVHCQA GISRSAT/CLAYLMRTNRVKLD EA/FEFVKQRRSISP/NFQLHGA SLLQFEFPRMLGPALFRAEAGK PRQMAVLDRGTSTTTVFNFVP SIPVHSTNSALSVPFRAPLTDLS QLVERPTGR
22958	53326	A	23091	13	287	
22959	53327	A	23092	1	492	
22960	53328	A	23093	1	636	
22961	53329	A	23094	1	506	PTRTWTRGRIPRLSAQPSRGAR GTMADPRVRQIKIKTG/VVKRL V/KEKVL/YEKEPK/QEEKIEKM RAEDGENYDIKKQAEIL/QES/R MMIP/D/CQRR/LEAAAYLDLQRI LENEKDL/EKEAEYKEAR/LVL DSVKLES/LKLFSGVVFALKPR GPILQSIIFDHVLCVQV
22962	53330	A	23095	1	786	
22963	53331	A	23096	183	1059	VLGAFIWQGLDPSPETAFDTHR ATEWGTNDQSLCLNSP*/DAPS AKHEYQASVSGSVSSKPEIDLQ LYDEVDRQDVPVKRNFARIVV NVSDTNDHAPWFTASSYKGRV YESAAVGSVVLQVTALDKDKG KNAEVLYSIESGSHPPYKTAAD VLLKAPPPGWRPTNTKPVHSTE AQPTQNRQTQQKHNGASRSP RHSFATSTRAGAGICGCKTRRW MTRWMEESRGLQTLPLSTRLEP GSSAAWLDPEEQASLQFSSQE APFLGEGGENHIKGVPHGTKE QQQPLNHRSSL
22964	53332	A	23097	1	1224	
22965	53333	A	23098	1	660	

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22966	53334	A	23099	129	595	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPWHSKPT WIMTL*FPLEKTGALSLTSDTS MFTVVVLTLGGPLSEA*/T/GG NYDSHFDVDKGTGTIIIVAKPLD AEQKSNYNLTVEATDGTITILT
22967	53335	A	23100	1	1782	MAARIEVIHELIRLLLMKTDL DAATAALLNVQPAKSGDNTSG APFPGKISQTLKDPHNGYHV FALAGSPKADDDTSIYMFYQK VGDNSIDSWKNAGRKFKDSK FDANDPILKDQTEWWSGATFT SDGKIRLFYTDYSGKHGKQSL TTAQVNVSKSDDTLKINGVED HKTIFDGDGKYQNVQGFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFRKESQKLQ SAKKRDAELANGALGIIELNND YTFEKSNEAADHFKHGGGATIK GRVADNGKPOLSSLTIDIRVIE ESIYPPAILPLEIFITASGEEYS GGVIGKIHATDQDVYDTLTYS LDPQMDNFLSVSSGGLIAHKKLD IGQYLLNVSVTDGKFTTADIT VHIRQVTQEMLNHTIAIRFANL TPEEFVGDYWRNFQRLRINIL GVRNRNDIQIVSLQSSEPHPLDV LLFVEKPGSAQISTKQLLHKINS SVTDIEEIIIGVRILNVFQKLCAG LDCPWKFCDEKVSVDSEVMST HSTARLSFVTPRHRAARQQIR GPPLHNPADT*TTARKYNC DKR
22968	53336	A	23101	184	13958	AMGRHLALLLLLLLFQHFHGD SGSQRLEQTPLQFTHLEYNVT VQENSAKTYVGHVPVKMGVYIT HPAWEVRYKIVSGDSENLFKAE EYILGDFCFRLIRTKGGNTAILN REVKDHYTLIVKALEKNTNVE ARTKVRVQVLDTNDRPLFSPT SYSVSLPENTAIRTIAIRVSATD ADIGTNGEFYYSFKDRDTMFAI HPTSGVIVLTGRLDYLETKLYE MEILAADRGMKLYGSSGSISSMA KLTVHIEQANECA
22969	53337	C	23102	56	331	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
22970	53338	A	23103	2249	2680	GEFLKTRFSIYFLEKYTTFPGE NLEHGFWDSSSTSPVLLHPGIPA SRJ/PVSSIFTKVPPKKSATKP/PV SIWGAPPLGPPGFWGCCPTGEQ RGVCHPSEPHPPVVDFRKKPPF LCVSLSLINIFKSNKFLLTTCNL VIFYTCSL
22971	53339	A	23104	739	1672	CQEAASEFGGLHTPAMFLRRL GGWLPWPWGRKKPMRPDPPYP EPRRDSSSENSGSDWDSAPET MEDVGHPKTKDSGALRVSRRA SEPSKEEPQVEQLGSKRMDSLK WDQPISSSTQESGRLEAGGASPK LRWDHYDSGGTRRPPVSPGG LGVPGPGAPLEKPGRRKLLG WLRGEPGAPSRVYLGGP EEC LQI STNLT LHLLELLASALLALCSR LRAALDTLGRGPLGLWLHGL LSFLAALHGLHAVLSLLTAHPL HFACLFGLLQALVLA VSLREPN GDEAATDWESEGLERE GEEQR GDPGKGL

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22972	53340	A	23105	122	2437	RLELKLPLWTMRFTMEMLLGH LSIFKITGKQKQLTRTAPGSPGQ LRSNQTTGNSLEPSGQPRSSQTT GNSLEPSGQPRSSQTTGNSLEPS GQPRSSQTTGNSLEPSGQPRSSQ TTGNSLEPSGQPRSSQTTGNSLE PSGQPRSSQTTGDSLEPSGQLRS NQTTGDSVQPNNREQPGTVRS APLQPNNREQPGTVRSAPLQPN NRGQRPTKQGGTTWNRQVSSA PTKQGGTAR/PSGQPRSNQTTG NSLEPSSQLRSNQTTGDSVQPN NREQPGTVRSAPLQPNNRGQR TKQGGTAR/PSGQPCSNQTTGN SLEPSSQLRSNQTTGDSVQPN REQPGTIRSAPLQPNNRGQRWD RQVSSAPTKQGTALGSPGSSAP TKQGGTALPSSQLRSNQTTGN SLEPSGQPRSNQTTGNSREPSQ LCSNQTTIGNSQDRQVSSAP/IQ TGNSQDRQVSPAPTKQGGTAG NRQVSS/PIQTGNSVQPNNREQ PGTVSGAM/VWVATPVKGP VETSAHKVSAAGLPKKKT/QPG VTGGAPRLTLNTLVLPKHSRTPS RHEAGSTQALYHNGQAQYALS FPHEAAPMAAFYVVTGIEVTTA LTLEEAPCTVEITALTLEEPPC TVFVWNTKTRNTRLVQDKGSN TKGFVQATATCCFRADCKASRPS PHPPSPHREWTSDLRHKQVSKF PGAHRLPGHPELPIQEAWRGE
22973	53341	A	23106	605	813	LFVFINFRENALLRWAYAR/IT NVYPNFRPTPKNSMLMGALCGF GPLIFIYYIITKTERVSIQTRCLVF
22974	53342	A	23108	273	936	AYSNNKVPWSNQK/PSPTKPA GLIFDFPAVKTVRNKVFVFINYP VSGYTEDLKKFLKPYTLEEQKN LTVCPDGALEFQKGPVYVACQ SPISLLQACRGMNDLDFGYSQR NPCILVKMNRIGLKGSEGVPRID CVSKNEDIPNVAVYPHNGIIDL KYFPYYGEKLHVGYLQPLVAV QVSFAPNDTGKEVTVECKIDGS ANLKSQDDRDKFLGRVMFKIT
22975	53343	A	23109	104	478	ETEVGGLVEASMSHNCTTALQ PGQHSQKENLQNKPIPREKY* VSIEFELIYFF/YCQVGYLQPL VAVQVSFAPNNTGKEVTVECKI IDGSANLKSQDDRDKFLGRV MFQNHSTVHMSRSVSSTE

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22976	53344	A	23110	3	903	LLSPVRAHTMTKNEKSLNQSL AE\WKLFIYNPTTGEFLGRTAAS WGLILLFYLVPYGFLLAALFSFT MWVMLQTLNDEVPKYRDQIPS PGLMVFPK\VTALEYTFSRSDP TSYAGYIEDLKKFLKPYTLEEQ KNLTVCPDGA\LFQKGPVYV ACQFP\ISLLQACSGMNDPDFG YSQGNPCILVKLNRIJGLKPEG VPRIDLCFKRMKDIPNAVAYS HNGMIDLKYPYYGKKTAMF/ VGIYQPIGLLVQVSFAP*QPLGK EVTVE/CAKIDGSSQPKKVQDD\ RDKVFGDEFMFQIHSTVH
22977	53345	A	23111	467	931	SRDSRRGTPLAGGRGRDFAGQ MGHRVQGRHGSRGRLPSGDAR VNAERAEPVGAGAGGPGGGSS VRGFCGRSWSEA/RGRRRAGG GVHNEP\RYRQFP\QLTQIPRCSQ SEFVSGLMWFWIF\WRFWHD K\KVLGHFPV\YPDPSQWTD\EE L/GIPDD
22978	53346	A	23112	1	390	VTIPTSLAELQGLPHIRVFLDNN PWVCDCHMADMVTWLKETEV VQKDRLTCAYPEKMRNRVLL ELNSADLDCDPLPPSLQTSYVF LGIG*ALIGAIFLHYRNNGPLTIS SEGGLASLLCKDSRGVPLL

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22979	53347	A	23113	3	1653	PQRIQRGVPTRGEEVAPGRRQE EEREQERGAERPDPCCVLSGGK GRGNRLREAPGGEGVSQVPA AAPLPRFHERKVFFQTLPAR ALRAQPEPSEAPSPSSGETR AAMPGGCSRGAAGDGRRLRLA RLALVLGVVSSSPTSSASSFS SSAPFLASAVSAQPPLPDQCPAL /CACRSEAAARTVKCVNRNLTE VPTDLPAYVRNLFTGNQLAVL PAGAFARRPPLAELALNLSGS RLDEVIRAGAFEHLPSLRQLDLS HNPLADLSPFAFGSNASVSAPS PLVELLNHIVPEDERQNRSE GMVVAALLAGRALQGLRRLEL ASNHFLYLPRDVLALPLSRHL DLSNNSLVSLTYVSFRNLTHLE SLHLEDNALKVLHNGTLAEIQ GLPHIRVFLDNNPWVCDCHMA DMVTWLKETEVVQKDR LTC AYPEKMRNRVLLELSADLDC DPILPPSLQTSYVFLGIVLALIGA IFLLVLYLNRKGKKWMHNIRD ACRDHMEGYHYRYEINADPRL TNLSNSGCLLEELEDPRPTTLH
22980	53348	A	23114	288	877	ASRLSLPTRTSMRSSSTSPSSSS SSSLCRFLNLNRVTDAAFNLL VWYYCTLTIRESLINNSRWG RAGPEGGEHGMGCQGPSKGR EQGAGG*WVVFCSR/VKGWV VFHHYVSTFLSGVMLTWPDGL MYQKFRNQFLSFSMYQSFVQF LQYYYQSGCLYRLRALGERHT MDLTVGESGVALASGHSFPLPS

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22981	53349	A	23115	1	1273	MAPLHSILGNRVGLCQASVRA CPGATVSSQCRASLRSLAWRG SELPANRGRTWPGPGGLRLQA APRLAYLGRATLLVLTPLYDLP PNVRFTSMSPASPHYFLVLGAPI FLLLRSTWSYHACRFEYATPN DRNTTYLAISGPTRRTYDVATF AYKDEYEKFKLYLTIILISFTC RFLNSRVTDAAFNFLLVWYY CTLTIRESILINNGSRPDGLMYQ KFRNQFLSFSMYQSFVQFLQY YYQSGCLYRLRALGERHTMD LTVEGFQSWMWVRGLTFLLPFL FLW/YNSGQLFNALTLFKPGPR DPQLQGVGRCLCCGPFLL/LFL GNFFTTLRVVHHKFHSQRHGS KKDLRLGLSPCRPRGRFLVPVC FWEQDWEQAPSSVRVSSGLFY SPLGFMGRGCGKEDPGPSCPQ
22982	53350	A	23116	238	398	
22983	53351	A	23117	1	386	
22984	53352	A	23118	13	580	
22985	53353	B	23119	39	1171	
22986	53354	A	23120	381	795	PPSSKAPSSKGPAAKIVCIYALI LQSEVNTITDKFNLIKAAAAY TVEPFWPSFFAKALASVNISSL CNAGVG/SMAPAACTAQAGGP ATSTTAASAFRNHNPRJAPKFR GVLAHEQYLSERATVWVWAPNP NPKSLF
22987	53355	A	23121	1	960	
22988	53356	A	23122	2	3952	
22989	53357	A	23123	1058	1494	KSVRLVNV/YLRTQKAVVRVSP EVPLQNLPLVICAKEVSPHVV LLRDNIAGELELSKSLNELGIK ELYAWDNRRVPSAVPMQGPWP AEHFLQVNEQPPAGSPSPCSSS SSSSGLRGGMQTANGPACALTP TCAQTDCCPTSH
22990	53358	A	23124	195	398	TDSSSALQPQHRGRPALRQRT PRRSP/SPGLSPPRGASPAS/SGA PARGVAFGGDEPPIGAEAMYSK P
22991	53359	A	23125	2	155	
22992	53360	A	23126	1	339	

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22993	53361	A	23127	150	1017	LGRWRQDQVPHGLECRSQSEW SCTDSRQHSYSDSRREQIGK MRYVSVRDFKGVLDIREYW MDLKRLPRKPRTEAGSGSLSS PGADTPVEAAVTVRLGLGSVD VGSFRAWQRGKSAAVGHTVSP RWPRWQGGSSALSMASLSTL TCSWGLRYSALPTTSAQREEG SALYRHLSPPSLRFPYPTVKWAT LAITRPPAPRSHSHHPQPRAL CPVVVLFQHPKTHGENLGDRW KEGSAVSSKGTAPAKLSSGRIR NALQNTLGEVSVARIQTHRGIF VETTEARL
22994	53362	A	23128	1	584	APIECGGIPSLPVLCSRANDQE GVRLLEPSEAMPKSELVSSSS GSDSDSEVDKLLKRRKASLL/P ENPVKKQKTGETSIRALSSF*TE PASSRDDNMFQIGKMYRVSV\ RDFKGKSA*FDIREYWMDEGE MKPERKGISLNPQQWEP SLKE QISGPLIDASKKTKISEPILIKPC TVPVVLICLVTVAVCF
22995	53363	A	23129	186	687	LLWARGLGRAKSAVPTVSTML GLPWKGGSLWALLLLLSQIL LIYAWHFHEQRDCDEHNVMAR YLPATVEFAVHTFNQSKSDYY AYRLGHIFNSWKEQVESKTV\F SMELLGRTRVWEYLKTTIDNC HFQESTELNNTFTCFITSTRPW MTQFSLNKTCLGFGH
22996	53364	A	23130	232	402	LFKAWECCFLIFLQVVITRLKLD KDRKKILERKAKSRQVGEKKG KYKEETIEKMQE
22997	53365	A	23131	637	758	NVEEKNRKKILERKAKSCQNK KEKGEYKEETIGTMRECGL

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22998	53366	A	23132	1	1095	IVFLLYLETCLFVMDCKPNEA LSDSSERLFSFGVIADVQFADLE DGFNFQGTRRYYRHSLLHLQ GAIEDWNNSSMPCCVLQLGDI IDGYNAQYNASKKSLVLVWQ FKRRKGPVHHTWGNHEFYNFS REYLTHSKLNTKFLEDQIVHHP ETMPSEDIYYAHFVPPKFWFI LLDAYDLS/ALGAWDQSSPKY GSVWKILEGSHNPINTGNWNSS SRDFSEA/RSLFQFNGRVSQAQEQ LNWLNEVLTFSDTNQEKVVIVS HLPALYPGPPFNDVCLAWNYRD ALAVIWSHECVGVSLGHGTHD GGYSEDPPGVYHG/NLEGVIET APDSQRFGTVHVPDKMMLKG RGRVPDRIELQKKEPSHC
22999	53367	C	23133	235	382	
23000	53368	B	23134	63	293	
23001	53369	A	23135	160	330	
23002	53370	B	23136	1	870	
23003	53371	A	23137	2	1013	
23004	53372	A	23138	1	1552	
23005	53373	B	23139	120	1034	
23006	53374	A	23140	1	584	RTRGRSLAFLLLAERGA VLWSGCRFRARLGLPGGLR VLVQTGHRSLTSCIDPSMGLNE EQKEFQNAAFDFAAREMAPNM AEWDQKELFPVDVMRKAQQL GFGGVYIQTDVGGSGHVRDLD SVIFEALATGCTSTTAYIRHPQ CPQSQHSFVQEGGTHYKAGHL CCRQWGPRACLPPGRPCHRGA
23007	53375	A	23141	2	412	
23008	53376	A	23142	47	487	
23009	53377	A	23143	77	459	GWKGIEHTLGRCLAQGVINY RMLLSWRRWLVAHPVF*SFSC VGPVGQS*RMTMLHCRHSDPV AKRLSCRRGDFASVVVLCPPPP RLRTLKHFLFFGGLPLSIDFVMT VDFCCHLHLTDFSSNFGF
23010	53378	A	23144	1	304	KVAGSPSPTPAGQQVLDVNSCL DSSVLDSSFLTFSGLHAE/AEGS TGGAALAYLGLKTLCTSQQAF AGQMKSDLFLDDSKSDLEEPW ELRKEGAPRSRDRE
23011	53379	A	23145	1	207	
23012	53380	A	23146	1	3009	
23013	53381	A	23147	3	298	
23014	53382	A	23148	1	636	
23015	53383	A	23149	1	795	

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23016	53384	A	23150	125	1527	SSPRQQTQLARVHP/DGRAQ/LA PSCLPGLGLCPVPVPCVNCNCPA CPCHEHCGEAP*GVA\AKRGAL RVHPPHPCGGPRAMTVTLHGQ DVLMLPGDLVGLQHDAGPGAL LHCSPAPGHPGPQAPYLSANAS SWLPHLPAQLKGTWACPACAL RLLAATEQLTVLLGLRPNLGLR LPGRYEVRAEVANGVSRHNL CSFDVVSPVAGLRVIYPAPRDG RLYVPTNGSALVLQVDSGANA TATARWPGGSVSARFENVCPA LVATFVPGCPWETNDTLFSVVA LPWLSEGEHVVDVVVENSASR ANLSLRVTAEEPICGLRATPSPE ARVLQGVLYVLLAGSSGYLVG FKFLESHGSDSGSANSFHCLISQ NEFKTL.LPDLTRAPRYSPPVEA GSDMVFWRWTINDKQSLTFQNV VFNVVYQSAAVFKLSLSADSAP RPRWRLQSPRVGRSLSPDPGFFG SPGPCQPRLQAFLI
23017	53385	A	23151	648	1387	ASTQSLLAWCPA.WLSIPSTWPS SFSSGCPG/CKAQPVVEVSRSSY VYLEGRCLNCSSGSKRGGYTFT LT.VLGRSGEEEGCASIP.LSPNRP PLGGSCRL.FPLGA.VHALTTKVH FECMGWHD.AEDAGAPLVYAL LL.QRCRQGHICEEFCVYKGLSG YGAVLP.PGFRPQFEVGLAVVV QDQLGAAVVALNRSLA.TLPEP NGSAMGLTVWLHGLTASVLP LL.RQADPQLVIEYSLALVTVLN ETYTESL
23018	53386	A	23152	2	654	DKHIWLSIWDRPPRSCTFRIQRA TCCVLLICLFLGANAVVYGA GDSAYSTGHVSRLSPLSDTV AVGLVSSVVVYPVYLAILFLFW MSRSKVAGSPSPTPAGQQVLDI DSCL.DSSVLDSSFLTFSGLHA EIVNTLADHQHRTDFGSGPSVLII TVSLRSYKFAISLCTTYLWVINT LADHRHRTDFGGSPWLLIITV FLRSYKFAISLCTTYLC

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23019	53387	A	23153	2	4072	SRDPAGSYHLNLSHFWRWSALQ VSVGLYTSLCQYFSEEDMVWR TEGLLPLEETSPRQAVCLTRHL TAFGASLFVPPSHVRFVFPPTA DVNYIVMLTCAVCLVTYVMVM AAILHKLDQLDASRGRAIPFCG QRGRFKYEILVKTGWGRGSGT TAHVGMILYGVDSRSGHRHLD GDRAFHNRSLDIFRIATPHSLG SVWKIRV\WHDNKGSLALGFL QHIVVRDLQTA\QSTFFLVNDW LSVETEANGGLVEKE
23020	53388	A	23154	1	10922	MPPAAPARLALALGLGLWLGA LAGGPGRGCGCEPPCLCGPAP GAACRVNCSGRGLRTLGPALRI PADATALTAMAKADGDVKKY GSKRGALALTHGHSLLRDVSH NLLRALDVGLLANLSALAEIDI SNNKISTLEEGIFANLNLSEINL SGNPFECDCGLAWLPRWAEQ QVRVVQPEAATCAGPGSLAGQ PLLGIPLLDSCGCGATLVGPHGPL ASGQLAAFHIAAPLPTATRW FGDGSAEVDAAGPAAS
23021	53389	A	23155	3887	14184	HVLCWVVTYMVMAAILHKLD QLDASRGCAIPFCGQRGRFKYE ILVKTGWGRGSGTTAHVGIHA VWGGQPERPPAPGTATEPSTAT VWDIFQIRHPAQPGVACWKIRV FGTTTGSALPRFPCSTSSGTC RRHAAPSSWSMTGFRWRRRPT GAWWRRRCWPRVPRSVFPLR HAALLRFRRLGAEQLRGFFDK HIWLSIWDPRPSYFTHIQRATC CVLLICLFLGANAVWYGAVGD SAYSTGRVSRNLNLSVY
23022	53390	A	23156	1	442	GGASGMGGITASTVNQ\SLSP LVLEVDPN\IQA VRTQEKQIK\ TLNNKFASFIDKVRFLQEQNM LETKWSLLQQKTARSNMDN MFESYINNLRQLETLGQEKLK LEAEFTTWGPPLMPPTATKQFN CFFFLVQNKTSASSANVK
23023	53391	A	23157	1	497	
23024	53392	C	23158	208	422	

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23025	53393	A	23159	81	1339	ELSSPRSSFSAPSRISA WFGPPAS TPASTMSIRGTQKSYKGSTSGP RAFKQAAS*QRSQPGFRISSSSF SRVGSNFRGGLGGYGGASG MGGITAVTVNQ/SRALLSPLVL EVDPNIAVVRTQEKEQIKTLNN KFAFIDEVGFLEQQNKMLGT KWSLLDQKTA/RSNNM/DNMF/ ESYNNLRRLQLETLAQEKLKLE AELGNMQGLVEDFKNNYED/IEI NKSTETENEFVLKKDVDEAYI NELYEEIEIRELQSQISDTSVVL DNRSLDTSIIAEVKTEISEMN RNISWLQAETGLKGGRISE GIADAEQRRELVIKIDANAKLSE LEAALQQTKKLLE/MENMSIHT KTTSGYAGGVSLAYGGLTGSG LSYGLSSSRSGAGSSFSRSTST RAMVVKKIKTRDGKLLTSLR
23026	53394	A	23160	1	651	MTAFNSGKVDIVAINDPFIDL YMYMFLYDSTHGKFGHTVK AENGTLVINGNPITVFQDQDPS KIKWAP/LAKVIHDFNGIIEGFM TTVHTITATQTINGPSGKLSRDG CRALQDIIPVSTGAAPVGVKVIP ELNGKLTGMFAHVPTANVSVA DLTCRLEKPA/KYDDIKK/INTHS STFDAGAAIVLKDHSVKLISWY DNEFGYSNRVVHLMAHNASKE
23027	53395	B	23161	1	382	
23028	53396	A	23162	3	1151	ASAHASAVRQSAIIFCVA HIAETPLGKVKVGVNGFGRIGR LVTRAAFNSGKVDIVAINDPFID LNYMVMFQYDSTHGKFGHTV VKAENGKLVINGNPITVFQERD PSKIKWG/DAGAEYRRGSPGLV FNQPRWKAGGSICKGGSQKGS ISAPSAECPPCFVMGCEPMKKY DKQAFKIIISNASCTNQLL*HPL AKG*FHDNFGNSLEGLHDHKS MAITANPRKTV/DGSPRGKLWP LMGRGALQNIIPASTGVA GKVIPELNGKLTGMFAVRVPTAN VSVVDLTCRLEKPAKYDDIKK VVKQASEGLKILGYTEHQV VSSDFNSDTHSSTFDAGA/GIAL NDHFVKLISWY/DNEFGYSNRV VDLM/AHMGFGQS
23029	53397	A	23163	160	236	
23030	53398	A	23164	931	1124	
23031	53399	A	23165	132	303	

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23032	53400	A	23166	20	171	
23033	53401	A	23167	1008	1262	HELQCSLLPVRHATAGHTNGQ NRLHWGHVAHSNYGAALKTN GVEVR*FTAAIARCDGNPYESF RKDVRADFQTRIDAIVRCLPK
23034	53402	A	23168	732	1162	RCIEKGRKGHQAPTGSTRPDG TILSACRSQQQGMFASAGV ARQMGSTGNLPHLV*PYFLGLS SKAQHTG*LHKKR
23035	53403	A	23169	2	1093	
23036	53404	A	23170	236	496	
23037	53405	B	23171	22	3084	
23038	53406	A	23172	305	522	LRDGRGSMSSSSPNSASGSAICP ASSVMPETVSVSRVMPNVTKP A/MTAKQTRIRNQMVAITYES DAWNRSYQ
23039	53407	A	23173	177	386	
23040	53408	A	23174	3	200	GAVAPMHPLAHPVPGAAAQPP PA*QPATPCHQPA*GQPA PPDV PGPESAGRSLHHAHICLAPNEQ
23041	53409	A	23175	171	535	
23042	53410	A	23176	190	505	VPTDRIRTLTSVCKRRCEVHQ LEDPRFEVYQVA/PRRD*SFETS VWNHMRKQ/PPLDVRQLAS*N VLHRQLDIMDSAVASMYSIHLS IKMGIGFSGVTTVVKGTPK
23043	53411	A	23177	349	1272	
23044	53412	A	23178	518	1451	VSSSIIMFGPLSQFPRQVQGVSSV KRPSNVVCPGLMFSFFSSAA*IP **PLI*QPGV
23045	53413	A	23179	2436	2894	TSPDVLRAQPRVPSVQGTSPSQ SCPGQRPHGPNSKAYGR/LSVM AQYYCNVIPLE/VPPSAFTPPP KVDSAVV/RLVPHATMPHPVK DVRVLSRITTEAFNQRRKTIKRS LGNLFSVEVL TGMGIDPAMRA ENISVAQYQCMANYLAENAPL
23046	53414	A	23180	1846	2557	IPVSEKQSGDWRFFSVVYNKA GGLIYQLDSYAPTGLRLEKTFIS YPLDLLLKLHDERVLVAFGQR GRHPEWGHAVLVAINGMDVNG RYTADGKKVLEYLGNPANYNP VSYLFAQPLTSNDKLMAL MFHSLFAIGSQACLPEQGGKPGQ IENAWKTDTFKLHCYQTLTG KFVVADLADPRQAGIDSLRKIYEI YSDFALKNPFSYLEMPIRCFLFD QNLKLALEVAEKAGTFPGPS
23047	53415	C	23181	34	225	
23048	53416	B	23182	105	381	
23049	53417	A	23183	1	837	

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23050	53418	A	23184	3	744	HEASCRSERRRQMAFDFTYDD RAYSSFGGGRGSRGSIAGHHGS RSQKELPTEPPYATAYVGNLPFN TVQGDIDAIKFDLSIRSVRLVR DKVTGKFKVGFYVFEDEVDSL KIEALTYD/GALLGDRSLRVDF AKGRKTKIRVAFGRKGGPDD R/GFRDDFLGGRGSRPGD/RR TGPPMGRVFRD/GPLRG/SNM DFREPTEEERAQRPRQLKPR VWRPLNQVANPNSAIFGGARPR EEVVQKEQE
23051	53419	C	23185	1	1038	
23052	53420	A	23186	1	1486	MGRNQSRKAENSKHESTYSPP KDHSSSQAMEQSWTENGFEKL GFRRKEALYYLDLTASCQSQEL FQLYAGMSVVGTSMPVQAVCP YCGNRIITVTTFPGALTWLLC TTLFLFGYVLGCCFLAFCIRSLM DVKHSCPVQRELFFYHRLRQ MELASSARTVVAPSRPCAGREG RGDANGKNSPTAGSAMSEPP PPQPPTHQA/GVGLLDTPRSRE RSPSPALRGNVVPSPLPTRRTRT FSVATVR/ASQGPVYKGVCKCF CRSKG/HIGFNYPPAGWAGPDIF PGTSLDVGGRSYVPSGKGDEV TLLKCAPIPTPKNEKLAGPWEV VHHSPWHPGT/KHET/WSG/HVI SFLGGLVESTPLSLCFVGDFA RRQQTLEDDILPHETGLQRGNG PSQVSPGGKGYGGAGVGCVF PAISTAYGPLQQLPHHLKSIKSH LKRRAHWWLSGGSNPIPGSGS RVGISSQLAQTHGLNPQNPS WSWRPQIPRSGLAA
23053	53421	A	23187	2	617	
23054	53422	A	23188	1	993	
23055	53423	A	23189	779	1210	AAAGSEAGRRRGADPTRGPHV LPGSRQRRP/PIFSLDLSGFFLF CSEFCPEIKSTNPGISIGDVAKE KKKLKEMWNSLNDSEKQPYFT KAAKLKEKYEKDVADYKSKG KFDGAKGPAKVARKKVEEDE QEEEEEEEEEEEE

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23056	53424	A	23190	116	522	KAPYSTNSLSLPPFILFMGSGY RKQPTTFQEPKPLPGAAARGPGC DPTQPPRHSAPRDHGGP/SPRCS PRPARPRASPAWLPAPRAPTPPSP PAPAAAPRSCRGHARASSGRSG TTATPRRRRGGLWNQSPMDIK G
23057	53425	A	23191	1	152	
23058	53426	A	23192	1	676	MWSAGRGGAAPVPLLGLLLA LLVPGGGAAGTGAELVTCGSV LKLNLNTHHRVRLHS/HDITYG SGSQQSVTGVEASDDANSY RIRGGSEGGCPRGSPVRCQAV RLTHVLTKGNLHTHHFPSPLSN NQEVSAFGE/EGEGDDPGTLW TVRCSGTA/HWEREA VRFQH VGTAVFLSVTGEQYGSPIRGQH EVHGMPCQ/QHNTWKAMEGI FIKPSVEPSAGHDEL
23059	53427	A	23193	1	1044	
23060	53428	A	23194	1	1083	MTATLAAAADIATMVS GSSGL AAARLLSR/SFLLPHNGIRHCAY TA/SLRQHLYVDKNTKICQGF GKQG/TPFHSQQALEYGTKLVG GTTPGKGGQTHLGLPVFNTVK EAKEQTGATG/SVIVPPPFAAA AINEAIEAEIPLVVC/YPRGIPQP GLGHSSSHKTCGPKDKAYWG PNC PGV/NPGECKIGIMP/GHIF HKKGRIGIVSTSGTLTYEAGH/Q TTQKLGLGQSLCVGIGGDPFN GTD FID/CLEILFERFLPQEGII L/GIEGGNA/EENAAEILEPLYSGS KF/ARPVVS/IIAGLTAPPGRRN GVMPGAIISGREKVGAKRERSS ALQSA GVVVSMSPTAGPRF YKEFEKREDRL

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23061	53429	A	23195	1173	2110	FFTELEETILKFIWNQKRACISK ARVNTNDKSGGITLPDFKLYNE AIVAKTTWYWKSRHIDQEK REEKKE*KKDPSVPETLKKKQR NFTELKIQCLSKKFAQKMLQTA RRKLIYEKVKHCHKEYRKM TEIRMARMATKAGNFYVPAEP KLAFVIRIRINGVSPKVRKVLQ LFLLYQIFNGAFVKLNKASINM LRIVEPYIA/WRYPNLKS VNELIYKCGYKINKK*/IALTDN ALTA RSLGKYGI CREDLIHEIYTVGKCFKEANN FLWPF/K/LSSPRGGMKKKTTH FVEGGDAGKREVQINRLIRRMN
23062	53430	A	23196	3	571	GTMEGVEEKKEVPAVPETLK KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRTIIRMA/RMARKVAGN FYVPARTQIWRFVIRIRGINGS EPQRFKVLQLLRPFKIFNG/T PFVKLQGGFRFNLDRCSRSHIL AWGIYPNLKSVNELIYK/RGYG QNQFDLHFFTEKRSHPGSQ
23063	53431	A	23197	2	340	PRVPRVRDSKMASVGEVSGP QYPVKDKLLAEVQTGGSPSPW NLMRGPSSPSGIFGAFQGLLR GTYNKYTNVKKGSDLGFTMV LVACYVLFYSYSFSYKHLKH ER/LRKYH
23064	53432	A	23198	2	48	PRVRLRC*MVDEYCGCEWGK* LNGGRVLWM
23065	53433	A	23199	123	693	QACIMREYKLVVLGSGGVGKS ALTVQFVQGFVEKYDPTIEDS YRKQVEVDAQQCMLIEDT AGTEQFTAMRDLYMKNQGQFALV YSITAAQSTFN/DLQDLRE QILRVKDTDDVPMILVGNKCD LEDERVVGKEQQNLARQWNN CAFL ESSAKSKIYNEIFYDL VRQINR KTPVPG/KAPQKSP SQLL
23066	53434	A	23200	461	1422	SPHGEPLLGCRRREMVGW SLH TESPLG/QWGSQILK LQNDLL
23067	53435	A	23201	232	331	TPL*KWLRGVMAVTVVTPQTG IIAIPDPHHEWGSTGYPR LPA

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23068	53436	A	23202	5	1223	GLDSGPESGLRAQPGLLAGKRK MSVLRRMMRVSNRSLAIFFFF SLSSSCLYFIYVAPGIANTYLFM VQARGIMLRENVKTIGHMIRLY TNKNSTLNGTDYPEGNSSDYL VQTTTYLPENFTYSPYLPCEKL PYMRGFLNVNVSEVSFDEIHL FSKDLDEIPGGHWRPKDCKPR WKVAVLIPFRNRHEHLPIFFLHL IPMLQKQRLFAFYVVEQTGTQ PFNRAMLFNVGFKEAMKDSV WDCVIFHDVDHLPENDRNYYG CGEMPRHFAAKLDKYMILPY KEFFGGVSLTVEQFRKINGFP NAFWG\WGEGDDDLWNRV\H YAGY\NVTRPEGDLGKYKSIPI HHRGEVQFLGRYKLLRYSKER QYIDGLNNLIYRPKILVDRLYT NISVNLMPELAPIEDY
23069	53437	A	23203	78	495	CTFEKAPPFQLGRGRMVPAKK GGEKKTGR\AINEVVTREYITNI HKRIHGVGFKRAPWALKEIR KFAMKEMGTPDVRIDTRLNKA VWAKGIRNVLYRIHVRLSRKR NEDESPNKLYTLVTYVTVTTF KNLQTVNVDEN
23070	53438	A	23204	138	360	KNQKRQLSGGHCADQTSLVLA RLAPLF\PTTMSDKPDMAEIEKF DKSKLKKTTETQEKNLPSKETT EQEKQAGKS
23071	53439	A	23205	145	728	KRQPTSAMKDPFSRSSTSPSIINE DVIINGHSHEDDNFPA\EYMWD GKMEGRNFNR\QIGRRELWGR KD\FLNRCFPKE\MLGEGKEG ALNWV\LFPSFEILPHQTMGPNP RTSFNDPCLSSDGSF\SWEDLVV KS\NLNPNAKEFVPGGEVRKYL SRRGPLLVDVAQFPHCEGSIRR LNCKSSLGHCVTL\AJAQSF
23072	53440	A	23206	530	707	
23073	53441	A	23207	1	515	MDFS\KVP\PHAA\FAQPP\ALT WGLAKGSGRGAGEGGERPDRR R\PAARTGTPA\WRPAGRRLPP RSPPPA\VPV\RPAL\PHV\PGKE TGKTRRRRHYS\PRPLRGAA AAAAAA\VAQTASPSWAEGGRS GAGGSAES\PAFSSPAL\PCPEGLL CPSAVPVPSKQSVSEVLAIF
23074	53442	A	23208	3	713	
23075	53443	A	23209	1	704	

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23076	53444	A	23210	2	1631	GLPRRPTRPPTRSGVSPWPVPGPH SGVLFPLLHCTGSLSQAVLTQ PSSLASAPGASVSKLTCTLRSDIN VGSPFIYWYQQKPGSPFPQFLLR YKSDSDNQQSGVPSRFSGSKD ASANAGILLISGLQSEVRRDDYY CQAWDSSTAHSDTGRGIVGRVP PVRQCWPLILLGLAMVAHGLL RPMVAPOSGDPDPGASVGSRS SLRSLWGRLLQPSQPRADPRC WPRGFVSEPSQLCYVFGTGTK VTVLGQPKANPTVTTLFPSSEEL QANKATLVCLISDFYPGAVTVA WKADGSPVKAGVETTKPSKQS NNKYAASSYLSLTPEQWKSHR SYSCQLQWGLGLGASQGGFLY EPVSCQVVFVGGGTLTVLGGP KAAPSVTLFPSSEELQANKAT LVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNKYAA SSYLSLTPEQWKSHRSYSCQKP NHASHGTSRMPVSAPVSGLSK CWSGTGDRSALQGMGPCHGI PDPMQQASDSGQPKAAPLGLS CSKPSSEELSGQGGPHWCVS
23077	53445	A	23211	1	959	VFLLLYLVAMPDPAKSAPAK KGSKKA VTKAQKKDGKKRRR SRKESYVYVYVVLKQVHPDT GISSKAMGIMNSFVNDIFERIA GEASRLAHYNKRSTITSREIQT VRLLLPGELAKHAVFIENLLNY RKYL VKSSEKDRNYPCPLGLK SKVDICTPYCLLLPQPRHYPG KDTKEETEDFPNSPPINREEDK RYTTVMGPCLRQAALLEGELLA CPVMEDQANWVHEPITNTF KEIRKSIRENGPASPFTRGLIEVI ADSSDLVASTQKLTPKETPSA PYNDISDLTNQDSWFGFPIWNN AGETDLSNNKTT
23078	53446	A	23212	3	463	
23079	53447	A	23213	74	464	
23080	53448	A	23214	41	490	
23081	53449	A	23215	2	369	PDPAANAPAAAKPAAKALPV FLLLSGGAGPAHPMRAPGC*G ELGYTEQLFQFLQATAQEEGIF EYTDPKLAISAVWTFRDLGVVLQ QTPSPAGPRLHLSPTFASLDNQE KLEQFIRQFICS
23082	53450	A	23216	124	301	

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23083	53451	A	23217	3	2426	PGVLSTATFRESGLSPCSKLLKHP GPRGRIQYSPPTAGQGRLENG AGHPQSTGPVATLSVAEYGTQ GGASGPARIPIGSRGCLLAGRA EASLWSSGFGMKLEAVTPFLG KYRPFVGRCCQTCTPKSWESLF HRSITDLGFCNVILVKEENTRLF SWALLRVLLKLLFNLVQLHKGQ MKMVQKAAQVGVGTSLWL SPEQGLPLVLLSTHKTLLDGILL PFMLLSQGLGVLRVAVDSRAC SPALRALLRKLGLFLPPEASLS LDSSEGLLARAVVQAVIEQLLV SGQPLLIFLEPPGALGPRLSAL GQAVWVGFVVQAVQVGIVPDAL LVPVAVTYDLVPDAPCDIDHAS APLGLWTGALAVRLRSWRWG CSHRICSRVHLAQPFSLQEYIVS ARSCWGGRTLEQLLQPIVLGQ CTAVPDTEKEQEWTPITGPLLA LKEEDQLLVRLSCHVLSASVG SSAVMSTAIMATLLFKHKQG VFLSQLLGEFSWLTEILVRGFD VGFSGQLRSLQHSLSLLRAHV ALLRIRQGDLLVVPQPGPLTH LAQLSAELLPVFLSEAVGACAV RGLLAGRVPPQGPWELQGILLL SQNELYRQILLMHLLPQDILL LKPQSSYCYCQEVLDRLIQCG LLVAEETPGSRPACDTGRQRLS RKLLWKPSGDFTDSDDDFGE ADGRYFRLSQSHCPDFFLFLC
23084	53452	A	23218	169	955	ASSQLPCSMACCATWAPLKM RWLCSTAWSTSSLPPSWSSL QASQPSCCHATSAPPACAGQCL ARAWPVLSTLCTCALGLLASIA MTFATQGKALLAACTFGSSELL ALAPYCPFDPTRIYSSSLCLWGI ALRCSAWAENVFAVRCAQLTH QLLELRPWWGKKQPTHMMRE NPELVEGRDLLSCTSSSEPLTL CRDDVLP RP DGQLRTLQATLL CDPGPGFLGAGLRGLKWTGG PISGAFQPSPTPAHLHLKIETL F
23085	53453	A	23219	1	344	

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23086	53454	A	23220	214	1355	FCSSWLRLSLADSSLWKMFVLVGLTGIIASGKSSVIQVFQQLGCAVIDVDVTARHVVQPGYPARRRIVEVFGTEVLLENGDINRKVLGDLIFNQPDRRSLNAITHPEIRKEMMKETFKYFLRGYRYVILDIPLFETKKLLKYMKHTVVVYCDRDTQLARLMRRNSLNRKDAEARINAQLSLTDKARMARHVLDNSGEWSVTKRQVILLHTELESLLEYLPLRFGLTGLAAIASLLYLLTHYLLPYAYTASAIPPSGAASRGPGARCSAIRKRAPRPTSAVSPPGAPRSPARGLRAIDRAAGTRNLNATLPPGPPAPSPSPSSITLHVFIQLQPDITRGREGTDFQWEKFPGRVLVADSRRLRCLAPATWLV
23087	53455	A	23221	2	1231	TPFLFRKGTADGSARTTVIHLGFTKGGKQRCVETQAAAAGVDVGRTAAGGRVKGESGVSSDDRPGLPVGQSQPEGGEQATDTVSVHATTSSQAWPGGADSKELSSKAEERETGKDQQTLEPLCLPLRDFPDSAPVMSSDSGHATESLHLASSDSKPPMPTPNEGPGSTVGHAGPRTVKADLCTEPQLALRGLQVSLPRLHLVGVIIAEHQASGLECGHAGSCSPDGSPRAPGATLCLS KPLSFRTKRCLPCWLPASAPVGPAGAPVHIPGAPVCIPGAPACISNAPVHIPGAPVGIPIGAPVCIPGAAVCVPNTPMCIPSPMCIPTPVCIPNTPVCIPNTPVCIPGAAVCILGAPRAHPWCSSCVHPGAPECYLGCGLTQADRLPEAVLDAGLQELPLFALCGQALPS
23088	53456	A	23222	2	408	
23089	53457	A	23223	62	251	

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23090	53458	A	23224	2111	3003	TQKAIACMCLGLCKKIHHLLSLQ CLISQIKMIMGAGWQ/SSGFTDE KETSQIKADPEKLLKQESLLE EDSEEEGLCRICQIAGGSPSNP LLEPCGCVGSLQFVHQECLKK WLKVKITSGADLGA VKTCEMC KQGLLVDLGDFNMIEFYQKHQ QSQIKTEATVVEHKDIYVNTET QLVPEARSVLLVGAGQMLLTG ANRALNSDYSSMRPKVKAQNE LMNSGLYLVLHLHLYEQRFAEL MRLNHNQVERERVVTRVLGG LSPNVSCGVVSGVGSFQWVRG LTDLKNEASDLHAQIPAE
23091	53459	A	23225	1	594	MIAAFNPGKVDVTITNGPFIDL NYMVMYMFHYDPTHGKFHDVP MFVGMGMNHKHNKLTVISNAS CTTNCLDPLAKVIHDFGIREG LMTTVHSIIATQKTVDGPSRKL WHDHSHGAFQNTIPASTGAAKI KKVVRQA/SQGPKLGILGYTEH QVVPLEFKSNTRPSTFEAGAGI AVNDHFVKLISWYGNEFAYSN KVIKPM
23092	53460	A	23226	3	232	QQTLLQPAALPCFPPTHTPPEVL PTAMNTTSSAAPP/SLGVEFISLL AIHLLSVALAVGLPGNSFVWSI LKRMQKRSVTALMVLNLALAD LAVLLTAPFFLHFLAQGTWSFG LAGCRLCHYVCGVSMYASVLL ITAMSLDRSLAVARPFVSQKLR TKAMARRVLAGIWLVSFLAT PVLAYRTVVPWKTNMSLCFPR YPSEGHRFAHLIFEAVTGFLLPF LAVVASYSIDIGRLQARRFRS RRTGRLVVLIIITFAAFWLPHY VVNLAEAGRALAGQAAGLGLV GKRLSLARNVLIALAFSSSVNP VLAYACAGGGLLRSAAGVFFA KLLEGVTGSEASTP/RGGSLGQ TVKSGPAALEPGPSESLTASS LKLANELN
23093	53461	A	23227	1078	2221	
23094	53462	A	23228	6125	6319	ASVVPVTALAMCSPKSGIGDG FAVLRVEDVAQK***KAALGV ASSPAWQQTREHVGQNSPL
23095	53463	A	23229	1	1347	

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23096	53464	A	23230	1	1124	MRECSIHVGGAGVQIGNACWE LYCLEHGIQPDGQMPSDKTIGG GDDSFNTFFSETGAGKHVPRAV FVDLEPTVVDEVRTGTGRQLFH PEQLITGKEDAAASNYARGHYTI GKEIVDLVLDRIKRLFGGGTGS GFASLLMERLSVDYSKSKLEF AIYPIAPQVSTAVVEPYNSILT HTTLEHSDCAFMVDNEAIYDIC RRNLDIERPTYTNLNLIGQIVS SITASLRFDGALNVDLTEFQTN LVVPYRIHFPLATYAPVISA EKA YHEQLSVAEITNACFEPANQMV KCDPRHGKYMCCMLYRGDV VPKDVNAAIATIKTKRTIQFVD WCPTGFKV*LGDMFAEQAAD AQNNLTGLEPHPLGRSLFHGL
23097	53465	A	23231	1	2918	MDVYCAHESLRHTKSPDATGQ TSQQRPEALQAFWPAFGSSPVT GSSPVTETTKGRWSSSRQVL WDRIPLAKSRPAISNRQSQRTNI PWWSCEPPLNLEREQPPRFAQP GTYASRWKALEMEKQOREQ VDRNIREAKEKLEAEMEAAH EHQLMLMRQDPLALVSCMQ QGQMSRSRSPKKVFKHLYELNL TKLQSLGSRSLRWKDSFVWGE EAGGKRPLVSLALHRSPLLL LFVPKHPKGRPDCTVQRS
23098	53466	A	23232	1	158	
23099	53467	A	23233	1	414	LGGLKGTWGETKPMAAAEEE DGGPEGNRERGGAGATKTL YTGNHLFSPQWLETRPERQEC VCKAGISREKVVGESLLTFS HFLRLKTPQICRLPV*LFLPP*GF QPFQDGGFHFSFGVGAFFPGF FNPSY
23100	53468	A	23234	1	663	
23101	53469	A	23235	2	667	SWAGGGFWFGACVCFVGGTE GYVGRNKTGHGSSRRRRSGAP NVPNRERGGAGRPKTPFECNIC LETARELVSLANLYFWTISH QVLETRPEIRQECVPCKAGISR EKVVPLVYGRGSQEAIPRLKT PPPPRGQRPAPEIRGGGFQPF DTGGHFPSFGVGAFFFGFTTV FNAHEPFRRTGVDLGQGH A/SSW/QD/SLLLFLAIFFF/WLL
23102	53470	A	23236	363	476	
23103	53471	B	23237	224	364	

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23104	53472	A	23238	1	1324	MRQRRRAELLSKDKRVRTDGN KCSPSAIGKRKRGTNDWIEGD NNQESQGLNCSDTLNRDLGPN TRGFLYAGLSGLDPSLPTPD MSSEVL EDNLDLTL SLYSGKDS SVKLL E EYADSESQASLQGRSR CWQHPPHAPLSYPPAASGSQLS LQGGKFP SAKPPLLGGYTCTAQR TQWALTKRSLRATRESVSRQQ GVYGLVGRKRTRHHRGVGLGL GIPSARPERPGTGEAGPTRLPG AAVARRRPARPVRGRGLGDPAP TAAQTSGPASP LPPPPR SYGDP HQNGYDPDPAPSASDLPPAA GDTRGSGGRRKKRRTGTARLN TPGRKA\PKQKAAAGRKGRAH QPAPRTPEPQRRRPIRPPNQTD LRHPHRRACRGPPPGAGGTA NPSTGANGAATARRTAGART RGARGASERAGRHGSRPASWL TATPPPGT
23105	53473	A	23239	1	433	PTRPSSPEETDGPWDPEGHGG PLTDPNAPVLALPPAIPGLSL MADGSSDAAREPRPAPAPIRRR SSNYRAYATELQDLCLRHAR VDKVDEERYDIEAK\VTKNITEI ADLTQKIFDLRGFKRPTLRRV RISADAMMQALL
23106	53474	A	23240	2	409	
23107	53475	A	23241	3	490	SSPEETVGPWDPEGHGGPLTD PPNAPVLALPPAIPGLSLMADG SSDAVRAAG*GVAGTPRARAR EPRPAPAPIRRRSSNYRAYATEP HAKKKSKISASRKLQLKTL LLQ IAKQELEREA EERRGEKGRALS TRCQPLELAGLGFAELQDLCLRQ LHARVDK
23108	53476	A	23242	149	846	VSAWRNGSSDAAREPRPAPAPI RRRSSNYRAYATEPHAKKKSKI SASRKLQLKTL LLQIAKQEL E REAEERRRGREGARSLAPRC/QP LELAGLGFADLPGLCCRFHA RVVDKVDEERYDIEAKVSKNITE IAN\LTQKIFDLRSKFKRPTLRR VRISADAMMQALLGARAKESL DLRAHLKQVKKEPKEKENREV GDWRKNIDALSGMEGRMKKW RELSLPA YCPCPEEGH
23109	53477	A	23243	1	487	
23110	53478	A	23244	80	511	

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23111	53479	A	23245	427	1417	KTMWKVEFGVRFSTIRLLLEHQ PKQTMYPILPK/PPLWPEEPKTE APKQTPRAPPKPKTSPRIPRIPQT QPEETDQSTQEPFTTKIPRTIEL AKTTQGLEMLSLIHNPKMHK DSTNEQIAASLQACYEQLLM YIRVTDVDSVGPNGKEAVTA PQAPTFLFWLNHKAQLAKDWA GKDVNITPTFATSKKENKPPNN LQICNVSKIHQRAKVAGKPEIK DKHIQKEMPLDAIEASKINLVKI FNEFLKAWKCRLSFEYRIPENQ GHKGSFYLLVGSSRTSWLLTEK IGSSKRVLRMPPMDILKTTQILL SFLWSINLTPRGKNNHLVAPAH
23112	53480	A	23246	3	1011	
23113	53481	A	23247	2	334	PIQSFFLVLKPPRLKGVYLSK SLSRWFFKVQAN*RSQPKAFS RLSCHC
23114	53482	A	23248	1	642	
23115	53483	A	23249	854	1150	KEDTNKWKNPICSWLGRINIVK MAIMPKVNL*IQCHPHQATNDF SSQNWKTTLKFIWEKPEKAL PSQS*AKRAKLGGITLPDFQTIT YKATVTKTA
23116	53484	A	23250	1754	2393	PSNRREFGESWPETQAPGALRP LLPAPGTPRARERAPGWPARPM EYIYPSFRYEESDLRGYTVFKI EVLMMNGRKHFEKRYSEFHAL HKKLKKCIKTPEIPSKHVRNVV PKVLEQRQGLETYLQAVILE NEELPKLFLDFLNVRHLPSLPK AESCGSFDETESEESSKLSHQPV LLFLRDPYVLPAAADFNPVVE GVLHGIFYPHLQPR
23117	53485	A	23251	1	265	AGNRLRFQLELEFVQCLANPNY LN/WYPQCLHMLELLQYEHFR KELVNAQCAKFIDEQQLHWQ HYSRKRMRQLQALAKQQQQN NTSGK
23118	53486	A	23252	1	987	
23119	53487	A	23253	1	491	RGRNFRARVSGLLLCQAGGVL VSSFVMAAAVAMETDDAGNR LRFQLELEFVQCYANHNLTIFLP QRIGYFKDKAFVNYLKYLLYW KDPEYAKYLKYPQCLHMLGA APNMEHFRKEAGWNAQCAKF IGWNRQVSTLGKHYSRKRM/R LQALAEQQQQNNTSGK

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23120	53488	A	23254	73	355	HEGQVHVLLASAHVDVAIVLG AGSMVEGEARPEQAAQHQQGI APLHLDAPGPSWTQSRSPNRNA NQNHTESEAT*SHPEQLPQTLW ECHAPRSP
23121	53489	B	23255	1	441	
23122	53490	A	23256	528	698	IIGQRFLHGPV/H/HHSHYDN/PH HSLHHHRCLHHCHLHHHRHHL HHHPLHCYHHHPQGNG
23123	53491	A	23257	1	403	
23124	53492	A	23258	509	4547	LYLTTSRREEHLKSLVETQDL ASPVLRVSICTKVEEAFRQAH VIVVLDSDTNKEVFTLEDCLRS RVPLCRLYGYLIEKNAHESVRV IVGGRTFVNLKTVLLMRYAPRI AHNIIAVALGVEGEAKAILARK LKTAPSYIKDVIWGNISGNYYV DLRKTRVYRYESAIWGPLHYSR PVLNLIQDSEWVKREFVAILKN LTTTGRQFGILAAHSIATTLKY WYHGSPGGEIVSLGILSEGQFGI PKGIVFSMPV
23125	53493	A	23259	56	290	
23126	53494	A	23260	468	993	VLLACFWPGSDFWPRSRRKTY GTAPQSCSYFYVALDCGGVSRL VIFVSWRNPQVAPTAHQNRPS RNPVSRPPNTQVARRKHYAL ADGYTERRWTNAPCAESSFPP NCPSAAPIDSYDK*PSRATLFT SHLTVEAFPVWSYLYPGETPRL HPRAHTRTVPAIRYPDRQTPN GLRGANTMHSQMDTLNGDGR THLAGQQRASPRTPARQYQYRI HTTSDLPGLVRKYASGCCLRIW YCCAWIERALSQVGGGVFGD PLSEQAECDDHGST
23127	53495	A	23261	1	3114	
23128	53496	A	23262	3	401	TSSLSLSGKSGRYIVFLRRSVGI QSPSAVATVRLLLAGSDRRFAA GSAGCAVLSRAERS*EPGCCYR IRRSFAFLRAGSIGNRDKPVAW PDTGSGDNTEVYFRAHQAGILP DTVLAGPAQRVAVSGGTPVDW
23129	53497	A	23263	2874	3062	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
23130	53498	A	23264	2766	3323	MPDLVEGREKSDKGAQPQPR QSRARTNGSGVRILHSLWRIIG IPLLGLYSLVCSRVLLACFWPG SDFWPRSRRTYGTAPQSCYSF YVALDCGGVSRVIFVSWRNP QVAPSAHQNRPSRNPVSRPPN TQVARRKKHYALADGYTERR WTDAPCRAESSFPNCPL*RY RIHIVDASVCGP
23131	53499	A	23265	968	1440	LSVVRSRIHMGVGVGVGCPVR YRNQDDHELQITHGNKILCGIV CDKGAQPQPRTOQSRARTNGSG VRILHSLWRIIGIPLLGLYSLVCS RVLLACFWPGSDFWPRSRRTY YGTVPQSCYSFYVALDCGGVS RLVIFVSWRNPQVAPSAHQNR PRRNPVSRPPNTQVARRKKHYA PADGYTERRWTIAPCRAESSFP NCPNSAAPIDPSYDK
23132	53500	A	23266	3	640	
23133	53501	A	23267	1	3140	MVYKMRYSQHYPYSIKEKQMK SEVLVKEKIGYGMGDAASHII FDNVMLYMMFFYTDFGIPAGF VGTMFLVARALDAISDPCMGL LADRTSRWGWKFRPWVLFGL PFGIVCVLAYSTPDLMSNGKMI YAAITYTLTLTYTVVNIPYCA LGGVITNDPTQRISLQSWRFVL ATAGGMLSTVLMPLVNLIGG DNKPLGFQGDLSPMFSTPEEIA RPGPYENDVHVVGASSLAAGH KTILPELVRSAEQHMGR
23134	53502	A	23268	750	1340	ILHAPAPPSASASHEQPEWSD KGAQPQPRTOQSRARTNGSGVR ILHSLWRIIGIPLLGLYSLVCSRV LLACFWPGSDFWPRSRRTYGT APQSCYSFYVALDCGGVSRV IFVSWRNPQVAPSAHQNRPSR NPVSRPPNTQVARRKKHYALA DGYTERRWTNAPCRAESSFPN CPFAAPIDPSYDK*PFRIVS
23135	53503	A	23269	93	699	RASVQKQLSTDDKGAQPQPR TQSRARTNGSGVRILHSLWRII GIPLLGLYSLVCSRVLLACFWP GSDFWPRSRRTYGTAPQSCYS FYVALDCGGVSRVRSYLPGET PRVAPSAHQNRPSRKPGTRPP NTQVARRKKHYALADGYTER SATNAPCRAESSFPPELVPQVP NTGFIRQVTRFDCFVNTPQAAA SGFW

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23136	53504	A	23270	1000	1530	QRYSDNPPNDKGAQOPQRTQSR SARTNGSGVRILHSLWRIIGIPL LLGYSLVCSRVLLACFWPGSDF WPRSRRKTYGTAPQSCYSFYV ALDCGGVSRLLVIFVSRNPQV APTSAHQNRPSRNPVSRPNTQ RVARRKHIALADGYTERRWT NAPCRA/VEPFPNCPEAQYRI
23137	53505	A	23271	242	711	LKQKRDKEDRSSRVSAVLLIK/ HRRPLPLPIGLKACHCSCTAKC LGGCESPRKGGQLLIFEGHVKI DLEIFTKSLWLTQQLIVKKETEK AVKHASNICIMRTGLTFQSHKIE DGLFGLLVIAEAWSYVCQST NPVDVYPLTAVPACCIASADV P
23138	53506	A	23272	2	459	CVNSQIGRGHKITTYPFSPRKS RKGMAQSQGWVKRYIAFCFK GFFVAVPVAVTFLDRVACVAR VEGASMQPSLNPQGSQSDVVL LNHWKVRNFEVHRGDIVSLVS AKNPEQKIIKRVIALEGDIVRFP *DFCMPMPHISCGPQSAGRNW
23139	53507	A	23273	1	474	
23140	53508	A	23274	358	948	PLTPFSRKSGRKGMAQSQGW VKRYIAFCFKGFFVAVPVAVTL LDRVACVARVEGASMQPSLNP GGEPV/ASDVVLLNHWKVTEF/ SEVHRGDIVFIG/APKNPEQKIIK RVICSLKGDIFQNHRTQKPDVK VPRGSHLGLGDHSDVDTVDFS NSFGPVSLGLLHAHATHILWPP ERWQKLESVLPERLPGTERRG MTA
23141	53509	A	23275	90	664	NKYRLQSPPLRLWDRASDPP APPEDPETAPAMEEDQELERKI SGLKTNMVEGERKTTLELV/Q AAGVTDRACTVFLHEEDHTLG NFLRYMIMKNP/EKVEFCGYT YG/HPSFQRAKLNLPHSRFRGY PPAVEPISREALNLMNVC/QP CAFTSFRASIKDYKESKSKQEM ESTFLVLLWQFYKGGTVL
23142	53510	C	23276	108	320	
23143	53511	B	23277	446	625	
23144	53512	A	23278	1	3042	
23145	53513	A	23279	1	3156	

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23146	53514	A	23280	518	2076	QQR*MCQNLMTHQNRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRPQYAEPS\HVEDKGH KYLVEANTGTENG YQGEESLF NKAYYGGGTNFFRKESQKLQ SAKKRDAELANGALGIELNND YTLKKVMKPLTSTNTVTDEIER ANVFKMNGKWYLF TDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTGLVLQMG LDPND VTFTYSHFAVPQAKGNV VITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGGQLTW LQVAKRAGLGGGSGRTVLRE RVRIEIASTHIALAVECVSVRV WKVPRLPSRQKYAKHASQLVS NQKSEEEYMKTFNISQQDLEL VEVATEKITMLYEDNKHVGA AIRTKTGEIISAVHIEAYIGRVTV CAEAIAIGSAVSNQKDFDTIV AVRHPYSDEVDRSIRVIPTYGT DEWEQWWNAFNEENLFCSEE MPSSDDEATADSQHSTPPKKKR KYIYVLVIAITMVMRFWQYING
23147	53515	A	23281	299	457	
23148	53516	A	23282	584	1185	QQR*MCQNLMTHQNRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRPQYAEPS\HVEDKGH KYLVEANTGTENG YQGEESLF NKAYYGGGTNFFRKESQKLQ SAKKRDAELANGALGIELNND YTSEKSNEAADHFKHVPQAKG NNV VITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QGGQLTVN
23149	53517	A	23283	1	3618	
23150	53518	A	23284	191	819	VNVTSGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELPSIVIF EPRESVNKYHLPILKTFARSISS VTVFEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMV VAGCIAFIDKLLNV LICFSVSVKNRVIFHSVDFECV

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23151	53519	A	23285	2	2556	WRKIYQAN/GKTKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSYTIIMGDFN TPLSLTDRSMRQKVKNKNTQEL NSALHQADLIDYRTLHPKSTEC TFFSAPHMHYSKIDHIVGCKAL LSKFKRTEIITNCLSDHSAIKLEL RIKKLTONCSTTWKLNLLND YWVHNEMKAEIKMFFETNENK DTTYQNLWDTFKAVCRGKFA LNAHKRQKERSKIDTLTSQKE LEKQEQTHSKASRRQEITKVRA ELKEIETQKTLQKINEFRSWFFE RINTIDRPLARLIKKEKNQID AIKNDKGDITDPTETQTIREY YKHLIYANKLENLEEMDKFLDT YTLPRNLQEEVESLNRPTGSGI VAHINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIIEEGI LPNSFYEASIIPLKLRDIAKKE NFRPISLMNIDAKILNKILAHRI QQHIKKLIHHDQVGFIPGMQG WFDIRKSINVIQHINRTKDKNH MIISIDAEKAFDKIQPFMLKTL NKLVLVLEVLVRAIRQEKEIKCIQL GKEEVKLSLFADDMIVYVENPI VSAQNLLKLISNFSKVSQYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKSIKYLGIQLTRHVKD LFKDNYPALNEIKEDTNKWK NIPCSWIGRINIVKELEKTTLNI
23152	53520	A	23286	1	3087	
23153	53521	A	23287	1	741	MLGKKKPVCEVGGDSGVPKKE FQEGRQVLFLKLRGQANKVG DNSIDSWKNAGR VFKDSKDF ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTI AQVKVSKS/V*HTQNQRSGRSQ NDF*RRRNIS*RSAYR*RL YIRROPYAERPSHVEDKGHKY LVFEANTGTENG YQGEESLPNK AYYGGGTNFFRKESQKLQSA KKRDAELANGALGIIELNNDYT LKKVVKPLITSN

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23154	53522	A	23288	849	1688	QQR*MCQNLMTHQNPQSGR SQNDF*RRRKNISERSAVYR*R QLYIRRPYAERP\HVEDKGH KYLVEANTGTENG YQGEESLF NKAYYGGGTNFRKESQKLQ SAKKRDAELANGALGIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTGLVLQMGDPND VTFTYSHFAVPQAKGNVVTIS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEPGQLAV
23155	53523	A	23289	1	3171	MVKGSIQQEELTILNIYAPNTG APRFKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYKIDHIL GSKALLSKCKRIEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLEKEKQEQRHSKPSRRQE ITKMRaelKEIETQ
23156	53524	A	23290	1	3255	
23157	53525	A	23291	1	3924	
23158	53526	A	23292	1	3139	
23159	53527	A	23293	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFFSAPHHTYKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRQERSKIDTLTSQ LEKEKQEQTHSKASRRQEITKIR AELKEIETQ
23160	53528	B	23294	1	3127	
23161	53529	A	23295	1	3325	
23162	53530	A	23296	1	3145	

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23163	53531	A	23297	191	819	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDIT*PSM*ISFELIPSVIF EPRESVNKYHLPLFKITFARSISS VTVFEVISGFTFFNV*SLFNSMI PRAPFANSASRFLALC*FWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVAVAGCIAFIDKLLNV LICFSVSVKNRVFIHVSDFECV
23164	53532	A	23298	1	3352	QQR*MCQNLMT*HQNRSGR SQNDF*RRRNISERSAVYR*R QLYIRROPYAEPSIHVEDKGH KYLVEANTGTENGYYQGEESLF NKAYYGGGTNFFRKESQKLQ SAKKRDAELANGALGIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTLGLVQMGLDPND VTFTYSHFAVPQAKGNVNVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNLSILEQGQLTV
23165	53533	A	23299	1841	2679	
23166	53534	A	23300	1207	1533	YVHCKPSGWTVRTFDKPRKRFI AFFIAGILFRAIKNHFLPRETLQ CLPYILTGFRRGQSEYFSIFSNM DLADTVML*GAIRFSDLVNEQ IQHTFLIPGETICRLSEVV
23167	53535	A	23301	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLDIYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKWKREIITNYLSOH SAIKLELRKLNLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLEKEKQEQTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
23168	53536	A	23302	1	3095	
23169	53537	A	23303	2	2678	

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23170	53538	A	23304	1	3335	MVKGSIQQEELTILNIYAPNTG APRFKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRILH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEITNYLSDHS AIKLELRKIKNLQSRSTTWKLN NLLLNNDYVWHNEMKAIEKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTTHSKASRRQE ITKIRAELEKIETQ
23171	53539	B	23305	1	2293	
23172	53540	A	23306	1	3810	
23173	53541	A	23307	255	1215	CVGQLAAAKR*RNSS*IQRLSR CVCSCGKPERR**HINLHVLSK GRRQLN/QTAGKTRAVSLKTAI SSTPTIRS*KIRKNGPVLPPLH LTEKSVYSTLTPTKAINLYSK PTREQKTDTKAKNLYLTKRTT AAARTSSVKKARSFSAALKNA MLS*RTAPSVS*S*IMITH*KK** SR/CITSNTVTDEIERANVFKMN GKWYLFDTSRGSKMTIDGINSN DINMLGYVNSLTPGYKPLNKT GLVLQMGDPNDVTLTNSHFA VPQAKGNNVVITSYMTNRGFF EDKKATFAPSLMNIKGNKTSV VKNSILEQGQLTVN
23174	53542	A	23308	1	4539	
23175	53543	A	23309	1	3229	
23176	53544	B	23310	1	3552	
23177	53545	A	23311	1	3139	
23178	53546	A	23312	1	3057	
23179	53547	A	23313	1	3215	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSLEREDIQTGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRLSR CDQLEERVSA MEDEMNMKRE GKFREKRIKRNQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTRLDIIQENFPNLARQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMMEKMLRAAREKDRSTRQ KVNKDTQELNSA

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23180	53548	A	23314	1	1921	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFESAPHHIYSKIDHILGSK ALLSKCKRTEIHTNYLSDHSAIK LELWIKNLQNHSTTWELNNLL LNDYVWHNEMKAIEKMFFETN ENKDDITYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTNHSKASRRQEITK IRAELEKIEQTKTL*KINESRSW FFERINKIDRLLARLIKKKREKN QIDAINKNDKGDTTDPTEIQTIR EYCKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPIGT AEIVAIINSLPTKKSPGPDGFTA KFYQRYKEELVPFLKLFQSEK EGILPNSFYEASILIPKGRDIT KKENFRPISLMNIDAKILNKKL AKRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSNVQIHINRAKD KNHMIISIDAIEKAFDKIQPFML KTLNKLGIKYLGIHLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKMCL* RRWTPCLLTAASLNRE*ERL VQPLLWRQMYCGPRHCRQVPQ HRRLNWSPSLRLS
23181	53549	B	23315	1	2907	
23182	53550	A	23316	584	1278	QQR*MCQNLMT*QNQRSGR SQNDF*RRRNISERSAVYR*R QLYIRRPYAERPSHVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFRKESQKLQQ SAKKRDAELANGALGIHLLNND YTLKKVMKPLITSNVTDEIER ANVFKMNGKWYLF*DSRGSK MTIDVPQAKGNVVTYSYMTN RGFFEDKKATFAPSLMNIKGN KTSVVKNSILEQGQLTVN
23183	53551	A	23317	1	3345	

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23184	53552	A	23318	2	3366	WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQEEELTILNIYAPNTGAPTFI QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIRTLHPKSTEY FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSDHSIAIKLELM IKNLTQNHSTIWKLNNLLNDY VWHKEMKAEIKMFFETNENKD TTIYQNLWDTFKAVCRGKFIAL NAHKRKQER
23185	53553	A	23319	1	2611	MGDFNTPLSTLDRSTROKANK DTQELNSALHQVDLIDIRTLH PKSTEYTFSSAPHHTYSTTDHIL GSKALLSKCRRTEIITNYLSDHS AIKLELRINKLTQNRSTTWKLN NLLNDYGVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQKLEKEQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKJNES RSWFFERINKIDRPLARLIKKKR EKNQIDAINKDKGDIITDPTEIQ TTIREYYKHYANKLENLEEM DKFLHTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKSPGPDG FTAEDQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASILIRKPGR DTTKKENFRPISLMNTDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIHKSINVIQHINRA KDKNHMIIISDAEAFDKIQQPF MLKTL SKLGIDGT YFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPSPLLFNIVLEVLAIRIQ EKEIKLISNFSKVSQYKINQKS QAFLYTNNRQTESQIMSQLPFTI ASKRIKYLGIQTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS VWGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTFKFIWN QKRARITKSILSQKNKAGGITLP DFKLYYKATVTTKTAWYWYQN

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23186	53554	A	23320	1	3099	MGELITPLSLDRSTRQKVNKD TQELNSALHQGDLDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYSLSHSA IKLELRINKLTQNRSTTWKLN LLNDYWIINEMKAEIKMFFET NENKDTTYQNLWDAFKA VCR GKFIALNAHKRRQERSKIDTLT SQLKELEKQEQTHSKASRRQE TKIRAELEKETQKTQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
23187	53555	A	23321	911	1539	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSVIF EPRESVNKYHLPFILKTFARSISS VTVFVISGFTFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
23188	53556	A	23322	191	820	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSVIF EPRESVNKYHLPFILKTFARSISS VTVFVISGFTFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
23189	53557	A	23323	965	5050	TWKGTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRINKLNQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETKENKIDTTYQNLWD AFKA VCRGKFIALNAHKRRQE RSKIDTLTSQLKELEKQEQTHS KASRRQEITKIRAELEKETQKT LQKINESRSWFFERINKIDRPLA RLIKKKREENQ
23190	53558	A	23324	1	2787	
23191	53559	A	23325	1	902	
23192	53560	A	23326	1	3640	

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23193	53561	A	23327	1	3686	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRLRSRCDQLEERVSV MEDEMNMKQEGKFREKRIKR NEQSLQEIWDYVKRPNRLRIGV PESDGENGTCLKNTLQDIQENF PNLARQAKVQIQEIQRMPQRYS LTRATPRHIIIVRFTKVE
23194	53562	A	23328	1	3433	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRINKNTQNRSTTWKLN NLLNDYVWHNMKAIEKMF ETNENKDDTTYQNLWDFAKAVC RGKFIALNAHKRQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEJETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAIKNDK
23195	53563	A	23329	1	3070	MEGEMNMKREGKFREKRIKR NEQSLQEIWDYVKRPNRLRIGV PESDGENGTCLKNTLQDIQENF PNLARQANVQIQEIQRTPQRYS SRRAATPRHIIIVRFTKVEKEM LRAAREKDRSTRQKVNKIDTQE LNSALHQADLIDIYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRINKNTQNRSTTWKLNLLN DYVWHNMKAIEKMFETNEN KDDTTYQNLWDA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met had	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
23196	53564	A	23330	3	2372	TTNCLSDHSAIKLELRRIKKLTEN HTTTWKLNNLLNDYVVDNE MKAIEIKMFFEINEKK\DTTSQNL WDTFKA VCRGKLIALLNAHKRRK QERSKIDTLTSQLKK\LEKQEQ NSKASRKQEITKIRAELEKIEITQ KKTLLQKINESRSWFFKINKIDG PLARLIKKKREKNQVDAIKNDK GDIITDPTMQTTIREYYKYLY ANKLENLEEMDKFLNTYTLQR LNQEGIESLNRPTGSEIEAIINSL PTKKSPGPDGTFKQFYQRYKEE LVYPEPRSESECLSNIREFLRGC GASLRLESIREDRNGRSQKT VH TEGDMNMNIKKIVKQATVLT TTALLAGGATQAFAKENNQKA YKETYGVSHITRDHMLQIPKQQ QNEKYQVPQFDQSTIKNIESAK GLDVWDSWPLQNADGTVAEY NGYHVVFALAGSPKDADDTSI YMFYQKVGDNISDSWKNAGR VFKDSDFDANDPILKQDQTE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT L KINGVEDHKTFIDGDKTYQN VQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSACKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG
23197	53565	A	23331	2	2987	APRFIKQVLSDLQRLDSHTIIM GDFTNPLSTLDRSTRQKVHKDT QELNSALHQADLIDYRTLHPK STEYTCFSAPHHTYSKIDHIVGS KALLSKCKRSEIITNCLSDHSAI KLELRRIKKLTQNRSTTWKLNLL LLNDYVWHNEMKAIEIRMFET NENKDTTYQNLWDTFKA VCRG KFIALNAHKRRKQERSKIDTLTS QLKELEKQEQTTHSKASRRQEIT KIRAELEKIEITQKTLLQKINE/SR SWFFERINK
23198	53566	A	23332	339	701	PDKEGNEIWDVDMYTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFISFNMDLADTMVFL*G AIRFSDLVNEQIHTFLIPGETIC RLSEVV
23199	53567	A	23333	190	502	

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23200	53568	A	23334	4472	8032	KKSGNNRLMRVHGKKRFLWQ KQGVCEVEIQARESARDGTD REDAESPHAEVTVPRGTRTEILT LWASDRDPASACGVTVPKGST THPGGMDRVCGVDTAVLHWM KQVQGISNLEVTGPRRRDMD EAGSRHSQQTNIGTENQTPHVL THKWQLNRNSACDKLHKPHSV PGGVAAGDVGCKTISNPGVCAI EYQVDGSPHIWEDVNKGVIIEE DRAPLMERSSSPAMEQSWMEN DFDELREEGFRSSNYSELRED
23201	53569	A	23335	1	2374	MVSISDLVICPPRHPKVLGLQGP PGLDSIDPSAGAGFLDWEIG MPGPGRAGHQALCKDCQCLE KTTTKAPGKMPKSTRSGPVRV RLADGPNRCAGRLECGMPDAG EQCVMTTGTSGRHCGLLGTGL WKGYTDLTHIPPGPGTPPQERTC QGDYHSGGTWTHSPLETTTRP GSSSPAIRRLPAQMLLLPARPPH PRSSSPEAMDPPPKAPFPKAE GPSSTPSSAAGPRPPRLGRHLLI DAN/GVYPYTYTVQLEEEPRGP PQREAPPGEPPRKGYSCPECA RVFASPLRLQSHRVSHDLKPF TCGACGKAFKRSSHLSRHRATH RARAGPPHTCPLCPRRFQDAAE LAQHSWGTPRGPLLAAACNCE VARGRLSPGPERLLHGYGGRE EEGGWGRAAGGLDRVEGFISS KAHHYLLIDTQGVPTVLVTRS HRGSQGPVGLQARKVLQLPRV LKGLRVHVLQRHSITHSEVPQ DFAGSLDSFQTPGESLRLVFRA LDTTQSSRISKAEPCLKEEPLSL GDLPYMHTTLCFCRKRASPGP GTLQRGALAWPDWASPRALPV PSLSSTTRSPAAPLFAVPLSGRT TQAMAFDGHIFQGQSQRSAGLT TTSRFLACQRLRLCAWWASRS PRCTLRPPVGLRPGVIHPRRLV YRDLKPNVMASGQPRDRPQP WFAWPPRPRFCGGCWLTTPK

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23202	53570	A	23336	853	1602	PGAAWSRDLRGCTCEPQPALR MLVLASPCQPLAFSSVETMEG PPRRTCRSPPEGPSSISGPQASS PPRPNHLLIDTQGVPTVAW LDEESQREPGASGAPGQK KCYS CPVCSR VF EYMSYLQRH RFSH SEVKPFECDICGKA FKR SQHL/ SARHHSIHLGGWVG GPTACRF C PRRFRDAGELAQHSRVHSGER PVSVSTLPSPLYGAETHAETHA VEASHEAGLPGAPGTHRTLQG ALDSCPDW
23203	53571	A	23337	1	1144	MGHHLMDKLVALGGLYYAIQ RHYATKCSVLKNDQILVIGLFM IQNVIRKHFANPLSALFLQQGI ELFAAIAEIHITVAERNHAITQI RLEAQITFDSLKEWHNAIRKSL DYEALQAFEFVVGATDRGFPAL SSEALVRVLVDANDNSPFVLY PLQNGSAPCTELVPRAAEPGYL VTKVVAVDGDSGQNAWLSYQ LLKATEPGLFGVWAHNGEVRT ARLLSERDVAKHRLVVLVKDN GEPPRSATATLQVLLVDGFSQP YLPPLPRAAPAAQAADSLTVYL VVVALASVSSLFLFSVLLFVAVR/ LCRRSRAAPVGRCSVPECFPFG HLVDVSGTGTLSSQSYQYEVCLT GGSGANEFKLPVLPNLSRDS
23204	53572	A	23338	1	1260	MVCYIQENLPFLKPSVENFYIL ITEGALDREIRA EYNITITVDTL GTPRLKTEHNITVLVSDVNDNA PAFTQTSYTLFVRENNSPALHIG SVSATDRDSGTNAQVTSLLPP QDPHLPLASLV SINADNGHLFA LRSLDYEALQAFEFVVGATDRG SPALSREALVRVLVDANDNL/ PFVLYPLQNGSAPCTELVPRAA EPGYLVTKVVAVDGDSGQNA WLSYQLLKATEPGLFGVWAHN GEVRTARLLSERDAAKHRLVV LVKDNGEPPRSATATLHVLLVD GFSQPYPPLPEAAPAAQAQAEAD LLTVYL VVALASVSSLFLLSVL LFVAVRLCRRSRAASVGRCSM PEGFPGRGLVDVSGTGTLFQSY QYEVCLTGGSETGEFKLPKPTP HLPPHRRGGKEIEENSTLPNSFGF

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23205	53573	A	23339	123	5794	SSSDSGSLKGACTEVKMEPAGE RFPEQRQVLLILLLEVTLAGW EPRRYSVMEETERGSFVANLAN DLGLGVGELAERGARVVSSEDN EQGLQLDLQTGQLILNEKLDRE KLCGPTEPCIMHFQVLLKKPLE VFRAELLVTDINDHSPEFPERE MTLKIPETSSLGTVFPLKKARD LDVGSNNVQNYNISPSHFHVS TRTRGDGRKYPELVLDTELDRE EQAELRLTLTAVDGGSPPRSGT VQILILVLDANDNA
23206	53574	C	23340	20	313	
23207	53575	A	23341	119	247	RSRCISASPRRPASFRKSIPEEED ESLNI*KGQVSILFFYIK
23208	53576	B	23342	55	288	
23209	53577	A	23343	1	3576	MAFLFEFSDLVSLLSIGTMLAY SLVAFSVLVLRYQPDENFSKNE KPKEEVVEMNSVPKAESPACVP EASSTPASLWSPVSTIPTPRWGR IVYGCAFLLVLLSMLCLVLAH WPKRLFSGELIYIAAAVLLVLI VGFTFTVWRQPSQNTPLYFKPP HISTSQNLSLPEHPMEYLLRTGI EPDVRGVLTVNALPAGPPVACS PLVSISAHVYLMQMATTETWA QCGVWMLIALECPNLKCLKPP WLHMLAMTMYA

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23210	53578	A	23344	3	1762	SVRPGPGHVRVRFSLSPPLR PWPLCPAARRTMGSILSRRIAG VEDIDIQANSAYRYPKSGNYF ASHFFMGGEKFDTPHPEGHLFG ENMDLNF.LGSRPSQFPVYTPAP HEPVKTLRLSLVNIRKDSLRLVR YKDDADSPTEGDGKPRVLYSL EFTFDADARVAITICYQASEEFL NGRAVYSPKSPSLQSETVHYKR GVSQQVSLPSFKIDFSEWKDDE LNFDLDRGVFPVVIQAVVDEG/ DSVVEVTGHAHVLLAGFEKHM DGSFSVKPLKQKQIVDRVSYLL QEIFYGIENKNNQETKPSDDENS DMSNECVVCLSDI.RDITLILPCR HLCLCTSCADTLRYQANNCPI RLPFRALLQIRAVRKKPGALSP VSFSVPLAQSLHDEHSCPFKK SKPHASPLASKKPKRETNDSV PPGYEPISLLEALNGLRAVSPAI PSAPLYEEITYSGISDGLSQASC PLAAIDHILDSRRQKGRPQSKAP DSTLRSPPSPHEDDEKLSEDV DAPPLGGAELALRESSSPESFI TEEVDESSSPQGGTRAASIENVL QDSSPEHCGRGPPADIYLPALG
23211	53579	A	23345	35	3134	RPREGPTWPQLPGSSPRRLFPW SPGSSSRGLFPWSPGSSSRGLF WSPGSSSRGLFPWSPGSSSRGLF PWSPGSSSRGLFPWSPGSSSRGL FPWSPGSSSRGLFPWSPGSSSR GSSRGHPGPPPGSSRGHPGPPP GALPVVTRVLLPGLFPWSPGSS SRGLFPWSPGSSSRGLFPWSPGS SSRGLFPWSPGSSSRGSSRGHPG PPPGALPVVTRVLLPGLFPWSP GSSSR/RTLPPVTRLLSGTLVP VTRVLL
23212	53580	A	23346	3	91	
23213	53581	A	23347	3	174	
23214	53582	A	23348	3	360	
23215	53583	B	23349	158	368	

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23216	53584	A	23350	3786	4928	PPPARTRPCASLTPEKAKWWRSS KPGLTRAPARGLSSPQTGSCS APASAG*VSGNSRSGTRRGLRP TRG*GPCGPSSRAAIISSPRAS/L RMSQRELGLWDPNNFEEPVAL QEMDTNSGVLLPFYDPSSIVY LCGKVLTAGQGEQGTGWRCG GPCPGAPLNRLLQGDSSIRYFEI TDEPPFVHYLNTFSSKEPQRGM GFMPKRGLDVSKCEIARFYKLH ERKCEPIHMTVPRKSDLFQDDL YPDTPGPEPALEADEWLSGQD AEPVLISLRDGYVPPKHREL RV TKRNILDVRPPSGPRRSQASDA PLSVRSALLHSGPIYISPNRPYTT RPLCPPPPQQHTLETLL EEIKAL RERVQAQEQRITALENMLCELV
23217	53585	A	23351	1	1898	MSRKGPRAEVCADCSAPVGPD FALAISELVSPDIFMQSHSENAIS VKEIVTIESISQGVGQIQLKGDI LPNPCHTPKKNSIHELL LERAQT PENKPGHMEQDEDSCTAQPEL AKDSGMCNPEGCLTTHSSIADL EEGEQLRGNKSSRAQGCTQNS KNDSSVADLAPKGKSDEAPPEH SFVLKEPEMSKGGKYSGSEA GSLSHSEQNATVPAPRVLEFDH LPDPQEGPGPEASNGLKVSQKS EGSQSSSRSPLEFLKEAGVPNQ TLSSGTPDPYFMALLGPKLNSR RPHLHPVSHTLDLGNPPLPQQ FAKQCRGRKGPEGKYPLHYLV WHNRHRELEKEVRAGQTLITQ TLSQANPTAITAE EYFNPNFELG NRDMGRPMELTTKTQKFKA KL WLCEEHPLSLCEQVAPIIDLMA VSNALFAKL R D FITLQIPFHILN ARITFGNLNGCDEPVPSVRGSPS SETPSPGSDSSSVSSSSSTSEAPR ENACPSALPGVASCRCGEISPAL FEAPRGYSMMGGQREAAATRDD DDDLLQFAIQSSLLEAGSEYDQ VTIWEALNSKPGTHPMSYE/R SPTGQGQVPAATCSG/R YDEQL RLAMELSAQEQEERRRRARQE EEELERILRLSLTEQ
23218	53586	A	23352	341	711	

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23219	53587	A	23353	57	719	TSDLMAEIIQERIEDRLPELEQL ERIGLFSHAEIKAIKKASDLEY KIQRRTILFKEDFINYVQRIQYSF KKDEIENSIVHRVQGVFQRASA KWKDDVQLWLSYVAFCKKWA TKTRL SKVFSAMLAHNSNKPAL WIMAAKWEMEDRLSSESARQL FLRALRFHFPECKLYKEYFRM ELMHAGKTGGRRNKLNKKPV WMWRILILKKSLRASWHGSST
23220	53588	A	23354	27	352	TESVVTIMSLNKKPKSEMTPEE REEEEFNTGPLSVLTQSVKNNT QVLINCRNKKLLGRVKAHDR HCNMVLEINVKEMLTEG/DRYI SKMFLAGDPVIVVLRNPLIAGK
23221	53589	A	23355	32	575	STRLDLPKCWDVRSILFNKP EMTPAEELQKREEVEFNTGPTP LCLTQSVKNNTQSAQSTCRNN KKLPGAA*RPFDRA SPCCPPGT CNMVLINVKEMWT*GTQEV GKGKEGSSKPVNKRDLTSSKM FPGGGGFSSVPCGNPFHSAG QIRGPPVLFDKNSHPLVLLKTA CHLVFENY
23222	53590	A	23356	103	713	VTSGCGKKKVVWDPNETNEIA NANFRSADPRLIKDGLIIRKPV TVHSRARLPEKTPLARCKGHG TLGIGKRKGTANARMPKEGHH GMRRMRILAPACSRRYRESKKI DRHMYHSLYLKVKGNVFNKK ADFSWEIHKAEGRARPRKEAS WLDQAEARRSKDQKGHGKRR EERLPGQRKEINQRLYSKEGR RPRNKNLTL
23223	53591	A	23357	1	2847	
23224	53592	A	23358	1	2823	
23225	53593	A	23359	3	2858	AMFGFQRRGLGTPRLQLWLLL LEFWEVGSGQLHYSVSEEAH GTFVGRIADLGLLELAELVQRL FRVASKTHGDLEVNQNGILF VNSRIDREELCGQSAECSIHLE IVDRPLQVHFVNVEVKDINDNP PVFSLREQKLLIAESKQSDSRFP LEGASDADIEENALLTYRLSKN EYFSLDSPNTNGKQIKRLSLJLKK SLDREKTPELNLLLTATDGGKP ELTGTVRLLVQVLVDNDNDPE FDKSEYKVSMLMEN

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23226	53594	A	23360	194	931	NSPVVPVMSAGQFVNKLQEEVI CPICLDILQKPVITDCGHNFCPQ CITQIGETSCGFFKCPLCKTSVR\ RDAIRFNSAVAIEIWWKEIQALQ ASEVQSKRK\EA\TCPRHQEMF HYFCEDDGKFLCFVCRESKDH KSHNVSLIEEAAQNYQGQIQEQ IQVLQKKEKETVQVKAQGVHR VDVFTDQVEHEKORILTEFELL HQVLEEEKNFLLSRIYWLGHGEG TEAGKHVYEIPLMPTVERSQEA
23227	53595	A	23361	2	381	AINWTSARPVSQCDWPCPPSQ VVCAGLPP*RVQCNPVKGP/N CPLAHTSEPTGHCLL*TRGMCF PSLCGQLCP*SGPPDCPSRALH HTGFCPVALLVAESQVRARAC GPEPHRAGRASRWCLHAG
23228	53596	A	23362	213	574	PQTHGTGNHSEGRQPITRSPEKP EPICPSKRAPQTQQP/PWAPSLC PPALGPCKGTRRPRVQVHRPTS SQKCPLPAWFHHLPLWPTSAAR SSSTETPTGQMRKLRLHPAAPR SANALSLGE
23229	53597	A	23363	21	456	
23230	53598	A	23364	2	98	
23231	53599	A	23365	64	241	PWPLASNPRGCLP*PSTLN*PTP SSQPGMSLDSLDRHPP*TRETAS GIGGQRPQSDPARTPHFISQTO
23232	53600	A	23366	209	353	

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23233	53601	A	23367	1766	3292	SSCPTRVLIMKGAGHPCYLDK PEEWHITGLDFLQGLQLWLMH MQQLMSLAVVSGRLSRGQCGT ERPSRRRAAAAAAGQFQRGHF QHIEERLETNVQNCQSPDTLCP THCSPVLNEPCPEVSVAVAPA SPDRMSGSDGLEEEPELSITLT LRMLMHGKEVSGIIGKKGETV KRIREQSSARITISEGSCPERITTI TGSTAAVFHAVSMIAFKLDEDL CAAPANGGNVSRPPVTLRLVIP ASQCGSLIGKAGTKIKEIRETTG AQVQVAGDLLPNSTERAVTVS GVPDAILLCVRQICAVILEGFSV QQQYGA VTPAEVTKLQQLSSH AVPFATPSVVPGLDPGTQTSSQ EFLVPNDVSRGWDGWRLIGCVI GRQGVTKINEIRQMGAHIKIGN QAEAGAGERHVITITGSPVSIALA QYLITACLETAKSTSGGTPSSAP ADLPAPFSPPLTALPTASPLAC WAHPMPSPSPTLIGFKAHALLG FTTCFPRAAAGLGLHRQDGSS
23234	53602	B	23368	1	363	
23235	53603	A	23369	486	947	LDGAGLLAPVKAHLQKKGPRL GTRGCAMPRLGSTPFLKGQCL ANSRNTLEAVSLTESSASRVPP APVLGSRPPHSPSPWP/P/YTYP VPPPPRMALVPPNMHGQGTVG LTSVPLACTVAMLGSYKQAGA FGPLANCYGGGLGHAQCWQGEF CPTQCP
23236	53604	A	23370	38	680	GSRLRLQAAAAARPALPLPLPP WEWKHLPHVPEAKWWLTTAR HSAAYRADPLRVSSRDKLT AASSQGNFEGNFESLDLAEFAK KQPWWRKLFQGESGSPSAEKYS VATQLFIGGVGTGWCTGFIFQKV GKLAATAVGGGFFLLQLANHT GYIKVDWQRVEKDMKKAKEQ LKIRKSNQIPTEVRSKAEVVSF VKKNVLT\TGGFFGGFLLGMAS
23237	53605	C	23371	30	200	
23238	53606	A	23372	14	161	

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23239	53607	A	23373	69	715	APALPGCEHMMAIRLKVCLL GDTGVGKSSIVWRFVQDHFH NISPTIGASFMKTVPWENDF KFLIWDTAGQERFSFIGLPL YYSRLQLAAVYSCGYLPSRDF IFITLKEWVVKRLKELGPNIV MAIAGNKCDSLDIRVPPPEGML KEYAESIGAIVVETSAKNAIN NEELFGQISIRQIPPLDPPMK NGKQWHDHQLRSQPMQASRRCC
23240	53608	A	23374	3	293	VTSTMAYRAQGQKVQKVMV QPINLIFRYLQNRRIQVWLYEQ VNMRIEGCIIGFDEYMNVLDD AEEIHSKTKSRKQLGRIMLKGD NITLLQSVSN
23241	53609	A	23375	3	393	HESCSQRQRAGCALCENSHPW RSRGPVQKSAEGLWCQPICT SSSRYLQNRJAGFQVWLYEQV NMRIEGCIIGFDEYVNLVDD AEEIHSKTKSRKQLGRIMLKGD DNITLLQTCPLPPRMVHGSGEIV
23242	53610	C	23376	129	425	
23243	53611	A	23377	470	635	ENSSSHHIKPFSSGCSIHGFSGH INVTSVTIL*PIKSCHIRCHF*CA QYMVADN
23244	53612	A	23378	71	566	PLFPPCLSPVAVAGWARGHMLG QSHQVVAAPLKHRIPTTELCLQ KCLSLIKTKFLNAYITVSEEVA LKHAESEKRYKNGQSLGDLD GIPIAEKDNFSTSGIETTCA SNMLKGYIPPNATVDQKLLDQGA LLMGKTKLNDFAMGSGSTDGV FGPVKNPWSYSK
23245	53613	A	23379	255	1042	ILAAARMGKQNSKLRPVEMQDL LESTDFTEHEIQEWYKGLRDC PSGHLSMEEFKKIYGNFFPYG/D ASKFAEHVFRFTDANGDGTID FREFIIALSVTSRGKLEQKLKW AFSMYDLGNGYISKAEMLEIV QAIYKMVSSVMKMPDESTPE KRTEKIFRQMDTNRDGTWVPH LALIYRTAEGGFVQRAVSIFY PPPSAGNAMVNEAAVFLEIPLG SSPGQVSAVCHSGRKL.SLEEFIR GAKSDPSIVRLQCDPSSAGQF

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23246	53614	A	23380	1	721	MDGNLRKIRFEKHAITEEFRTT EPGLAALRLPSTWIRGVRTSES KREVGKGGQSQQYENRDTEGE GHVMTKARDWSKAAASQRLP ANHLLRLCIDGFRSHSLPEEGP KKPCQHHAQEPEPTRSGRLPQ AHEGSISDCCTSEQGSMDIGSV EPGTGYNNLVCHLLSTLEKRSI WAGVSRFSRYHLRLPLARKIG NPLTPCASQLLLPLPSTTQKRQS GHALYSFPYRPQPKNDNLVMP
23247	53615	A	23381	80	562	DRAMWGDWLWLLPPASANPGT GTEAEFEKAAEEVRHLKT/RSPS DEEMLFIYGHYKQATVGDINTE RPGMLDFTGKA/KWD/AWNEL KGTSGDVAEAYL/NQV/EELK KKYGDMERLDLVTVPVYPKP ETIPFFFSNTVDGWEFRENNPV KPAQTQRLLTHTGS
23248	53616	A	23382	380	1041	EVTINSGFIFIMLFMEHPEHYTI MHKWILTWILPTLLYRSCFHIIC LVGTISLACND/MTPEQMATNV NCSSPERHTRS DYMEGGDIRV RRLFCRTQWYLRJDKRGKVKG TQEMKNYNIEMIRTVAVGIVA IKGVESEFYLAMNKEGKLYA KKECNED/CNFKELILENHYNT YASAKL/WTNGGEMFVALNQ KGIPVRGKTKKEQKTAHFLP MAIT
23249	53617	A	23383	127	549	SSPKMAATMKKAAAEDEVNVT EDQ/QKINKFARNTSRITELKEEI EVKK/KQLQNL/EDACDDIMLA DDD/CLMIPYQLGDVFISHSQE ETQEMLEAAKNLQEEIDALES RVESIQRVLADLVQLYAKPFG SNINLEADES

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23250	53618	A	23384	1	2050	MEYESMVISFDDRVMEKTEYG PIFTVFAMGNRMFTVTEEGIN VFLKSKKVDVELAVQNVYRTA SIPKNVFLALHEKLYIMLKGGKM GTVNLHQTGQLTEELHEQLEN LGTHGTMDLNNLVRLHLYPVT VNMLFNKSLFSTNKKKIKEFHQ YFQVYDEDFEYGSQLEPCLLRN WSKSKKWFLFEKNIPDIKAC KSAKDNSMDSDEDPVNLQSR ALVCEMLHVQRSSDADAIGPH ADHSLSNRWEVILADEHGIAD DMISRYALSEKSQLVSTQVIKS ASSKSVNKSIDITSVFLNWYN EKKMIRAYATVIDGPEYFWCQF ADTEKLQCLEVEVQTAGEQVA DRRNCPYIGDPICIVRYREDG HYRALTINICEDYLVSVRLVD FGNIEDCVDPKALWAIPSELLS VPMQAFPCCLSGFNISEGLCSQ EGNDYFYIITEDVLEITILEIRR DVCIDIPLAIVDLKSKGKSINEK MEKYSKTGKSAALPYENIDSEIK QTLGSYNLDVGLKKLSNKAQV NKIYMEQQTDELAETEKDVNII GTKPSNFRDPKTDNICEGFENP CKDKIDTELEGVSQKAQESMC TEDMRKSSCVESFDDQRRMSL HLHGADCDPKTQNMNICEEF VEYKNRDAISALMPFSLRKKKA VMEASTIMVYQIISQLNYRPTL
23251	53619	A	23385	3	602	TRPPTRPGLSPDPTSPTEADRGV CERPHRCFLLPQITHPSSGRRL CLLSPTSFDFSLYESQSDRAIF GVGTEPDQEPPIPPYHEQVPVSV YHPTNPSQTWVATQLTEEEQIRI AQRIGLIQHLPGVYDPWRDG SEKKIRECVICMMDFVYGDPIR FLPCVHEWYHLDCIDDWLMRS FTCPSCMEPVDALLSSYETN
23252	53620	A	23386	33	512	TAARCOGGPPTHVPFVGTACP TRIPGHAPARQCREYYY*YYVD F/WKEPRRCHAILLPWAGLEV GMPPSHTQLGMHPAPPPHLEV KAQGPSNRQRDTGCRWCSCR ASALGGGRQDSRLRERGGGYD H/HCPICRSLKIQLKCHPASGPQ TVLGLRLASVS
23253	53621	A	23387	1	1731	
23254	53622	B	23388	1	706	

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23255	53623	A	23389	1	1986	MGIGEGPTTSEGCRESVEYSHQ KSELPLSGDSQVPGPIGNCNDP QGSVSSQCDAAAGQCQCKAQVE GLTCSHCRPHHFHLSASNPDGC LPCFCMGITQCCASSAYTRHLIS THFAP/GDFQ/GFA/LVNPQRNS RLTGTEFTVEPVPEGAQLSFGNF AQLGHESFYWLPEYQGGDKG EAYFARMRRAHQNRSTLSEEQ LRAAVTAGRIPEPPEGRDWAQR ASQFSLSYEGFSLPGSLYYWQ LPRAFLGDKVAAYGGKLRITL SYTAGPQGSPLSDPDVQITGNNI MLVASQPALQGPERRSYEIMFR EEFWRRPDGQPATREHLLMAL ADLDELLIRATFSSVPLAASISA VSLEVAQPGPSNRPRALEVEEC RCPPGYIGLSCQDCAPGYTRTG SGLYLGHCELCNNGHSDLCHP ETGACSCQQHNAAGEFCELCA PGYYGDATAGTPEDCQPCACP LTNPENMFSRTCESLGAGGYRC TACEPGYTGGYCEQCGPGYVG NPSVQGGQCLPESELHFPVSQ PSDAGVYICTCRNLHQSNTRSRA ELLVTEAPSKPITVTVEEQRSQS VRPGADVTFICTAKSKSPAYTL VWTRLHNGKLPTRAMDNGIL TIRNVQLSDAGTYVCTGSNMF AMDQGTATLHVQGSAAEAGERS MYSISVLLKYTS
23256	53624	A	23390	3	13319	PASGR.LRAARSRRGASERESG AGRAMGWRAPGALLALLH GRLLAVTHGLRAYDGLSLPEDI ETVITASQMRWTHSYLSDDDEYM LADSISSGDDLGGSDLGSGDFQM VYFRALVNFTRISIEYSPQLEDA GSREFREVSEA VVDLTLESEY.LKI PGDQVVSVVFIKELDGWVVFVE LDVGSEGNADGAQIQEMLLRVI SSGSVASYYVTSPPQGFQFRRLGT VPQFPRACTEAEFACHSYNECV ALEYCDRRPDCRDMS

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23257	53625	A	23391	41	1323	HYLVFFLP SLRRYTVSLSPNSTS YQLLVPGPSY/SALPISSAASLY AGA/GGSGSRMSVSHSTSLRDG ISSGGLA/TGMARGLGGMGGIQ NKKETTQSLNDSLAVRVSLET ENRKLESKIREHLEKKGQVVRD WSHYFKTIEDLRAQIFANTVDN VRIFLQIDNARLAADDFRVKYE TELAMRQSVESDIYGLHKVIDD TNVINGCSFFMKKNHGEEVKC LQAQIASSGLTMEVDAPKSQDL AKITADISTRYDELARKNREEL DKYWSQPIEESTTEVTMQSAKV RAAEMTFMELRRTVQSLIEDLD LMRNPKASLENSI.REVEACYA LQMEQLNLDP/GILLHLESELTO TRAEGQLQAQKYKALLNIKNK LEAEIATYCLLEDGKDFNLGD TLDSSNPMQTIQKTTTSRIVDG KVVSETNDTKVWRH
23258	53626	A	23392	1	771	SCSWTPSAAWPPNASLHSC LKR RNQDHL LWDWRFDFPSMA SKCQSPLL PQQKKPRPLPALGP EKTSASAGLPKKGEKEQETIE HIHEVQNEMDR LNEQAKRSEL ISKIPDFWVTIFVNHPEVSALPG EEDEEALHYL TRVEMTDFDDIK SGYRIDFYFDENPYFENNILAKE FHLNESGDPSSKSTEIKWKY GK DLMKRSSQTQNK AHRKRQHEE PESFFTWT DHSDVGADELGEV IKDIWPNPLQYYLVPDM DNEEG EGEEDDDDEEEEGLEDIDEEG DEDEGEDEDEGEKGEDEGE
23259	53627	A	23393	732	1656	
23260	53628	A	23394	3	923	ARRLVVWFWDFFNSMAPKRQS PLPPQKKKPRPPALGPETSAS AGLPKKGEKEQQAIEHIDEVQ NEIDRLNEQASEEILKVEQKYN KLRPFPQKRSLSAGIPNFWV TTFVNH PQVSALLGEDEEAL HYL/TRVEVTEFEDIKSGYRIDF YFDENPYFENKVLSEFHLNEIS GDPSSKSTEIKWKS GKD LTKRS SQTQNKASRK RQHEEPESFTW FTDHS DAGADELGEVIKDDIWP NPLQYYLVPDM DDEEGEGEED DDDEEEEGLEDIDEEGDEDEG EEDEDDDEEGEGEEDGEDD

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23261	53629	A	23395	732	1656	SCSWTSPAAWPPNASLHSLCKR RNQDHL LLWDWRFLDFPSSMA SKCQSP LL PQKKKPRLPALGP EKTSASAGLPK KGEKEQQETIE HIIIEVQNEMDRLNEQAKRSEL ISKIPDFWVTIFVNHPEVSALPG EEDEEALHYLTRVEMTDFDDIK SGYRIDFYFDENPYFENNILAKE FHLNESGDPSSKSTEIKWKYK DLMKRSSQTQNK AHRKRQH PESFFT WFTDHS DVGAD E LGEV IKDIWPNLQYYLV PDM DNEEG EGEEDDDDEEEGLE DIDEEG DEDEGEDEDEGEKGEDEGE
23262	53630	A	23396	3	924	ARRLVVWFDFPNSMAPKRQS PLPPQKKKPRPPALGP EETSAS AGLPKKGEKEQQE AIEHIDEVQ NEIDRLNEQASEEILKVEQKYN KL RQPFQKRSLA SAGIPFW VTTFVNHPQVS ALLGEDEEA LHYL TRVEVTEFEDIKSGYRID FYFDENPYFENKVLSEFHLNE SGDPSSKSTEIKWKS GKLTKR SSQTQNKASRRQHEEPESFFT WFTDHS DAGADELGEVIKDDI WPNLQYYLV PDM DDEEGE EDDDDEEEGLE DIDEEGDED EGEEDDDDEEGE EGEDEGED
23263	53631	A	23397	1	1393	MGKQKGGGPQAWA EGLGRE WMRMPQEGKGSQRKSTQKQT KREIDAYIVAKERSYETVLSF GKRGLNIAASPAVQAATKVLW APSPPAAPIPPLRPFGLQLCCQG AQRWQPGSREVKGRLCQARLA ETSSIAGNLRVQSYERPVDPGV TMDPLLPGRTIVFAAGDHTLW RAPVSSCAQRSGVWSLDNMGV NSGSVPFHGVRIQASQLISFN FSFCEADLKTPLHGFLIPAGPK EEVTVKKEKREDRDRQREGH GRGRGRPEVIQSHIFEQGPAE MMKKKGNWDKTV DVS DMGPS HIINIKKEKREDEETKQILRML EKDDVDHHA LSEHLVTTATFSI GSTGLVVYDYQQVECGHVRA DLKTQDLYSHAQFGDNNYPGG VDWYRAGGLQSDTEDECWS DTEAVPRAPARPREKPLIRSQSL RVVKRKPVPVREGTSRSLKVRTR KKTVPDSVDVS
23264	53632	A	23398	297	584	

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23265	53633	A	23399	2	149	CMKFGAVTPIGGPPLGDQSPVL LLFAL*KRSTYNLGSSDPQAQGI SHQF
23266	53634	A	23400	1	170	PAGIRHEERSTYDLWSSDRPGQ GTSHQF*IRFQIPWNSGPRLSE* LLPRSSRLSS
23267	53635	A	23401	1	1077	
23268	53636	B	23402	289	1359	
23269	53637	A	23403	3	2233	
23270	53638	A	23404	1	1491	
23271	53639	B	23405	76	511	
23272	53640	A	23406	1	2706	
23273	53641	A	23407	273	862	
23274	53642	A	23408	1	1080	
23275	53643	A	23409	134	675	MHYFHSSVQIGLPLTRRSQVLIL PQPLLNPILLSPLLTPVPAYS FIL/PTSPPPARQFPLKKVAEAK GIVKQLKTDARTSPRKPTGPSQ TLWVTLTVEDLKHAFITPLHP SSQPLFAFTWDPDTHQAQQIT RAVLQVFTDSPHYFSQAQISS SVTYLGILLIKTHVLSLLIMSG
23276	53644	A	23410	1	895	MEVHKHPFNTALRHSQGCEL VWAEKHRNQIFFPKSTASPKQ WDTGRHNSDAKQQEPGGREER NTMEMETKETHFIRGPKTLASV TDWEGSLPLVFNHCRGTSIIHP RFKGVPRPRDACLGPSPLAASP AFLGKGQHALKGLKPVITRLLQ HGLLKPINSPFSPILPVLKPKDK AYKLQVNLRLINQIVLPIHPVVP NPYTLSSIPPSTTHYSVLDLKH AFTIPLHPSSQPLFAFT*TDPT H*AQQITWAVLPQGFTRQPLL QLSPNFILICYLSRHSNHNKTRA LPADRV
23277	53645	A	23411	1	930	MIQEHADKQVQRLQGVLGSI TAASRARLHPGEINNHVAHTEP VWWSLHMDAYEIWCRGSDRR TSLGRSIPPLALCSLRRHILRPQ VLRSTSPRNISPISNPGHLSDYTP TFQGCQTMQGRLPWSFTLSGK SRFSGEGATQRYPIPQQAALKG LMPAITRLLQHGLLKPINSPYHS PILPVLKPKDKPYKLVQDLRLINQ IVLPIHPMPVNPNYTLSSIPASTT HYSVLVYVKHAFTIPLHPSSQP LSTFTWDPDTHQAQQIT*AVL PQVFTDSPHYFSQAQISSSVTY LGIILHENTRALPADHV

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23278	53646	A	23412	299	1028	RLGSFSSNHPYLQGRQYPIPQQ ALKGLKPVITCLLQHVLLKPVN SPYNSPILPVQKLDMPYRLVQD LCLINQIVLPIHAMVNPYTLT SIPPSTTHYSVLDLKPFAFTIPLR LSFQPLFTFSWTDPDTHQAQOI TRAVLPQSFTDSPHYFSQAQIS* RLGSFSSNHPYLQGRQYPIPQQ ALKGLKPVITCLLQHVLLKPVN SPYNSPILPVQKLDMPYRLVQD LCLINQIVLPIHAMVNPYTLT SIPPSTTHYSVLDLKPFAFTIPLR LSFQPLFTFSWTDPDTHQAQOI TRAVLPQSFTDSPHYFSQAQISS SSVTYLGIPGFAILTKPLYKLT GNLADPIDPKSFPHSSFRSLKTA LETAPILALPVSSQPFSLPTAEV WAAQSEFLHKNRDRTE
23279	53647	A	23413	157	202	RSECARWMEK*CPWL
23280	53648	A	23414	184	482	EGVSVFLLSPYQGPQVSRRC S/RQVSQRCPHRRGRPCPQVS RSHGPSWVGHPGMPLYGS/EQF YCGAPLAGPPNGSRGESLKIS VWIFPCRDGFGNFN
23281	53649	B	23415	13	862	
23282	53650	A	23416	1	11342	MATRWFFYYGHPPRDARVPRIV AEAKEKNLTPGKIEVDVTIEAQ IRQEFDLAERDTGGFVKFFRITK KKLQEFFLGEEEEQVPHVSPVE LGAKPTAFNAFIANAVGKTLAV QHASKLAPPEMTVTHERFYG NYAVWITDVPDRNHRJIEVHVI REISGRTSEYVNNLLAQPTPFK VFDWLTETQAKEFVRRLNNTQ GVISVYNKLEDGIPVKVAVKAT EPTNKEKLEAASTKLKAMGAV ATDAYEFHTDLNENE
23283	53651	A	23417	7597	7883	LSSLAWVWQWNHRISVLFHNS SVRTNLVPQFNQLVITESNSCPE FFNQTSAFFKT*VESGCM/CLQD *GIEWFRLRLDVYNSRLVFLTG ATDYCTG
23284	53652	A	23418	3	1573	
23285	53653	A	23419	6692	6793	GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS
23286	53654	A	23420	1	17727	
23287	53655	A	23421	6687	6785	VNTGNRTWWEPLFRK*KKTQR EDTTEKKTGR
23288	53656	A	23422	1	2856	
23289	53657	A	23423	1	7194	

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23290	53658	A	23424	7460	7561	GASVAPSIGS*STGNAIPSCFLQ QNVIVIPQS
23291	53659	A	23425	1468	1857	
23292	53660	A	23426	1	1985	MEPVGIDIIAISWIGAPEYDPNV KRAINAKVEATQKTLQREQEIQ QRVAEANMEREQAKGVADAIR LRGEALTENPNVMQLEAINKW NGLVPFITSSPGMGKSAIVRQIA EDFGKLIDHRLSTSAPEDLSGL PRFKENGRAEFAPFDELFPLEG DAVPEGFNGWLLFLDEFNSAR KEIQAAAYKLVLDGMTGQKKL HPYVAIVCAGNKATDRAITNNL STAMQSRLIHLEMETDFDVFME DVAIPNKWDERVIAFLNANPNK LNDFFPDHQEKTFCCSR TWEFV NKIVSILPPGPINSEMTLLLAGTI TSGVATSFVQFTQVYSNMVSL NEILDNPCKARMPEDNLLWA VVTSLINNTDEDNHSKIFDYVE RMPFTFKVLVYRSRKTDSMT DAQLTREYDRCAKAFMGKTA AFFGSLCCLKFRWVKDGCOT AQTDGEHLEWNPWFESLLPE SRVTVMHLEWHVGLLHVS MGSRDPEVWNYACDIYINNQLI QDGYSGFIGIENCWKDPKYAGW AEEQIYHDLMSKHPRPPKASGA FGTSGGDMKPKSTKASLKLGS GSLPGVLPKMEEVITQFLKPV VPWQVLLERFFNDLQETYYSW QRPNRRYPDMYLPSSMDDDCR LEHLAYFL*NEADLTGLLVLK* TDDQS VSGQNLLQSDEQLQIY
23293	53661	A	23427	2365	2784	
23294	53662	A	23428	5789	5980	DQNMRFDFNTFETYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL
23295	53663	A	23429	1	6819	
23296	53664	A	23430	376	2052	SKVCGNDGFADDLKHLILFTGA QSGEDIVPFQLEDGHSLSGEVVL LHGGSGVESGQR/CGRTSAGSC Y*SPGKICCCNLLVTKTEGFFAP VPIQLENTNQVTNCSDNW
23297	53665	A	23431	2	2189	
23298	53666	A	23432	2	1583	
23299	53667	A	23433	2142	2242	GASVAPSIGS*STGNAIPSCFLQ QNVIVIPQS
23300	53668	A	23434	3	1188	
23301	53669	A	23435	470	862	
23302	53670	A	23436	1	1352	

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23303	53671	A	23437	1837	1955	SKCSIGLYQRYPSYNGC*NSGCI CRVY*CCREHRGYVRN
23304	53672	A	23438	1447	1565	SKCSIGLYQMYPYNSGC*NSGC ICRVY*CCREHRGYVRN
23305	53673	A	23439	773	823	
23306	53674	A	23440	3	1529	
23307	53675	A	23441	1	1794	
23308	53676	A	23442	236	427	DQNMRFDTNFETYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL
23309	53677	A	23443	8510	8611	GASVAPSIGS*STGNAIPSCLFQ QNVVPIPOS
23310	53678	A	23444	516	669	ATSELKRKASLGLMEPDVSRK* ARCSSLPSSSIGDGRYISGYRL GRCHE
23311	53679	A	23445	410	593	FLNLIQPOGKRKLLLRKRSLLP KN*CQHSKQHKLSISSVVILNIT NS*PNKVKLMPILAM
23312	53680	B	23446	1	2286	
23313	53681	A	23447	1418	1723	CNTNIIFNCHFPTKLGICICKAMK VVSPLIHNSIVILLNQITIDFFSTL AQICTFICLTYSKQTTRIASFQ KVIEEFLSLAPIEKVELKEHS*YI SISEKV
23314	53682	B	23448	1	6167	
23315	53683	A	23449	1	3199	
23316	53684	A	23450	1	5733	
23317	53685	A	23451	709	1099	
23318	53686	A	23452	5039	5230	DQNMRFDTNFETYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL
23319	53687	A	23453	664	993	
23320	53688	A	23454	1	19859	MASIDSIACVNPRQVRKFVEHC IRSGLVPFITSSPGMGKSAIVRQI AEDFGLKLIDHRLSTSAPEDLSG LPRFKENGRAEFAPDFELFPLEG DAVPEGFNGWLLFLDEFNSAR KEIQAAAYKLVLDGMTGQKKL HPYVAIVCAGNKATDRAITNNL STAMQSRLLIHEMETDFDFVME DVAIPNKWDERVIAFLNANPNK LNDFEPDHQEKTFCSSRTWEFV NKIVSILPPGPINSEMTLLAGTI TSGVATSFV
23321	53689	B	23455	74	240	
23322	53690	A	23456	143	384	
23323	53691	A	23457	1	3267	

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23324	53692	A	23458	2	550	KRSSEHIQRIDRDVSGTLRKHF FRDRYGTQKRELLHILAYEY NPEVGYCRDLSHIALFLLYLP EEDAFWALVQLLASERHSLQG FHSPNGGTVQGLQDQOEHVVA TSQPKTMGHQDKKDLGGQCSP LGCLIRILIDGSLGLTLRLWDV YLVEGEQAFMPITRIAFKVQK RLTKTSR
23325	53693	A	23459	72	630	
23326	53694	A	23460	1	2835	MDALMLALGALMLALGLGDP KSAQVSDPDGAEPGPGRATGT DPLVQIHVKLGISEALSIPGGRL YRDLWSLTPVCLHIPGIAHHGP FTLGRMDVVEVAGSWWAQER EDIIMKYEKGHRAGLPEDKGPK SFGSYNNNVDLGIVHETELPP LTAREVKQIRREISRKSKWVKM LGEWDTYKNSRKLIDRAYQGIP MNIRGPMWSVLLNIEEIKLKNP GRYQVRSARAQPTGQAVSQAQ VSSWRERQDHPGELGVKI

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23327	53695	A	23461	1	832	MGWRARWLMPVISALWEAED PIPELTRLLQQSQDPLLMGLFP TNPKEKTQEEPPGQSRAPVLT VSKFKVLGALLHLGNIQFAASE DEAQPQCPMDDAKCEGQGVG WAGPVRKASLEQLQLVLSHTT PHYIRCIKPNSSQGAQTFLQEE AGAGRRRQRRRQKQRRRRRQ LGGGGDGGNGSVGDDGATRGS RGCALEKECVATPRRGLLFSRP HKLAFVGGSVTSVGPKPAP MDVVEVAGSWWAQEREDIM KYEKGHRAGLPEDKGPKPFRS YNNNVDDLHGVQDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMQLARQV SRLESGHFYDAHNPFLPPSMS KQAKKTGVPSEGLCRPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFTGKR AVSATQLIGLQILLGEVLQKV LTASYPAQSSVPLTSGPVRQIM KEKGRSSEHIQRIDRDISGTLR KHMFFRDRYGTQRELLHILLA YEEYNPEVGYCMDLSHIALFL LYLPEEDAFWALVQLLASERHS LQAARAPAAIGAHADQAQIS LGLTLRLWDVYLVEGEQALMP ITRIAFKVQKRLTKTSRCGPW ARFCNRFDVTWARDEDTVLKH LRASMKKLTRKQDGLPPPAKPE
23328	53696	A	23462	3	497	SSECLTMAWIPLLPLILCTVS VASVELTQPASVSVSPGQTASIT CSGDVLAKKKYARWFQKPG QAPVLVIYKDSERPSGIPERFSG SSSGTTVTLTISGAQVEADY YCYSAADNNGWVFGGGVTKLT VLSQPKAAPSVTLFPPSSEELQ ANKAHTGVSQ
23329	53697	A	23463	1	393	FRSGSELVKAGLRAFFENAED LEKTSNKLKLGKFTHSRTQIKG VSQINITYTTVALLPILTSIFEHV TQHFGMDLLLDGVQISCYHIL CSLSYSLGTGKNYVEILGMPDT VEDMCPDIPQLECLMKEIN
23330	53698	A	23464	319	508	
23331	53699	C	23465	94	222	
23332	53700	A	23466	1	636	
23333	53701	A	23467	1	483	
23334	53702	A	23468	1	1797	

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23335	53703	A	23469	1	4275	
23336	53704	A	23470	1	1848	
23337	53705	A	23471	122	14928	ARSWRRRWRTRTKRRRRKSAA AVSARRAAAGGSRGAGGWGT ADASGAMAEAGGEGEDEIQFL RTEDEVVLQCIATIHKEQRKFC LAEAGLGNRLCFLEPTSEAKYIP PDLVCNCFVLEQSLSVRALQEM LANTGENGEGEAAQGGGHRRL LYGHAVLLRHSFSGMYLTCLTT SRSQTDKLAFDVGLREHATGE ACWWTIHPASKQRSEGEKVRIG DDLILSVSSERYLHLSVSNNGNI QVDASFMTLWNVHPTC
23338	53706	A	23472	134	1063	RPPGLTRSPSPAPARSPTRRQS TRRRSGATTSCQRLWATWNG CD/VCLNQSLREIPTDDKGFTAI HFAAQWGKLACQLVVEEYKF PVDLLTNSQTPLHLVIHRDNT TVALPCIYYLLEKGADLNAQTC NGSTPLHLAARDGLLDCVKVL VQSGANVHAQDAMGYKPIDCF KIWNHRACARFLKDAMWKKD KKDFAREMTKMKMFKSQTL MEHNYLIEYQKEHKILREAAIR KWLHGKLLHPGHSLSVNTKQAR ATALSKTPEQRESQRSRSHPSV DARLQCIPQTEMPKPIYRKPTV KRPHNVEC
23339	53707	A	23473	1	1280	MAGLGFVGHGAPGLLLLLLV LPPRALPEGPLVFVLFVRHGD RAPLASYPMDPHKEVASTLWP RGLGQLTTEGVRQLELGRFLR SRYEAFLSPEYRREEVYIRSTDF DRTLESAQANLAGLFPEAAPGS PEARWRPIPVHTVPV AEDKLLR FPMRSCPRYHELLEATEAAEY QEALGWTGFLSRLNFTGLSL VGEPLRRAWKVLDTLMCQQA HGLPLPAWASPDVLRTLAQISA LDIGAHSVGPRAAEKAQLTGGI LLNAILANFSRVQRLGLPLKMV MYSAHDSTLLALQGALGLYDG HTTPPYAACLGFEFRKHLGNPAK DGGNVTVSLFYRNDSAHPLPL SLPGCPAPICPLGRFYQLTAPAR PPAHGVTVCHGPYEAIPAPVV PLLAGAVAVLVALSLGLGLLA WRPGCLRALGGPV

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23340	53708	A	23474	133	672	AVGWESGKWDSDGRGQGGGQE QMWSCQSDMLYPPDQVGA WG LPGPTGPKGDAGSRGPMGMRG PPGECPCQCPTAPLAIPSTRWAL PCSWPPGPPGPPGPPAPVGPPHA VGSMSVSPGIPAGGGGGGVAI STVPATIKTRRQEVSPELPRP/PG PAPPPGPDVRPWL.LRPPGPMGK LSPGQG
23341	53709	A	23475	135	677	AVGWESGKWDSDGWGQGGGQE QMWSCQSDMLYPPDQVGA WG LPGPTGPKGDAGSRGPMGMRG PPGECPCQCPTAPLAIPSTRWAL PCSGPPGPPGPPGPPAPVGPPHA VGSMSVSPGIPAGGGGGGVAI STVPATKKTRRQEVSPELPRP/P GPAPPPGPDVRPWL.LRPPGPMG KLSPGQG
23342	53710	A	23476	220	745	TVIQRITGLHSVGPDPQQLRE AKLGTMVRLVLLPTPRRTTEVR TGPEREISMVLEAILGSLLETAC DHRQTTPSSKQA/GSSRLREGT SAGQPCL/LRLRLGPRAGGRRRC CRDIERSSSSSVCGRKCKRKKR KRGMCQSRHKHGCRRPQEGPR CNDGRALCSPRPQTTPGPLSTA
23343	53711	A	23477	1	2433	
23344	53712	A	23478	3	803	FPGRFRVRAVAGGSHCLFNS CCCCTSASLPARERHEWPGPAA AAAAAAAAAARRSQTQREGLFA GWGGGFAMSDDDSRASTSSSS SSSNQTEKETNTPKKKESKVS MSKNSKLLSPRAKGIGKELVAD ITLDPPPNCSAGPKGDNIYEW STILGPPGSVYEGGVFFLDITFTP EYPFKPPKVTFRTRIYHCNINSQ GVICLDILKDNWSPALTISKVL LSICSLTDCNPADPLVGSIAATQ YMTNRAEHDRMARQWTKRYA T

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23345	53713	A	23479	372	1839	GEAGGTEAEPENGAGGPRVPG WWGWSSTSSPRGCWDSGRSAA AIMDFLWDKRTGLAARKMPHP RRYHSSERGSRSYCEHYRS/R K/HKQRRSRWSSSSDRTRRRR REDSYHVRRCRSTRFSRSSQH SSRKAKSVEDDTEGHLIYHVGD WLQERYEIVSTLKGKGTGFRVV QCVDRHRRGARVALKIKNVE KYKEAARLEIKVLEKINEKDPG KNLCVQMFDFDYHGHMCISL ELGLSTDFDLKDNHLPYPIH QVHHMASQLCQAVKFLHDNK LTHIDLKPNILFVNSDYELTY NLEKKRHERSVKSTAVRVGDF GSATFDHEHHSTIVSTRHYRAP EVILELGSWQPCDVWSIGCIIFE YYVGFTLFQTHDNRQHLATME RILGPIPSRMIRKTRKQKYFYRG RLDWDENTSAGRYVRENCKPL RQYLTSEAEEDHQLFDLIESML EYEPARQLTLGEALQHPFFSRL WAEPNKLWDSSQDISP
23346	53714	A	23480	28	941	QSARPSLKRARSQRGRPLPSRA LVFLFLFFFFFFNFLPIHTQPSAH KDMITTNAGPLHPYGPQHLRLD NFVPNDRPTWAYTGLGLFSVT GGLRSWTTWAVVQGRAAGCPI GDFGRATVPCCWVLQCVGFH LVIEGLVPFSNYERPFCGDSLL NLKLWKEYGQGETARLHPGG DKFHSVALGTITSFA\WGEPSL WVVI\FLQLHPLARFILQLVVS VGQIYG\DVFYFLKEHPRRDS KHGKPGFTPLLLPGFSFVFHEM PLWLVPAPGSPCLDA\VKAPS THAPEHAWNAKGPKPKSKKN

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23347	53715	A	23481	1	1386	MWRNLKLPDRLLNGFDQNADS DMDNEVQAEVVTGDDEELIGN WSKGHSCYILAKRLAAFFPCPK DLWKFELEERDDLGLAEISS EAFKSVSYEKAAHWNPLESTC RHASLALAVVLQRRDWENP/G VTQLINRLAAHPPFASWRNSEE ARTDRPSQQLRSLNGEWRLMR YFLLTHLCETLVKVKDAEDQL GARVCVLERQIFDLGYQWAPI LANFVHIIVILGLFGTIQYRPRY ITGILSFPKHQESLSLKFTCLTEA ERDTDALLHLENACRESTATQR IQGFLLKDKKRKKQPPQQKQ QQWAKVQLGPWLQRVQAPSL GSFHGVLSLRVHRSKELRFRNC CLDFRCMEMPGCPGRGVLQA QNPRGEPLLGQCRREMCSSP YIVPTGALPSGAVRRRPPSSRPH NGRPTDSLHCVPKKAADTQHQ PLKAARRAAVPCATGSELKP
23348	53716	A	23482	3	732	SPLTPTATSGNPSKASSPGGLGS LVSTASSLPAGEKNSPRTGPGP RRAGAGIPNSGPDVTEGYPYNL CGRQGRWGGLIISLASEMKLQT LQTSVTTAKATLLELFVPLGGL VASLASEVRLQIFPRGGHLQSA KCGLLHLFSLPSTRSGRRKANR PMAVTVLLVLRDCADLLAVK AVIHICYQDQWPLRGSSRPANTP PPKASVSRPPGHRGVRRGSPL LQVGARRVGAEPALLELQSPS
23349	53717	A	23483	1	234	
23350	53718	A	23484	1	256	MLNLQGEWLELEEDAQKAYI MGLLDRLEVVSRRRLKVARA VLYAQDGEKFCPKRDCTNNS/ RY/NSI*MIQMMRFGTLELMRL
23351	53719	A	23485	1	3333	
23352	53720	A	23486	1	2661	
23353	53721	A	23488	3	433	

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23354	53722	A	23489	3	990	EKMNTADQARVGPADDGPAPS GEEEGEGGGEAGGKEPAADAA PGPSAAFRLMVTRREPAVKLQ YAVSGLEPLAWSEDRVSVST ARSAIVLELICDVHNPQGDLVIH RTSVAPLNSCLKVGSKTEVA ECKEKFAASKDPTVSQTFMLDR VFNPEGKALPPMRGFKYTSWSP MGCDANGRCLLAALTMDNRL TIQANLNLRLQWVQLVDLTIYIG ERLYETSYRLSKNEAPEGNLGD FAEFQRRHSMQTPVRMEWSGI CTTQQVKHNNESRDVGSVLLA VLFENGNIADVWQFLPFVKGES ISSCNTIESGITSPVLFVWEYE HNNRKMSSGLIVGSFAGPIKILPV NLKAVKGYFTLRQPVILWKEM DQLPVHSIKCVPLYHPYQKCS SLVVAARGSYVFWRLLLISKAG LNLHNSHVTGLHSLPIVSMAD KQNGTVYTCSDDGKVRQVIPIF TDVALKFEHQILKLSDFVGSVR THGIAVKPCGAYLAHTTEGMIN QLHPVNKNYQVQFVTLKTFEE AAAQLLESSVQNLFKQVDLIDL VRWKILKDKHIPQFLQEALEKK IESSGVTYFWRFKLLRILYQS MQKTPSEALWKPTHEDESKILLV DSPGMGNADDEQEEGTSSKQ VVKQGLQERSKEGDVEEPTDID SLPTTGADAGGREPMGRNSW GNSKGIKIRSCWEMRLTREHMK
23355	53723	A	23490	1218	1446	RCTDSQVRSPTPLHLAAQACSL ETTVCLLCSKADYTLSEKRGW MPIHFAAFYDNCVCHIALCRKDP SLEAEATAE
23356	53724	A	23491	2	632	NMAKTYDYLFLKLLIGDSGVG KTCVLVFRFSEDAFNSTFTITIRI DFKIRTIELDGKRIKLQIWDTAG QERFRTITTAYYRGAMGIMLVY DITNEKSFNIRNWRNTEEHAS ADVEKMILGNKCDVNDKRQVS KGS/GENKLALDYGIKFMETSA KANINVENAFFTLARDIKAKMD KKLDGNSPIQGSNQGVKITPDQ QKRSSFFRCVLL

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23357	53725	A	23492	1	1018	MVFYHVQAGLELLTSGPHCP DSQAADKAESATLLSRARLGA YCACASLERRWPHFSGREC MAKTYDYLKLLMGDSGVGK TCVLFRFSEDAFNSTFISTIGIDF KIRTIELDGKRIKLIQWDTAGQ ERFRTDHNRPYRGAMGIML VYDITNEKSPDNIRNWIARNIE EHASADVEKIMILGNKCDVND KRQVSKERGEKLALDYGIKFM ETSAKANINVENAFTLARDIK AKMDKLLGPAPHGHTLLGKGE EFAGVAGASAGSASLGLTPKQ TRPCPVNPQASREHTAFSIPKLG QKDNMEGNSPQGSNQGVKITP DQQRSSFFRCVLL
23358	53726	A	23493	1	130	
23359	53727	A	23494	1	1392	
23360	53728	A	23495	445	649	YPSLTNSKLLVHHFMELCWD KCVEKPGIALDSRTENCLSC WDRFIDTYLATSRAFIQVQKG GQ
23361	53729	A	23496	210	397	VITYAPGKKAQRTQK/APKTKTK KPHLSPCPSP/WRSRSCQPMQQS WSGAQVHIPQPPHTTCITWA
23362	53730	A	23497	55	286	QASSSPPISSVTCRKALPPGQTK KGLVASGDPEPVSMTSSPTPS LAPEHSSRASLEPSSSA*PSLAT* SRAGGSQA
23363	53731	A	23498	780	1022	QAMHGRSPGVTVRASGLRNEG DGPLGSVPTQARATGAPGHSAT PSPA WRA WSSSSKAS/WLPDA AGPPTPPWSGPSPTSW
23364	53732	A	23499	1	782	
23365	53733	A	23500	275	688	

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23366	53734	A	23501	1166	2271	LRCILTLISRWC*VSTVANLPP GISKWGANWQRCMEKE*CWSP AVTWICITCAQRSQ/IGDSSPYPG ATSFNEYVKANLTWRGPVEQH PLVNYLDHERGTLNPTARHYL PVLYVLRILWARTPLPIGRRTT VSKVKMKRILRAMRQKQQVL PLLVLGLDELMSAPSIPA ARMAQLDSRECRKLLNQAMA CRTSLEVEHLLAQFRMTQQDA PLVTAEITLES DWSKEEV LK GMTDNLLLAGRCRYPRKLEAD LWAREAVFSTGLGFSFAIPHSK SEHIEQSTISVARLQAPVRWGD DEAQFIIMLTNLKHAAGDQHM RIFSRLARRIMHEEFERNALVNA ASADAIASLLNMNWTVKEHHE
23367	53735	A	23502	1	2604	
23368	53736	A	23503	306	468	TRHCDRRQPRRGHRRAGT/CNQ I*KGCCCVRTKQLSPSLVSNF CPCSSFLKNS
23369	53737	A	23504	102	509	AAQQGTMARSL.LLQILL.LSL ALETAGEEAQGDKIIDGAPCAR GSHPWQVALLSGNQLHCGGVL VNERWVLTAAHCKMNEYTVH LGS DTL/E/ADRKAQRIKPSKSF RHPGYFTQTHVNDLMLVKLNS QARLSSMVK
23370	53738	A	23505	1	1032	MMQATVGFEDGDAATSQVSPS VNKVHSSYFLDFFEEYIVIAFKI LRRGPDISCQIINGEDCSPHSQP WQAALVMENE/LFCSGVLVHP QWVLSAAPVSRKYNRPLLAND LMLIKLDESVS ESDTIRISIASQ CPTAGNSCLVSGWGLLANDPT SRLLPPLPCRNPVQPLLPPPEKP RTAPDTLGSSPVKSRGTSSGSS FLLPAPSPFPFRPHHGTPTSCG QDQVDPALAGGSLGSPAGEAL PRLAAPERLSRHGKIPSPAPAD LTAILALETAGEEVFPPLTSCA WMSSSSPPGLIEGLQGLTGKHFH AVRWHPRLQEKRLQSVSPDSR IPGARRPAAR
23371	53739	A	23506	303	393	

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23372	53740	A	23507	391	1170	GSFFFFFYFAYSPMPKNSKVV KRELDDEVTSVKDLLSNEDA ADDAFKTSELIVDQEEKEDTDV EGK/SEVEDERPAWNSKLQYIL AQVGFSVGLGNVWRFPYLCQK NGGVVEPECEQSSATTYYWYR EALNISSSISESGLNWKMTICL LAAWVMVCLAMIKGIQSSGKV NTYDRVTMSATVLALQEQQWT FSPIRSGNHLTGSGAQRTPCRI RRGGSQLRVCDGGKQQWWTV SQSSARAITNTDQKSVQLQDLIE
23373	53741	A	23508	45	546	EGGGSRSLSWFRELIGQPVSQFIE PVAAGGAVALNVQ/RSCGVVS AAPACL*SRPHSWRWGGPACW RTPGG/LASRSSSSA SILMSSSRA SFTRSLSLSTHKDQGLVCSGSS GATGAGSCLWPPISHTVKLMF LYSTVSTLKPVMGMVVTISPSSL SL*RIVVFPAASRPT/YEDAHFFF CQKGP*RGSSSLQHPGPP
23374	53742	A	23509	1367	2142	VRRPQGCGLGKRSLSRVCAVLP WGIWP/WSLAVGPQYSSLGSP ILCASIPGLVPKQLRFCRNYVEI MPSVAEGIKIGIQEQHQHFRGR RWNCTTVHDSLAIFGPVLDKG YFGYLETTITVPDSVVSTKAETP DKGVCGRELGRGGWLPQLQS LDEISMGWALCSRLQIKATRES AFVHAIASAGVAFVTRSCAEG TAAICGCSRRHQGSPGKGWKW GGCSEIDIEFGGMVSREFADARE NRPDARSAMNRHNNEAGRQV GSPPARVLGKKEPPQGVCPGS LGHMARSLAVGPQYSSLSQPI LCASIPGLVPKQLRFCRNYVEI MPSVAEGIKIGIQEQHQHFRGR RWNCTTVHDSLAIFGPVLDKG YFGYLETTITVPDSVVSTKAETP DKGVCGRELGRGGWLPQLQS LDEISMGWALCSRLQIKATRES AFVHAIASAGVAFVTRSCAEG TAAICGCSRRHQGSPGKGWKW GGCSEIDIEFGGMVSREFADARE NRPDARSAMNRHNNEAGRQ

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23375	53743	A	23510	2094	2619	ASPASPAPCSGIPRT*SPYPSPSR TQAPRARGPAIHHPGPRGCT ALPRQGPPTPGSARAPPIPAHR APTSPTLNFLCLASSRQSMPPAPR PPPVPATNPVTPGCGRPPPTLGC RNPQTLRPPGLPSPALLRRPLP PPARVGMPPHPQPLPTTPACWR PVDWARAEGAGRAVC
23376	53744	A	23511	3050	3317	PARTSPASGPP**DLISALWTPS QPRAPTRQSLNSLSSAPSSSTIG PSPSPAPGAPPLPWLPSPSSSL PRLSQVSRRPHSHLHPQ
23377	53745	A	23512	862	2954	AEHTLLVCFNLSTLTSTHVES FGQLRGSQIGHPRRNKMPYA WSIPQDPLKPERDPGGPLGVS LSLPVNQYGESEPMGDDDDYD EYSKELNQYRRSKDSRGRGLSR GRGRGSRGRGKGMGRGRGRG GSRGGMNKGGMNDDDEFYDE DMGDGGGGSYRSDHDKPHQ QSDKKGKVICKYFVEGRCTWL YHTTGNCGNDDCMFSDHPLTE ETRELLDKVEMTGSSVFDYIHP GDHSEVLEQLGLRTPTPGPPTPP SVSSSSSSSSSLADTPEIEASLTK VPPSSLVQERSFFVRMKSTLTK RGLHVKASGYKVIHVTGRLLRA HALGLVALGHTLPPAPLAELPL HGHMIVFRLSLGLTILACESRVS DHMDLGPSELVGRSCYQFVHG QDATRIQSHVDCEHLHPPSL PTTPQTRASHSLVPGSPSSGLPT VPPAAPTAAGTPFISIGRAARRLS DASGLLDKGQVMTGYRRLQ RAGGFVWLQSVATVAGSGKSP GEHHIVLWVSHVLSQAEGGQTP LDAFQLPASVACEEASSPGPEPT EPEPTEGKQAAPAENEAPQTQ GKRIKVEPGPRETKGSEDSGDE DPSSHPATPRPEFTSVIRAGVLK QDPVRPWGLAPPDPPPTLLHA GFLPPVVRGLCTPGTIRYGAEL GLVYPHLQRLGPGPALPEAFYP PLGLPYPGPATRLPRKGD

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23378	53746	A	23513	1319	2211	GSKVYGSFLFHINHGPNFNMVEVL VDSWPEYQMVIRPQ/ETVRGE EKVQGNLDTFHHPTQEMTDDM DSYTNVYRVFSKDPQKSQEV KNSEIHNWKQLQIQGFQESLG EGIRAAAFSNSVKVEHSRALLF VTEDILKLYATNKSILGSAET GHPDDELESETPNFKYAQLNVS YSGLVNDNWKLGMMNKRSLRYI KRCLGALPAACMLGPEGVPVS WVTMDPSCIEGMGSVEKYRR RGNGTRLIMRCMKYLCQKNIPF YGSVLEENQGVIRKTSALGFLE ASCQWHQWNCYPQNLVPL
23379	53747	A	23514	234	858	SVPLQESPLPPPTHQADC*SPC GAQGGWVTLAVASASS*AHTA SPLRSPQAQGRASPAPPQIHL TTPSFSSQGT/SHGGLGSTPGA DDPNTSSS/PPPGGSTPRWSAGD SAHSGGEVDGWS*SP*SVPSY GT*SPFCWPSSGQRSFHGIASG WEPDGPIDGSSRWEPCGKQES ETGVEGRQHFPKQLCLGSCRA VASPRVARA
23380	53748	A	23515	1	3582	
23381	53749	A	23516	628	4254	RLPESRAHDVAGADERPWPVH AGIFKSPAAGAAMSPAAAAAG AGERRRPIASVRDGRGRGCGGP AGAAALLGLSLVGLLLYLVPA AALAWLAVGTAAWWGLSRE PRGSRPLSSFVQKARHRTLFA SPPAKSTANGNLEPRTLLEG DPAELLMGSYLGKPGPPQAP APEGQDLRNRPGRRPPARPAR STPPSPPTHRVHHFYPSLPTLL RPSGRPSPRDRGTLPDFVITPR RRYPHQTYQYSCPGVL
23382	53750	A	23517	1	392	KVHMNGLRYALYIMGPALTRG CHQVLMIMLCCVEIERILT/VMM KEAYFGEVDIMDDLPTGNISA NVTGRLYKCGVINHTVDLRRM KT/EKWQNNLLPSRQGFIVLTT SAGIMDHEEARRKHTGGKILGF
23383	53751	A	23518	227	352	

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23384	53752	A	23519	3	507	SFRAATMVRMNVLDALKSIN NAEKGKQVLRPCSKVIVRF LTVMMKHGIGEFEEIIDDHRAG KIVVNL TGRNLK VGVQWRDLG YCNLC L PGSSDSSASASLVAEIT ICGVISPRFDVQLKDLEK WQNN LLPSRQFGFIVI.TTSAGIMDHEE ARRKHTGGKILGFFF
23385	53753	A	23520	279	653	ARAQRFSSQVDV FYLIQSVIFCR LALAEFEIIDD PQSLGKLL*TLT GRLKQ/CLGVISPRFDVQLKRP WKKWHEIIL/SPNPAKFGFIVLT TSAGLHG/HHEGRQDRKHTGG KILGILYRDVHIIFT
23386	53754	A	23521	1	392	KVHMNGRLRYALYIMGPALTRG CHQVLIIMLCCEVIERILT/VMM KEAYFGEVDIMDDLPT/GNISA NVTGRLYKCGVINHTVDL/PPY ENGK WQNNLLPSRQFGFIVLTT SAGIMDHEEARRKHTGGKILGF
23387	53755	A	23522	108	371	LSYIGKFEIIDDHRAGKIVVNL GGLNKC GVISLRFDVQLKDLEK WQNNLLPSQFGFIALTT SAGI MDHKEAR*KHTAGKILEFFF
23388	53756	A	23523	252	378	
23389	53757	A	23524	3	518	HASAFRAATMVRMNVLDAL KSINNAEKGKQVLRPCSKVI VRFLTVMMKHGYIGEFEEIIDDH RAGKIVVNL TGRNLK VGVQWR DLGYCNLC L PGSSDSSASASLV AEITCGVISPRFDVQLKDLEK WQNNLLPSRQFGFIVLTT SAGI MDHEEARRKHTGGKILGFFF
23390	53758	A	23525	279	709	ARAQRFSSQVDV FYLIQSVIFCR LALAEF*NPLMTHQSLGKFVFN PHRAGLNKCGVISPQILTVQLQ RPWKK WAGLILL/SRQVLGFV VLTTSAGIMDHEEARPKTPRR GKSWGFFFLGDVNYILFYKLLKC LMDSGASTWSF
23391	53759	A	23526	207	564	SMAKEAISINRSLWAGPAKISSP AETVIESLISLFQKYVVGKGGYN CTL SKTEFLSFMNAELAAFTKN QKDPGV LHRMMKKLGTNN DG QLDFSEFLNLIGGLAMACHDSF LKA VPSQKRT

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23392	53760	A	23527	1	407	FREKQSQELSQYGAMGAGQSF NSQFLQHGGPRGSPVPAGMNP TGIGGVMGPGSLPLAMNPTRA AGMTPLYAGORLPQHGYPGPP QAQP/PAPTGGQENLL*GVSR AVSARSLGPPFRAIPVSHLAGNP TPPMNP
23393	53761	A	23528	3	315	
23394	53762	A	23529	1	763	DYEEITDPTCSWKVPVVKPDM HIKEEPDGPALKRCRTVSPA LMPSVMEMIAALGPGAAPFAFL QPPSVPAPSDYPGQGSFLGPGT FPESFPPTPTPTLAEFTPGPPPI CYQSDIPSSLLTSEKST/SLPLQA RR/PPAGHLDPHTNPGTGLHTS NLGAPPGPQLHHSNPPASRS LGQASLGPTGELAFSPATGVMG PPMSGAGEAPEALDLLPELT NPDELLSYLGPPDLPTNNDDL LSLFENN
23395	53763	A	23530	1	2901	MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARIVP GFIRIARPRDGSFAYESVPWQQS ATQPAGSLSVVTTVWGVGNAT QSQVLGNPMGPAGSPGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQQGVYSRGGYP GAPGFTTGYAGGPGGLPLPSH AARPSTDFTAQAAAAVAAAA ATATATATATVAALQEQSQSE LSQYGAMGAGQSFNSQFLQHG GPRGSPVPAGMNP TGIGGVM
23396	53764	A	23531	80	412	KPGNGACAGREWCDDGGGA NWRDPGLPVGDSGVWDRVLE LLGPRSPRPLDVGGPAAGTPGV LSR/HLPVDCGLGPEALLCSSAP AARRPSLCGGHGRVMRGFLRG CGFRP
23397	53765	A	23532	1	192	RPLDVGGPAAGTPGVLSR/HLP VDCGLGPEALLCSSAPAARRPS LCGGHGRVMRGFLRGCGFRP

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23398	53766	A	23533	1	2094	RPLDVGGPAAAGTPGVLSRPCPS TAALAPKPFCAAPRPQPDAPAC AGATGGSCADFDGSGVDFVRRR SSGLWGPQPPLFPVKNYTEMFQ DPVAFKDVAVNFTQEEWALLD ISQKNLYREVMLDTFVNLTSIG KKWKDQNIIEYEQNPRRNFRS VTEEKVNEIKEDSHCGETFTPV PDDRLNFQKKKASPEVKSCDSF VCGEVGLGNSSFNMNIRGDIGH KAYEYQYEGPKCKCQQPKKA FRYRPSFRTOERDHTGEKPYAL LKNDGKKPLFYHSSIQRHMVV HSGDGPYKCKFCGKAFHWLSL YLIHERHTGKPYECKQCGKS FSYSATHRIHERTHIGKPYECQ ECGKAFHSPRSCHRHSHMGE KAYQCKECGKAFMCPRYVRRH ERTHSRKKLYECKQCGKALSSL TSFQTHIRIMHSGERPYECKTCG KGFYSAKSFQRHEKTHSGEKPY KCKQCGKAFTRSGSFRYHERTH TGEKPYECKQCGKAHERHTTG EKPYECKLYGKALSRLISFRRH MRMHTGERPHKCKICGKAFSS PSSFQRHERSHTGEKPYKCKQC GKAFTCFHFQYHERHTTGEK PDGCKQCGKAFSAKYIRIHGR THTGEKPYECKQCGKAFHWVS SFHRHERTHAGEKPYECKHCG KAFTCSIYIRIHERIHTGEKPYQ CKECKGAFIRSSYCRKHERTHTI

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23399	53767	A	23534	48	1317	CGLMDELVHDI.TSALEQTSEQ NKLGEELWEEMALSPRQRRQL RKRGRKRKRRSDFTHLAEHTCC YSEASESSLDEATKDCREVPV TNFSDSDDTMVAKRHPALNAI VKSKQHSWHESDSFTENAPCRP LRRRRKVKRYTSEVAASLQKK LKVSDWSYERGCGRFSAKKQR LSRWKENTPWTSSGHGLCESA ENRTFLSKTGRKERMECETDEQ KQGSDENMSECTSSVCSSDT GLFTNDEGRQGDDEQSDWFYE GECVPGFTVPNLLPKWAPDIHS EVERMDSGLDKFSDSTFLPSR PAQRGYHTRLNRLPGAARCL RKGRRLVGKETSINTLGTERTS HIISDPQKDFWLPASAGKRERN QFNPLSPLYSLDLADASHRRR SPAHC SARQANVHWGPCCSRDI KQEAETSGHSIFV
23400	53768	A	23535	225	403	
23401	53769	A	23536	1	403	REQEFHMAPGEVITVIRLIRS LEHRNFKPVVYHGVNLDQTV KEFIVFLKQDIPLRTNLPFPFRN YKYDALKKIHHQAHSKTNELVL SLEDDERLLLKEDSTLKAAGIA SETEIGIFREEDYRNYKANPISS
23402	53770	A	23537	2	239	
23403	53771	A	23538	2	214	
23404	53772	A	23539	1	1341	
23405	53773	A	23540	1	1677	
23406	53774	A	23541	1010	1509	
23407	53775	A	23542	1	6355	
23408	53776	A	23543	223	10504	VKMPIGSKERPTFFEIFKTRCNK ADLGPISLWFEELSSEAPPYNS EPAEESSEHKNNNYEPNLFKTPQ RKPSYNQLASTPIIFKEQGLTLP LYQSPVKELDKFKLDLGRNVP NSRHKSLRTVTKMDQADDVS CPLLNSCLSESPPVLQCTHVT QRDKSVVCGSLFHTPKFVKGR QTPKHIESLGAEVDPDMSWSS SLATPPTLSSTVLIVRNEEASET VFPHDTTANVKSYFSNHDESLK KNDRFIASVT
23409	53777	B	23544	137	709	
23410	53778	A	23545	1	1974	

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23411	53779	A	23546	207	1622	MACCLSDVEVKESKRINAEIEKA AAAEETRRDAREL/RLLLLGT GESGKSTFIKQMRIHGAGYSE EDKRGFTKL VYQNI FTAMQAM IRAMETLAKILYKVRSTRANA L/LIRGGGTLEKVTTFGAFSYVQ LPLKDLFGRDPGIE/CAYERQP RSYQLSDSAKYVLTVDRIATL GYLPTQQ/DVPAGSRVPTTGIE YPPDLNIIIFRMVDVGGQRSIE RRKWIHCFENVTSIMFLValse YDQVLVESDNENRMEESKALF RTIITYPW/QNSSVILFLNKKDL LEDKILYSHLVDFPRSSMGPO R/DAKAAREFILKMFVDLNPNS DKII/YTSHFTCPHRRRTSRFVF PAVKDTILQNL EYKPLGSAP GPGRRDGDGTQDL PSTEPAAA RAGGAESGPGPLPAGGDFFFF IFLTNGFYFTVIRGCTSLPPYTSR TFSFVNGKGSFLALTYGSLFS KKKKKKKE
23412	53780	A	23547	1	401	KKVPGRLSEMSFSLNFTLPANT TSSPVTDCGPSLGLAAGIPLIV ATALLVALLFTLIHRRRSSIEAM EESDRPCEISEIDNPKISENPRR SPTHEKNTMGAQEAHIYVKT VAGSEEPVHDYRPTIEMERRR
23413	53781	A	23548	584	1071	PCRLPLHLILVEDLSFSLNFTLP ANTVSTAAPHQAT/PEKTSAEF TDCGPSLGLAAGIPLIVATALL VALLFTLIHRRRSSIEAMEESDR PCEISEIDNPKISENPRRSPTE KNTMGAQEAHIYVKT VAGSEE PVHDYRPTIEMERRRGLWWL VPRLSLE
23414	53782	A	23549	25	654	LFLQMKDTSPIIFVRKELTIRQC TKKVPGRLEMSFSLNFTLPAN TTSSPVTGGKETDCGPSLGLAA GIPLLVATALLVALLFTLIHRRR SSIEAMEESDRPCEISEIDNPKI SENPRRSPTEKNTMGAQEAHI YVKT VTKSEEPVHDYRPTIE MERRRGLWWL VPRLSLGMMP TSNQGSHTQWHLGTGLKTQGF VLGEERCQAAS
23415	53783	A	23550	108	413	RRSGSMALWRAYQRAAAHP WKVQVLT/ALLGRKAALLAP CQ*LYLPQTQASWTEGHASCS SSLQEATSCPSAFCA*NSKATKQLV ERRGLQEHRGRTLT.MVVS

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23416	53784	A	23551	1	146	
23417	53785	A	23552	2	442	GREARRSRSMALWRAYQRALA AHPWKVQVLTAVASGEEGSTA GMPMPVAIPADPGLLD*RTRFLL TPRSHFLPLCLLRMKLKSHKRS LMGLGDIISQQLVERRGLQEHQ RGRTLMTMSLGGCFVGPVVG WYKVLDRFIPGTTKVD
23418	53786	A	23553	3	675	RHSRFGAQGSMAWWRAYQRT LFALPWKIVQVLTAGSLMGLG DIISQQLVERRGLQEHQRGRTL E/TMVS LGCGFVGPVVGWYK VLDRFIPGTTKVDALKKMLLD QGGFAPSFLGCFLPLVGALNGL SAQDNWGQTTAGELG/RDYPD ALITNYLWPAVQLANFYLVP LHYRVAVVQCVAVIWNSYLS WKAHRALSLPHSIVSTLQVMQ LDPWNGSDNPPQKWA
23419	53787	A	23554	512	1227	LQGHLMGIMAASRPLSRFWEW GKNIVCVGRNYADHVREMRSA /VWLSEPVFLPKPSTGVRAQRA RPILMPAYTRNLHHELEL/ALVI GQRCRAVPEVAAMDYVGGVY ALCL/DMTAWDVQASARKKG LAWDSGE/DAFTASCPVQVSL PKEKIPDPSQ/LKALGFKVNGEL RQEGETSSMIFSIPIIYSVSKIIT LEEGDILTGTGKGVGPVKEND EIEAGHTRAGQYDHLKVEKAQ
23420	53788	A	23555	192	436	RTSDHECFREGQICSVCLRERL NLNPEEACLLSQAPCMLFVLQY LNTVIPYEKKASPPSVDELQML \TNILFAMKEDNEKVP

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23421	53789	A	23556	94	1252	ARMEAPLVSLDEEDFLRPSCS EDPEEKQCFCYGSSPHHLEDPSL SELENFSSEIISFKSMEDLVNEF DEKLNVCFRNYNAKTENLAPV KNQLQIQEEEEETLQDEEVWDA LTDNYIPSLSEDWRDPNIEALN GNCSDEIHEKEEEEFNEKSEN DSGINEEPLLTADQVIEIEEMMM QNSPDPEEEEEVLEEDGGETSS QADSVLLQEMQALQTFFNNNW SYEGLRHMSGSELTLLDQVEG AIRDFWEELVQQLARRDELEF EKEVKNSFFTVMIEVQNKQKIE QRELMKKRRKEKGLSLQSSRIE KGNQMP/LKRFSGEGISNQLQSG IRQTFGSSGTDKQYLNTVIPYEK KAYPPSVEDLQMLTNLFAFM KEDNEKVPYFA
23422	53790	A	23557	391	1169	GSFFFFFKYFAYSPMPKNSKV KRELDVDTESVKDLLSNEDA ADDAFKTSELIVDQGEKEDTDV EGK/SEVEDERPAWNSKLQYL AQVGFVSVGLGNVWRFPYLCQK NGGVVEPECEQSSATYYWYR EALNIISSSISSEGLNWKMTICL LAAWVMVCLAMIKGIQSSGKV NTYDRVTMSATVLAHQEQWQT FSPIRSGNGHLTGSGAQRTPCRI RRGGSQRLVCDGGKQQWWTV SQSSARAITNTDQKSVQLQDLIE
23423	53791	A	23558	321	568	CLWCGASWPRRHSSPGRPAD HRGDRP/EGPDTQGPGRPEPSTE PAFNPQSSLDQGGGPAAPVD DDTRRGHGGVCGDGAGAEA
23424	53792	A	23559	510	690	LRSPQIRGVAAPFLGSPVPFPGG FRVQGGMAGQPSAPPALQTD PYSKAHSVTPKSTPRVT
23425	53793	A	23560	25	480	
23426	53794	A	23561	84	292	VRAVQSLHFFPWR/ISCPSES TRSIHVDR/PRNSASLSAFP VSAGALINGEAWVRMGQVPIP KAP

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23427	53795	A	23562	1138	1924	CRSSATWTPWTTTTCRCRDLTK TYSLEAYDNWFNCLSMVLVATE VCRLLSPGSAMLRSPTATQVV KKKHRTRMLEFFIDVARECFNI GNFNSMMAIISGMNLSVVARLK KTWSKVKTAKFDVLEHHMDPS SNFCNYRTALQGATQRSQMAN SSREKIVIPVFNLFVKDIYFLPQ NP\SNHLPNGHINFKKFWEISRQ IHEFMTWTQVECPFEKDKKIPIS YLLTAPHPTARKLSSPSFESE PENHMEKDSWKLTRLTLLNRA
23428	53796	A	23563	3	260	
23429	53797	A	23564	1	1386	
23430	53798	A	23565	137	611	MKVNLDGSQLNACVFCRKH DCPNKYGEKKTEKWNLT YYCLLMSSGIWQRKEEGVY GFLIEDIRKEVNRASKLCCVC KKNGAFIGCVAPCRKRSYHFP CGLQRECFQFTGNFASFCWDH RPVQIITSNNYRESLPWHLLG NLFEPIPSY
23431	53799	A	23566	181	486	DPQGEAKGAAPAEGGGPV*W N\GLQGPAVGPGRDGSPGANGI PGTPGIPGRDGFKEGKCLRE SFEESWTPNYKQCSWSSLNYGI DLGKIAECTFTKMRS
23432	53800	A	23567	600	888	QYNGMCSPPGAVPGR\EGSPG ANGIPGTPGIPGRDGFKEGKCL RESFEESWTPNYKQCSWSSL NYGIDLKGIAGRNCWHILAPVP NIVSLYFGS
23433	53801	A	23568	91	1170	ISLHRRPGPTCSMESPASSQPAS MPQSGKSKRKKDLRISCMSPK PAPNPTPPRNLDSTFTITIGDRN FEVEADDLVITSELGRGAYGVV EKVRHAQSGTIVAVKRIRATV NSQEQRLLMLDLINMRTVDC FYTVTFYGFALFREGDVVICME LMDTSLDKFYRKVLKDNMTIP EDILGEIAVSIVRALEHLHSLKLS VIHRDVKPSNVLINKEGHVKM CDFGISGYLVDSVAKTINAGCK VKHGHESLN\PDNRRKGC DVKS HVWSLGITMIEMAFRLFYESW GTFPFQQLKQVVEHPSPLPAGR FSPEFVDFTAQCLRKNP AERMS YLELMEHPFFTLHKTKETDIAVA FVKEILGEDS
23434	53802	B	23569	111	193	

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23435	53803	A	23570	312	696	RP*SAHPEPGDCPSPPHPPRCGG VAQTAQVPDAPAPV*AG/QHSR SYMEDHLKKNRLEKEWEALC AYQAEFNSSFVAQREENVPKN RSLAVLTSQPTRNQCLPFLQHG PGDICTPVSISSIVLCHRV
23436	53804	A	23571	1	2974	QAAGMGPPPLLLLLLLLP VLPAAPSSVPRGRQLPGRGCL LEEGLCGASEACVNDGVFGRC QKVPAMDFYRYEVSPVALQRL RVALQKLSGTGFTWQDDYTQY VMDQELADLPKTYLRRPEASSP ARPSKHSVGSERRYSREGGAAL ANALRRHLPFLEALSQAPASDV LARTHATAQDRPPAEGDDRFSES ILTYVAHTSALTYPGPRTQLH EDLLPRTLGLQPDDELSPKVD S GVDRLHMAALSA
23437	53805	A	23572	1	3202	ASRRLPRGHGLSAGQAAGMG PPLPLLLLLLLLPRLPAAPSS VPRGRQLPGRGCLLEEGLCGA SEACVNDGVFGRCQKVPAMDF YRYEVSPVALQRLRVALQKLS GTGFTWQDDYTQYVMDQELA DLPKTYLRRPEASSPARPSKHS VGSERRYSREGGAALANALRR HLPFLEALSQAPASDV LARTH A QDRPPAEGDDRFSESILTYVA HTSALTYPGSR TQLREDLLPR TLGLQPDDELSPKVD SG

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23438	53806	A	23573	1	1459	MPLTSQDVDPQKTA A WVPNTNRD STVPSDPWDCKRRPWPLLVLRP LAPGTKAPPGQNGRGRQKGS PCSRRLLEPAGPLGPASVRCIR TTTTQLLIITSLRFPSLEAAVGY GSNTCIFANACQMFIMITWPY LQCIPYSVLLKDLERNLRELE DLIEAVYTDIIQKGLDQRNQLL EVDFCIGRDIRKKDINNIVKTLH EWCDCGEA\ALLGIEQQVLRAN QYKENHNR/TLQQQVEAEDVVI LPQSGNDCRGLRFVSSLIGGVR CVHLKHKGDVAVWEAIEEGEA LPGKYRLKGGRSVWAAAVRA VCMDQVTNIKKTLKATASSA QEMEQQLAERECPPHAEQRQP TKKMSKVKGLVSSSPLGPAGA AGTHQAWVRWGGDTKGFPPL STCSEFQTCPSPHQRLPTLLVLF QKNCYSPSPTPSPFCSLQTQGL HQCHPKTGSDTAQLPSRRFLSL CKGLVSLPVFLLLPFRHFVRLVIK
23439	53807	A	23574	2	396	
23440	53808	A	23575	1	1014	
23441	53809	A	23576	110	212	
23442	53810	A	23577	1	747	
23443	53811	A	23578	323	495	GRAGKWHQTPE*SLRKAM*MF QILMMKMIVALARATSGTEAV AGRSWASGLRRSGRV
23444	53812	A	23579	26	229	
23445	53813	A	23580	1	574	
23446	53814	A	23581	889	1189	
23447	53815	A	23582	170	625	GAAVAALVRPNGGTAASHVCR EMRPLRPLQSRRCRRRTGISN MRALENDFFNSPPRKT VRFGGT VTEVLLKYKKGETNDFELLKN QLLDPDIDKDDIINW/LLEFRSS VMYLTKDVE/QLISILRLPWL NRSQTVVEEYLAFLGNLVSA
23448	53816	A	23583	166	455	RWKPSGTWPRNPMERPGH*ES VPKPGD*AKKSGGETRGRKEG NEHRETFSQIPDCHLNKKSQTG VKPKCKSVCGK VFLRHSLDRH MRAHAGHKRS
23449	53817	A	23584	3	3706	

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23450	53818	A	23585	1	1970	MVTDKAA AAGTHGEARPCWG SGSRVHTYRGAGERAMRVHRP MPREDSEVRREADGGKHEQRS FGDLHPTAAPAPAAASGCGTQPG RVKQPGWEQHREAPQORQPPV RPHGSHQLVTVRYERRPGGKE RARLRPGLGCPSGRTPOGRAPQ GTALPTAAAAAIFPSAALTSGQ RNASLPKFYFRGGTWTGTSQSEA LCGKLSNQLGLEPLVPRIRLILS CGTCSGCSPPKDPGHPEAGNG PSRDFQLPSEERDSVAFEDVA VNFTQEEWALLSPSQKNLYRD VTLETFRNLASVGIQWKDQDIE NLYQNLGIKLRSLVERLCGRKE GNEHRETFSQLPDCHLNKKSQT GVKPKCSCVCGKVFLRHSFLDR HMRAGHGRSECGGEWRET RKQKQHGKASISPSGARRTVT PTSMRPYETKVCGKA/FIS/PIYF QIHQRTPTKRSYKCREIVRAFT VSSFFRKHGKMHTGEKRYECK YCGKPIDYPSLFIQHVTRHTGE KPYKCKQFGKAFISAGYLRTHE IRSHALEKSHQCQECGKLSICS SSLHRHERTHSGGKLYECQKC AKVFRCPSTLQAHERAHTGERP YECNCKGKTFNYPSCFRHKHT HSGEKPYECTRCGKAFGWCSSL RRHEMTHTEKPFDCQKQVKS
23451	53819	A	23586	86	390	LQSGDLPWENPLSSCSLLREKD PPTTSGPQTTSRNPISPNPELA THAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP ELLELPWKVL
23452	53820	A	23587	1	502	MLLTQSLFGGLFTRTHMKFGA VTQIRGPPLDGKSPVLLLFALER QRRHVLMSDPKLRCSRTGKA AFPWCLIIAEMPDPYSPTFQRCQ TTQGRLPWSFTLSSKSRSFSG ARACYKCKQSDHQAKECPQPG IPPKPCPICAGPTGNRTVQLTW QPLPELELPWKAL
23453	53821	B	23588	1	663	
23454	53822	A	23589	233	496	
23455	53823	A	23590	2	378	ERQRRHVLMSDPKLRCSRTG KAAFPWCLIIAEMPDPYSPTFQRC CQTQGRLPWSFTLSSKSRSFSG EGARACYKCKQSDHQAKECPQ PGIPPKPCPICAGPTGNRTVQLTW QPLPELELPWKAL

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23456	53824	A	23591	3	452	VRPRRDACLGPSPLAASPAFLG KGQVQPLISLCPDPLFPHNPLIS LRPNPLCPHDLVSLCPDPFPAF LEAHKNFQTPEPQQGPPIPEPPP PGACYKC/HEI*PPQGMPAAQ DSS*AMS/LSVRDPTGNQTVQL TWQPLPEPLELWPKAL
23457	53825	A	23592	1352	1540	
23458	53826	A	23593	177	383	EAMEPWKGVPGLGRVNTQIAP FSEAEQPREIH*GSRKVRKAAQ GLNEGPRELFWQPLPEPLELW KAL
23459	53827	A	23594	1478	1744	
23460	53828	A	23595	23	178	SCLEVCDEQGPEKTRQRALRG VSSVTEDTLNICRLCWQPLPEPL ELWPKAL
23461	53829	A	23596	1	282	
23462	53830	A	23597	34	241	SGDLPWEINPPSSCSLLREKDP MTSGPQT/TSRPNISPNPDPTG NRTVQLTWQPLPEPLELLPKAL
23463	53831	A	23598	121	286	AASFYSSPTSLTIPQLSPFNLGV TLQSLPSLNFNSFLFWQPLPEPL ELWPKAL
23464	53832	A	23599	144	488	GYEIWCRDSQGTTFPWEINPPS SCSLLREKDPPTSGPQT/TPR NISPISNLVSGFLLSPPSLTIPQ PLSPFNLGATLQSLPSLNFNSFH FLVETKETRIFIRGAKIPAPVTD
23465	53833	A	23600	471	677	
23466	53834	B	23601	67	555	
23467	53835	A	23602	1	1440	
23468	53836	A	23603	860	1209	IPGNCRDSSGVGIKERETNAGS QHMH/KNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAPNPVYEKKPK KEVKKRWNRKMSLAQKKD WVAQKKASFLRA

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23469	53837	A	23604	1	966	MGFVKVVKNKAYFKRYQVKF RRRREGKTDYYARKRLVIQDK NKYNTPKYRMIVRVNTRDIIICQ IANA\RIEG\DMIVCAPYAHELP KIWV*RVGLTNYAAA\YCTGLL AGPAGFFHRFGMDQIYE\GQVIE LTGDEYNVESIDGQPGCLHPAY WDARPLPRTYPLAIKVFQCP*R GA\VDGGLVLFPHSTKTIPFGY DSVESKIEFNAES\IHRKPHPWAQ NVARLHAPTLMEEDEDA\YTK KQFSQYIKNSVTPDMMEEMV/Y RKAHAAIRENPVYEKKPKKEV KRKRWNRPKMSLAQKDRVA PKKASFLQSSRGLLESLTPAIFP
23470	53838	A	23605	1	644	ANSSPVNPVFFDVSIQGEVVG RMKIELFADVVPKTAENFRQFC TGEF/RVSFRCV*LLCLLQRGVL GLQ*GYR*TTCPW*MIAGDSDR RKDGVPIGYKG\STFHRVIKDF MIQGGDFVNGDGTGVASIYRG PFADENFKLRHSAPGLLSMANS GPSTNGCQFFITCSKCDWLDGK HVVFVKIIDGLLVMRKIENVPT GPNNKPKLPVVISQCGEM
23471	53839	A	23606	638	1391	CPAYKGAHQVCVYCTLPPL QTRRVRRNPTLPTSASGSEPW RLANSSPVNPVFFDVSIQGEV VGRMKIELFADVVPNTAENFR QFCTGEFRKDGVPPIGYKGSTFH RVIKDFMIQGGDFVNGDGTGV ASIYRGPFADENFKLRHSAPGL LSMLTWPGKLTAGIFGFHQANS GPSTNGCQFFITCSKCDWLDGK HVVFVKIIDGLLVMRKIE\GMPC IFQPTWTHFLPVITTCALSALGSM LAAERGTKN
23472	53840	A	23607	2	591	ARAEFGTSRVGAMAVANSSPV NPVFFDVSIQGEVGRMKIEL FADVVPKTAENFRQFCTGEFRK DGVPIGYKGSTF\HRVIKGF\MI QGGDFVNGDGTGSRPVFTRGP ILQMKIFKL\RHSA\GLLSMAN SGPSTNGCQFFITCSKCDW/V WDGKHVVFGK\IIDGLLVMRKI ENVPTGPNNKPKLPVVISQCG
23473	53841	A	23608	6	424	

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23474	53842	A	23609	3	470	DAWVSGRLTELPSCFFPPPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKKDGKKRKRRESYS VYVYKVLKQVHPDGTGSSKAM GIMNSFVNDIFEIRIAGEASRLA HYNKRSTITSREIQTAVRLLPG VELCKHAVSEGNTAVTKYTS
23475	53843	A	23610	93	421	
23476	53844	A	23611	2	1173	DHAAPRRRSRASVATVTRAGR CPTMSVRVARVAVVRGLGASY RRGASSFPVPPGAQGVALLR DATGAEEEEAPWAATERRMPGQ CSVLLFPQGGSQVVGMRGGLL NYPRVRELYAAARRVLGYDLL ELSLHGPQETLDRTSQVQSPGT GIPRRVRAHVLHLSPOVIENC/V VS/AGLAFSPSFCALIFPNALL/F WPGLYAVKIRAEAMQEASEAV PSGMLSVLGQPQSKFNFACEA REHCKSLGPNVNGQICKGGFLGH CSAETSFLPQALRFLQKNSSKF HFRRTMLPVSGAFHTRLMEP AVEPLTQALKAVDIKKPLVSVY SNVHAHRYRHPGHIHKLLAQQ LVSPVKWEQTMHAIYERKKGR GFPQTFEVBGPRQLGAILKSCN
23477	53845	A	23612	187	425	
23478	53846	A	23613	1	1258	MKAYLLGGAAPLPWFPGQAV FRPCPPAGLWRTAQLVELEHG PVPREDLIPCSRPFISFLGPERV DGLAFPRIQALGIAAARGMEPK GAPGKSDSGNSRSAGGRVLGC QGAALVEVCSAGRGPPVRLAV GCVLLRAPERGWRRGEGAARG IPAGRSSSELGALSPOVGVRS DINGINWHPGVQTDFFSLKRSQ GLYAVKIRAEAMQEASEAVPS GMLSVLGQPQSKFNFACEARE HCKSLGIENPVCEVSNYLFPPDC RVISGHQEALRFLQKNSSKFHF RRRTMLPVSGAFHTRLMEPAV EPLTQALKAVDIKKPLVSVYSN VHAHRIQIPGHIHKLLAQQLV SPVKWEQTMHAIYERKKGRGF PQTFEVBGPRQLGAILKSCNMQ AWKSYSAVDVLQTLHEVDLDP

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23479	53847	A	23614	2	1050	GRCPTMSVRVARVAWVRGLG ASYRRGASSFPVPPGAQGVAE LLRDATGAE EEPWAATERRM PGQCQVLLFPQGSGVVMGMR GLLNYPRVRELYAAARRVLGY DLLELSLIHGQETLDRTVHCQP AIFVASLAAVEKLHLHQPSVIE NCVAAAGFSVGEFAALVFAGA MEFAEGLRFLQKNSSKFHFR TRMLPVSAGAFHTRLMEPAVEP LEKLLKAVDIKKPLVSYSQR PTRIRLQAFPGNIQSCLAQQQLG LPK*KWEQTMHAIYERKKG/R RGFPQTFEVGPGRQLGAILKS CNMQAWKSYSVAVDVLQTL VLDLPQEPKMTGRGLKNDP LCPPEERL
23480	53848	A	23615	600	905	QAPASGSPWLSGGPQQVEDAG AGYGFAFGQPPPPRTQPRSAC SRRAAG/TPVPRAPPASAG/PK ARAPRSLGCGSLGRFSTGV KCIFFPETENAAAGCF
23481	53849	A	23616	390	722	QAPASGSPWLSGGPQQVEDAG AGYGFAFGQPPPPRTQPRSAC SRRAAG/TPVPRAPPASAG/PR AAAPRSLGCGSLGRFSTGV KCIFFPETEMSYLLFRNTVSR C
23482	53850	A	23617	1	673	MGQVKGHKLCDFTLLSPDGG AAEGRCLELWGQAKEVEETIE GMLLRLEEFCSLADLIRSDTSQI LEENIPVLKAKLTKIMRGYAK VDRIKAFVKMVGHHVAFLEAN VLQAERDHGAFPQALRRWLGS AGLPSFRNDPTAPLRQVFEASP DPRLARTVTIQTQPPVRVSGPL SGQRKEKSLQKGAQVFQTNVP ETLLEGAISPAPACGGPLTSGD GFRHVRK
23483	53851	A	23618	1	651	
23484	53852	A	23619	195	497	DQFLENTKKCDGLNQLSFDPA NNNKPLEFGRARGPLVTEGLIE NGGESSKKRRRTNSSADNSRT LNVDSMTLPMSPATAWATA MNNFGMAPVRJVGH

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23485	53853	A	23620	241	1823	NDDRKFVTEHTMQDRFRW LWVYEIGYAADNSRTLNVDS AMTLPMSDPTAWATAMNNLG MAPLGIAGQPILPDFDPALGMM TGIPPTPMMPLGLIVPPPIPDM PVVKEIHHCKSCTLFPNPNLPP ATREPPGCKTVFVGGPLPENG EQIIEVFEGCGEIIARKSKKNF CHIRFAEYMYDKALYLSGNR ELKKFLNKEDNYFRKINLTALY KTVLEERCEKRRGGYRIRLGSS TDKKTGRLHVDFAQARDDL EWECKQRMRLAREERHRRRMEE ERLRPPSPPPVHSDHECSIVA EKLKDDSKFSEAVQTLTWER GEVNRRSANNFYSMIQSANS VRLVNEKAAHEKDMEEAKEK FKQALSGILIQFEQIVAVYHSAS KQKAWDHFTKAQRKNISVWC KQAEIRNIHNDLGMIRREEE MEMSDDEIEEMTETKETESEL KKLEGIVDGSVEVSAEALRKL NEYERQVKEEQKVGYRIWGTI HNKGEGKKEFAEELEKSSSER
23486	53854	A	23621	996	1512	RPVHLASPAKEQGGTRKGRRA PARLPVPTTGRGLEKGPESQAP PSFRQATGRFSRSGSGGPTPSK NSRDCSHTPQLPTPRGNPVVFP PGHPEPSRPVEMPAPGEPRTQ LCRERTRKACPPKPRPPLGLPG DPTGPVTHHAPPVSPTGASGQE RRAEPGAVSYAHASATK
23487	53855	A	23622	293	1140	PRGILHQDKNLVVINKPYGLPV HGWPGWQLCITDVLPIAKML HGHAEPHLHLCHRLDKETTV MVLAWDKDMAHQVQELFRTR QVVKKYWAITVHVMPMSAGVV DIPIVEKEAQGGQHHKMTLSP SYRMDGKMKVVRSSRNAQV AVTQYQVLSSTLSSALVELQPI GIKHQLRVHLSFGLDCPILGDH KYSWNR LAPQKLSVGTLLKLL GLEQSKARYIPLHLHARQLIPA LGSGKEELNLVCKLPRFFVHSL HRLRLMPNEDQNNENAEKCL

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23488	53856	A	23623	1	1328	MAVDLGSHTPGSSGVTAATFR GRLVNTREESVVLGAGGEVL SGVPGTWDALGPGASFGIKGM FPKGTVMSTSPMCEGPVPRRK PCASSVQQNSRSRKKAGRKTP TLAGRHVPVKIKKEAIQKPLP ASSFSPALTRSGAIFGPCALTS APVLEYPLQKVVENAEFKVFN NRDEESKRQKQAEFRMLTSAIR GPAGPRGHSSTRKPPSNPPPPGA CFKCGNEGHRSRQCPNPGTTSQ EALIALTRALTLAAGQQINIYS NSHYVFHIVHSHSSIWKERGILT AKNTPAINGSLINKLLKAARLP QKVAIHICRGHQTPDNPILAGN VLADQVAKQVALQPVGQQLS LSLFSPLYSSEEKEDFRAQNLQ KQGPW/LQSQGARLLVPAACAS KVAEAGRKPAGRHVPLKIQKE AIWSSPFSVPMATRAAASTSPT
23489	53857	A	23624	475	622	IHSKVLFSASSSSC*NTNNSWFR ASIKKNPEKQKNMNMQSAIPQHG LWKI
23490	53858	A	23625	17	992	GRGEVLRRGRGQLDAVLSRE HCGGSRQSEQPWSRRSSSSSR RRLRSAEPAMALSMPLNGLK EEDKEPLIELFVKAGSDGESIGN CPFSQGLFMILWLKGVVFSVT TVALKRKPADCQNLVPGTPPP/ LILFSSEVKTDVKNKIEEFSEEV/ CPPKYLKLSPK/HPRSNTAGMDI FAIKFSAYIKNSRPEANEALER GLLKTQLKLDY/LNS/PLP/DEI DENSMEIDIKFSTRKFLDGNEMT LADCNLLPKLHIVKVVAKKYR NFDIPKEMTGWIWRYLTNAYSRSR EFTNTCPSDKEVEIAYSVDVAKR LHQVKSRLLEKVSFMSPP

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23491	53859	A	23626	1	1128	MALASGEGLPVALSHGRRNGG QERVYPYLKLRDTCAYRVAWRC NRLARAKVKRTSYRSGYNGGF EPGVEPDCVLLALGVENDLV RISSKAKEYSLYEFSFPLRVSRE CEECECRKEPWFNPQKPSVLIT SGQILGQEEQKTLFPGLILSLVF QFNVENSDLRCLSLAENLEISAL LSLSCSSVIRLILINLEVTISPPITI LKHAPPLTSLAASSSSSGIEKKIH NNFRQGPFPSSATRSTFLMNH TFDYSVVVSNIVPRLNLYPQVL DVLQSLHKIHLASNAKWITQGG PAKPDILGLEILHRYPDWEKE ERKKKKRKRVSPEKSITTHNKP TSSGIFY/RPRRCGCDLGRPPAP GPHPSPPHSPQPSRCPPV
23492	53860	A	23627	3	453	SLGKDIRPRSARAACKGVGLWS GCFGKMAGSGVRQVTSASTF VKPIFSRDMNEAKRRVRELYRA WYREVPNTGER*RLVRPAVLK HSYVANRSF
23493	53861	A	23628	3	695	PYASRRKFRVDPRVRAWSGCF DKMAGSGVRQATS/TASTFVKA HFSVGMDMNEAKREGARVLTAP WYRLEVNTVVRVHQQLDITV KMGRDKVREMFMKNAHVITDP RVVDLILVIKGLIELEETIKVL KQRTHVMRFFHETEAPRPKDF LSKFYYVGHDPKLSFSGKDAR WILFLGAQIKLTIQWSLCDRIPL MNQFSAASFCLSKWGPWVLIHI TCSFPFSWKCVCCCKLD
23494	53862	A	23629	82	441	SLPINVPVPTACTLQAGLLRPPG SDVRTPMLPPSAPSQPSYPTSRP PLWPTWPA GPVFRSQPLAQPN LPRSYHQQAPGGQTPVALGLE\ CPKATNQPFGLQRDPKSPAKV PPFEESL
23495	53863	A	23630	3	504	DRSSSSTMTSGDGFNPLRKFK LVFLGEQSVGKTSLITRFMYDS FDNTYQATIGIDFLSKTMYLED R/TNVNSFQQTTKWIDDVTER GSDVIIMLVGNKTDLADKRQVS IEEGERKAKELNVMFIETS/AKA GYNVKQLFRVAAALPGIMPS VLFQIHPQALTRYLC

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23496	53864	A	23631	416	1239	GGGRSSSTMTSGDGFNPLRK FKLVFLGEQSSIGKTSLITRFMY DSFDNTYQATIGIDFLSKTMYL EDRTIRLQLWDTAGQERFSLIP SYNRDSAAAVVVYDITNVNSFQ ANYKSGIDDVRTERGSDVVIIM LVGNKTDLADKRQVSIIEGERK AKVELNVILMETSAGVYNVK QLLSTCKQPALPGMESTQDRSR EDMIDIKLEKPPQE/QPVSEGGFLF LTNLPCHLQPPFFKLTFGWPPPY SFIDCSVNIGLMPFFPSNNVLRFI IAACPAWR
23497	53865	A	23632	1	493	PKPATAPPPSL/RARFLCPQRRP ERAR/PRARGASPRPEKTAGAR KRRRGSCERPHPGG/RPPAPG*I SSRPTLGFFWILNFFLLKKLGRI KDVPWQDSTKEHLSVCRGLRG TWSVPSADPLHPAARRTCFRV PPTTGAREWWHLPPPALQRP DSRQCHRI PVC
23498	53866	A	23633	1	560	MESIWAGLWTAQDITVLADDF EFILWTLKRRPERAR/PRARGAS PRPEKTAGARKRRRGSCERPH GGLRRLPGARDQAPRSDAG RSPGRRLRRLPALLCAGPLSPGRE PRRWEPRAGVARPAGQQWGFF WPGNQQGASICSLLWFLLECG SRSTGGPCSGTELGHFSRERPTV LLSRLGTVKRP
23499	53867	A	23634	32	327	LTQRLFGLFTRTHMKFGALTR IG/DLPWE/INPLSSICSLPEKDP PMTSGPQTDQPKHLTNFKSAA RRSSRTSSHRNLLHVLEIWQLD QGMPAARD
23500	53868	A	23635	2	424	LTPFSDSAHLHPGEINSPVAHTK PVGGLFTRMRVTFGAKTQDRS TPIQETSPSSPS/PVTS GPQTNQ PKEHLTNFKLKGKQSFHSSHASL ATLQSSSLATLQSPCPSNSNSFS SLVETRRRPGAVARLQSQLSGR LRGRIA
23501	53869	A	23636	31	246	TAILLTQSLFGGLFTRTHMKFG AVTRIGDLPGWGINPLSSCSLR EKDPLTISGPQTHQPKHLTNF KSGPH

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23502	53870	A	23637	125	464	TAVFLTQSLFGGLFTRTRMKFG TMTRI/RGDLDPWEINPLSSCSLL HEKDPPTTSGPQTNPQKKHLTN FKSRKVERTKGLKTHLTKLSH QLKKAWTILLPLSLRIQACPR NAT
23503	53871	A	23638	1064	1304	TAMLLTQSLFGGLFTQMCMKF GAVTRIG/DLPWEINPLSSCSLL HEKDPPTTSGPQTDPRKEHLNF KSGACYTCRKSGH
23504	53872	A	23639	539	747	TAMLLTQSLFGGLLTRTRMKF GALTRIG/DLPWEINPLSSCSLL HEKDPHTPSRKIHIRPQGNHESQ KGL
23505	53873	A	23640	709	950	TALLLTQSLFGGLFTRTHMKFG AVTQIGDLPWENQSPVLLCSLL REKDPPTTSGPQTDQPKHLTN FKSGKWSFHSSPAF
23506	53874	A	23641	1	1257	MGKKVLGIASQLLGAVRCEPD GRRVLPEDWPECLSLVTHGTW FTRQGDKNIQMADNSFSDGVPS DFVEAAKNASKTEKLTQDQVMQ NPGVLAALQERLDNAPHTPSSY IETLPKAVKRRJNALKQIQVRC AHIEAKFYEEVHDLERKYAAL YQPLFDERREFITGDVEPTSDM ESEWHRENEEEKLAGDRKNK VVITEKAAATAEEPKNKGIPEF WFTIFRNVDMSELVQYDEPI LKYLQDIKFHFQPNDCFANSVL TKTCKMKSEPDKADPFSAFAGPE IMDCDGTIDWKKGKNVTVKI IKKKQKRKGPQTVRTITKQVSN ESFFNFFNPLKASGDGESLDKD SEF/ASDFEIGHFRER/PQAVLY FAGEALKDDDNFDEGEDEEDEL EGDEGEDEDEVEINPNKEPSQ
23507	53875	A	23642	132	1277	
23508	53876	A	23643	1	515	RVRHRSVSVGSTHASAHAYGE GSLRIIPVTRSPVLTMNHIVQTF SPVNSGQP/PNYEMLKEEQEVA MLGAPHNPAPPTSTVVIH/IRSET SV/DPHVV/WSLFNTLFMNTCC LGFIAFAYS/VKSRDRKMVGVD TGAQAYASTAKCLNIWALILGI FMTVLLHIIPVLVYQAQR

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23509	53877	A	23644	243	643	NHTVQTVFFSPVNSGQPQRM CIKEEHEVAVAGGPHNPAPPTS TVIHIRSETSVADHVVWSRVQ TPSSMNPCLGFLAIRLTP*SLR DRKMVGVDVTGAQA\YASTAK CLNIWAHDSGASVMTILLIVIPS
23510	53878	A	23645	3	1498	RCNFLRSSRIRVHPTPAASTMP KFDPNEIKVVYLRCCTGGEVGA TSALAPKIGPLGLSPKKVGGDIA KAMGDWKGRLRITVKLTIQNRQ AQIEVVPSASAMIKALKEPPRD RKKQKNIKHSGNITFDENGNIC STDMR/HRSLSRELSGTTKEILG TAQSVGCNVGDRHPHDIDIN SENDKQPRKSKMRTSFSPQIPG HEHFHYLLLLQHVCQLALTL RARKEGSSTHHQLSTYYFKEG NSKEPKIQRNTELKKEEGG GGSGKAPGSEIKLESPACSGASL GEMTAWTMGARGLDKRGSEFF KGPLPNTCGHFWEVMEQKSR GVVMLNRVMEKGSVEFVTEL FFYVALPKMFPVHYIVILLASKL EEVTFNFPPLDCTPFLQNYLR VAFQEVNSGCTGKTLVVPYIT TEDVCQICVEKFKVGDPEEYSL FLFVDETWQQLAEDTYPQKIK ELHSRPQPHIFHVYKRIKNDPY GIIFQNGEEDLTTS
23511	53879	A	23646	361	918	GCTGSRGTVPLSALGPQRJGPP GSCLQKSWVNDICRQPG/DW KGP*GFTVKLTHSRGTQAPDCT RVP/VLSPCP*FIQSPREPPKRPE KKPEKTFKHQLGIFTFLNEICST LLRQMRVHRSLSPEKLSWNPT* RDSWGIAQFSGAVNVDG/RH/P HD/IDDIQQWVWLWKCPRQLST KENIFNKGII
23512	53880	A	23647	1	642	

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23513	53881	A	23648	894	2438	VETKRIQPQPPDEGDHSDKED EQPQVVVLKKGDLSVEEVMI KAEIKAAKADEEPTPADGRIIY\ RKPV\KHPSDEKYSGLTASSKK KKPNEDEVYQDSVKKNSQKLII NSSLLSFDNEDENDTEKSMENL TGKIRKLQLRIVDPTFLPKLSNK GKDPVAVARLETGKGNKGAFR VLRDISRWATLCTSPQHSSEA KNIIPIYQATQFQNEVHKWYKK KGGKIKSKRKALFFLTQDIQKK LQKLALGPNTPTPDILKIASLVF YNQDQEEKERAAQNERQKEKL YWL.SYKSASPFQVALRILSQET THKDELPTDLPNNPEVQAPGIP GNTIMAMPVAIQLKDPSSYPGR IIVPEIASWIHRTQVKLWKSPE TSELEPTPSVIEYTREALEDLKF LFKQKDNSSAKTPGRAYAASPR DWTSEIAELHIFYQWDPNLKG MFKPASLLAKVKQDFPDHKE PIFAIFSNITLMGIAPICVTGKTI KKRTRQHHTTPKSNLREQASQ GSLNWEKN
23514	53882	A	23649	200	1727	RTATSLDSVLKSDYMTWKYR VSFFYILSCRLLKK/QCTDNEHV YMEISKLYKYPCKEWWKEAS KVRQYEVTVVWSKRGDYILK HIPNMHKDQFALTASEAHLKYI KEAVRLDDVAVHYRYLYKDK REIEASLTGLTMRGIQIFQNL EEKQLLYDFPWTNVGKLVFVG KKFEILPDGLPSARKLIYTYGCP MRSRHLQLLSNSHRLYMNQ PVLRRHIRKLEENEKKQYRESYI SDNL.DLMDQLEKRSRASSSS AGSMKHKRLSRHSTASHSSHT SGIEADTKPRDTGPEDSYSSAI HRKLKTCSSMTSHGSSHTSGVE SGGKDRLEEDLQDDEIEMLV DPRDLEQMNEESLEVSPDMCIY ITEDMLMSRKLNGHSGLIVKEI GSSTSSSSETVVKLRGQSTDSL QTICRKPCTSTRHSLDDIRL YQKDFLRIAGLCQDTAQSSTFG CGHELDEEGLYCNSCLAQQCIN IQDAFPVKRTSKYFSLDLTHDE
23515	53883	A	23650	182	423	RLSIMASSLNEDPEGSRTYVKG DLFACPKTDSLALHCISEDCRM GAGIAVLFKKKFGVQELLNQ HYKEKGLRTSGLYG

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23516	53884	A	23651	1	249	
23517	53885	A	23652	435	494	
23518	53886	A	23653	163	578	RVTWLK KHLNSGNSDSVCMAS SLNEDPEGSRTYVYKGS LFEGP KTDFLAPCISED CRMAGITVL FKKKFGGVQELLNQKKSGE VAVLKRWRWGLYIFTWTKRK RAFAQSPLYENLT EFRGQLKS HLSEEWSH
23519	53887	A	23654	1	2238	
23520	53888	A	23655	26	1941	RDAGTKWQRLGHLSCICRQQA AREIIMHFQAFWLCLGLL FISI NAEFMDDDDVETEDFEENSEEID VNESELSS EIIYKTPQIGEVYFA ETFD SGRLAGWVLSKAK/KVD MDEEISYDGRWEIEELKENQV PGDRGLVLKSRAKHH AISAVLA KPFIFADKPLIVQYEVNFDQDID CGGAYIKLLADTDLILENFYD KTSYIMFGPDKCGEDYKLHFIF RHKHPKTGVFEKHA KPPD VD LKKFFTD RKT HLYTLVMNPDD TFEVLVDQTVNKGSLLEDVV PPIKPPKEIEDPNDKKPEEWDER AKIPDPSAVKPEDWDESEPAQI EDSSVVKPAGWLDDEPKFIPDP NAEKPD DWNEDTDGEWEA/PQ ILNPACRIGCGEWKPPMIDNPK YKGVWIPPLVDNPNYQGIWSPR KIPNPDYFEDDH/PILLTSFSALG LELWSMTSDIYDFNFIICSEKEY ADHWAADGWRWKIMIANANK PGVLKQLMAAAEGHPWLWLIY LVTAGVPIALITSFCWPTKVKD RHS DLEYIIPDICIPQTKGVLEQE EKVEKAALEKPM DLEEEKKQ/N DGEMLKEEESEPEEKSEEEIEII EGQEESNQSNKSGSEDEMKEA DESTGSGDGP IKS LRKRRVRKD
23521	53889	A	23656	297	398	
23522	53890	A	23657	286	430	TAGARCSSRTSSPGSCFNQKS GHWARNARSPGFLSRVPSVN WIHI
23523	53891	A	23658	405	524	ARMSVACLPGFLFICLRGDFKQ NLTA YCWKC YQL* RSLGTHS
23524	53892	A	23659	1	657	
23525	53893	A	23660	22	334	ALKHFC LSLIFS VTTMKFLAV LVLLGVSI FLVSAQNPTTAAPA DTVSSLLVLLMMKPLDAETTA AATTATTAAPTTATTAASTTAR KDIPVLPKWVGDL PNR

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23526	53894	A	23661	1	270	
23527	53895	A	23662	1	284	
23528	53896	A	23663	111	281	
23529	53897	A	23664	229	363	
23530	53898	A	23665	250	586	PVRHGAFQDKSSDKKVQTKG KRGAKGKQAEVANQETKEDL PAENGETKTEESPASDEAGEKE CQCLINNHIPCLISGPCLPSCTIQ RNINIFYVFNASFLVALETFLKK
23531	53899	A	23666	3	478	APAVGLSSSGGRRSGSOKAARF REGCRRAAARMQQAAGTRLPR RHPARAFPAATMPKRKVSSAE GAAKEEPKRRSARLSTKLPAK V\EA KP KAAADKSSDKKV\Q TKGKRGAKGKQAEVANQETK EDLPAENGETERLEEESLLIEA GEKEKPKS
23532	53900	A	23667	1	252	
23533	53901	A	23668	328	414	
23534	53902	A	23669	1	3156	
23535	53903	A	23670	1887	2036	
23536	53904	A	23671	3	212	
23537	53905	A	23672	22	539	YEGIVMKPLIIVNPADICG\RT CE\ACVVAHPSEQELNADVFL PRLKVQPIWTVSAAR*CCPFSS ENAP\CVGA\CPVGA\TMGEQV VQTNSARCIGQSCVSA\CPFGM ITIQLPGDTRQIVKCDLCEQR EEGPACVESCPTQALQLTERK LRRVRQQRIVVSGENPL
23538	53906	A	23673	135	302	PIHMKTRQPRDQFSADCVFLQS TCPVPC*RNRL*TPGGYWRTRR DYLRCDRSVHV
23539	53907	A	23674	175	794	LSTHSQPIADAADPPPHLHTGEL LCSAHQADFVSAEPARPANN NAATTAPVHAVAITPPAYPDCF RTLPKLSHQDSTQRLYGIAL LLRISTSGPPSRLKVQRLDSISA PV/MCHQCENAPCVGACPVGA LTMGEQVQVQTNSARC/IGQSC VSACPFGMITI/QLPGDTRQOI VKCDLGCALRDCVAVLRQRN SRVVLDACTRA
23540	53908	A	23675	2	434	LISLPFPDLSLAHRPPSSAPTEPQ GLFTVAAPTGPASPATLAHL LPTPAMYSLLETENKPNVGTPT QAAGTGGPAAAG/GRKMALEN PKMHNSEISKRLGADWKLLTD AEKRPFIDEAKRLRAVHMKEYP DYKYRPRRKTTL
23541	53909	A	23676	3	264	

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23542	53910	A	23677	1	2377	MDDTFLNYKYKNKCGPKHIKK KEEEEEEDNNSNDSKNKDKTLT TGSSGSAKIFLMRGRRQLLLP TSLCLLSVQRSPGSHSGPPQS MNPRLSPQGYLKNDFLDVIG MCDIACHLVVELVGNNGNFL AHAFHVEVVAQQNQRENAA RPNGGSVMIGQGASLRTCQSRV LRVARGGSPNPGSEQGLFTV AAPAPGAPSPATLAHLPPAPA MYSLELETKNPVGTPTQAAAGT GGPAAPGGAGKSSANAAGGAN SGGSSGGASGGGGGTIDQDR VKRP/MNAFMVWSRGQRKKM APENPKMHNSEISKRLGADWK LLTDAEKRFIDEAKRLRAVHM KEYPDYKYRPRKTKTLKKD KYSLSGLLPPGAAAAAAAAA AAAAAASSPVGVQRLDTYTH VNGWANGAYSLVQEQLGYAQ PPSMSSPPPPALP/MHRYDMA GLQYSPMMPPGAQSYMNVAA AAAAASGYGGMAPSATAAAA AAYGQQPATAAAAAAAAAAM SLGPMGSVVKSEPSPPPIASH SQRACLGDLRDMISITGRENIFV VGDPAAACLLPIEMEETFLPWPL GFEDRLHLEGRPVQEIPIFLRK VPNCGQWLLQTPSVEPADPWE NPQAFPPSLQEQPCLSLIVGIF VEAFGGGRGWGSKGKKPKRYR TVEWMRIHQPSICCLQETHLTR
23543	53911	A	23678	1	399	

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23544	53912	A	23679	3	1216	LGNKRAGLRADGEAPSALPY CYFLOKDAEAPWLSKPAYDSA ECRHAAEAALRVAWCLEAASL SHRPGPRSGLSVSSLRPTRKMA TTFLAHEKIWFDFKFKYDDAERR FYEQMNGPVGASRQENGA/T VILRDIARARENIHKSLAGSSGP GASISGTSGDHGLVVRASLEV ENQSLRGVVQELQQAISKLEAR LNVLGKELRLAHRGTAPQTQH VSPMR/QVEPPAKKPATPAEDD EDDDIDL/VGRDNEEEDKEAA QLREER/LRHYAEKKAQESLP LGGQVPPSLLDVK/PWDDSDM AQLEACVRSIQ/LGTGRSWGAS QMVA VGYGIRKLQIQCVVEDD KVGTDLLEEITKFEEARARSV DIASFSTRSEALKCVYVAHVRE GPCTRSKDLRPAKKKKKK
23545	53913	A	23680	1	2066	MAAALRAPTOVSAASSRPLPS PPTEGRVKGFQPGPHCPAQ LCSGDDGSDNELEQKREVI PHEAPVAEHRQQTGLRELVAI PKRKEETTAIVQVFVAFEDVAI YFSQEEWELDEMQRLLYRDV MLENFVAVMASLGCWCGAVDE GTPSAESVSVEELSQRTPKAD TSTDKSHPCIECTPVLRLQMI ELHASPCGQKLYLGGASRDFW MSSNLHLQLQKLDNGEKLKFKVD GDQASFMMNCRFHVSGKPFTF GEVGRDFSATSGLLQHQTPTI ERPHSRIRHLRVPTGRKPLKYT ESRKSFRKSVFIHQQRADS RKYKCECGKSFSSGFLRHR KAHGRTRTHECECGKFSR THLTQHQRVHTGERPYDCSEC GKSFQVSVLIQHQRVHTGERP YECSECGKSFHSTNLYRHSRA HTSTRPYECSECGKSFHSTNLF RHWVRVHTGVRPYECSECGKAF SCNIYLIHHQRFHTGERPYVCSE CGKSFQKSVLIQHQRVHTGER PYECSECGKSVFSQSSGLFRHRR AHTKTKPYECSECEKSFCKTD LIRHQTVHTGERPYECVCGKS FIRKTHLIRHQTVHTNERPYEC DECGKSYSSQSSALLQHRRVHT GERPYECRECGKSFTRKNHLIQ HKTVHTGERPYECSECGKSFSSQ

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23546	53914	A	23681	1	468	MAAQVQGA VRV VRA VAAHEEP DKEGKEKPHAGVSPRGVKRQR RSSSGGSQEKGRPSQEPLAPP HRRRSQPPTSWAAA VNDM/PAP TVPGPVEPLLPPPPPSLAPAG PADDAPLAPSTSGLFTFSPSLTA SAAGPKHGTQGAQAQAPSPRP RW
23547	53915	A	23682	950	1326	RPESQRANGVDSGPNLKTVPQP DTRKGSVLK WSKRGKPLAVEI EESHCLCLPLRTECLGIKPIVH LFSCTRPVIVPSLELNYDVDSIA HMFVADLLMITLPSYDIPFYC LVFQNLVLVEFYLY
23548	53916	A	23683	271	918	NQGLRDLGLRCLVNMFTSS ILGKGHRHSLVSIKQEHSLARK AAGVPLPKVGYC/QGFSPCDSL KYGSWDEKDLTVPPDTHKGS VLRWISKRGKPLAVEIEEG/HCL PELPPGELECPG/ILKHGLYHWS SSEMGEINRPMVG/ARHVYSNA ALLFFTLALRIFQRRNINLGLRA HPGIVPPELNYDIDSSAH/FF LADLLIITLPSYIIFC
23549	53917	A	23684	1	942	
23550	53918	A	23685	346	1753	TWIPLSRTGRFPVFCSSSRVY AISFHKRWKEGRGCRTRGE MGWEGRSRSLKELNTRNDWNP GERELDFWKITRFKEAASWTL EALIEAGSTARRRVWLEDGR TCEILSVLCTSSLSNCASLDCV TYKALSTTRLYDSVYWNKKPE RSSSPATEQSWTENDFDKLREE GFRRI/NYSELKEEARTHGKEVI NLEKK\DLRLTRJTNAEKSLKD LMELKTMAREL RDECTSFSSQF DPLEERVSVMEDQMNMKIQE EKFREKRIKRN/EKQSLQEIWDY VKRPNLHLIGVPESDRENGTKL ENTLQEIQENFPNLARQANIQI QEIQRTPQYSSRGATPRHIVR FTK VEMKEKMLRAAREKGRVT HKGKPIRLTADLLAETLQARRE WGPIFNILKEKNFPRIAPAKL SFISEGEIQYFADKQMLRDFVTT RPALKELKALNMERNNWWYQ PLQKHAKW
23551	53919	A	23686	73	327	GALQPTAALWEPLSGLAKAAA RSLSLQGGVEGDARAGTGAAR GACGPGAGVPGGRGLGGPALGA AGRPGP*LPSRGAGLGTAAARHA

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23552	53920	A	23687	322	402	DQEPNTSGHIGNLEQCLGHGYQR*LFP
23553	53921	B	23688	545	3063	
23554	53922	A	23689	1	579	MKHEKRDRCAELTAILLNEQAS PMCTIVLGYTGTSTITLPTTSCH FAPRLSNSQQHSSYQVGHKPE YCVRNWWVLGLTDFKNEAAD PHNSGGQLASPSGSRGTGAAGV VPASPAPCARTPQPLGGRWDW AP*GTGGGIRRGSGCTGTHGG GGRLRHGGLQSGGLPRGKA ARREIESSAGYSNSSKCSII
23555	53923	A	23690	399	592	KCIHFGPTPKFVCGVIVVTAVP /TFGM*TVYV**LPFSILAQNVG *RDDCDPGWKLNLFYAKKKK
23556	53924	A	23691	3	268	DRV/RPLRKNFQRNDQTAFTV HENPLLCYRCWYPGKQEQQK IKPQRGGKNRAEKLETLSRAP LLFQRNAVPHQQRNKAGWRM TLTS
23557	53925	A	23692	29	484	CSFFLVSMVFTFWHDFAAAGTS CSFFCLVLSFRSSFRAGLVVTKS LSICLSVKYFISSSLMKLSLAGY EIVG*KFFSLRMLNIGPHSLLAC RVSAERSAVSLMGFSLRVTRPF SLAALNIFSFISTLVNLTIMCLG VALLEKYLGCILCVS

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23558	53926	A	23693	182	2076	MQEWLRLTARKTELSRDSRSC GQLKTSLLISLLVESTQGRH*SF L/VWTQTHSGGDGWRVAKAW RPKYHDTQLGGEKEEPQGHHA SDCRWRAQPHCRTLSAAVVNV AGFTVTVELRCLTLMKMREKD HHLCDNDIVLFPPDTAFPLDCL LSCHISTVHGLLRWNAIYQLAS RSESHPERSEGGTPDRNGHPAL SLASFNGAQDRTTVQSLGEKP GLPEEMA AFMAGTEKEQNELG IEFFQLIIPASKRTHSENALFSHS GDDTECSRSGQSPPSYSRGPP RRTFILATQPLCSKEAQTSPHEQ PTRTEKNRGSHLYHKSPCDHAS PGMSVTMSGMQALPRQLTTL TFYPPAFRSIKIFRIMILKTEMLH THARSQEALLKDSSKTMHLSTL PSCVRKSNYHHRERKIKTKEAF PAKIHRSRNQGMKVEVAPLTIT SSDPLAEFLLPVTVTLCASLEV LAPEGGMLSPGDATMIPLNWK LTLPPGHSGLLPLSQQVKKRV PVLVGVIDLDYQDEIDYSSMK ERSSSPATEQSWMENDFDELRE EGFRRSNYSELREEIQTKGKEV ENFEKNLEECITRITNTEKCLKE LMELKTKVRELREECRLRSRC DQLEERVSA MEDEMNEMK
23559	53927	A	23694	933	1118	RVERRRLQTIKLRATGGNSNQ RQRS*KL*KKFRMYN*NNQY REV LKGADGAESQGSRTT
23560	53928	A	23695	2	250	WCHTKLDGLSLFGESVALEEA GGQTALWLMRFLSRKANYVD KITTREVGHR*LMSSRLHSR* WAASSVCSSCVLLPSSHS
23561	53929	A	23696	1017	1230	
23562	53930	B	23697	62	1069	
23563	53931	A	23698	216	582	ILVPTLFWLGEFLLRDPLL*W ASI*G*PD/AFSLAALNIFSFISTL/ RESNDYVSWSCSRGVSL*RSLL YFLNLNVGLPCQIGEVLLDNIL QSVFQLGSILPVTFGYTNQMQL WFFHFIHFIHH
23564	53932	A	23699	434	681	TLACLARLKGFSWIIISCRVFSNL VPFSLSLSGTPIRRRFLGT*SHI SWRLCSFLFILFSLNFPSPRISFV SSSITD TLSSS

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23565	53933	A	23700	290	1231	RSFRAIGEVSIGSRGWGGGYAAQ LQSPSRLPVLGGGKGGSRGV GQGSSRAEVLGSQRERSGTCC AEAAAAAAQLIAGTGSSLPYQG PGQNQTAIAPTCAPLSPCKAAA VIMGNIFGNLLKSLIGKKEMRL MVGLEDAAGKTTILYKLKLGIV TTIPTIGFNVETVEYKNISFTVW GCGVARDKMRPLA/WRHVFQNT QGFDILWSDSNDR/ERVNEA/R EELAMKNAGAETSLRDAVLPFL/ FGNKTDLRNAMNAAGUQDKL GLHSLRHRNWYIQTATCATRG NGLYEGHLWLANSPVKQEVES RTALTAKHPNRP
23566	53934	C	23701	164	208	
23567	53935	C	23702	1	381	
23568	53936	C	23703	43	276	
23569	53937	C	23704	1	462	
23570	53938	C	23705	38	121	
23571	53939	A	23706	77	202	QKNYTQRPLPLHGLELEVTCR CWSWQPLLEPLELR/RLSD
23572	53940	A	23707	123	209	
23573	53941	C	23708	1	411	
23574	53942	A	23709	1400	1809	SSNPLSRPPLPTPTVPCPLRLSL LRACCCCLFLPLRFFSCPLLCLF/ LCFFFSVCSPAHNFKMPKPQW SGIPTGPPPSGSCFKCQKSGHW A/RNACSPGFLLSHVPSVWDPT GNQTVQLAWQPLLEPLEL*P/R LSD
23575	53943	B	23710	76	358	
23576	53944	B	23711	1	606	
23577	53945	C	23712	272	388	
23578	53946	A	23713	1	259	PGVRGAQGGPSIPRQCEESAIGP KFAWISSFHWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGFIWQPLPEPLEL*P/RLSD
23579	53947	A	23714	684	917	GDFGLRQWGLNIQSCHLQTGT P/LPLFLIEYPLFLSPA*L/PWPELP TLCCIGVVREGISVLCQFSKGM LPVFAHSV
23580	53948	A	23715	618	683	
23581	53949	A	23716	306	710	DRVSLTLPRLGVPQWPDPSLQ RPPGFKRFYCLSLPSS*DYRHEP LLPAYFFPYRIIGWSRL
23582	53950	A	23717	2	88	

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23583	53951	A	23718	972	1967	FPPGRGRGPRPAGCSRGRARA CPKPVVDHVVRPNAFMVWSR AQRKMAQENP/QMHNSEISKR LGAEWKLLTESEKRPFIDEAKR LRAMHMKHEPDYKYRPRKPK TLLKKDKFAFPVYGLGGVAD AEHPALKAGAGLHAGAGGLV PESLLANPEKAAAAAAAAAAR VFFPQSAAAAAAAAAAAGS PYSLLDLGSKMAEISSSSGLPV LNMPMHINSLGKNLALNLFV YNDANSMLDLCYDGVGKGPI CFCATQGYEDIFKAGYGSVVD YYNDGSDLTTPLEIATVPTFSN HPLMSQRPSTWRQNPPLAKRLP LTEDSDGDDH
23584	53952	A	23719	2	144	RPQRRP/LPPTGSPLKHPGGAS GAAGAPIGEPQHPGAVVSRA WSLCS
23585	53953	A	23720	219	897	PGRAGGTLGLGSRRDGTREKG VEETPHRLHARTDTPAGCCGS PIGAPAAPEAPPCCFEG/PRWVE GVKKASPLPAELIGWLWNFPL ARPVRPPLSPGPPRRPPEGVCG SWPGRSEGERGKAKNTAESTPR QNLHRKYTIIVTHYQRNRKGQ NISFSLVCEFHPSLADWTTVTA LTWTSKDNLSLTTESWLREGN VHRGMDEYVRAQSFLIMTLE NSGGSVVSK

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23586	53954	A	23721	937	2730	TNPHCHDHYYHHHHHCHHCH HHHHHCHHHHHHHHHHCRDH HYHHHHHCHHCHHHHHHCHH HHYHHHHHHCHDHHHYHHHH HCHDHHHYHHHHHCHDHHYH HHHHHCHDHHYHHHHCHDH YHHHHHCHDHHHYHHHHHCHD HHYHHHHHCHDHHHYHHHHH HHHHYHHHHHCHHCHHHH/P HHHHHHHCHHHHHYHHHHH HHHHYHHHHHCHHHYHHHC HHHHYHHHHHCHHCHHHYH HHHHCHDHHYHHHCHHCHH HYHHHHHHYDHHHYHHHHHCH HCHHHHHHHVHHHHHHLCHH HYHHHHHHHHHHYHHHHHH HLHCHHHHHHHHHHHHHY HHHCHHCHYHHHHHHHHYHCH HHYHHHHHHYHHYHHQH YHPRHHYHHHHYHCHHHHDYH HPRHCHHHHHYHHQHYYPIII TTTTTTTTTTITVTTTTTTTNT TAPTTPVTAITTTTTTTTTTT TPITTTTTNITTTTVTVTITTF TTTTHPYHHHHHHHPVTITTT TATITTTTTSITTTTIVTTII TTTAATHHHYHPYHHYHHHH HHHHHTHSYHHHHHHHHHCF HYHHHHYHHH
23587	53955	A	23722	2348	2571	
23588	53956	A	23723	4919	5142	
23589	53957	A	23724	2	370	
23590	53958	A	23725	588	701	
23591	53959	A	23726	295	521	
23592	53960	A	23727	2837	3061	
23593	53961	A	23728	272	436	
23594	53962	A	23729	239	514	
23595	53963	A	23730	105	367	TGRPPELLHLRSLSPPLL/CSSP/ TPPPQLPPPVSLASGYLLHPL ARYPACLPPIRRARTEQRGGEQ PGVGASPLPIGRWPGTEAT
23596	53964	A	23731	999	1145	
23597	53965	A	23732	1084	1893	

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23598	53966	A	23733	1605	2296	HSIHSSVDHPENRIYRRKIEELS KRFTAIRKTKGDGNCFYRALAAI PYLESLLGKSREIFKFKERVLTQ PNDLLAAGFEEHKFRNFFNALR AGRAQFYSVVELVEKDGSVSSL LKVFNDPGASDHIVQFLR/LCF TSAFIRNRADFFRHFIDEEMDIK DFCTHEVEPMATECDHIQMTA LLQALSIALQVEYVDGWIPALT QHVFLAATPSVYMLYKTSQY NILYAADKH
23599	53967	A	23734	529	1830	AGYGDRTMLARKSIIEEYVLA RIAENLRKPRIRDRLPKARFIA KSGACNALAHKNIREQGRFLQDI FTTLVDLKWRTLVIFTMSFLC SWLLFAMWWLVAFAHGDIYA YMEKSGMEKSGLESTVCTNV RSFTSAFLFSIEVQVTIGFGGRM MTEECPLAITVLILQINVLITNA VMLGICFMKTAQAHRRAETLIF SRHAVIAVRNGKLCFMRVGD LRKSMIISASVRQIVVKKTTTPE GEVVPQHLDIPVDNPESNNIFL VAPLIICHVIDKRSPLYDISATDL ANQDLEIVILEGVVETTGITTO ARTSYIAEEIQWGHFVSIVTEE EGVYSVDYSKFGNTVKVAAPR CSARELDEKPLPSLFRPSQKSEL SHQNSLRKRNSHRRNNFHRRN NSIRRRNSSLMPVKVQFMTPTE GNQNTSES
23600	53968	A	23735	968	1243	
23601	53969	A	23736	541	1010	SVTSLCKVTSVCLTSAASCRH RRSVEEYLVSKLPM/WSRRRK AAALTESV/CIVFWLASWMMMS RWLHYPDWVTTHAQVLMNVV SVMQADCRMNLLIEFLRWLMR KIFHNILRHFSQLLNVPITRPF WILRPF
23602	53970	A	23737	766	1910	LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFSICFVI CSRTLILKGSSLMYVFCLPNTAI GGSSRVDRCAATSRGSSRVDL TL*KYSLVGPSVPLVSSV**SDW PLKLLMTMMS

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23603	53971	A	23738	581	1434	KLPMGVAVVKLLHLHPKVIIVFW LASWMMSRWLHYPDVWVTHAQ QVLMNVVSMQADCRMNLLEI FLRWLMRRASDICSHGD*EPL L/YAVFGKQNTYIRLEPFKINV EQITKHIEKLQCGGVVKQLSRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQV WIDRKAGECLLHEYEDLVPIRD TLRLFPGGRYLPRAKHVAPSEP DPEQDEQLRFCKRHLYGKQP RSPVERVWDHGPTRIVGLIISLG PRSHSYRRSDNQTTGTVPLVSS
23604	53972	A	23739	515	774	LFPRLLSCLTTPPHCSFICFVIC SRTLILKGSSLMYVFCLPNTAIS GTTVPLVSSV*LLVWDHGPTRI VGLIIRLGPRSHSYRRS
23605	53973	A	23740	322	763	CRMC*LFPRLLSCLTTPPHCSFSI CFVICSRRTLILKGSSLMYVFCLP NTAIVMALSPRGWRSKFGMPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPCVGRDVKSTLE VLRGDSVEKTSRVVWSGNERDQ ELLTEDALDDL
23606	53974	A	23741	1	127	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEK*RRL SPLHSLMMTARKRGK*PGAGE
23607	53975	A	23742	9	437	WLGLGNWKERLGTQTRMIWS QKTARRLCRTFGIPAYSMCI/CI GMAERMWCDNRNRERTVSSSG GNRLPNPDWAPGPPRIVGLNIS LGPTVPTRIVGLIISLGPRSHSYR RSDNQTTGTTVPTRIVGLILVLGP WSHSYRRSDY
23608	53976	A	23743	766	767	LUTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFICFVI CSRTLILKGSSLMYVFCLPNTAI GGSSRVDRCAATSRGSSRVDL TL*KYSLVGPSVPLVSSV**SDW PLKLLMTMMS
23609	53977	A	23744	573	1085	VCHQILTHLPALLSGARMWWD QLWRGRP**RRCQQPCCGG*WH CFWATAHHSPLDSTLNLHLCLP RGP
23610	53978	A	23745	2	379	WLTRSSCSWRLPPRRKKKGAL V*PVWLPGGVAVLLQLGCCV LQDVSCCKRLCYNRKQSEIVL MS*ITMWKLFPRPPLPFSTCIC *KTCGKGRSK*KVDILVLSIRF SAIKLEPLDCHENAWL

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23611	53979	A	23746	575	576	TGIDSDQLNGRDWRRALSVSPA PDSGFPRCNGDEQAGI*LLGTG WAEKCHRLAFPPAGSTAGR
23612	53980	A	23747	1	723	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPMERIGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVCSWKEPPGNSL NVSRMVWDHDPTRVVGIIIGL GPRSHLYCRSDYQQRSTSVCG CMPAVDCCCVLLIHNLRTVM WTKYLVTOAVPAR*PGCIRCKC
23613	53981	A	23748	1	1101	
23614	53982	A	23749	5	205	YCSSLSTFAITSAFLPDRRITT PPATSPSPFSSAMPRRISGPWTF ATRRR*TGTFPSLAFKTM
23615	53983	A	23750	1	761	
23616	53984	B	23751	56	2188	
23617	53985	A	23752	627	1272	
23618	53986	A	23753	448	2218	VRRQRSDPERSDARMVRFCLN YI*RKNPFILH*LFR*TLRQTKPD NSAGKCVKI
23619	53987	A	23754	171	959	AASRGPDAPGLEMAGNCSWEA HPGNRNKMCPLSEAPELYRR GFLTIEQIAMLPPAVMNYIFLL LCLCGLVGNGLVLWFFGFSIKR NPFSIYFLHLASADVGYLFSKA LFSILNTGGFMGTADYIRSVCR VLGLCMLLTGVLLMPAGWDE RGVRSEAWCTVETGRVHRSR VRVSRNTARDPANGLGHLQSS LGMPALEPGPTLGSALRWEFLQ TASPQLPVQPLHPAAA TPQPSL RGRGRGPKARALGLGPRSTSYR
23620	53988	A	23755	664	838	
23621	53989	A	23756	2732	3007	
23622	53990	A	23757	1522	1706	CHYFACMWSGCEVYS*SAPG** C*EDLSGLVRCRCLHNSAETPI* FAANADTSPRGFLCR
23623	53991	A	23758	537	795	ADCLPHMGRPCLID*GPCRTE*P RCAVVCLLWIAAVSCLSTT/SLR TG/DGPKYLVTQAVPARYPGCI RCKCVAVDELASSDMRLPCS
23624	53992	A	23759	2074	2276	
23625	53993	A	23760	36	206	ECWIWCELGAELHHQP*ASSH WKSSYRQSSLPSCRASQRTLH LLQGWAVLGPLE
23626	53994	A	23761	444	725	
23627	53995	B	23762	1	1212	

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23628	53996	A	23763	11	972	RFSKSLD SGVQLASPSGSRGTG ATGGAHSPARAPALHSPWAV DGTRGRLAGTAGLWSPRAFHF FKVSLSLPFCVSPFPFPGPLGPS PRKHQMADDAGAGVGGRRPR GPRMG/NRGGFRRGFGSGIRHQ GCGCGQGGQGRGVGGGKAE YKEWMTVTKLGHVLKDIKIS LEEIVLFSFFKTSLSLKDEV LKI MLVQKQTHTSQCTRFKAFVAT GDYNGHISLGKCSKEVATAIC GAILAKLSIVPACRGYWGNIKIS KPHITPCKVAGCCGSLVCLIS VPRGTGIVLAPCEGDRGLRKSS PASLSPECKDGGSHRSF
23629	53997	A	23764	2	260	LLEECRSLRSRCDQLEERV SAM EDEM NEMK*EGKFREKRISPKR APERSAKHGKEQPVAAAKSC QNVNTIETRKKLHLQTSKITS
23630	53998	A	23765	3	1150	
23631	53999	A	23766	1	1521	
23632	54000	A	23767	1	753	
23633	54001	A	23768	1	3351	
23634	54002	A	23769	1	1740	
23635	54003	A	23770	1	1353	
23636	54004	A	23771	1	1932	
23637	54005	A	23772	1	1221	
23638	54006	A	23773	1	1214	MAKKQNRKTGNSKKQRASPPP KECSSSPATEENWTENDFDEL EEGFRQSNYSELWEDIQTKGKE VENFEKTL EECITRITNTEKCLK ELMELKTKAQELRKECRSLRSR CDQQQERASVLEVLVAR/QL GRKRK*RVFN*EKRSNCPCLO TT*LYI*KTPLSQPKISLS**ATS AKSQDTKSMYKNHKHSYPTTT DKQRAKS*VNSHSQLLQRE*NT *ESNLQES*NWISSLHLIQSISQD GLKT*TLDLKPSKP*KKT*ALPF RT*A WARTSCLKHQKQWQQRT KL TNWI*LN* RASA/PAKESTV/S SEQATYNMGENFHNLLI*QRAN IQNLQ*QTNLQEKNKQPHQKV GEGHQQTLLKRRHLCSQKTHE KMSIITGHQRNANQNHNIPSH TSYNGNH

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23639	54007	A	23774	1157	2085	QGRPTDFADFGTTIKQDFRLIG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTLPNTQTASPR ALADSLIAAGTTGFTGKRAVS ATQLMTQFSPAREQSWRN/DF DELRKE/GFARSNYSKCLKEL MELKTKARELREECRLSRCD QLEERVAMEDEMNMKREG KFREKRIKREQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIHQENFNLARQANVQIQE IQRTSQRYSSRRATPRHIVRFT KVEMKENMLRAAREKGWVTL KGGPRLTADLVAETLQARRE WGPIFEFP
23640	54008	A	23775	1	1707	
23641	54009	A	23776	1	1899	
23642	54010	A	23777	1	2781	
23643	54011	A	23778	1	831	
23644	54012	A	23779	1	3264	
23645	54013	A	23780	1	882	
23646	54014	A	23781	1	1853	
23647	54015	A	23782	1	550	
23648	54016	A	23783	1	831	
23649	54017	B	23784	64	3436	
23650	54018	A	23785	1	1422	
23651	54019	A	23786	1	773	MGKKQSRKTGNSKKQSATPPP KERSSSPATEQSWTENDFDEL EEGFRRSNYSLEQETQTKGRE VENFEKNLDECITRTNTEKCL KELMELKAKAWELREECRLSR SRCNQLEERVSVMEDEMNMK REGKFREKRIKREQSPQVIRD YVKRPNLRLIGVPESDGKNGTK LENTLQDIHQENFNLARQANI QIQEIPRTS/QRYSSSEHSIIGLIGR FPS*RTDMFRAPKKREQKRNRR KIQKEEGGRTAPTGI
23652	54020	A	23787	1	2775	
23653	54021	A	23788	1	2712	
23654	54022	A	23789	1	1590	
23655	54023	A	23790	1	547	MGKKQNRKTGNSKKQSASPPP KECSSSPATEQSWTENDFDEL EEGFRRSNYSLEREDIQTGKGE VENFEKNLEECITRTNTEKCLK ELMELKTKARELREECRLSSR CNQLEERVAMEDEMNMKE D/GNRYDDRRQ/RKEEIMKSW RFCCRHLIRVVRGWGPSKYLWI TMVVTLAGNPQ
23656	54024	A	23791	1	710	

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23657	54025	A	23792	1	895	
23658	54026	A	23793	1	1938	
23659	54027	A	23794	1	1413	
23660	54028	A	23795	985	1219	LCSGVSVERCTESYLHSSHCLVQ QAGVTGDEGGSCY*DPPSHHRS HPRKLLKLC EQEFSVTSAPWRK CRSLHGRFPGLP
23661	54029	A	23796	1	3570	
23662	54030	A	23797	1	634	
23663	54031	A	23798	1	4551	
23664	54032	A	23799	1	4721	MHPSQRTPYQSRSPATIFATVST FKSHKSNLETKHPQQVPLSSLG LAANISSEIESEAEDNGKWES VDRTSFFPALTSFQQSMHKKI MTVFKSV EPEDGLGRPTLAFHE DRCQLSIQNSLDAGGGCPSMA APPAEVHELASGLISAAAALLSP AASGRVSKHQHIPTGFPDPPKA LHKGKLTTRKDIYTENPSVHHH HQRPKVDKTTKMGKKQNRKT GNSKTQSASPPPKC SSSPATEQ SWMENDFDELREE

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23665	54033	A	23800	I	2152	MDILGWASRAHKWKGRATGT HVFNLMEYLIISLQCCASEQAA SPEHGASFRVWKSGLGFQKLILS LICPQCLQSLTRETWMRFKSKK TKGPDRLRLVMDANKWEFRRH ALRPALTFPNEGDDLVEALPV ALPPEAHVGGVVLPAALVRGA HGEQLPAIPGPEEFALPAVQAR AARPERQVVVIVVNEAGVDP GVEGLAPVPVLPVGRLEATAPK QPPRLPARLRLAPSGRKLNAK CPRLRWGFFVQDGDGTCLACL SEGDDGCCQEAPLDHRPRLRG LAGSAGAREAREPRLRPGDWG NRIARVRAPEEAAAALSRPARV AAALAKTHRREHRARSQKLV SSVQQKLTTRKDIYTENPSVH HHHQRPKVDKTTKMGKKQNR KTGNSKKQSAFPPPKCASSPA MEQWTWDNDFDELREEGFRGS NYSELREDIQTGKEVENFEKD LEECITRITNTEKCLKERMELKT KARELREECRLRSRCDQLEER VSAMEDEMNMKREGFKREK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGKLENTLQDII QENFPNLAQANVQIQEIERMP QRYSSRRATPRHIVRFTKVEM KEKMLRAAREKGRVTLKGGPI RLTAVLSAETLQARREWGPIN ILKEKNFQPRISYPAKLSFISEGE IKYFIEKQMLRDFVTTTRPALKE
23666	54034	A	23801	I	2109	

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23667	54035	A	23802	1	2544	MSVHSWKPSWIRPIRSLSPKRPL GTQGTSEVPPDTHICQTKFHSL SGPLLLSVHPVGKLSAVVGRVF IHILSQRERRRRVISAFPSEVPG SSHQGVDPDSGCRSVGAHPVREP KQGEALPHSGSPREGKLTNRKD IHTKNPSVHHHHQRPKVDKTT KIGKKQNRKTGNSKTQASPPP KECSSPATEQSWMENDEFELR EEGFRQSNYSELRKDIQTKGKE VENFEKNLEECKTRITNTEKCL KELMELKTKARELCEECRSLRS RCNQLEERVSVMEDEMNMK REGKFREKIRIKRNEQSLQEIWD YVKRPNRLIGVPESDVENGTK LENTLQDIIQENFPNLARQANV QIQEIQRTPQRYSSRRATPRHIIV RFTKVEMKEKMLRAAREKDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEII TNYLSDIISAIKLELRINKLTQSR STTWKLNLLNLDYVWHNEM KAEIKMFFETNENKDDTTYQNL WDALKAVCRGKFIALNAHKGK QERSEIDTLTSQLELEKQEQT HSKASRRQEITKIRAELEKETQ KTLQKINESRSWFFERINKIDRP LARLIKKKREKNQIDTIKNDKG DITTDPTIEIQTIREYYKHYAN KLENLEEMDTFLDYTLPRLNQ EEVESLNRPIGTGSEIVAINSLPT

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23668	54036	A	23803	1	1886	MKENFKHRHVAVFISSQEAQE DSREEDRLERSRFYFLFLELSY KTTGLNREPTVSLNSKSGTPMD QNEHSHWGPAAKGQACASSEL RIILVGKTGTGKSAAGNSILRKQ AFESKLGSQLTKTKCSKQGSW GNREIVIIDTPDMFSWKDHCEA LYKEVQRCYLLSAPGPHVLLLV TQLGRYTSQDQQAQQRVKEIF GEDAMGHTIVLFTHKEDLNGG SLMDYMHDSDNKALSCLVAA CGGRICAFNNRAEGSNQDDQV KELMDCIEDLLMEKNGDHYTN GLYSLIQRSKCGPVGSDERVKE FKQSLIKYMETQRSYTALAEAN CLKGALIKTQLPKVDKTTKIGK KQSRKTGNSKKQSTSPPKERS SSPAMEQSWTENDFDELREEGF RRSHYSELPEDIQTEGREVENFE KSLEECITRITHTEKCLKELMEL KTKARELREECRLRSQCQDQLE ERVSAEMEDEMNMKREGKFKE KRIKRNEQSLQEIWDYVKRPN LRLIGVPESDAENGTKLENTLQ DRIQENFPNLAQRANGFCRFRN HHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINRWSH DRFPDWKAGTGLKSAIFAW
23669	54037	A	23804	1	4134	
23670	54038	A	23805	1815	1849	

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23671	54039	A	23806	1	4016	MGKKQNRKTKGNSIKTQSAFFP PKECSSSPATEQSWMENDFDKL REEGFRRSNYSERLADIQTKGK EVENFEKINLEECITRITNTEKC LKELMELKTKGSRNYVVECR/S LRSRCDQLEERVSADEDMNE MK*EGKFREKRIKRNQSLQEI WDYVKRPNLRPIGVSESDGEN GKLENTLQDIIPENFPNLRQA NVQIQEIQRTPQRYSSRRATPRH ILVRFTKVEMKEKMLRAAREK GQVTLKGKPIRLTADLSAETLQ ARREWGPINILKEKNFQPRISY PAKLSFISEGEIKYFIDKQMLRD FVTTTRPALKELLKESLNMERNN WTSKQIIQEDGYSEEGWLCRA VIYSHTLQAIMAIVKATGNLQT DFANPFHTDDARQQFAMSYTV VGQGALPEDLSRCHLQTEAVQ RHPESLGCPLDLLHGMPVSSCF GYPQDTSSTV
23672	54040	A	23807	2059	3153	
23673	54041	A	23808	6	188	
23674	54042	A	23809	3	1014	VACRPLPRRRAQPATFIPRVAV KMALVASVRVPARVLLRAGAR LPGAAGFRTERAAGGGDGA/RP VFGSQRVLVEPDAGAGVAVMK FKNPPVNSLSLEFLTELVISLEK LENDKSFDRDILTSD/RPGVFSA GLDLTEMCGRSPAHYAWVLE RPVQELWLRLYQSQ/LVLSAI NGAICPAGGICLVALTCDYTILA AGNPRYICIGLNETQLGIIAPF WLKDNPWRTPIGHRAAESALQ LGLPLPPAEALQVGIVDQ/VVP VEEQVQSTALSAIAQWMAIPKP MAHKLTAKIMRKGGQPPAWS RKGYADVQNFVFSISKDSIQKS LQMYLERLKEEK

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23675	54043	A	23810	1	2665	MTTSIRQFTSSSIKSGSLGGG SSRTSCQLSGGLGAGSCRPGSA GGLGSLGSSSYSSCYSGSGG GYGSSSFEGVDGLLVGGEKAT MQNLNDRLASYLDKVRALEEA DTELVKIRDWYQRQAPGPAR DYSQYYRIIEELQNKPPPSDDL TLPSPLILATVDNANILLQNDN AHLAAADFRTKFETEALCLSV EADINGPCRVLDELTLARADPE MHLENLKEELAYLKKNHEEMN APRGQVGGEINVMGAAPGVD LSRILNEMREQYEKMAEKNRK DAEDWFFSKTEELNREVA TNSE LVQSGKSEISELRCTMQALEIEL QSQLSMKASLEGNAETENRY CMQLSQIQLIGSVVEERLAQLL CEMEQQNQEYKILLDMKMRLE LEITTYHRLLEGEAQTVQHTP GSPCVPEWAHDCSLPAQLDE WSCQAQRGICGHRRENCWERIP SQSCFYRPTARSLTSLGTMST CSHQFTSSSRSMKSGCSIGGSIGG GSSRISSVLAGGSCHAPSTYGG ASCGLGGGYGGGFGSSSSFASG FGGGYGGGLGAGFGGGLGAGL GGGFAGGDGLLVGSEKVTMQH LGDRLASYLDKVRALEEANAD LEVKIRDWYQRQRPSEIKDYSP YFKTIEDLRHKIIAATIENAQPIL QIDNARLAADDFRTNYEHELAL QQTVEAGVNGLCREMLALRGQ
23676	54044	A	23811	222	548	TLPCGDHHHSQDPARLPSWHD LLQERSEKCGSQDWQRDSVQP GVSYQFCCVPWPAGRSQPQRH CWGCCGTEASYDSGI*SLSTPG GGQLQGSV*GPDGAGLQNSHR
23677	54045	A	23812	2	165	
23678	54046	A	23813	1	665	
23679	54047	B	23814	1	1673	

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23680	54048	A	23815	1	331	ARQLRTSAMTMPVNGAHKDA DLWSSHDKMLAQPLKDSVVEV YNIKKESNRQRVGLEIASENF ASRAVLEALGSLNNKYSEGYP GQRYYYGGTEFIDELETLCKQRA LQAYKLDPQCQWGVNVQPYSGS PANFAVYTALVEPHGRIMGLDL PDGGHLTHGFMTDKKKISATSI FFESMPYKVNPDGTGYINYDQLE ENARLFHPKLIAGTSCYSRNI.E YARLRKIADENGAYLMADMA HISGLVAAAGVVPSPFEHCHVVT TTTHKTLRGCRAGMIFYRKGV KSVDPKTKKEILYNLESLINSV FPGLQGPHNHAIAAGVAVALK QAMTLEFKVYQHQQVVANCRA LSEALTELGKYKIVTGGG/CVISG GAGKPG*FSHQDGTGTSQDGG RRPFLHHTLSY
23681	54049	A	23816	3	1709	SHPTPRETPGTGVEGQATPSVLG AAPASQAKATPTLGRPHASDR GEVAQLDEWSCQAQRGICGHR RENCWERIPSQSCFYRPTARSLT SLLTGMTSTCSHQFTSSSRMKGS CSIGGSIGGSSRISSVLAGGSC HAPSTY/GGGGLCVSFSRFSFGGA CGLGGGYGGGFGSSTNFWS\GF GGGYGAGLGAGFGGGLGAGL GGGFAGGDGLLVGSEKVTMQH LGDRLASYLDKVRALLEANAD LEVKIRDWYQORQPSEIKDYSP YFKTIEDLRHKIIAATIENAQPIL QIDNARLAADDFRTKYEH.EI.A LRQTVEADVNGLRRVLDLTL ARTDLEMQIEGLKEELAYLRKN HEEEMLALRGQTGGDVNVEM DAAPGVDL SRLNEMRDQYEQ MAEKNRRDAETWFLSKTEELN KEVASNSELVQSSRSSEVTELR VLQGLEIEIQSGLSMKASLENQ I\VEETKGRYCMQLSQIQLIGISV EEIQLAQLRCMEQSQSQEYQIL LDVKTRLEQKYCHPTAALLEG EDAHLSSQASGQSYSSREVFT SSSSSSSRQTRPILKEQSSSSFSQ
23682	54050	A	23817	2	365	

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23683	54051	A	23818	1	464	RRWRICSTWTRSFATAWLPPAP SANFPRTRDSQGRGAPAGFAL APILEFFLWDTSSQKFLQKPHCF MHGRERAKMGRRAQQESAQA ENHLNGKNSSLTLTGSETSAKL PRCR/QGGWAGDSVKASKFRR KASEIEIDFRLRPQSLNGSDYG GDIP
23684	54052	A	23819	384	805	
23685	54053	A	23820	3	392	MKYSAIQTLDGEIDLKLLTKVL APEHEVR*VQWWQFPGLSTL AIPINPAELPGLALCLP*RPWNG REKVSLLQREKALSLSYPAKPF LAEDDVGWWDHLEFTEVSSEV LTEWDPLQTEKEDPAGQARHT
23686	54054	A	23821	63	785	GPIRGPGWPGFGGWGGATPPAP TSRLRLRAAGLAPRRRAKMGR RAQESAQAENHLNGKNSSLT LTGETSSAKLPRCRQGGWAGD SVKASKFRRKASEIEIDFRLRP QSLNGSDYGGDIPINPDLEEVEQ EEDFVLQVLAAPSIQIKRVMT YRDL/DNDLMKYSAIQTL DGE D/IDLKLLTQK/VLAPEHEVRER NPSWQDDVGLGTWGPICSTEV SLRRSFTEWDPLQTEKEDPGG QARHT
23687	54055	A	23822	1	441	MSFNCSTRNCSSRPIGGRGICVPV AQVTTTSTTDADCLGGICLPSSF QTGSWLLDHCQETC/CGCQPLG GISSVCQPVGGISTVCQPVGGV STVCQACGVSRTYQQSCVSSC RRIPAKCVGASERIKTPRPASCF QDLPAACLSLNSSS
23688	54056	A	23823	1	538	PTRLPQQATCSPLSDIMSFNCST RNCSSRPIGGRGICVPVAQVTTTS TTDADCLGGICLPSSFQTGSWL LDHCQETCCEPTACQPTCYRRT SCVSNPCQVTCRQTTCISNPCS TPTAGRSP/CVSSGSQPLGGISS VCQPVGGISTVCQPVGGVSTVC QPACGVSRTYQQSCVSSCRRTC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
23689	54057	A	23824	832	1885	AEWDAADKAHVGPGRSPRQPL PHVGRRAAHTTGRGRRTAGC APAPARTLCILSILGPWCVLPHL PTLCLGQAQAASCSQGAHGCF AGCSCT/GTSASHPV/CCKCPLH PVCITLADVHGCTSGFSVISLPQ TCAPWTSWRKWSLSDSWQVD ACPESCCEPPCCATSCCAPAPCL TLVCTPVSCVSSPCCQAACEPS CQSGCTSSCTPSCCQSSCQPA CCTSSPCCQACCVPCCKPVCC VPVCCPKPVCKPICCVPVCSGA SSSCCQSSSRQFACCTTSCCRPS SSVSLLCRPVCRSTCCVPISCC APASTCQPSCCRASCVSLLCRP TCSRLSSACCGLSGGKSSC
23690	54058	A	23825	1	3097	MDEKRTRIQFEEADVPAYPKV ATVPQSEKKPSKYPLCSADAAV STTPPGSPPPPPPLPEPPVLKVL SLKPAAPSPATAATTAATASTA ASSTASSASKTASPLEHILQTLF GKKKSFDPSAREPPGSTAGLPQ EPKTTAEDGVAPPLLDPIVQQF GQFSKDKALEEEEDDRPYDPEE EYDPERAFDTQLVERGRRHEVE RAPEAAAAREEEVAYDPEDETI LEEAKVTVDLPLNRMCAVRR NSVERPAEPVA
23691	54059	A	23826	67	442	VKFFCLYLQSNKPMKNFKQG SNNQLLMRSFWLLCGIDYKKPP PPAPGPESVAPALSGPPPAHS RGPRAVVRA/PPPPGPRHSPA PPPPGTPEPSVATYSIKASKRVS QQDRCHNLKMSQE
23692	54060	A	23827	3	657	GERSRRWGPACGPAEAKTTP CDAGAAGAAPGAPGHAGNPL GSGPDYD/GEATCMHLHPDDPC PAGAGCCPGSFEVAFDAAEK MKKSLHSLKKGCYSRVCDLPL DCPGCDSDSGRQAMFSCIVNFQ LPKEESPIPGSQEESGPSHSEC DSVGVDWRGQRVSRKQLQAPNH SLVLLVTSLFQETTKSHLNRTN DAVSPRKFKRLGALYWGKVEA
23693	54061	A	23828	141	246	
23694	54062	A	23829	1	609	
23695	54063	A	23830	1619	1752	

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23696	54064	A	23831	54	470	CSTMNPSEMQRAPRRQRHRS RAPSAHKMNRMMVMSSEQMKL PSTKKAEPPTWAQLKKLTLA KKKVLNTKVTQTPENMLLAAL KTVSTVSAGVPSSESDHRR AMMTTVVLSKRRGKCGEKKEI SDCYCVYVERS
23697	54065	A	23832	213	572	IQWYPYQDITDFLHRIRKNFFKF HMEPKKSLHCQDNPKPKQSW MHHTT*LQTMLQGYSNQKRMP PHLGSEERLCPAAPSGR*GAPLP GRCAIFQV*SDLSAGVPSSEE TATIENG
23698	54066	A	23833	296	583	
23699	54067	A	23834	2452	4557	
23700	54068	A	23835	3	266	
23701	54069	A	23836	31	499	ARVTAAVSAAVAKRVRWDG FDCSGYYSLTILLVQPTKRP GRTYADYESVNECMGCVCKM YEEHLK\RMNPNNGPSI/THNTTS QLFDFD\DLADLSCLVYRA\DT QTY\QPYN\KD\WKDEDPTVLLS SGKAQQAREIIVGSHWGGWG GAWDTGV
23702	54070	A	23837	3	323	
23703	54071	A	23838	366	892	PCVYSQFPAGEQCLKLHSPA SPPALEASEAQTRKAPECGSGV PEVAGGSCPCLLCLPRHQAVP TQGPPTYSPCTSHQPHIFRPAA PHHLGLLQNPNAASCIQCLYP AGVATTMPRRKAEGDAEGD/K AKVKDEPQRRPAKLSAKPAPPN PEAKPKNAPGVTLSLRGATRF

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23704	54072	A	23839	201	1412	LWKSRLTFKLAMSRVSPPPPA EMSSGPAESWCYTQIKVVKF SYMWDPSITLAFCREEMGEVI KSSTFSSGANDKLKWC/LRVNP KG/LDEESKDYLVTFTCYLVSC PKSEVRANFKFSILNAKGEETK AMESQRAYRFVQKDWGFKK FIRDFLLDEANGL/LPDDKLT FCEVSVVQDSVNISSQNTMM VKVPECLADELRGLWENSIRF TDCCLCVAGHEFQAHKAILAA RSPVFSAMFEHEMESKKNPSL KSMDEVPEVFKE/MMCFIYTG KAPNLTKMA/NDLLAAADKYA L/ERLKVMCEDALCSNPV/SVEN AAEIL/LADLH/SADQLKTQAV DFINYHA/GDVLETSGWKSMVL SHP/HNLVAEAYRSLASKQCPF LGPTQNALKQSLKILLCC
23705	54073	A	23840	1	575	FRHRKIY*NLKQEDSINVTEM TSIRASVDILIPDPKDDMDT DKQEKKEVPKCGFLPGNEKVL SLLAMVKPEVWTLKEKCIIVIT WQHLPKIEDGNDGFAIQEK VLERVNAVTKVEAFQTTIS/K MDYRALVHERDEAAYGELRA MVLDLRAFYAELYHISSNLEKI VNPKEEKPLMYPTRD
23706	54074	A	23841	1	1092	
23707	54075	A	23842	130	397	EGVHSQVNLFPKIGNQTHVPAS HGTDALPPTLQMDYRALVHE PD*AAYGELRAMVLDLRAFYA ELYHISSNLEKIVNPKGEEKPF
23708	54076	A	23843	20	334	VRLPGSTHAGGDRSSMAKPCG VRLSGEARIQVEVLRLNQLFQEA NEEFLYRFLPQKIYLNQLQEDS LNVADLTSLRAPLDMPIPPPP KDDMETDEQEKKEGK

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23709	54077	A	23844	1	898	MKQKVAAEAGRGQILQAKVLP SGTL SRLAEALFGVQTYDQDA YGF LTPSAQSMKVFCCLWKL V CKQLEGDVAQGLAIDGDVKKH SGLEWQVETIQNLVDSYMAIV NKNMQDLMPTIHLMINNTKE FIFSELLANLYSRGEQNTLMGE SAEQAQGRNEMRRMHVLR APSIIGDIKTIVSTPTGSPKSSPT TQCRLPAVPPAPGLRSPAPGPL PAASTLGEAPVVPSTPGASPDPL GPPPVPSRPSRGQPQDRMP GLAGDLTVGFLEPTLQAIIRWS LLLRPPANSPEQS
23710	54078	A	23845	99	429	FSDAAAVARQPSFGKALGAPQ ADTQPTSPMPRCPPGSETKPK KAAGKDKSSDKKNKTKKQMK AEKGGKEKQAEVADQETKDL AENGDTENKESPASDEATEKDT KSD
23711	54079	A	23846	1	390	TWMFIAAVFRIASTWKQPRYFS VGKQDQKRTSRKLQQTCSRGA *WLEGLTNRKE*HQYQRKGH PRKNTIQRSP LKTKANILNGQ KLEAFPLKTGRQRCPLSPLFN MVLVLARSIRQEKEIKVFK
23712	54080	A	23847	522	733	ASAADTQANRVWSGPP/RKLQ QTCS*GS*LLQGKLTNRKDIHT KTPSVHHHHQRPKTLNQQRSK ETKKAIT
23713	54081	A	23848	46	330	
23714	54082	A	23849	1	873	MAEKKDPTKEPEKKHLLAWM NKLLEYLDPKYKNDNTDGS VVHKIIACDKVSPPPSAMIGSF PRPSSEADAGAMLCVQPARTKI LGILGLKATSLQYLRLHTGKPL LPKIDESTKMGRNQPKKAENSK NQNAASSPPKDHNSPVREQNR MQNEFDELTEVGFRDRSSKR NSVVIKALPRHLINQGRSQEWR LGIGARDSPKTSGRRGKSPAGP NRTTVPEDEQA/GSRPRPIPTRQ ADPRTPPPTRSEKE/AQLSLATD QMCPSLAPLIK*PQES**WKQRI SI*MEHL
23715	54083	A	23850	1075	1350	AJITANVFKFVSDIRGLVCNMEL EGSNCFIDVCSWTSEMKSOGTS RR*KIT*GNSSGSLPRDTQRSGH RNSSLCCERSKYGGSRVDIRRK VF

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23716	54084	A	23851	1	956	MEVLARVFRQEKEMKGIHIGK EEHKLFLFADNMTLCLLEKTKDS VKKLVEQPSSFGSVDWLCLSSC SGSTHTPRPADVSPGSLPGPGQ TFGTREPPQAVSTKEASSNLH APERTVAGLFTTEQVRALEGV FRHHQYLGPLERNWLAREMQL SEVQIKTWQFQNRMRKHKRQM QDSQLNGPLSGSLHGPPAFHSP SSGLANGLQLLCPWAPLPGLS/L WLPGLSGFWLQRQMDQEAALSS WASCCGQPLAYHPPRPGSGAH KLGALSTGPRGLCALPETGDA FEETPTTCLPHKRSVPQIASDAY PEDSAVLFTSWRHLS
23717	54085	A	23852	1	846	MEAFDANYTFQSGPSAAGLLV FAGGPLQALCAWVSAVEAAEQ WILQPSFGSVDWLCLSSCSGST HTPRPADVSPGSLPGPGQTFTGT REPPQAVSTKEASSNLHAPER TVAGLFTTEQVRALEGVFRHH QYLGPLERNWLAREMQLSEVQ IKTWQNRMRKHKRQMDSQ LNGPLMGSPGAPWLSTHIFLA LAKGLQLLCPWA\PLPGSPGCP LGSFWGTP/QMDQEAALSSWA GCCGQPLAYHPPRPGSGIDLPK GTQLSLRLFQDISSTRGDHRS
23718	54086	A	23853	3	239	
23719	54087	A	23854	10	1154	RRAGFGGVRASGAMGTTPGLQ TDCEALLSRFQETDSVRFEFT ELWRNMKFGTIFCGMRN\LEK NMFTKEALALAWRYFLPPYTF QIRVGALYLLYGLYNTQLCQPK QKIRVALKDWDEVLFQQDLV NAQHFAAYIFRKLRLDRAHFH TAMPKLLSYRMKKKIHRAEVT EEFKDPSDRVMKLITSDVLEEM LNVHDHYQNMKHVISVDKSKP DKALSLIKDDFFDNKNIVLEHQ QWHKDRKNPSLKSKTNDGEEK MEGNSQETERCERAESEKIKS KA\FSVVIQASKSRHRHQVKLD SSPLDSASGGQVKATRKKEK KERLKPAGRKMSLRNKGNVQN IHKEDKPLSI.SMPVITEEEENES LSGTEFTASKRRQH

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23720	54088	A	23855	16	447	VNCDKANCSTTCFNGGTCFYF GKICPPGLEGEQCEISKCPQPC RNGGKICIGKSKSVCEPGCGAH GTCHPEPNKCQCQEGWHGRHCN KRYEASLIHALRPAGAQLRQH TPSLKKAEERGDPPESNYIWVE LPTSGNVLSYTKFI
23721	54089	B	23856	103	1989	
23722	54090	A	23857	3	1295	SGRGVSRHMADYLISGGTGYV PEDGLTAQQLFTGAAARDRLT YNNFLILPGFIDFIADKVDLTSA LTWKITLKMPLISSPMDAVTEA DMAIAMALMGGIGFIHHCTPE FQANEVRKVKKFERGFIMDPV VLSPSHTVG/DVLEGMKMRHGF G/NPITETGTMGSKLDSHKQLLC GAAVGTREDDKYRLDLLTQVG VDVIVLDSLQGNLSYQMAMVY YIKQKYPHLQVIGGNMVTAAQ AKNLIDAGVEGLHVGMGCSIC ITQEVMAYSWPQGTAVYKVAE YARHFDHGEHGKALALGASTV MMGSLLAATTEVPSPKYFFSDG VWLKKYRGMGSLDALEKSSGS QKQYFMEGDKLKIAQGVSSSIQ DKGSIQKFVSYLIAIGIQHGCQD TGVCNLSVLLSMMYSGERKFE KWTMLAQIKGGVQGLHSYKK
23723	54091	A	23858	770	1008	LAPSPCVRSKGRKESPDSSR/RPL WLRPIAPALGPSRRGLAPDSR LNPHRSLLGTGNVDVNVIMAA LQGLGLAAVWWDRRR

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23724	54092	A	23859	1	1489	MTRWSSYLLGWTTFLLYSYESS GGMHEECVFPFTYKGSVYFTCT HIHLSLPWCATRAVYNGQWKY CQSEDYPRCIFPIYRGKAYNSC ISQGSFLGSLWCSVTSVFDEKQ QWKFCETNEYGGNSLRKPCIFP SIYRNNVVSDCMEDESNKLWC PTTENMDKDGKWSFCADTSNL GMGVGPTPRHHRRASTRHSRPP PADPDGGERPRTADDRQDDA TEDDGTRCRGRQTRTQATNAN ANHKKSNRTKPPRHKPNKAK RHTKKETPQNT/CGTDKNPDS GRPKLFRACITSTGTGRELWT RSREHPAK/QGRRSGKQRLRPW DRMLSPDWHRAQRIAQVWKPE QEDGLSIGFGDQPGPHSDTSSR QQVRRSKATEMHVGGRVDFD DFVELMTPKLLAETAGMIGVQ EMRDAFKEFDTNGDGEITLVEL QQAMQRLGERLTPREISEVVR EADVNGDGTVDGEGDIDGAWG RHGTQGPWWPGLGDVVRGEPL
23725	54093	A	23860	283	490	GDIWMGTQPKPYHS/PPGPSPN/ PCPPHFNQSMSPSPKSPKVFNS FPALTQKVHTSKVSSETRQVPS HL
23726	54094	C	23861	82	222	
23727	54095	A	23862	27	454	VDGRIAGEITRRGSRARPRPGPQ CPPGRPGTAMIKAILIFNNHGKP RLSKFYQPYSEDTOQQIIRETFH LVSKRDENVCNFLEGG/LVFVE TLDKCFENVCELDLIFHVDKVH NILAEMVMGMVLETNMNEIV TQIDAQNKL
23728	54096	A	23863	1	403	RGRSARPRPGPQCPCPPRPGTAM IKAILIFNNHIGKPRLSKFYQPY EDTQQQIFRETF/HLGSKKEEK WNLKGGLLIGGSDNKLDYRH YATVYFVFGGDFSKRELGLN LIQEFGEPLDKCFEKVWELDLIF
23729	54097	A	23864	215	599	

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23730	54098	A	23865	2	683	GRIAGEITRRGSRARPRGPQCP PGRPGTAMIKAILFNNH GKPRL SKFYQPYSED TQQIIRTFHLV SKRDENV CNFLEGG LLIGGSDN KLIYRHYATLYFVFCVDSSEVS ELGILDLIQVFVETL DKCFGNV CELADLIFHVADKVHNLAAEMV MGGMVLETNMNEIVTPIDAQN KLEKSEAGLAGAPA'RA'VSAV KNMNLPEIPRNINIGDISIKVVP
23731	54099	B	23866	94	726	
23732	54100	B	23867	94	1146	
23733	54101	B	23868	1	360	
23734	54102	B	23869	1	1371	
23735	54103	B	23870	1	639	
23736	54104	B	23871	280	2391	
23737	54105	A	23872	3	244	
23738	54106	B	23873	103	285	
23739	54107	A	23874	70	378	MPLRILLMHGEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEILQIKTK HYTTKEQEKEEQGIKLVQGSNN D/QEQEKKGEYKNTGEKNSMK
23740	54108	A	23875	5	156	RKKGGG/EEEEEGEEEEEEEE EEEEEEEEEEEEEEEEEEVV LTPGTGAEDFKKH

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23741	54109	A	23876	1	1808	MEVLSIDNLAGHKVFYQKESH WKQKQKDLMSGKRLSAAANPLP ALLLPVLWTTGQAPSPGGDP ILQLWDDAQMQAGSPRTKKKG CTRNQQAARLSFQSRGGQGS LTKMIFEQRFGGGKGESKDAIA IIVVDIVTLQPCRTVEWVPTRPF RSLQGHFQGLRRQMMVMVE GVVWVLSAMDLTSPRDCLPFC VSLPVLLLSAPLCSCTAGGSPV TSPHHFVVEGGLGRVRRCYNE PVVTTLGWESVCWVSFWLLLR IRYSTGQAACHAESQELNPRG FGCLGHRNVTWVKCLLPALQP EGSVPFLELLEPFIFASASKTFV AANLVTWVACFLLVQAQFQSL EYRQGVGIPVADRTGDAPTLGL SYEADVAEGHGFLLDQESVIQII PEPLPQFYLCLLDAELTGVQGE PALPSMQIFSSPEAATGVHNDR GAEHFPVSRQPSAELGLRPMQA SQERKINFPGPSGFPKRNKT LSRREKKEEEKKEEEEEEEE/E GEEEEKEEEEEKEEEEEEEEE GEEEEEEEEEEEEEEEEEEEE KWLYQYDPEDKAQSKQWLSR GGSGPVKAKADWWRAKEIHSL QPRQVIPGIPSM
23742	54110	A	23877	459	636	IPGGSNGLEAEGPPPPPLVAAV LA/AGSGGLAVASCAFTICALR WPGVPCSRVPIWTPS
23743	54111	C	23878	183	254	
23744	54112	A	23879	103	335	LGSGDLPWEINPLSSCSLLHEK DPPTTSGPQTDPRKEHLNFKSG ACYTCRKSGH*AKECLQGIPIK PHLICVGP
23745	54113	A	23880	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPKHLTNFKSAA ED
23746	54114	C	23881	80	106	
23747	54115	A	23882	317	427	
23748	54116	A	23883	353	511	
23749	54117	B	23884	1	320	
23750	54118	A	23885	1	624	
23751	54119	A	23886	224	355	
23752	54120	A	23887	872	1003	
23753	54121	A	23888	1	603	
23754	54122	A	23889	2	214	
23755	54123	A	23890	459	601	DVDRHVRGSNFHHNEIRSLAAT PRAPGTLAQGLTDSFPDLLGLA AED

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23756	54124	A	23891	2	267	QWDGWWGARKGMEWEDDLPLE FGRPTASLLSDRPPQPNSSRGSDV PFLAPPSLPCHSSACLAATPRAPG TLAQGSLTDSFPDLLGLAAED
23757	54125	A	23892	72	299	
23758	54126	B	23893	1	1470	
23759	54127	A	23894	134	1276	
23760	54128	A	23895	2	847	PPPPRVLRITGGGASLTAQAPGT PRRPQGEPEVTPGRSLGLRSSCQ ASVSLLLPVIVACASLEPGRGR AFRDEGAWNTRVSAAVISSQA QLLSSILVNSRRLSFSAHHTAFG TVVALGEYAFRMFRLSARLFGVE VTRPTNS/RLSMKVVKLFSE/IW PLAKKKETYDWYPNHHTY/AL ELMAGRLRFLGTLTEDEAFRDF MGMEAKTDLKEAFVKGKGNP KEREKGKRAAKKGNSCLVPSR RGDFLSSVAERRKLHLSPFHIG GDVIFLNGSLFGRNTSHLLGEI
23761	54129	A	23898	3	1224	MRRNKPRQRGVREARPAGGAG PGWRGARCSGAGEGGGGERRG SPPAALALAPASGPRRNFPDA RCLIVQIHHQGAFLLAGSASLS AVTGVPGEARFTEDYCPEEK MFGFHKPKMYRSIEGVCISGA KSSSSRFTDSKRYEK/DFQ/SCFG LHETRSGDIGNACVLLVKRWK KLPAAGSKKWNHVVVDARAGP SLKTTTFEPKIKVKTLSGNRIK/S TQISKLQKEFKRSNSDAHSTTS SASPAQSPCYNSQSDGSDTEM ASGSNRTVPVFSFLDLTYWKRQK ICCGIHYKGRFGEVLIDTHLFKP CCSNKKA-AAEKPEEGPEPLPIS TQEWTECPDLSLVVSWRPPSS LPAGCSLHGLAADWTTDMITV TTSKCREPSCQEGSFQRRKAF PKRLPKMAEVQVLVL
23762	54130	A	23900	69	355	
23763	54131	A	23901	316	830	VLSLQTLHPPMTLQLSRYSRGW GLSSDRPRGAKAKVPSCFGTAP R/GPEAAPRLLAHHLVPAGRG/S ARAPAPGWRLGSPGAGRKGR DFRLPASGLAVSGEWDPIPWGY VGEVGGCSCQWFSFGVQKRR RRKVWLGQPDLPGPSALADK GPALAKADGQRVNVASVGLQP

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23764	54132	A	23902	1	1044	MSYKVTQEISKELRWISAVLVT WDLRGETGTRVCIAMGVSRMQ YSIMAKIVGSGNNLELNPAADK LDNLGAQCGLASVKVSARAAP PFAPATLVALLEARAELPLPPP PGVSLRCVEAPDVRGRGRGGG EGSGVTRLLLP PPPSGASFLQR GRPVT PALFQAGWGRAADRP PADLAGGAGGRSGRRMLPRS PGAALDRSALEDGIVEGYGPL GEPEEGSRSSFLESKVAFNYCN KVAFDLDFGNEAVEQCHTMSDR KAVIKNADMSQDQDAVDC ATQAMEKYNIEKDIAAYIKKEF DKKYNPTWHCIVGRNFGSYV PHTEKHFYFYLGQVAILLFLK
23765	54133	A	23903	33	427	
23766	54134	A	23904	72	777	EWKQAGEGGGQRRGSPPAVL ALAPASCPREMSYLPNTNPPGSI LICWLGVSLSHRSAGGSAIY GSIYYPEEKMFVFKPKMYRSI EGYICIRAKSSSRFTDSKRYEK DFQSCFGLHETRSGLCNACVL LVKRWKKLPAGSKKKTGIMCN QSDDGSDTEMASGSNRTVPVFSF LDLTYWKRQKICCGINYGKRF GEVLIDTHPFKPCCSNKKAAAE KPEEQGPELP ISTQEW
23767	54135	A	23905	234	989	PKTSDQAYYCPEEKMFGFHKP KMYRSIEGCISGAKSSSRFT DSKRYEK\DFQ\SCFGLHETR\SG D\ICNACVLLVKRWKKLPAGSK K\NWNHVVDARAGPSLKTTLK PKKV\TL\SGNRK\STQISKLQK \ENFKR\HNS\DAHSTHPQVPSP AQSP\FTVNQFRWTS\DTGVG FPGSNRNHPVFSFLD\TYWKR QKICCGINYGKRFGEVLIDTHLF KPCCSNKKAAAEKPEEQGPEP LP ISTQEWVTEVFM
23768	54136	A	23906	3	1059	

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23769	54137	A	23907	1	1697	MRPCALCWRSAVTAAPERAVL ESRGGAPDTPRRLHSFTQTRSL PQAAGPHTRLHPHQGHAMHR GGGRVTDTRRHIPNADVPRYK LTCTGGVTTFVALYDYESTRET DLSFKKGERLQIVNNTKGDW WLAHSLSTGGTGYIPSNYVAPS DSIQAEWYFYGKTRRESERLLL NAENPRGTFVLVRESETTKGAYC LSVSDFDNAKGLNVKHYKIRK LDSGGFYITSRTQFNSLQQLVA YYMSHCPPFSAAGWYGGGCP EEPQKHADGLCHRLTTVCPTSK PQTQGLAKDAWEIPRESRLLEV KLGQGCFCGEVWMGTWNGTTR VAIKTLKPGTMSPEAFLEAQQV MKKLRHEKLVQYAVVSEEP YIVTEYMSKGSLLDFLKGETGK YLRPLQLVDMAAQIASGMAYV ERMNYVHRDLRAANILVGENL VCKVADFGRLARLIEDNEYTAR QGAKFPIKWTAPEAALYGRFTI KSDVWSFGILLTELTGKRVVPY PGMVNREVLDQVERGYRMPCP PECPESLHDLMCQCWRKEPEER PTFEYLQAFLEDYFTSTEPQYQP
23770	54138	A	23908	1	736	MDPGAALQRRAGGGGGLGAG SPALSGGQRRRKQPPRPADFK LQVHIGSRGVGKTSMERFTDD TFCEACKSTVGVDFFKIKTVELR GKKIRLQIWDTAGQERFSSITSA YYRSAKGMLVYDITKKETFDD LPKWMKIDKYA/SEDA DLLL VGNKLDCE/TDREITRQQGEKFA QQITGMRFCESAKDNFNVDIEI FLKLVDDILKKMPLDILRNELS NSILSLQPEPEIPPELPPRPPIHVR
23771	54139	B	23909	84	441	
23772	54140	A	23910	6	254	
23773	54141	A	23911	1	230	
23774	54142	A	23912	3	187	
23775	54143	A	23913	3	143	
23776	54144	A	23914	3	481	
23777	54145	A	23915	1	711	
23778	54146	A	23916	55	381	

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23779	54147	A	23917	240	875	GLSAESTPTSIMSMTLGWDIR GLAHAIRLLLEYTDSSYEKKY TMGDAPDYDRSQWLNEKFKL GLADFPNLPYLDGAHKMHPEA TPFLCYIARKHNLLGETGRRE KISSWDILNENQAMDVSQNLAR VCYSPDFEKLKPEYLEELPTMM QHFSQFLGKRPFVFGDKITFVD FLAYDVLDLHRIFENCLDAFP NLKDFISRFVSCGIM
23780	54148	A	23918	64	774	CLSAESAPTSTMPMTLGWDIR GLAHAIRLLLEYTDSSYEKKY TMGDAPDYDRSQWLNEKFKL GLADFPNLPYLDGAHKITQNSA ILRYIARKHNLCCGDRRREKIS CWDILENQVMNHNMEVLRLC YDPDFEKLKPKYLEELPEKLKL YSEFLGKRPCFLGDKITFVDFL VYVDVLETKQVFEPKCLDAFIQ NLKDFISRFEGLEKISAYMKSS RFLQELVFSKMAVWGNK
23781	54149	A	23919	163	317	LSPNNYYRKLQPKVKLE*RYHR LALFSFPTKLTPKVSLLCCRFL EMGYIF
23782	54150	A	23920	62	255	VRLTAQKSLGPLTSTHSLWGS ARARHREPVGSVCGCDPCEQLL LLVSQLRAPGVDSAAAGRPV
23783	54151	A	23921	173	467	KSRFCFFGVVLKPKKLHIR*WI GATL*NQP*TIFQTDGDCSHQSL GPLPACDLWDQLHLRSKGGGS VCGCDPCEQLLLVSQLRAPGV DSAAAGRPV
23784	54152	A	23922	35	548	PRSCPSLSPGLSCLLQRLVNYQI SIKCSNQFKLEVCLLNAENKVV DNQAGTQGQLPAVGQARWGS GCRGAHTWPLAVIGAADCTG QRGWEGV*AFPGLTEPVSSLFC GQDGD/CSPHSM*VLSHVVLWL LNLGLCSLVLGSVCGCDPCEQL LLLVSQLRAPGVDSAAAGHPV
23785	54153	A	23923	1	599	MSPAGLVNYQISVKCSNQFKE VCLLNAENKVVDNQAGTQGQL KGRPDGAQAV/VGAHTWRFGC RRCC*LHRSHWGL*LLHTPCGR PHCARHREPVAHSLLCRAISGS EPHFQCSVQ*PQLCVPRVAT PLGELSDGDCSHQSLGPLPA CDLWDQLHLRSRQGGSVCGCD PCEQLLLLVSQLRAPGVDSAAA GRP
23786	54154	A	23924	290	528	

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23787	54155	A	23925	274	571	KSRFCFFGVVLKLPKKLHIR*WIGATL*NQP*TFQTDGDCSHQSLGPLACDLWDQLHLHSRQGGSVCGCDPCEQLLL\VSQQLQAPAI DSAAAGRPV
23788	54156	B	23926	204	410	
23789	54157	A	23927	29	330	YLGVELVKSAYPFFQIHLSPSCMWL CGLFLFYIDFL TLMCGDKPLICKKHQLSASTCA/CTIC*GAL TLLMEIEQGQCDLSCASREVSTARSLAELFSGP
23790	54158	A	23928	259	699	ETSHQVMDRSNPVKPALDYFLNRLVNYQISVKCSNQKLEVC LNAENKVVNDQAGTQQGLKV LGANLWWPYLMHEHPAYLYS WEDGDCSHQSLGPLACDLWDQLHLRSRQGGSVCGCDPCEQLLLVSQLRAPGVDSAAAGHPV
23791	54159	A	23929	245	695	
23792	54160	A	23930	302	745	ETSHQVMDRSNPVKPALDYFSLNRLVNYQISVKCSNQKLEVC LNAENKVVNDQAGTQQGLKV LGANLWWPYLMHEHPAYLYS WEDGDCFTPKALDPLACDLWDQLHLRSRQGGSVCGCDPCEQLLLVSQLRAPGVDSAAAGRPV
23793	54161	A	23931	2	293	VFCHTDLRKNLTVDDEGTMKVEVLPALTDNYMYLVIDDETKEA AIVDPVQPKVVDARKHGIV KLTTVLTHHHWDHAGGNEKL VKLESADLGIRLF
23794	54162	A	23932	1	441	
23795	54163	A	23933	1	630	
23796	54164	A	23934	3	265	
23797	54165	A	23935	3	1062	SAVQPGPVMVVGRCGRSRLAALGAACARRGLGPALLGVFCHTDLRKNLTVDDEGTMKVEVLPALTDNYMYLVIDDETKEAAIVDPVQPKVVDARKHGIVKLTTVLTHHHWDHAGGNEKL VKLESLKVGDDRIGAL THKITHLSTLQVGSNLNVKCLATPCHTSGHICYFVSKLGGSEPFVVFTGDTL FVAGCGEVL MKGLRDEMCKALLEVILGRLPDPVGSASLRAGRVYCGHEYTIKQTSKFARHIVETGNAVAIREKLPWA/KEKYSIGEP TVPSTLAE/EFTYNP/ FIKVREERCKQHVAGETDPVITMRPVRRKDKQFKM/PRDLRPPLHLQQDLGIKALLDRLF

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23798	54166	A	23936	107	750	SHLWSPVSEPLQACSFC/VIRDK YRYFACLMRARSEHTNEKDM MKAIRLLKEAEEEFWYHQHPQ PCIFPDSPRGTSYVTHECYKVPE WCLDDWHPSEKAMYDPYFAK RKQWKLLRRRESWKREVKQLQ EETPPAGKEECKLHEGMNYYV LTCIPGAIKQYLACRSYKTPGP RDSCEWVQSDNQCWWWLDSDG AHGLVTSFKGVMMTVEATTM AAVF
23799	54167	A	23937	3	718	PASTISCVSTRSRAVSRLSARP GKVSAMASLASGPYLTHQKQ VLRLYKRALRHLESWCVRQDK YRYFACLMRARFEHKNQDM AKATQLLKEAEEEFWYRQHPQ PYIFPDSPWGHPYERYDCYK VPEWCLDDWHPSEKAMYPD YFAKREQWKLLRRESWEREV KQLAQEETPPGGSF*LEALPPGP KRKVLPLWVYIVTRPRERP MLERERPHLSCLQVKYVTEHG
23800	54168	A	23938	269	488	TDGVIFIGLSWSPRRCGLGIRD AERIFFALDQASCGFTIHPHIDA AETPRGLTMHLCRRCQRGQSQ AEKLP
23801	54169	A	23939	1	1560	MVHLGAPVMALNLQGGKHLCD STASSLLPRRRESNSDDTARED ARQKRPAINTDMRTQELQTRET GQGTARETEVATPLSGPSAGDS PPAAASEMSCGQLVLALLLFFL LVWNTGTGKSGSGRVARLAQLA HDCDGGALGLCYAVLDQRSV VQATPQAPKPGPVQPLTVQGL QPVHVAQESSGNEITARRQSAR SRPRGDRTPASRRVTRRPKHAP ERAPIQQGNIVTVRAPTARKKW RPAVGTPTGAHPVCTAKGTGG RPTPTQAHTRYTERDPIRNSAEL TGSRRPCTGRERSGVEACKAAV HNLLVAQTGSSGLIINYPLDDIQ DAIAVEAACTNPALFLDVSQD TPINSIIFSHEDDVWRTPLVAPT NLNTRSSQPARHHRAGAVRRH HMTVARSATAHARLRRHAKPQ GRERIKPSGAREGSEPLGGESGI RTPRGRERDPNPSGAKAGSEPG RIPETLPRCKGETEAKCWARGN FHTAQGSWPRGGRSRWEPLA PALSQQAHHGELPLPAAARSHR
23802	54170	B	23940	98	229	

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23803	54171	A	23941	1	256	
23804	54172	A	23942	289	433	VLWSCAAEDFDWL VYRPIGSA LSCLRGIPWAIGMWETGFP*VL WSCAAEDFDWL VYRPIGSA LSCLRGIPWAIGMWETGFP LLSVLS
23805	54173	A	23943	450	1260	LCACVVGGEKRSGRPRIGCAGA GKDPFWRAVGVAAQAAAVVA CGAASPYRNRAVSVSDHSQS RGPGLSLSGGTVCMDGKKT RTADSSSEDEEEYVVEKVLDR RVVKGQVEYLLKWKGFSEHN TWEPEKNLDCPELISEFMKKY KKMKEGGNKVKRESESSKR KSNFSDSAEDIKCKKKREQSD IARGFERGLEPEKIIGATDSCGD LMFLMKWKDTDEADLVLAKE ANVKCPQIVIAFYERLTWHAFA PEDAENKEKETAKS
23806	54174	A	23944	3	267	AMVGGGGVGGG LLENANPLIY QRSGERPVTAGEEDEQVPDSID AREIFDLIRS*AWPLTPQAYW YPGPSSCQGCYRCFLES LTMRN
23807	54175	A	23945	1	942	
23808	54176	A	23946	3	470	AMVGGGGVGGG LLENANPLIY QRSGERPVTAGEEDEQVPDSID AREIFDIRRCWARAGSGGLRW GEQ*YRAAGGAASQGVPGRG F*VGKGAESLFLHFPQ/LIRFLN DP/EHSLTLEELNVVEQVRVQV SDPESTVAVAFTPTISHWSMGT
23809	54177	A	23947	2	604	ARSHRISGGGSAMVGGGGVGG G LLENANPLIYQRFGERPVTAG EEDEQVPDSIDAREVFDLIRSH QMTPEHPLTLEELNVVEQVRV VQVSDPESTVAVGFPKPTHSGT CRHIGPPLIGLSIKVK/LRLSLPS AFSRWDVAHLPGDPLPQEHHA VEQATLQIKEAGWATALGRTH HLLEVVNQCLSSPAGTWAFF
23810	54178	A	23948	1	1002	

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23811	54179	A	23949	89	2587	STSRDRRLSKRSRTTMAAQPRG GDYRGSFLLSILGTPWEAWAG RILYSVSEETDKGSFVGDIADL GLEPRELAERGVRRIISRGRTQLF ALNQRSSGLVTAGRIDREEICA QSARCLVNFNLMEDKMNLYPI DVEIIDINDNVPRFLEEINVKI MENTAPGVRFPLEAGDPDVG TNSLQSYQLSPNRHFS LAVQSG DDETKYPELVLERVL DREERV HHLLVLTASDGGDPRSSTAHIQ VTVDVNDHTPVFSLPQYQVT VPENVVPGTRLLTVHAIDLDEG VNGEVITYSFRKIIPKLPKMFHL NSLTGEISTLEGLDYEETAFYE MEVQAQDGPGLSTKAKVLITV LDVNDNAPEVTMTSLSSSIPED TPLGTVIALFYLQDRDSGKNGE VTCTIPENLPFKLEKSIDNYRRL KVTTKNLDRETLSLYNITLKATD GGTPPLSRETHIFMQVADTNDN PPTFPSSSYVYIAENNPRGASI FLVTAQDHDSEDNAQITYSLAE DTIQGAPVSSYVSINSDTGVLY ALQSFIDYEQRELQLRVTAHDS GDPPLSSNMMSLFLVDQNDNP PEILYPALPTDGTGTMELAPRSA EPGYLVTKVVAVDKDSGQNA WLSYLLLKASEPGLFAVGLYTG EVRTARALLDRDALKQSLVVA VQDHGQPPLSATVTLTVAVAD SIPVELADLGSLEPSDGPYNYDL
23812	54180	B	23950	165	335	
23813	54181	A	23951	217	859	GSAMAQQRALPQSKETLLQSY NKRLKDDIKSIMDNFTEIJKTAK IEDETQVSRATQGEQDN YEMH VRAANIVRAGESLMKLVSDLK QFLILNDFPSVNEAIDQRNQQL RTLQEEDCRKLITL RDEISIDLY ELEEEYYSSSPGSLVVSQQLSEQ QLLSSAWTAWPKVTLSSLAPGP QYSVNGPAAIIAHPGT CASAGIS SLLPEPVLVLPVF
23814	54182	A	23952	1	1263	

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23815	54183	A	23953	70	2530	PGVSRLVSKLRRARGMGSGAG ELGRAERLPELFLFLTLFCPAL CEQIRYRIPEEMPKGSVVGNLA TDLGFSVQELPTRKLRVSSEKP YFTVSAESAELLVSSRLYREEIC GKKPACALEFEAVAENPLNFY HVNVEIEDINDHTPKFTQNSFEL QISESAQPGTRFILGSAHDADIG SNTLQNYQLSPSDHFSLINKEKS DGSKYPEMVLKTPLDREKQKS YHLTLTALDFGAPPLSSTAQIH VLVTDANDNAPVFSQDQVYRVS LSENVYPGTTVLQVTATDQDE GVNAEITFSFSEASQITQFDLNS NTGEITVLNTLDFEEVKEYSIVL EARDGGGMIAQCTVEVEVIDE NDNAPEVIFQSLPNLIMEDAEL GTHIALLKVRDKDSRHNGEVT CKLEGDVPFKILTSSRNITYKLV TDAVLDRQNPEYNITVTATDR GKPLSSSSSITLHIGDVNDNAP VFSQSSYIVHVAENPPGASISQ VRASDPDLGPNGQVSYCIMAS DLEQRELSSYVSISAESGVVFA QRAFDHEQLRAFELTLQARDQ GSPALSANVSLRVLVDDRNDN APRVLYPALGPDGSALFDMVP HAAEPGYLVTKVVAVDADSGH NAWLSYHVLQASEPGLFSLGLR TGEVRTARALGDRDAVRQRL VAVRDGGQPPLSATA TLHLVF ADSLQEVLPDITDRPDSDLQA
23816	54184	C	23954	75	149	
23817	54185	A	23955	442	618	CQRLRSWVSQPSFSFSPFTE* NILCLFVYLEVEFPSCCPGWSN NWKSSGKALEAN
23818	54186	A	23956	1	245	

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23819	54187	A	23957	30	1079	APCASFLTPLAAASVGKVLG LRGAAPMASVLSYESLVHAVA GAVGVSVTAMTVVFPLDTASIF DFSVDPKRKSKTTHMVVLEIK EEGLLAPYRGWFPVVISLCCSNF VYFYTFNSLKALWVKQGHSTT GKDLVVGFGVAGVVNVLLTTPL WVVNTRLKLQGAQFRNEDIVP TNYKGIIDAFHIIIRDEGISALW NGTFPSLLLVFNPAIQFMFYEGL KRQLLTFAPQLSSLDVFIIGAVA KAIAITTVTYPLQTVPLFPQFGR HRLNPNERTLGSLRNILYLLQLI FRTPSREPFYTSVTLVLSVA YPMMPLSNITSAYRIGVLEKGG GSGKSDNSDDDDNDGGV
23820	54188	A	23958	1375	2451	VPRVPFAINVLTHSRQRYRRNL RFYADDPTRV/GGPTYHWVRE AEEERVVDNRMHDRFCELRTA AGHPVEGGRPLVIKITHPAET ALQRFKFLMYQVVASDLDTGL LSPDHTLSPYAKETLKLTLTARGI NFVFATGRHHVDVGQIRDNL KSYMITSNGARVHDLGDLNIFA HNLDRIASDLFGVVNDNPDIIT NVYRDDEWFMNRHRPEEMRFF KEAVFQYALYEPGLLEPEGETK ALLTPGKLKNFLVEKMRTLGT AACPPYHIAFVIGGTS AETNLKT VKLASAHYYDELPTEGNEHGQ GSAMSSWNRNCWKPRNSVLA RSLAVNTSRTTFALSCHVTAH PARSAWASPV
23821	54189	B	23959	1	1386	
23822	54190	A	23960	1375	1609	VPRVPFAINVLTHSRQRYRRNL RFYADDPTRV/GGPTYHWVRE SVEERVVDNRMHDRFCELRTA AGHPVEGGRPLVIK
23823	54191	A	23961	433	741	
23824	54192	A	23962	12	224	
23825	54193	A	23963	3	2053	

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23826	54194	A	23964	1	2408	MGGADIAGPRREHNAKHPTVG LGSAAQTTCLPGPKQKGDPTRH QPVDKRNVDGPRQHFWCWRV EIHKEKRMKTGPLNESELEWLD DILTKYNTDHAILDVAELDGLL TAVLSSPQIEPEQWLVA VWG GADYVPRWASEKEMTRFMNL AFQHMADTAERLNEFPEQFEPL FGLREVDGSELTIVVPPGGRTA TNALSCGSLFGEETSPRGPADS TSQSIGGSGPHDCAKGIALVAA NGGDIRDYEGVDRSAKPQLPMI AINTTAGTASEMTRFCITDEAR HIKMAIVDKHVTPLLSVNDSSL MIGMPKSLTAATGMDALTHAI EAYVSIATPTDACALKAVTM IAGISTFFASSRMALMQASAPSA SFLPVTFTPIAAAQSRRAAAT GYRDRWLCHGDVLLQICANTQ DTVIHALRDIKHNSCPDDCSVQ HDAVIDDGCDFIDYLGGETVV ALNTPRADDYHPVMVLCAKTD KAHRNVIHTSKLCFITLTPESQ RSHGKSSKRVSFCFPVLLKH RRIVAQKYAELAYDLFHLGFD VLIIDHRGGQGRSGLLADPHLG HVNRFNDYVDDLAAFWQQEV QPGPWRKRYILAHSMGGAISTL FLQRHPGVCDVAIALTAPMFGIV IRMPFSFMARQILNWAEAHPRFR DGYAIGTGRWRALPFAINVLTH SRQYRRNLRFYADDPTRIVGG
23827	54195	B	23965	1	3357	
23828	54196	A	23966	14682	14931	EIGPGPRPLPSPLP*ATSTSVLAA SGRPERTRHAGIKIVLEDIFTL WRQVETKVRKIRKMKVTTKV NRHDKINGKRKTAKEQSPLLQE SLFATGDSHNLRLALDVGLLA NLSALAEIDISNNKISTLEEIGF ANLFNLSEINLSGNPFECDCGL AWLPRWAEQQVRV/AAARGS HVCWAWLPGWPASAWHPLAG QWL.W*GVCRLPP*QQLRHRS SVLFSCPRRPA/CSQRPAAPAS PPARASQSPSRA

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23829	54197	A	23967	1	714	MVKLSIVLTPRFLSHDQGQLTK ELQOHVKSVTCPCEYLKRVINT LADHRHRGTDGFGSPWLLIITV FLRSYKFAISLCTSYLCVSFLKTI FPSQNGHDGSTDVQQRARRSN RRRQEGIKIVLEDFILWRQVET KVRAKICKMKVTTKVNHRDKI NGKRKTAKEHLRKL SMKEREH GEKERQVSEAEENGKLD MKEI HTY/MITPSARKPLCNVRMAA AEHRHSSGLPYWPYLTAETL
23830	54198	A	23968	111	216	ALLFPISWTSTPLGTQQAQCVC* PTPMPMKRPVPS
23831	54199	A	23969	1	4710	
23832	54200	A	23970	3544	3723	RSIRSPPRCPPSRAPARRSAAA PPRR*PPRAPAAPRPGPP/CMAR PPPARPTAGSRVPLL
23833	54201	A	23971	3	1119	EFGTSHRHRGTDGFGSPWLLIIT VFLRSYKFAISLCTTYLWVINTL ADHRHRGTDGFGSPWLLIITVF LRSYKFAISLCTTYLCVSFLKTI FPSQNGHDGSTDVQQRARRSN CRRQEGIKIVLEDFILWRQVE TKVRAKIRKMKVTTK\ATRLTK IKERRKTAQDHWRLKLSMKERE HREERQVSEAEENGKLD MKEI HTYMEMFORAQAALR\RAED/Y YRCKITPSARKPLCNVRMAAA EHRHSSGLPYWPYLTAETLKNR MGHQPPPTTQHSIINDNSLSLKT PPECLLTPLPPSALPSADDNLKT PAECLLYPLPPSADDNLKTPEEC LLTPLPPSAPPADDNLKTTPPKC VCSLPFHPQRMHSRN
23834	54202	A	23972	1	1149	

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23835	54203	A	23973	93	1165	HRRSAAEAPAAAVMPFFPGKS HKSPADIVKNLKESMAVLEKQ DISDKKAEKATEEVSKNLVAM KEILYGTNEKDPQTEAGAQLAQ ELYNGLLITLVLADQLIDFEGK KDVAFQFNILRRQIGT'RTPTV EYICTQ'QNILFMLLKGYESP/IEI ALN/CGIMLRECIRHEPLGKIIL WSEQFYDFFRYVEMSTFDIASD A/FATFKGLLTRHKLLSAEFLEQ HYDRFFSEYEKLLHSENNYVTKR QSLKLLGELLDRHNTIMTKY ISKPVNKLKMMNLLRDKSRNI QFEAFHVFKAFVANPNKTQPI DILLKNQAKLIEFLSKFQNDRT DEQFNDEKTYLVKQIRDLKRPA QGEA
23836	54204	A	23974	3	158	
23837	54205	A	23975	3	1071	GVRASGRAVPRAVFAGMKRPC EETTSSEDMDETIDVGSENNYS GQSTSSVIRLNSPTTTSQIMAR KKRRGIIEKR/RRDRINLSSEL RLVPTAFEKQGSAKLEKAEILQ MTVDHLKMLQATGGKGYFDVA HALAMDFMSGFRECLETEAAR YLSSEGLDSSDPLRVRLVSHL STCATQREAAAMTSSMAHHHH PLPHHHWAAAFHHLPALLQP NGLHASESTPCRLSTTSEVPPAH GSALLTATFAHADALRMP/ST GSVAPCVPLLSTSLLSATV/H AAAAATATAAHSFPLSFAGAFP MLPPNAAAAVAATAISPPLSV SATSSPQQTSSGTNNKPYRPWG TEVGAF

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23838	54206	A	23976	1	1416	MPGNLTRKESSPLTDHCHTS SQFSHRFNAISFPFAELGCDHV ASAAADPLGVPGVATQWAGGL SAALAAPRRPHSCRRLLQVLGAL GILKSAGRNVNFRFCGPLSIRGKP KTPLWEQEKPKLQTGSAGSQQ KRVMLKPSRGADRVLGRGSQR PAETDRETTDLRQKRKMKEGK ERTLRAARGETRRSNGNLARQ TVPEGCRSQTALQVVRNART PPCIPNLDRPPEACSSGSTGGM MPLRVASPSVASGESSHLSGR GDRGLVRCKVEELRFQPVAFPE FIPPTSPRADSESGDWCCTVLA NPSKTGGGWEQRKTECPQGR TQNPQQRGS/RNLVLLTAGQES TPRRSQLTRSPAERRTEEQGE DRKNRNLGCNLFPRVPRHARD SQRALRASTQAPKSTFAFPGI HSGAVCSKRRICGVQGEPPFLPF ASQCSSCLKILPSGPTKELTSY LLHSGCGFLDKLRV
23839	54207	A	23977	3	139	
23840	54208	A	23978	141	734	GSOLRRPAFGVRVALEESKGLI RKDCSRGRACAGANACARRRR PPTMSGAAWRGTPLALVRSSRT RGVVAWQWSATRSPSDSCFP VARDKEDGEPKTKHLREEEEE GEKHRELRLRNYVPEDDLKK RRVPQAKPVAVEEKVKEQLEA A'SPEPVIEEVDLANLAPRKP DLKRDVAKKLEKLRRTQRAI GRLLDP
23841	54209	A	23979	3	585	GTVGGVCGPRRSSASPEQDQ DRRKDWGHVELLEVLAQARALF TAVPLSEEDRATVLKAVHKVK PTFSLPLQLPPVNTSKLLRDVY AKDGRVSYPKLHLPLKTLQCLF EKQLHVELASRMCVVSVEKPT LPSKEVTHARKTLKTLRDQWE KALCRELRETKNRLERQVYEG RFSLYPFLCLLDECEVVRMLLQ

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23842	54210	A	23980	1	3778	MRRRGVPGWPGAACVMSALC WGRGAAGLKRALRPCGRPLP GKEGTAGGVCGPRSSASQPE QDQDRRKDWGHVELLEVLQA RVRQLQAESVSEVVNRVDVA RLPECGSGDGLQPPRKVQMG AKDATPVPCGRWAKILEKDKR TQQMRMQRLKAKLQMPFQSG EFKALTRRLQVEPRLLSKQMG GCLEDCTRQAPESPWEEQLARL LQEAPGKLSLDVEQAPSGQHSQ AQLSGGQQRLLAFFKCCLLTDQ
23843	54211	A	23981	101	805	HMYTSMKPSSQPRSWISTPHPK ACSSLSFPLSLDNWMNNINLREVI CTSRDGDKFWRMPECYIRGSTI KYLRIPEIIMVKEEVVAKPR GRGGLQQQKQKGRGMGGAG RVGSPSSGIVPGAGRQPHVAS LLLGVALAALPRRLPNLPGPPS CPLAMNRGPGRGAPRHGTQSS QCASWRSSGHIKSPQAPVSPM RGNGGAHLRSLATTLTLGRGS IQSQGRPPPEMMNWH
23844	54212	A	23982	133	1069	RIAWGQDRSCLQGPFATYVP GLILCSLQGWYGVQAGQDLQG LPRSQGWARRPGGLITCSPSP QDGDGKFWRMPECYIRGSTIKYL RIPDEIIMVKEEVVAKGRIGR EGPCQQAESQK/GVVRMGGA\ GRCVFGGRGRGMGPITG\RGH PDKKPGRQAGQTVSAHPDRL RPLLARVGDFRSTVSENNLLQK GRGRPPRGEPPFRVLVTPSLFKV KAPFFLPKRNQILRVKCLLCCF FGFCETGPSQKLGWNPLERVLC LKAIFSSPFASFGSKASHFRRG LFLHFLGSLSEASNQTGRFLIK
23845	54213	A	23983	1	326	PVSLECYTVPPEDNLALLQLYF RTLVTGA/LRPRWCPVLAYVTL WPHVNSFISQRPRIVDIDGKM GTLSCIQPFNRCLARRRTLCPNG RQETKEQKACLPGSRLFELF
23846	54214	A	23984	2	341	

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23847	54215	A	23985	114	712	DLISALMIWFHVIHTPYVCYI PTLPLSTSFPLSQLPVSLCYTV PPEDNLALLQLYFRTLVTGALR PRWCPVLYAVAVAHVNSFISQ DPQSSVSYSIFGRKGASN*AA SGPAGEEVSVKQGWVVPAL GSVPPLPVLLDEVKAARRSM LQKTWLLADEGLRQHLLHYKL PNSTLPEGFELYSQMPPLRQHY
23848	54216	A	23986	357	2771	FESSCPVGSVPVAGPTPSLYKV PCATAMKLLRLVLSAGRNI RLSSFDLRSRLCRIIAEAPQEL ALPPEEAEMLSTEALRLWAVA ASYGQGGYLYRELYPVLMLRAL QVVPRELSTHPQPLSMQRIASL LTLLTQLTLAAGSTPAETISDSA EASLSATPSLVTTWTVQVSLQPL VEPCLRQTLKLLSRPEMWRV GPVPAACLLFLGAYYQAWSQQ PSSCPEDWLQDMERLSEELLPL LLSQPTLGLWDSL RHCSLLCN PLSCVPALEAPPSLVSLGCSGGC PRLSLAGSAPFFLTALLSLN TLAQIHKGLCGQLAAILAAPGL QNYFLQCVPAGAAPHLTPFSA WALRHEYHLQYLALALAQKA AALQPLPATHAALYHGMALAL LSRLLPGSEYLTHELLSCVFRL EFLPERTSGGPEAADFSDQLSL GSSRVPRCGQGTLLAQACQDL PSIRNCYLTHCSPARASLLASQA LHRGELQRVPTLLPMPTEPLL PTDWPFPLPLRLYHRASNTSPG\ LSPTDTMGVTAMIRVLQWVLVL ESWRPQALWAVPPAARLARLM CVFLVDSELFRESPVQHLVAAAL LAQLCQPQVLPLNLNDCGLRG LTSFPDLYANFLDHYEAVSFGD HLFGAMVLLPLQRRFSVTLRLA LFGEHVGAALRALSLPLTQLPVS LECYTVPPEDNLALLQLYFRTL
23849	54217	A	23987	291	454	KAETGSLPYTLCKNQFKMD*RL TC*T*NHKNPRRKP*YHSGHR HGQRLHDENT
23850	54218	A	23988	1	613	

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23851	54219	A	23989	807	1345	RCEERLLPLNLAVIALPSGLER WSFFAVYNGHPGSQVAKYCCCE HLLDHIADNQ/DFTGSAGAPSL NVKNGIRTG/CPEPEVHDTERSE EDDHFIILACDSIWDVMGNEEL CDFVRSRLEVTDDEKVVYNEIV DTCLHKGSDNMCVIFLWFPN APKVSPEAAKKEAELGKYRLN SILSDQ
23852	54220	A	23990	344	636	SSLSLLDIWVGSKSLL*IVPQ*T YVCMCLYSSMIYSPGLIYPMVG WLGQMVFVLDPGSIATLTST MVELVYSPTNSVKVFLFLRLSS TCCFLTF
23853	54221	A	23991	1	2793	
23854	54222	A	23992	18	409	SSVVEFVDPVRVAPALLPQLPES SSHGSVLPTMAVCLDKGHKMT KNMSKPRHSCRRGRLTKHKFM WDMIREVCGFAPYERHAMVLL KVSCKDKALKFIKKRVGTHIRT KRRQEELSNVPAIMRKADAKK D
23855	54223	A	23993	1	609	MHPRGPPPPAQEESHTDESPGID HQLARRAGRVGRTGGFSQLL AQNTNSMLSSPASCTSPSPDGE NPCKKVHWASGRRRTSSTDSES KSHPDSSKIPSRRPSRLTVKYD RGQLQRWLEMEQWVDAQVQE LFQDQATPSEPEIDLEALMDLST EEQKTQLEAILGNCPRPTEAFIS ELLSQLKETPETQPAISEISLRDH
23856	54224	A	23994	1	204	
23857	54225	A	23995	1	418	MWNRLCNVVTISIGWKSLEGSE EDRKSSQWGTLP SGAVRRGPPS SRSKNGRSNSSLHPVPGKATGT QLEPMRAVMGDESCKATGTGL LHALGAHPLHRLKQHSIMMF QKVQVEPLRKEPHHWQRL*PF SSE*NHGPSR
23858	54226	A	23996	104	253	

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23859	54227	A	23997	666	1436	WRPCFWLQAKKEAPAP/PAKAKVKALAKAKAVLKD VHS HKKKKDKRSPTFRGVPKTLCTRA/KPKCLQKTA PRKNKLDHCAITK/PLTTKSTTKKIEDNNTLVFIVDV KANKHQFKQAVKKLYD TDVA KNITKRWDVTSIITSYIHLRLA SRLALEDLLAGLMNCKLGTFW NEESGERVETRPESRFKQSKLI YTIKNPGRKKYGAEKRAFWC HTDLLLHDHDEQVNHFFSSPST FTKCKRRKPFLREFVWIK
23860	54228	A	23998	2	301	
23861	54229	A	23999	1	242	MGMVRKQALERTEWALVCRQAWSSRMGYSTTVSPTQCQYTC SRGLLDSQLQLYKCTQALPEIH SLGHVCPSLITVKYSHYVLAATA LFIWDDNNESLRTGLLSVSTCK SGRD FMRISGMVSLTSEVDNV EVFHYFPLHIQGGKFWAVGAI MTIFVISIYYEPGAHWHHMWK LLKVYSLESQKREEDISKRLPNF LKSSRRPWEDLILMLRKSPEMS KEYRASPLSLSAALRSKDRQSR HRCVTSTFHIREVRCKSKSGLPLCMHETA AHIC*TEGQQKGSGLLYIP*TSPEIFSASES DPPMAC
23862	54230	A	24000	2	948	CGTPTVVPCTGTSRRVRTATVE PTWKCRAAQPPPPP/PPLWVK LPPPDSTKPELQLEELDADSS WMP L HGSCPTGKLAVDARSSL FTEPAFPYWKMKHTFQNILS WSKFTNLTVSVTQLWLLV VMA QTSYPHSLVGRKQVILHSSCLY SLDNKTS LAGDDHDDDDHDDN DSSPAEKGPPPTKSLDKADEQS HLR LA VLELGFYKPVNLLVA MTGCLLQLMMKKEQCGTHGG EGSTLEGSRPDVPQDLFSPTLGF YGSTLSADLGENVILKLYLPSF PLQESEPSAEHGENLWALYVGF EERSEASLAKAP
23863	54231	A	24001	265	513	
23864	54232	A	24002	513	796	TGTA WTPPPPLTTGAPCTPPPR CTARGRT/PGDHLGGGPAATA GGPRTSPMSSGGPSAPGMRPPA SSPKRNNTSLNLSGLEPTFSFRIT FGFM

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23865	54233	A	24003	1268	2097	TPELTGAISLSTLGDPSFRRQPS AQMGHLLSTSLSTPPTTSNSETT QPFAFATVTPSSSVLPGLPQTSF SGMGPSAELMASTSPKQQLPQF SAAFGHQLSSHGIPKDLQPSHS SIAPPTGFTVTGVKLQTFVAVSVT VLKATCLELFVPPGGFVVSLS GVKLQTVTPLHFGSNHPSAFYY YRLSFEMDKGKKRQFGVEKEK CGSLGGFVMLGNEEMIRRAVT LIAWTKIPFLGIREAKNPGSENI RLATILEAPPPSWELWEQGGPG APYYQP
23866	54234	A	24004	3	1163	GEVTSWNRGRGLRIWRYFLFGP VQKTMRLLSRLTYCWLEQDG RVSWRI.GLEIGSLPTVPVRLCP ANRSPPMVCGTTGRSSNSSTE KRMCTCSSRAALHFLKGPEGG TLMEEIRALIKEPPESSLTPSTRG GHSEKAPSKNHQAATVNTTSL RISHISHTHLIHCTGKEQHEPY EDAATRSRPEADLSRHERLTCR HLDLGLPDMQNRQCVPGSQGL RPVGGLEGPRHWCLVRSSRLG VLPRRPQGCEDDAGGLQRQDC GQWRELVLPTPP/VCPGGASP HPKPLPDLDPFGSSRCFCLLP TCPAAPPAGSPSPCSQSPGCLPP VPTPSVLECCQTVLLEDSPQS HRNSAPHLQPGIWSHIPGSHWP CLVLAAGSTSSV

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23867	54235	A	24005	1	2502	MEARVERAVQKRQVFLCVFL GMSWAGAEPLRYFVAETERG TFLTNLAKDLGLGVGELRARG TRIVSDQNMQILLSSLTGDLLL NEKLDREELCGPREPCVLPFQL LLEKPFQIFRAELWVRDINDHA SVFLDREISLKILESTTPGAFFL ESAQDSVDGNTSLSNYTISPNA YFHINVHDSGEGNIYPVLVNLQ VLDREEIPEFSLTLTALDGGSP RSGTALVRILVLDVNDNAPDFV RSLYKVQVPENSPVGS MVVS SARDLDTGSNGEIA YAFSYATE RILKTFQINPTSGSLHLKAQLDY EAIQTYTLTIQAKDGGGLSGKC TVVVDVTDINDNRPCELLSLT SPIAENSPETVVAVFRIRDRDSG NNGKTVCSIQDDL PFILKPSVEN FYTLVTEKPLDRERNTEYNITIT VTDLGTPLRKTEHNITVLVSDV NDNAPFTQTSYTLFVRENNNSP ALPIGVSATDRDSGTNAQVIY SLLPSQDPHLPLASLV SINADNG HLFALSPWTTMPLRAFEFRNNS PALHIGSVSTAETNIQVTSLLP PRNPHLPLASLVSINTDNGHLF ALRSLDYEALQEFEFVVGASDR GSTALSSEALVRVLVLDANDSS LFVLPQNGSAPCTELMPRAA AEPGYLVTKNAWLS*QLLKAT EPGLFGVWAHN/GTDRLLSERD TAKHRLMVLVKDNGEPPRSAT

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23868	54236	A	24006	1	1960	MEARVERAVQKRQVFLFCVFL GMSWAGAEPRLRYFVAETERG TFLTNLAKDLGLGVGELRARG TRIVSDQNMQILLSSLTGDL NEKLDREELCGPREPCVLPFQ LLEKPFQIFRAELWVRDINDHA SVFLDREISLKILESTIPGA ESAQDSDVGTNSLNYTISPN YFHINVHDSGEGNIYPVLV VLDREEIPEFSLTLTALDGG RSGTALVRILVLDVNDNAPD RSLYKVQVPENSPVGSMSV SARDLDTGSNGEIAVAFSY RILKTFQINPTSGSLHLKAQ EAIQTYTLTIQAKDGGGLSG TVVVDVTDINDNRPELLSSL SPIAENSPETVVAVFRJRD NNGKTVCSIQDDLPFILKPS FYTLVTEKPLDRERNTENIT VTDLGTPLRKTEHNITVLV NDNAPFTQTSTYTLFVREN ALPIGVSATDRDSGTNAQVI SLLPSQDPHLPLASLVSNAD HLFALSPWTTMPLRAFEFRN PALHIGSVSTAETNIQVTSY PRNPHPLASLVSINTDNGHL ALRSLDYEALQEFEFVVGAS GSTALSSEALVRVLVLDAND LFVLFPQNGSAPCTELMPRA
23869	54237	A	24007	1	966	MGHHLMDKLVALGGLYYAIQ RHYATKCSVLKNDQILVIGL IQNVYRKHFANPLSALFLQ ELFAAIAIEHITVAERNHAI RLEAQTFIDSLKEWHNAIRK DYEALQAFEFVVGATDRGFP SSEALVRVLVLDANDNSPFV PLQNGSAPCTELVPRAAEP VTKVVAVDGDSGQNAWLSY LLKATEPGLFGVWAHNGEVR ARLLSERDVAKHRLVVLKDN GEPPRSATATLQVLLVDGFS YLPPLPRAAPAQAQADSLTV VVALASVSSLFLSVLLFVAV LCRRSRAAPVGRCSVL

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23870	54238	A	24008	1	2673	MEVMGNMGSKILITGITSTKRK VALLAKKRERKIISQRKDVTD RAKRQSEESIGKETVVGIGLI SKDSAAAIICESRWLSHFER LIQRRMEARVERAVQKRQVLF LCVFLGMSWAGAEPLRYFVAE ETERGTFLTNLAKDLGLGVGEL RARGTRIVSDQNMQILLSSLT GDLLLNKLDREELCGPREPCV LPFQLLLEKPFQIFRAELWVRDI NDHAPVFLDREISLKILESTTPG AAFLLESAQDSVDGTNLSNYT ISPNAVYFHINVHDSGEGNIYPEL VLNQVLDREEIPEFSLTLTALDG GSPPRSGTALVRILVLDVNDNA PDFVRSLYKVQVPENSPVGS VVSVSARDLDTGSNGEIAAFS YATERILKTFQINPTSGSLHLKA QLDYEAIQYTLTIQAKDGGGL SGKCTVVVDVTDINDNRPPELL SSLTSPAIENSPETVVAVFRIRD RDSGNNNGKTVCSIQDDVPFLK PSVENFYTLVTEKPLDRENT YNITITVTDLTGTPRLKTEHNITV LVSDVNDNAPAFQTQSYTLFVR ENNSPALPIGSVATDRDSGTN AQVIYSLLPSQDPHLPLASLVS NADNGHLFALRSLDYEALQAF EFRVGATDRGSPALSSEALVRV LVLDANDNLFPVLYPLQNGSA PCTELVPRAAEPGYLVTKVVA VDGDSGQNAWLSYQLLKATEP
23871	54239	B	24009	1	993	
23872	54240	B	24010	1	4056	
23873	54241	B	24011	1	906	
23874	54242	B	24012	1	4318	
23875	54243	B	24013	41	1935	
23876	54244	A	24014	3	328	GWQSGPVLGGLCGTAGQSCGD GDGIWWAAQAAGDPAHLRL LTHGQSSVPEAPVRAHQPALP QPRSAARECGR/AGRSTTNSL RKRVAESYMIVAPPMPSSWSS SG
23877	54245	A	24015	114	567	VKKPHSAEWVPLWGLQPGWR QPRCNSGSEKELRRPVNSQEI LSPVTMRKPAVSVCCDLTLREA APPFQRHERTYTGEKPYKCKQC GKAFGFCYQTYILEKAQTGKQP YE/AHERTHWKQNHDCQTFGK AFSSSSI.CIHEKHTGEKLYE

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23878	54246	A	24016	170	491	PAQHQRGLWQSPTHQALTLMLSVHREDWKPVLTINSIYGLQYL FLESKNRWLGLERLGFPCPSGLIT PPTCTGHRSP/NPEDPLNKEAAE VLQNNRRLEFQNVQRSMR
23879	54247	A	24017	1	1062	
23880	54248	A	24018	2	700	RRPTRPGGGSGGGGRMIKLFSLKQKKKEESAGGTGSSSKKASAAQLRIQKDINELNLPKTCDISFSRSQTTLNFKLVICPDEGFYKSGKFVFSFKVGGQYPHPPKVKCETMVYHPNIDLEGNVCLNILRGDWEASPLRLNSIYGLQY\LFLEPNPEDPLNKEAAEVLQNNRR/VCFEQNVQRSMRGGLHPAPPTFERCLKIGLAHTHPPPRPQALASPAKYLLGAMG
23881	54249	A	24019	302	884	PMAPLSSQPTLFPNTLTQAQQVQLTKGLRKWMVQHGGDGVVVEENRTTVPGAPSQTCFVTSF/EVNAPAIQSWCKKQVLDLEEGLWPELLDSGRIEIVSDWWGARHDSGCMYRLLVQLLDANQTVLDKFSAVPDPIPQWEQQCLPFTFTHVFFQHSRWGVRFCVFSEH RGPETHSSGAGPLLSPEQLQC
23882	54250	A	24020	274	866	SLLNLPSSWDYGVVSYEQANCKGEQVFVEKGEYAHWDWWTSSQRTDFSSLR/RPSKVDSQEPKV\YLYENPNFTGKKMEIIDDV\PSFHA/HGYQEKVSSVWVRSGMWVGYKYPGYRGLQYLLKKG DYKDSNF/GARHPQV/QSVRCI HDMQGHQCGAFHPLGTQEELAGQKEQMEQVPFWLARGDICE LSGKKSVI
23883	54251	A	24021	179	374	AASIGRSMTEKAHAGPRPGRN*ADAPSSDTLFPDALLSNQAGRLACWLFSGPQTKNDHFIFK
23884	54252	A	24022	1	141	

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23885	54253	A	24023	1	506	PHSPLWKTL CSPSSGVCCGFVT LFCNDRFACLFQLTPPPSPAWM TAAASLLASLLPALPPLNLQDA KFVEERRKQLQNYLRTVMNKV IQMVPEFAASPKKETLIQLMPFF VMGLQVGMVGLFHFVMMMDQ PQPSLTRADESPCDRVLSPCAA HRKQRDCCLSWKAEPE*FLVK* KTL CSPSSGVCCGFVTLCNDR FACLFQLTPPPSPAWM TAAASL LASLLPALPPLNLQDAKFVEER RKQLQNYLRTVMNKVIQMVPE FAASPKKETLIQLMPFFVMGLQ VGMVGLFHFVMMMDQPQPST RADESPCDRVLSPCAAHRKQR DCCLSWKAEPE
23886	54254	A	24024	1	396	
23887	54255	A	24025	1	1176	MVPGDLSQTSQSLSDFEISN RALINVWIPSVFLRGKAANAFH VYQSQIAGVSGIARKRALIPFGK STFSYVCITNIKLTALPSWDYT CHFNLPKAQKPGPEPTKILTIME WLALLQGDPGSWIQKEFIVGKR GGKMDNILWDQRDVQPPLRLP HQLLHSGGGPLISFRNGGPILV WELRRKGASGKEIVGSRVFRES DEVLVWKNPKTLQKEDEEVNS THPMHTYPCTHCQVFCVTAIEI NTYLQACIVLEMSMLPPGERPLF LLRLTTVLEVTVFDSQWSRPYH VSADPSAWKHHHHYHHHHY QLSSSPITITINHPSPLSHASPS P/CHPSPSPAVHHHHQPSITITSR PSPSPAVHHHHQPSITIIRPSSITI INHPSQASSHHHHQPSIPFIVSH
23888	54256	A	24026	1349	2125	
23889	54257	A	24027	670	972	KTDEWNIYRRYTEFRSLHHKLQ NKYPQVRAYNFPPKKAIGNKD AKFVEERRKQLQNYLRSVMNK VIQMVPPSSLPAPKKETLIQLM PLLRSTSTPPRRAL
23890	54258	A	24028	1	699	

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23891	54259	A	24029	221	864	VDCPRSFSAVVVWQGRFWLLS FIPGGFLGMLTFFASGMNWTVT LLGFLAGNLEVEPSDTIENVKA KIQDKEG/PPDQQLIFAGKQL EDGGTLDYNIQKESTLHLVLR LRGGMKIFVKLTGKTTITLEVE PSDTIENVKAKIQDEEGIPPDQ RLIFAGKKLEDGRTLSEAIFLDV GLLSCTRVSSCGAFLGWSVVI LIPVISTRDDTSTTK
23892	54260	A	24030	2	864	PSFRLA WPEGR LALLGELVCVP VVGGMENGRILVSA DRSGGHI CLKTLTGKTTITLEVEPSDTIEN VKAKIQDKEGUPPDQQLIFAG KQLEDGRTLSDYNIQKESTLHL LVLRLRG/GMQIFP*RP*PAKTI TLEVEPSSHHRKF*RARFQKKE GIPPDQQLIFAGKQLAEDGRT LSDYNIQKESTLHLVRLRGGM QIFVKLTGKTTITLEVEPSDTIEN VKAKIQDKEGIPPDQQLIFAG KQLEDGRTLSDYNIQKESTLHL VLRLRGGC*FSSHGIRSAQ
23893	54261	A	24031	1	124	
23894	54262	A	24032	97	296	
23895	54263	A	24033	71	269	AAGYRCPRHGARGRTAATRR CHPSPAVARPAGCSGPP*CYAL SPDPARTRRGDPTPPCRLPRA G
23896	54264	A	24034	206	667	STRGLPKCWDYRREPPRAKS SFLTAQACEAQKTSATRRKD CFLQPTFWLLPFLVLEKGAPSA CRGKRYVRAVWLSLSTGAILQP YPKLQVSNWL*CARDQEMPEG CL*QSCQTL SLLVLPKEKDV *EISPWTPAPPEHQYTVRTFQSP
23897	54265	A	24035	3	190	GTFKNDLILLISKSY*APLPSD FSHSDTSS*KPSKSLKTYSPPPF SAKTSLLQCPRNILY
23898	54266	A	24036	197	474	SPLSHRGASELLSSLHLRSSCS PKMAETPEAGFQIVHSASPPQG TAPGNPWAAGAGG*HCEPGQL AGPYRAASFFGQA WPPHPRAK LGVS
23899	54267	A	24037	164	323	GQEKITLANMVIPRLY*KYKKI SWAWWHAPVVPATWEAEAGE LLEPGRQLQ

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23900	54268	A	24038	582	1166	HCEPGQLAGHILGQPLSSGRLGH LMASHKLSNNYYRTRDGRRES VPPSIIMWSQKALVSG/KPAERV YGDANHTVGNMCA SRLGGYL GFSIRIVVFIWYLGLSVVVNML VGRQCDWQGLVYGGPELLVFS GNMPGEVARGKHRNEKAPLSM RPASQCRVFCVLKGCSESRHK EQPTDTTIFKNCNTHCEGPWLH
23901	54269	A	24039	1214	3878	
23902	54270	B	24040	62	1242	
23903	54271	A	24041	74	408	
23904	54272	A	24042	790	1877	DEIVDPGSMKWSYKSQLNYKT KRPSVFVLTALHTRPDILILGTLE SGHSRNLTCSVPWACKQGTTP MISWIGASVSSPGTTARSSVLT VLLPQSPQDHGTS\LTQCCTLPG TGVTTTSTVRLDEAYPA\WNLT MTVFQGEGTASTTLRNGSALS LEGQSLHLVCAVDSNPPARLS WTWGSLLTSPSSNGLVLELP RVHVKDEGEFTCRAQNPLGSQ HISLSLSLQNEYTGKMRPISG MLGAFGGAGATALGFLSFCIIF VGVRSRCKKTARPTMGVGD GMEDTINAVRGSASQGTPELN PRQKEQAPQNHGSANALANPP RPEEGEIQYASLSFHKARPQYP QEQAIGYEYSEINIPK
23905	54273	A	24043	183	1176	VHQLVFPRQHQRHSVFPKANSS WIHQLFPQ\QHSYGPSAVSAGQ HQLMVHSLFPQATPAHASISLV FRQGTGHLHRVHQRRIPSAQH RHRLHQRRLLPSAQHQRHRDS VCFPFRAHTRPHCDSIQRQHQL MRSIGLFSSGKTDPTVTLLKEA AAEHEICLCRHPVNLRETKAH LGNAAHAVFPRGNQKKPEMCP YLPTHKLVVPTPLIPLEAALRN IAHSRSIPPKKFSPTPDTSDDY LVFNSFPYSKLTTPKTGGQENL GSTRPIPCNGPPTRGPHNGAKY PGDVSHPGVGTWVANRLTG QYEENGKSFLLICTIATFQVNA
23906	54274	C	24044	178	342	
23907	54275	C	24045	86	283	
23908	54276	C	24046	91	177	
23909	54277	C	24047	11	169	
23910	54278	C	24048	209	673	
23911	54279	C	24049	164	208	

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23912	54280	A	24050	182	255	DAESRRSWQPLPEPLRLPRLSD
23913	54281	A	24051	146	456	LKNHNRSEKPCPTLTDIPPQK KCKWVPLALSADITL*KSFSWL ILAQKAPPLSTL*PPLLPAEQM SFDLILFYLPKSYKVAPPLSSFT ESLFLGLSPAPR
23914	54282	C	24052	90	215	
23915	54283	B	24053	1	1059	
23916	54284	C	24054	129	215	
23917	54285	C	24055	19	347	
23918	54286	C	24056	228	260	
23919	54287	B	24057	406	602	
23920	54288	C	24058	7	375	
23921	54289	A	24059	322	400	FLLSRVPSV*DPTEENTVQLTW EWLP
23922	54290	A	24060	818	1078	ILDVFSYTMKIEPSLRSPISPH YNL*QLPP*LDP*ESGYKTPLSA LLLTFLLYISSFASHKVSSSSVD PLPTCAYLPIGQAHVH
23923	54291	C	24061	1	411	
23924	54292	A	24062	1	861	
23925	54293	A	24063	425	484	
23926	54294	A	24064	1844	2097	HSAGTKLRLVNFLTTLRLVNS VMRLKKSFMVMVQRMVSIPKV WSISLGLLSFVPSVWDPT/ENR TVQLT*HPLPELELGPRLSD
23927	54295	A	24065	729	807	LFSCSCPPKPPRP*LTAEGGLC IFL
23928	54296	B	24066	1	1317	
23929	54297	B	24067	509	810	
23930	54298	A	24068	1	385	MDLPSTVRVTRSSASVMVQGG SEAIRQRQSSAAKPRRSGKESKS LGPEFQGLWEWLPEIYFSQFRR LGNPKSRHQIQCLMGACFVV TERLSFQDSDLAEPRHSYPLQ VKRLDLPTVLETDLEKLDPF TTIPSPVETLQCLFVSLRIKSRVP *FWISQPEL*EINFWQPLPEPLE LWPKAL
23931	54299	B	24069	1	774	
23932	54300	A	24070	350	640	SLQGCLSDNSPTFORCQTQGR LPWSTLGSKSHFSGGVARACY TCQKSGHWAIRNASSPGFLLSR VPSVSDPTENRTVQLTWQPLPE PLELWPKAL
23933	54301	B	24071	85	331	
23934	54302	B	24072	1	1844	
23935	54303	B	24073	1	1169	

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23936	54304	A	24074	63	220	NLTGNIWNREWYSHFDLLD PVGFGSGSIAKMPKRKLFKCHSV *GHWRSKSE
23937	54305	B	24075	497	898	
23938	54306	A	24076	3	678	GGGFSRDRRTIALQPGQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGKIFYFIPKAMG AMEGSGQRRTLDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWVFFQTQRMKFGAVT RIGGLPWEVNPPLSSCSLLRE/KD PPTTSGPQSNQPRKH/LTNFKSG A/CYTCKRSGHWAKCECLPGFL LSRVPVVDPTEN/RTVQLTWQ PLPEPLELWPRLSD
23939	54307	B	24077	522	873	
23940	54308	B	24078	329	530	
23941	54309	C	24079	147	439	
23942	54310	A	24080	3	3889	
23943	54311	A	24081	2	394	
23944	54312	A	24082	1	197	
23945	54313	A	24083	1	205	CLRAGPHALYLLC/NIPEFTFL/S RADFAARSQLVDLLTDP/FQ/QEL EELLQVGA VTLIRILPCLPCLP
23946	54314	A	24084	134	182	SCFIPSSQPVAGTERSRFLGPQY FQTPHNPSGPGGLGNQLMR*AF
23947	54315	A	24085	257	481	
23948	54316	A	24086	415	630	
23949	54317	A	24087	123	340	
23950	54318	B	24088	49	270	
23951	54319	A	24089	1	900	RSRVREVVALLRRGLACIPSLG VWRFPVSGVLA VSDRWCLAVS DRWCLARATLSCFCGAMPYQ TRRQENDLRTASIAV*RRKQQN DH*KQRRWQNIQRKGPKRYIVI AGNSQSHQPMIFSMRLKLPKVT CRDVLPEIRAICIEEIGCWMSY STSFLTDSYLKYIGWTLHDKHR EVRVKCVKALKGLYGNRDLTA RLELFTGRFKDWMVSMIVDRE YSVAVEAVRLLILKKNMEGVL MDVDCESVYPIV*ASN*GLASA VGEFLYWKLFYPECEIRTMGGR EQRQSPGAQRTFFQLLL

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23952	54320	A	24090	1	812	MARTPGAELAVAKYPKKGSQA VHRHSRKQSEPPANDIFNAKA AKSDMQHREVRVKCVKALKG LYGNRDLTARLEFTGRFKDW MVSMIMDREYSVAVEAVRLLI LILKNMEGVLMVDVDCESVPIV LFYPECEIRTMGGREQRQSPGA QRTFFQLLSFFVESKLDHAA YLVNDLWDCAQTQLKDWEGL TSLLEKDQSTCHMEPGPGTFH LLGESPGISAIVQGAIEKSGERSS PPPKRIGSMKEGPMVLPLALDT QCWFPEVPLD
23953	54321	A	24091	152	1209	MPLKNVQNITHFPLEKELALPL LIFSPLHWCSGYLSLPLNPKP HFSNPLLLQVILPALTLVYFSIL WTLTHISKSDASPGECGS*MG* WEQRNLCPSILPLQSPCPTAA VEFEGTRMVAFCELCQSCUSD VDTEIP/ESR*VLAQSGRKKAEY PCPPFFRRN*QCHYLPWETFCPF KHFFFSPLQAFVLLSDLLIFSP QMIVGGRDRLPLVFFPEATLQ SELASFLMDHVFQPGRPGQW CSDSIPGAQ*GLGLGCSKSI*GR KLKSVIPFCLPCEPGDSQEDHLQ IERLHQRRLLAGFCKLLLYGV LEMDAASDVFKHYNKVHQGPS LGFTKPLVMPRFSAAATV
23954	54322	A	24092	37	625	SLMLLTPHFHPPEECPPPIATAH HLLPFLSTWELFLQQLQEVVV KHAEPVLEAGAHALYLLCNP EFTFFSRADFARSQ/LV*DLLTD RFQQ/LEELLQGRELGAGTMG DTPNKGWGGCKTGGMWDL MSSGGKCYCGIFFSILPSQIED EVYNLGSHTETPLCLLQVSGFP PLPHPVFTGVCVGLCSFPV
23955	54323	A	24093	2	198	PNDRSRVTREMSAPSRSLGRFL SVGVWHAPPSLALVPPCRCTRRL KTYHGRGAPLRVELPTCMYRL SNVQGRSGGAPAGVGHLQSLV DEWLDSYKQDQ/DAGFL/ELVN FFI*SCGM*RNSGDYPLTAPGL SWKKFQGSFCEVGTLCVCRQ YILLHDDFPMDNLISLLTGFSDS QVCAFRHTSTLAAMKMLTSLV RVALQLSLHQDINQRQYEAER NKGPGQRAPELESLEKHKEL H*YQAKNLSRARCSTCGASH
23956	54324	B	24094	211	3841	

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23957	54325	A	24095	1	1798	MSLLAFKILVGFEGSKARVQT DLFYRSLVLFLLQICFPLSCFG NWKGEEGGMQRVVLGKNEKI ASPHRLPAPTARFAVSLQNLRI LGAFAQFGPVLFVLWRPLDRDN ASPOSEFLNSCGITAYLVGKRE GGVERGGGGRSSERCRTL SFS PRHSHVFSRPFCKILKKSPGAN GGRCRARGGGLHGARAANPPT PIAEPARLPACLSRAEPEPQAAE PAPPPVGVVRSRPLSHRRHPVV CPAAPIRLINKRLAHSARPAGIC CVSRSGLSALAAAGTASMFQLP ILNFSPPQVAGVCETLEESGDV ERLGRFLWSLPVAPAAACEALN KNESVLRARAIVAFHGGNYREL YHILENHKFTKESHAKLQALW LEAHYQEA EKLGRPLGPVDK YRVKKFPLPRTIWDGEQKTHC FKERTRHLLREWYLDQPYPNPS KKRELAQATGLTPTQVGNWFK NRRQRDRAAAAKNRSQTS PWA EAFRFPECGRSLAKHFAEEPGLI PQAQMLLTILFAFRSGRPDPTRS REHLLRRKPQADAPLEM LQQQ VLSQGSGRALRAEGDGTPEVL GVA TSPAASLSSKAATS AISITS
23958	54326	A	24096	3	1034	GLHGARAANPPTPIAEPARLPA CLSRAEPEPQAAEPAPPPVGVV RSRPLSHRRHPVVCPAAPIRLIN KRLAHSARPAGICCVSRSGLSA LAAAGTASMFQLPILNFSPPQV AGVCETLEESGDVERLGRFLWS LPVAPAAACEALNKNESVLRAR AIVAFHGGNYRELYHILENHKF TKESHAKLQALWLEAHYQEA E KLGRPLGPVDKYRVKKFPLP RTIWDGEQKTHCFKERTHLLR EWYLDQPYPNPSKKRELAQAT GLTPTQVGNWFKNRRQRDRAA AAK\NRLQQQVLSQGSGRALR AEGDGTPEVLGVA TSPAASLSS KAATS AISITSSDSECDI

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23959	54327	A	24097	3	1024	GTRVGVAVRSVRLLLGPGAGL RGGVVLKVSPPCRGRRVPVR AEGARGRGPINKVPGASSGAA VGAARLTAPLLAKAMASKLLR AVILGPPGLGKGAPVCQRIQAN FGLQHLSSIGHFLRENIKA\STE VGE MAKQVYREKVFLVPDIIV TRLMMSELENRRGQHWLL\DG FPRTFGQAEALDKICEVDLVIR LNISFETLKDGLNRRWIHP\PSG RVVYNL\DFNPPHVGIDDVTGE PLVQQEDDKPEAVAA\RLRQY KDVAKPVIELYKS\RGVLHQFS GTETNKIWPYVYTLFSNKITPI QSKESILT\AQWEEPGRCGSFIP IVWCSNWCCCPNLEA
23960	54328	A	24098	2	178	
23961	54329	A	24099	96	340	FGALTRIG\DLPWEINPLSSCSLL PEKDPMTSGPQTDPQKEHLTN FKSAARRSSRTSSHRNLLHVLEI WQLDQGMPAARDS
23962	54330	A	24100	3	155	
23963	54331	A	24101	1	162	
23964	54332	A	24102	1	1032	
23965	54333	A	24103	167	476	TAMLLTQSLFGGLFTPTHMKFG AVTQIG\DLPWEINPLSSCSLLR EKDPPTTSGPQTHQPKHELTNF KSDHHGCRASGNSHSGRMLLIF SPSRGLYACSCVKT
23966	54334	A	24104	371	772	
23967	54335	A	24105	146	312	OKRSIPNSSPIP*SHLLANCTK/ DHHFLNGSKSFQPLLSCKFS* GQHLFQGALCT
23968	54336	A	24106	76	441	
23969	54337	A	24107	1	1284	
23970	54338	A	24108	150	371	EESRAAGIPWPSGQISGTC SKL CGRRFRWNAWPLRFRHLEVLV CWRCGCGLSHSGKELQLFSLI VHLEGEVN
23971	54339	A	24109	280	351	
23972	54340	A	24110	1	483	
23973	54341	A	24111	129	363	FGVVTQIG\DLPWEINPLSSCSL LCEKDPPTTSGPTKKHLTNFKS SKRPLFTLFSNLPHYPSTSFQFS WRYTSISPFPS
23974	54342	A	24112	2	111	
23975	54343	A	24113	3	808	

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23976	54344	A	24114	497	815	TALLLTQILFGGLFIWTRVKFG ALTWIGADLPWEINPLSSCSLLH EKDPPTTSGPQTDQPKKHLTNF KSACFERIKACYHSPATAWPFK AYKLSLQFPHTCPKTR
23977	54345	A	24115	1	753	
23978	54346	A	24116	1	513	
23979	54347	A	24117	625	701	IHVAHKLAVVMGCKRGCLSL FYFQLIWSHKGWVRSGEASHR EMAGLLLLCSS*PPSPCETLPRS EPSL.CDSRSAESRTKTSNLSCIP ASLQQVCGPREFIWSGNHCHPF LPITRCYGCCLYHYCMENSIL
23980	54348	A	24118	458	605	VVEEGIEDKRVYRLGTTGWIGK TIWLVRRRS*TNL*DLSGFWTG KMGEL
23981	54349	A	24119	566	769	IKEKGGLFSFSASNWLKQVTSS FLCSPPLSLLKSSKLLANRDY RMCGPVPANGNRTQQ*SKHVR
23982	54350	A	24120	345	664	GEIAASQEPAGGFGSSAQPCPL PWTGPPTTQAPGH/CNSAPSSRD NASSNGRRQRVPTVPGGGLIL QREHILLPLGPALRAAGKEPAT AATIPESPGGDSDDSR

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23983	54351	A	24121	2	2204	IDMIFTGPPSTPKHKKSQKGS AFTFPQQSPRNEPYVARPSTSEI EDQSMGKFKVERQVQDMG KKLDLFLVDMHMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTIHCNYSYETGPPPEPYSF HQVTIDKVSYPYGFADHPVNL RGGPSSGKVQATPPSSATTYVE RPTVLPILTLDSRVSCHSQADL QGPYSDRISPRQRSITRSDTTP LSLMSVNHEELERSPGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDTDPTPSGSMPLSST GDGISDSTVPLFLSSEILQKQVG QSITSMGLFLSRGSPMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFSLLSVTSYS SFAFHKFSVAVYNISNLKTVDP AKFPTRYCYCLNNRNTDLSDF ALLVDHGNSTSYLTEIFKSTSIL SVNQSNESDCIFCVMTGKSGR NLSDFWEIEEKYPINITYFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIGDLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARPTFLGQGQVPLNPF SFTLSGKSCFPRRQEPNRLFPH PNLLSLCPNPLFCPNPFSTLE GKNHHHPFVSQVFSGLP LWEHSPMAHRLRVQPRQQPPDI HKQVISLQSGHSLLVKSQSWSQ DPIKQLPHHHKNTASVCINPSV
23984	54352	A	24122	2102	2529	ETTMSFIFSLLYPRFMHLSFLVS PALRSISRRALAAFRGRSLDLQ PAMPEPTPS/CGLLCVPSPPMS AAPCSKVPSHLFAFMSCNTAK VCSFTAASETTSPPGGTNNR RATLRAVTLTRRSATLTRSAA SHRSSTV
23985	54353	A	24123	299	567	TAMLLTQSLFGGLFTQTRMKF GAVTQIADLPWEINPLSSCLL IEKDPPTSSGPQTDQPKHLTN FKSGETKEMHFIRGPKTPAPVM
23986	54354	A	24124	684	822	KVKRQSYSQNTFYYPICSRH*IK LQKLNSGPQTPQQLINLAIV

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23987	54355	A	24125	1163	1826	TVLLLTQSLFGGLFIWTRMKFG AVTR/IRGDLPWEINPLSSCSLL HEKDPPTTSGPQTNPQKELLTN FKSVPTPSVAESFQSSFSTDPSD PSSPPQAAPRQAKPGPNSSSASA PRPYNPFITSPHTWSGLQFHSA TSPPPPAQQFPLKKVAQVKGT KWLKTDAAARSPQKPTGTITDAL DNSHSGGPIMDRPLLKSPKQF LRLLVFSKTFISLTILNLQE
23988	54356	A	24126	636	922	TATLLTQSLFGGLFTRTRMKFG AVTRIGDLPWEINPLSSCSLLRE KDPPTTSGPQTHQPKHELTNFK SDKGDMFYPWTQNSSAGHGLG RQPSLGV
23989	54357	A	24127	728	1013	MKFGAVTRI/IRGDLPWEINPLSS CVLC/CREKDPPTTSGPQTDQPK EHLTNFKSGKRPAFYSLQPPSL SLNLFLLSILAPHFNLSLLISIPF IFW
23990	54358	B	24128	1	3993	
23991	54359	B	24129	105	420	
23992	54360	B	24130	45	2866	
23993	54361	B	24131	1	1680	
23994	54362	A	24132	1257	1403	
23995	54363	A	24133	1	2130	
23996	54364	A	24134	1	725	
23997	54365	A	24135	2825	4123	RAADGVITLEDNDPCVKKDSRR FPYEDRLDLVLKGTADIPRLTV HRGSEYIISRAFPCYFIKEQSVI NHCYTEIDLKIFRQYLAPALGV THRFVGTPEFCRVTAQYNQDM RYWLETPTISAPPIELVEIERLRY QEMPIYASRVMFIFRPDNTALP RNDTPQMVKLFMDRFQVVKDI GVIELKVVEDQRTAVVMIFRA FVKEGAVIVIRFDNKEVAFQAM SGNLTVPRTSDYKARDIFFQY RFLTRISTGHGVANNHQIRLRL ELAGIVPLNQLNALLKVYPLS KLCNSPKKQCQLESFRLTQWV VKKPISNRQSGLGIVLPGLFRV LSPGNLSPKGTVILPNEVQPGF LGNLVGPI/RGWIGLS*IYLPHGF TG*QNSAGLADH*RASASPERA GVYPIHNERCAHRASRY*YK/W HPDVSAAADHLLG

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23998	54366	A	24136	137	1199	ISSGGPRELGLKMHVPGSQLSQ LPPGLDSTFEAAIVGNLLDNAF EASLRSDGKNIVELFLSDEGD DVVIEVADQGCGVPESLRDKIF EQGVSTRADEPGEHGIGLYLIA SYVTRCGGGITLEDNDPCAPLT LLIVEDETPLAEMHAEYIRHIPG FSQILLAGNLAQARMMIERFKP GLILLDNYLPDGRGINLLHEL QAHYPGDVVFTTAASDMETVS EAVRCGVFDYLIKPIAYERLGQ TLTGFPQRKHKMLKSIESATQKQ IDEMFNAYARGEKDELPTGID PLTLNAVRKLFKEPGVQHTAET VAQALTISRRTTARRYLEYCASR HLIIAEIVHGVGRPQRIYHSG
23999	54367	A	24137	2	243	RPGRGLGQRGIWEPAAIILDSV AQQQGAWLPHVADFRWRVDV AISTSALARSLQPSVLMQLKLS DGSADLEKRCERRLQD
24000	54368	A	24138	1	1483	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPPEARITRRWRIG EAAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPIV GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNPDQGT SMYHGWVVDLHIHAEDTL LPLF YLGEKDDVTYAIKPTCWPLDI IPSCLAHLRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPSDLRYLQSC EWGDTGIFLKWSCIPAEKGLQT SGAWVEAADIPLLPGSPRRLSP QAGSRGGQGPKHGQQCLKMP GPAPGLQGGSNRDP/AP/GPAV ERAPAAALSSTTIWMPMSLCP WRPVLAACSTMTVRGRSTMYL PTTTGNAGCTWPKASLATRWL SSPMGRQARSLMLGAQVTL SW DRSMPPWRRGRSSGRNLSTI

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24001	54369	A	24139	727	1498	GICIWDRPPGLADQRRSHSHGW WGELATPLPWIII/HLSDSHSGV RVSFGLGAQLPPEVAAMARLLG DLDRSTFRKLLAKFVVSSLQGED CREAAAAVLGSAPTCCRVAAGC LLAGMHTLLQQAIRLPPTSLK PDTFRDPAPGALHPPRPGRGL/G QRGIWE/PSGPSFDSVAQQARV AWLPHVA/DFR/WRVDVTISTV ALARSLLQ/PSVLM/QLKAFQNG SSIPA FEVPPQPKFQELRYSVA/ LVVLKEMADLEKK/C/ERNLQD
24002	54370	A	24140	1	312	
24003	54371	A	24141	2	524	
24004	54372	A	24142	144	494	AGSCPFAAGPGLSGRCFVLR FILIQNRAGKTRLAKWYMQFD DDEKQKLNEEVHAVVTRDAK HTNFVGVSGTFKIIPLPLCWPLL LASVWMFNDNKPGLYLGPPFH NFRGRS
24005	54373	A	24143	1	428	
24006	54374	A	24144	108	422	
24007	54375	A	24145	3	387	
24008	54376	A	24146	3	337	TRLMLLDRSQGKVVYGLVGR* RFQMQMDVLEGLNLITIRNRN KLRVYYLTWLRJIKIMDNDPKLE KKHDWTTAGYMEGCGHYRVG KYERIKFLVIALKSSAEVYAWA PKPY
24009	54377	A	24147	1	340	ERTRMNKQHNSTLAKSRPGNT GPEPLMPQASPGPPGLSQTPP MHRPVPEQEGPHKSLVAHRVP LKPYAAPVPRISLQDQDPTRN LAAFPASHDPDAIPAPTATPSA RGAV
24010	54378	A	24148	335	869	ATPTLLISQKSHFWPQLSSVLLK LTSGEISLQSSPSPICRMKKRR LSPLASGLS*VKSGEWCEVLS RAPLFP/HNPSQAAP/EWEMQG TRPSIPHPLGLAGLPQLQQGRL WGYRNPASPFRTRVAARDCAAG KQVRTGPDARLEGSRPGVRAG LGWGRGYSERVQTCAKSSVSPS
24011	54379	B	24149	158	5640	
24012	54380	A	24150	1	1854	

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24013	54381	A	24151	1	1510	MPCGKGQNLQVPVPSKVLPLGLG EGCKEMWLRKVYIGGEVWVGK SPEPEFPSLVNLCQSWKINNLM STVHSDAEGMLSYFLFEELMRC DKDSMPDGNLSEEEKLFLSYFP LHKFELEQNIKELNLADQVDT THELLTKTSLVASSSGAVSGVM NILGLALAPVTAGGSLMLSATG TGLGAAAATNIVTNVLENRSN SAARDKASRLGPLTTSHEAFGG INWSEIEAAGFCVNKWKAIQG IKDLHAYQMAKSNSGFMAMV KNFVAKRHIPFWTARGVQRAF EGTTLAMTNGAWVMGAAGAG FLLMKDMSSFLQSWKHLE/DG ARTETAELRALAKE/LEQELD RLTQHHRHLPQKASQTCSSSRG RAVRGSRVVKPEGCLATSQPH QHQQERGDRPREDTNEKRG EKWSDFGSVLKGEPTGFVHGL DLWCEGKKSQDNGGLWPEQL AGWSCVHLKWTGGSRSLPVP VLDAACTGTLSPLDTSWRYHPS SIPLPKQLQHGF
24014	54382	A	24152	3	515	VGQTAGAAPGPVQFLSSAWVA LHETELPPLTAREAKQIRREIS RSSKVVVDMLGDWEKYKSSRK LIDRAYKGMMPNIRGPMWSVL LNTEEMKLKNPGRVYQVRSARA OPTGQAVSGAQVSSWRERQDH PGELGVKIMKEGKRSSEHIQQ MDLDVSGTLRRHHIFDRDYG
24015	54383	A	24153	1	1317	
24016	54384	A	24154	1640	4841	TITGSSPLAGGHHSTCRGRMDM VENADSLQAKERKDILMKYDK GHRAGLPEDKGPEPVGINSSIDR FGILHETELPPVTAREAKKIRRE MTRTSKWMEMLGEWETKHS SKLIDRVYKGI PMNIRGPVWSV LLNIQEIKLKNPGRYQIMKERG KRSSEIHIIHIDLVRTTLRNHV FFRDRYGAKQRELFYILLAYSE YNPEVGYCRDLSHITALFLLYL PEEDAFWALVQLASERHSLPG FHSPNGGTVQGLQD
24017	54385	A	24155	1640	4056	

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24018	54386	A	24156	479	3902	GQVDEDVSVKMDTVPVYNLSC ILNEMRDQDKLVEKSYKDAK GCFSSMGEPSLIDPCLEVICYGT QLAQLQGLIRSMEQQLCELCCD AEHQDHEHQVLLDVKTRLEQEI ATYSRLLEVEDAQQGPIVMRA MTSECHWCLAPIRSPDCVCVLR QLHTRSGLIHKRFGKLGFLPER HNPGQLIHQNSGCCSRMYPFD RKLGISVALNIPGGRSYRDLWC LTAVHHIPGIDHRLFTLGRM DMVENADSLQAQERKD
24019	54387	A	24157	780	983	QHQSILGHKYQRSHRSL*AEPE* LECHQPDLAEPADGPPLTRYG IVNAEMGLEQLPKGPSLKEAK
24020	54388	A	24158	773	2016	DWPTLRENKREPTLKYWGLVP LISGMPTWFFFLSACGNLIPSG GIRVPMENMLRVFRAVEEHCP WFPEKGTLSEQWDSVGAQFQ ELVPTGNYVPITVWGDWALLL QFSESGDPLPLQLSSPTGPSLS DQPLPSPTPPPPDDVENSISNSG DFGLTLPPGDLLFPPEPLAAS AAPNRTALGHIYANSSLFKPLQ HLPLESANGSGAKLQFTYNSAG PSPSSAAPRPVVSVQPVTLP TQAASLYPSSHMDTSNHQCTSA SSAPPMPLSHTLIPSDETTCNVF NYPLKKPTGRELREAKNKGSPQ KVHEKTPNGNRCISTEERPHEN KGFNHLLEWLAEKTTIHLDC WFIKDVNREQPDGRDAGDKR LCVKFLREIAANTYKTEVGAAK VMEILLHSHGATTIAN
24021	54389	A	24159	365	675	
24022	54390	A	24160	1	1191	

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24023	54391	A	24161	363	1434	QQGVCSGEKGGHWAPRQVGV YLLPGRVGVCSRVSPSPFGDG LD\$GLARRGS\$V\$ALASGLVEE PMLGPPPHPTPRFKA\$V\$AKSKE DLVSQGFTTEFTIEDFHNTFMDLI EQVEKQTSVADMLASFNDQST SDYLVVYLRLLTSGVYLQRESQ VLRALHRRVDGTVQRSSAKQE VEPMCKESDHHSHHCAGPGPS ACPSRVGVHGT\$AARA\$APPIRTS F/H*GVSP\$KVYLLYRPGHYDI LYKLGLGSSPLGCPGCPLLARA LGHCYRGFSVVVNGPISPPSSCH MTPPPCFIKGGAGGPECVRVPA LLPAWLLCLLPPPRWVPLLF YLLSF\$P\$NR\$RFEGPGLLEAPPA SLGSASFPS
24024	54392	A	24162	2	888	VFRSRHQGCLKMAAEEPQQQN QYPLGSDSEGVNCLAYDEAIM AQQRDIQQEIAVQNP.LV\$ERLE LSVLYKEYAEDDNIYQKQIQID LHKKYFVHPQDQGLTGTCFYS GFRD\$PTWEGTCWIDSKELQRF QGLVS/SQRSKGKTLVSQGLSL EFHNFEGFSTTTFI/VDLIEQVEK ADLCRRPCLASFNDQSTSD/VL VVYLRLLT/SRAYLQRESKFFE FNEGGRTVKE/FCQQE/VEPMW QGEATTSTSLALAQALSVSIQV EYMDRGE\$GTTNPHIFPEGSEP KVYLLYRPGHYDILYK
24025	54393	A	24163	3	819	EGATMAAPPQPVT\$H\$FDMDG LLLDTERLYSVVFQDI/CHRYD KKYSWDVKSLVMGKKALEAA QI\$H\$DVLQLPMSKEELVEESQTK LKEVFPTAALMPGAEKLIHILR KHGIPFALATSSGSAS\$FDMKTS RHKEFFSLF\$H\$IVLGDDPEVQH GKPD\$DIFLACAKRFSPPPAME KCLVFEDAFNGVEAALAAGMQ VVMVPDGNLSRDLTTKATLV NSLQDFQPELFGLP\$SYLEGRA SVFRQPPTLMVHTAGGKGKEIS NSSIPTCAVILAS
24026	54394	B	24164	115	594	
24027	54395	A	24165	4	160	SIIFPAIPVSLK*IKPNCPEPPPDH LLQAAWGCVSLGQGLSYSALN TLLYFT

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24028	54396	A	24166	88	2280	VPLYDRMGGTGLLIPSPFRSL HAATDAHSCKNRHSLTGKTDS LWQQDTKLQTRPKATQGKGES GGCGPHRPLLLLRTKSTPESKS AHDPPVAPAQAGASGCGRGAA QKGFKAACAVDGGQDRDTPG VPAAGPPTSSGRGDRGPSSRRR TRSQTPESTGRPGSRQFQAAPP PSHHSRPAHAPFPGFQMYRGPL YSSSPAPATPNTSAYESPRFCST SYISSSPRFCTPSYICSSPRFCSTS YICSSPRFCSTSY
24029	54397	A	24167	2	352	WRITLIVLGMSCLSGYPK*MHLT HLIHC*S*EARSLVTLHIPLTICG EPRNIKLVCGP*IQWKK**KKI MNSRLSPFSRSRY*TSNLLGLP *LRGLSPVERELKLWTRHKL
24030	54398	A	24168	2	252	NKSSVFATSCSLDPSIMSLM*W TSVISCRSKK*SRSLRIRL*HKA KELIYPLPVRESMWGYCQLLS MSMPIMHAGTGEMTTG
24031	54399	A	24169	1505	1680	RTSSSLVTL*TLHEPAGT*VLTP GSTTGITVSGTVLFLILLSCFLSS TPFRLKLACLS
24032	54400	A	24170	681	932	
24033	54401	A	24171	1740	1950	HHHHLLQMSWSAGMQAWHW PSFYNVVTGKTLA/LPNLIALQH IPLSPAGVIKRPAPIALPNSCA ALLSSQ
24034	54402	A	24172	1	652	GKLTEARTRCCMQLTSDRHRH TALNHTTCSHHCSGVMAGRL GPITVLSGDGPKGMRALTMW HTLARPTGDLEAPRHGRPRIT ATQPDHAPPATSRNRAAPHN HTP/PHPQTAH/PTATHSHLTYR TPRPPTARTPL/HPHSHQQYPY Q/PTQSPYLLHPPAPPISLHPS TTRATVNAPDTRPTIYARESVPF GRLLNLGRQGMELANILQVH GP
24035	54403	A	24173	267	400	RFLHCGNLAGLLVGLFSFKLGE YEGGLPLAALTAGKGLFFLPLE SRLRLHRRPKRSPASFG*VSRH THAIHFN
24036	54404	A	24174	422	452	
24037	54405	B	24175	131	1047	
24038	54406	A	24176	2	199	LGLR/CARLEARARPPWATVRE KLWLFHGHPTHMRCSSWRGLFQD DLGLQKPLSGSSSAYRGCE NS

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24039	54407	A	24177	440	1746	RNLQCVFQGRIKEGIPVLALS/L RPSPI/VLHTATKQKNSCOHLE EDVDQTKWRDTPSMDKILME EVKLEEQLEAVEEDKQALAD TEGSEQSSQKLVEEGNMYSIQG FCKDSLEVADVLEKATQCVPEE EIKDNNPHLKNLCETLTMSEEL SQMVDCCRLPQDVSVLGVALH WVTPQMLCVPVNEDIPEVSDT VLKAITAPPRVPIGRTSGDVTGT GVRRRRVSSAMSQHRAFRDVT VTVQCLELGCFLRLVELASQFL KRPRSPESNEKVPEIEVTVEASA KMSHPTLYDATRSPWGMFQSQ SVLLSCAHHSLLRGATLDRCGS IDEESEWYGMDTFECTGVGVSI RRATEPERSSGSAAALDSHRSM HPIVNHACEGSTLRCPYENLMP DALSLSPILSSRSGDASPPQAEILP VVGPFMRMRCLTVDPPLDVT
24040	54408	A	24178	391	656	

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24041	54409	A	24179	1	2150	MEDSTSPKQKENQEELGETRR PWEGKTAASPQYSEPESEPLE AKQGPETGRQSRSSRPWPSPQR AKTPLGGPAGPETSSPAPVSPRE PSSSPSLAPARQDLAAPPQSDR TTSVIPEAGTPYPDPLEQSSDKR ESTPHHTSQSEGNTFQSSQQPK PHLCGRRDVSYNNAKQKELRF DVFQEEDSNSDYDLQQAPGGS EVAPSMLEITIQNAKAYLLKTSS NSGFNLYDHLSNMLTKILNERP ENAVDIIFENISQDVKMAHFSKK FDALQENELLPTYEIAEKQKA LFLQGHLEGVDQLEDEIAENA LPNVMESAFYFEQAGVGLGTD ETRYRFLALKQLTDTHPQRCRF WGKILGLEMNYIVAEVEFREGE DEEEVEEDVAEERDNGESEAH EDEEDELKPSFYKAPQAIPEES RTGANKYVYFVCNEPGRPWVK LPPVIPAQIVIAKIKKFFTGRLD APIISYPPFGNESNYLRAQIARI SAGTHVSPGLGFYQFGEEEGEEE EEAEGGRNSFEENPDFEGIQVID LVESLSNVVHHVQHLSQGR NWFNSIQNEEEEEDEEKDD SDYIEQEVGLPLLTPISEDLEIQN IPPWTTRLSSNLIPQYAIIVLQS NLWPGAYAFSNGKKFENFYIG WGHKYS PDNYTPPVPPVYHE YPSVPEMAEMDDPSVEEQAF RAAQEAVLLAAENESEDEDE
24042	54410	B	24180	1	489	
24043	54411	A	24181	39	423	RSPTPDAASRSQCSSRRRRGVS KEVFSVSMARTKADWPANRTG G*STPRKPTGPTKSPLRKSAP/A PTGGGERNPRLQGLVTVAAP* NLDGYQKVHNSFLIRKLSLPSV WVREIASGLLKQNLRFQERQ
24044	54412	A	24182	3	384	
24045	54413	A	24183	1	434	MLQNVTPARAEWQRKTALQG VEDPVPARPPISSPEDLLRSGET STAPTQRQVPQPVHE/SHRPTQ DSPGARRKPTSERGHTEQRAAP DREARPATRGWGLRPGGWLG GSEHAAAAPGSDHPRGRCRH HTILQRPLLSGKTES

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24046	54414	A	24184	15	286	LPSRGAWLGTCSPPCLSLPPP WAPVRPEPPR*APPPAPRRPVPS TTQGLSGPHCFYEL*HSPRRSA ASLLKPARPRAHQEERTTPDAP P*EL*HSP*RSAASLLKPARPRA HQEERTTPDAPP
24047	54415	A	24185	2	214	CLSLPPPPWDPVRPEPPQ*VPSP APQHVPSTTQGLRSVGARRGT GRQLHLQSRGIIHWVKPAGLL SLGL
24048	54416	A	24186	308	311	LPSHGAGLGTCSPPCLSLPAAP WAP/RVARASPTSAATPQHVP PSTTQGPLGSPSTLRKL*SFALC NKSCCCLFGSTLPL*AVTLTA KVCSTPKA\ARP
24049	54417	A	24187	1	669	MMNEGSGISLSCDLGTALQLL SQAIVECLKLFQMLNRSTILGSG GQQPSSHSTKLRPDSGAQLAS PSGCTGAAGGAACQSRITVCSH SSALGWSMGLGAVEQGVVLV GEAQAAQEPMEGVGGSGMAG CRSRALPHGKAARKARAEHST GGLALLGDPVHSPQPLARVLSP SLPRASAGW/PAPSAGPPSPHP PGTPAGPQAPHAAPVPARASPS TPPCKL
24050	54418	A	24188	157	395	RCSSCQREMTPTYGK*NVQKRL KTTKNGSM*LKSHILSTPEQPA SPTSS/PPLLQPAAPAPLMPRPS PPPGISVA*YPGM
24051	54419	A	24189	2	287	CLSLPPPPWAPVRPKPPR*ATPP APRRPVSTTQGLRSAGARRGT GRQLHLQLPCGIIHWVKPAGLLS LVGTWRTFMSSSGIVNTPISTLC LAQGL
24052	54420	A	24190	500	724	
24053	54421	B	24191	1	2154	
24054	54422	A	24192	688	1215	SRLAPALLSPVVVDGTGRCGA VGGAHWGGLGRTGAHGGGGR LRHGGLRVSPAPREGS*GPPR YRAQRWWAGT/DWRTQYTLRS CWPGTLPK*REMTPTYGK*NV QKRLKTTKNGSM*LKSHILSTP EQPASPTSS/PPLLQPAAPAPL MPRPSPPPGISVA*YPGMPWTC PFYWQ

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24055	54423	A	24193	308	1131	VLQLLRRTWWSCLRAWSDWL IVPPGGLVVSASGVKLQTFVAV SVTALKEARLDLFVPPGGLVVS LASGVKLQTFVAVSVTAHKSSV DPKNSGQALASPSGSRTEAGG AACQSRVVRSHSSALGWSMGL GAIEQGGAALVRGGSGRTGPME WVGSGSMAGCRSRLPRGKA AKAQREIEHSAGGPALLGDSVH PPQPLARVLSPPLPASRACWL LRVRGPPSPRPPTAGPQAPH AAPVPARASPTPLVHLTNDV LRVKVKWAFFTLHK
24056	54424	A	24194	192	818	SWCLSRVAVGDSMTSEVIED\E KQFYSKA\KTYWKQIPPTVDR HAWGEGPNKTGTSCALDCGAG IGRITKRLLLPLFREVDMDVITE DFLVQAKTYLGEEGRVRNRYF CCGLQDFTPEPDSYDVIWQIW VIGHLTDQHLA/ESFLRPCKGQ ASAPNGHIVIK\DNIA/QEGVILD D\VDSSVCRDLVVRRINCSAG LSLLAEERQENLDP
24057	54425	A	24195	1	233	FFFFETESRCVARLECSGAISAH CNLCPLGASNSPASASQ/CSWD YRCVP SRLANFLYFSTDGSPC WPRMVSNNLTS
24058	54426	A	24196	240	476	LLPQYRRVLLIYSGIQLPLGLGL RRRMCPGIYSFLDLFLVYLRRG VYSIL*W*FV FVVLVPWFSAPS GHLRSSLCCLF
24059	54427	A	24197	288	677	NLPEDVVPDDKPHQPLLRAVC LFVISKDLFLESPPESPIWRMYP NSTVHIQRLELALLC/CHCPRAL PASAHSCHSLERGLPICKE**CM PCSEYTIASQRQAGGAPAILPEC DSRRRTTQATSEPGSHI
24060	54428	A	24198	99	399	LLCHGFEHPPLAQRSLLLPIV*S LLLSTRQSHSPSSFVPLLARSCG SWVSPAEEAEPQILQKGKCSCL IVPLEALCQRGTRLSLWLPLTF PSFQLWPV
24061	54429	A	24199	1	586	LSFFKVFSSFAIGSNILFSSEKFI TDHLKPSSPTCQSHLSSSFVPLL ARVAFRWGFGVDVLSFVSFSPN SQDPQLQVCGVCWRSTPDRLP GYHQRSGGCGRTADIEPQMLR LIVRLEVLSQLRSTRPQRCSA/L LGASQLGCC/GVRDLLEEAVC PFSDL/KLHAGKTTLFLKAVRQ/ SHLSLQRLLLSFVCLCPT

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24062	54430	A	24200	1	822	
24063	54431	A	24201	1428	1801	RSAGIDPE*FFSG/PRRIHTASCL PSQRSSNRACSSSVTRIVSILSRF IGIITPMNRNPRFWRNSTSWTR MNRQTSVNRFTTLLMSFTAAA SRVSVMTVKTSDDTCSSRRRSQ LKKYHLSISTQVL
24064	54432	B	24202	1	2040	
24065	54433	A	24203	176	564	AWPEKWSYTTATRTTHFWMRS RSIMSTTKAFSTNSASDSLEEP SSRKTRSSSLQ*KSCNGGSEM SSTYRVVGLTGASLSASALNSLI DSRSNR*VFSRNTLANITRRNQ LKMPLAPDPDGSSGSPFQ
24066	54434	A	24204	1	774	
24067	54435	A	24205	1	1807	MPLRAFNPVSSFRWARGMTIV AALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGEK QAIHAGMAADALGYVLLAFAT RGWMAFFIMILLASGGIGMPAL QAMLSRQPNFDHWTADRHGD LCRLGEHMERVGMDCRRRPIPC LPFRVASRCMEPHLDLNGSRR HLANGFTTFRIGANQFLRRTVN AQTNPWQNISIAISSSTRTRIS GSVGSWPRSGNAEVSALHHYV PDLHRRMLATLWNTYICINEA LALTLSDFSLVPPHPYRQLFTLT TFHNRACSSSVTRIVSILSRFII TPMNRNPPYTEASVTKEKTAL NMARFIRSQTLTLEKLNELDA DEQADICESLHDHDELRYSLC ARFGDDGNSYDHDYAKLACLQ VEGRGGGTFAHELLAVEYAGW ISPAFLKVMHWMNRMRLDAR NRDRYKQWKQDFHDSYNRQS AGHILSQCANLAATTSEYFIHKP HRLIAAETGYSQSTVVRAFREA VNGILSVEIVIGDHRERRADL YRFTPSFLVFAQQAKNALIESKS KISSAATKVRLLAPISPTSPMG KIGLATSGS
24068	54436	A	24206	291	851	
24069	54437	A	24207	2	694	
24070	54438	A	24208	2	331	HLSTIEPEDYNLLFRRVSLKLSV WLPTWQSKSNGWSKKCLWMH LKSNNPLNALLPPAGF*SATMPK CSAWAKTISSPGCVITEF*SQPV NAGTSPNKNNTLVGISPLKKP
24071	54439	A	24209	1	4455	

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24072	54440	A	24210	698	1088	LTSKFIAAVCMRRISLCGKGS QNTD SGIAATPCSCVSD*QNST SRIRM*PWMCPMPMKRSAT*N ITLRC*RAAPISSRVK*/MSM Y/NHLQSAECGGHRPFVPQEE SILLLLHLIANRSSACHSIR
24073	54441	A	24211	1	1902	
24074	54442	A	24212	1	2898	
24075	54443	A	24213	1	2604	
24076	54444	B	24214	1	1254	
24077	54445	A	24215	1	2946	
24078	54446	A	24216	698	1285	RFWRNSTSWTRMNRQTSVNR FTTLMSFTAAASRVSVMTETA MTMITPSLHACRSKAVAAALLP MNC SLWSTQAG/CSP/DVSAEG KPD IYRLSNRKITTCYSAES/LL KLSVWLPTWQSKSNGWSKKCL WMHLKSNL NALLPPAGF*SAT MPKCSA WAKTISSPGCVITEF*S QPVNAGTSPNKNTYLVGISPLK KP
24079	54447	A	24217	1	1986	
24080	54448	A	24218	1	2262	
24081	54449	B	24219	1	1014	
24082	54450	A	24220	1	1155	
24083	54451	A	24221	5	386	
24084	54452	A	24222	1922	2146	SSSAGISCWSSSPTPGSIPSRVGS AAA*GWTTSSSTGSANPSASR KPAAAIRASMPNCRSGEARWP LWSGSL
24085	54453	A	24223	1091	1435	
24086	54454	A	24224	1	2919	
24087	54455	A	24225	1324	1502	
24088	54456	A	24226	1	2901	
24089	54457	A	24227	5	253	
24090	54458	A	24228	1227	3031	

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24091	54459	A	24229	1	1940	MNRQTSVNRFTTTLMSFTAA SRVSVMTVKTSDDTCSSRRRSQL VCKRMPGADKPV EGRGGGTFA HELLAVEYAGWISPAFRLKVN QTFIDYRTGRLQPAIPQSLPEAL RLAADLAEQKQRLQKMLMD APKVEFAERVATASGV LIGNYA KVLGLGQNYLFTWLRDNGILIA TGERRNVPKQEYISRGYFTLKE TVIDTSNGSRISFTTRITGKDVV RTTSIVMLAKVTF LSCITMSDFT FSGYELACFVTHSGLSR SAGHIL SQCANLAATTSEYFIHKPHRLIA AETGYSQSTVVRAFREAVNKG I LSVEIVIGDHRERRANLYRFTPS FLAFAQQAKNALIESKLKISSA ATKV KAVLAKTLALFNFLSTPP CQNDTPSPCQDDVAIKNKKSQ VKKTKRSVSGGAGTTSLKKLTS WIAKAKAKADNLR LSKKRTQK HEFKQKVEAAARKYAYLKNKR SPDIGGISNFDNLPHCMTVNEA LNAVLAKNKDNEQWGA VAGA YIADITDGEDRARHFGLMSACF GVGMVAGPVAGGLLGAISLHA PFLAAAVLNLNLLGCFLMQ ESHKGERRGELLKIVVLPGDHV QGEITAEAIKVLKAISDVRSNV KFD FENHLIGGAIDLQGGGGK PRCVSKSLMLHCTR
24092	54460	A	24230	1	1230	
24093	54461	A	24231	1	799	MKPRTYTVSVTAVKDGVS GVC SFRCSDVSRVSSFQWVRGLADF RSEAADLHNSGAQLASPIGSR T GATSGAPCQSRTHAPALLSLW AVDGTGRHGAGGSTRRQGGSG TQEPMVAGKAQAWRAAGFSG SGDGVGV SILVPWGGTCIGSFR QANSWISGGAFSDAGCDSDR L GKDWNLSLEGSEERKMWESLE LPRDLKSSDRKMWESLELPRD LLNGFDQNA D TICTMKSLRLW SQMEMKNLLGTGVNVT LVM L* QRDWRHLLLV
24094	54462	A	24232	416	775	
24095	54463	A	24233	548	882	PGGHQYPPCHLEEKETD LPLY TAVEEKG LSYIIPGSLVEKPLT STNSSGTPIQSNITSL* IPLAGIMS MAASQN*AI*WPLAPTMQSFTC TT*RLS*SHRRS WWHRGCT
24096	54464	A	24234	144	570	

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24097	54465	A	24235	254	1117	LSRMKRLRTLVSVTVLKDVVS GVCSFRYSVDVSGVSSFQWVRG LADFRSEAADRLGLKLQTFVVS VTPHKGSDPKSDQQRDLQR VKEQNFNRNVKGDPAALAHEDD VNGTESGAPRKHGDRDLDDV ITNPHIEAILENKDWIEDASGLM SHCIAILKICHTLTKLVAMTM GSGAKMKTSIAVSDMIVVAKW NSPRVDDVVKSMYPPLDPKLL DTGTTTLLSVSHLVLVTRNA CHLATGGLDWDQSLSAEEH LEVLRREALVASEPDKGLPGPEG FLQEQAISAI
24098	54466	A	24236	472	844	RTDGLVWMSFLVFSFNSQD PQLQVCWSLLEVHSRCLPGYQ QWRLLCPHEITGESMSKLHIIQK YTSSCCLFKSSISERGSSTPCPSW LGSGEGLSTLHATDFSFSAPMA QRGKSSLVLSLE
24099	54467	A	24237	206	456	
24100	54468	A	24238	50	392	LGLLPFFHRCPTQRGGI*RGSLA TAALLSCGGLCPVGS/SRHLCL/ PVRGKRPTQASVMGDALPPTK LECPRSASGCCAGSDNFKPVDL SLLSSMGLGSTELDLAPWLQP PFQ
24101	54469	A	24239	1	204	SFSVQFCSLVGDPLG*SSCDPLE EKRCSGFWNIQPFCAGFSPSLW DYLVLVFDVDDLQMRSLSGCPF
24102	54470	A	24240	1	375	MCNAQVLEYMGKSSSLTSDL QLVRDALRSLRNSFSGHDPQHH TIDSLQGISSLMERLHVMTQ KKQERKPLVIPRQT/VWWSGP PANSNRPAEAGPDC*KEN*RDA LRSLRNSFSGHDPQHHTIDSLQ GISSLMERLHVMTQKKQERKP PLVIPRQTGSGVDLQQTPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL
24103	54471	A	24241	1	674	MVVYACSPSYLEAEVGGSLSLE VEATNPKNSSKKFLDLISEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFYFGI YLTKEERLKPSSKKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTPPLVIPRQ T/VWWSGPPANSNRPAEAGPDC QKEN*QTERNSINIKKKDIHTKT PLCI

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24104	54472	A	24242	1676	1768	
24105	54473	A	24243	270	471	PSREYQDANPWLKWKYVSRT LNKSDCYASGYK*A ¹ CLLC ² SVYS HGKAAGECTLSAGSKNGLA ³ EVI KK
24106	54474	A	24244	23	200	AQMKAHGRSRSS*RC ¹ DEEHWR ACRAQEPPCSQSQRERSKRTCR QGT ² VASKVKCHSEAR
24107	54475	A	24245	3	270	ASTSHVPQPCGLDDLAIRHSAV RLNRERVHSTAVLP*EYTKQRR QGHL* ¹ PDYPYKKEGAATNEDAL LLRWERGRGARLHIPGCKAPQL
24108	54476	A	24246	135	275	
24109	54477	A	24247	365	583	
24110	54478	A	24248	2906	3114	
24111	54479	A	24249	108	405	NLHTPYRQSLGQGEPLDDYV NTQGAS/LFSVTKKELGAGSIEE CAAKCEEDKEFTCRYFHCRC ¹ TF LSIPQVTSF ² LCFPLPL ³ LKSSK LLANRD ⁴ KYRM
24112	54480	A	24250	1	386	
24113	54481	A	24251	1	808	MSYSQCVSPDKAHGILPGYHC WLF ¹ RDQGL ² LKSKQHVINPAKAST GFFLQDTLMVLEIKTIRNYYK HLYAHELERLEEMDKFLDTYT LRL ³ LSQEV ⁴ IDS ⁵ PNR ⁶ PIM ⁷ SSK ⁸ IESV KGYTHQ ⁹ QFCH ¹⁰ KSTLNK ¹¹ GDRVI DNL ¹² TCPPYCCVWF ¹³ LAGT ¹⁴ GPHI LYLSRLVSNLEL ¹⁵ FKRGKGRGEQ RKEEVT ¹⁶ CGMLR ¹⁷ KS ¹⁸ LV ¹⁹ SD ²⁰ LPEP GGVTSEGCETAKVTACSSLWE LCHREVLTPYCPK ²¹ DT ²² CRK ²³ WLE TPVRRSCPVR ²⁴ SRIST ²⁵ CL ²⁶ RK ²⁷ KFG HILAEQLSCA* ²⁸ RCL** ²⁹ FL/YGCFY FQDHECVLKEES ³⁰ TSFGRINHV LTLKEPLVPE
24114	54482	A	24252	833	1245	ANMFP ¹ AF ² AA ³ VAAGA ⁴ ATEAAA AAAA ⁵ AP ⁶ LAP ⁷ ARRAAAA ⁸ ARG PPL ⁹ RLP/WSCAEV ¹⁰ MYHPQPYG ASQYL ¹¹ PNPMAATTCPTAYY/RA GAPTWPAGESPDGQ ¹² PAGGGGG GHREYRSGARRRPAGTRGAED ALGSAGASLSRK ¹³ PK

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24115	54483	A	24253	145	766	TGCIREKFHLPEGSLIIVSSRRKH LQRLAFQAKVSSMMLPLQGAQ MLQMLEKSLR/KSLPRNPLKVY GTIVFHINHG/NPFLKAVV/DK WPDFN/TVV/CPQ/EQDMDRW TLDHYITIVYQIYKDPQNCQEF LGSPELINWKQHLQIQSSQPSLN EAIQNLAIAIKSFVKVQ/TQRILY MGRLETAK/ELTPFLAGNQRIIS PSGWAKPKAM
24116	54484	A	24254	215	550	VGFRSCLVMSGRGKGGKGLGK GGAKRHRKVL.RDNIQGITKPAI RRLARRGGVKRISGLIYEETR VLKVFLENVIRDAVITYTEHAK RKTVTAMDVVYAL/KRQGRTL
24117	54485	A	24255	3	292	TLNLNLAHAHCGPCLLWFQLSF RSPSTSAVGRCCRPSADFHPSRS SRVSAVLLIQ/QRCPLPILQLKA CHCSCATAKWLGSPPKETFEEII HPSPS
24118	54486	A	24256	1	789	
24119	54487	A	24257	3	256	TLNLNLAALSSGPCLLRLELSFH SPSTTAVCCRHRPAADFPPFGR VSSLLLIQ/QRCPLPILGLKACQ CSCAAKCCVRPNRAEQ
24120	54488	A	24258	3	212	
24121	54489	A	24259	2	491	
24122	54490	A	24260	20	272	
24123	54491	A	24261	160	876	
24124	54492	A	24262	623	796	GANSWNLTGTLAVKAGTVENP I*VFATHVESAGPR*LDPRTGSL AVRTKGRHWDQGA
24125	54493	A	24263	242	659	TSNSPPQTRPHVCHGPRQYLLQ LSSRDLEFLVQIAVRSLCPGLR IRSPVFAVASTTFGTLRGKV KDFGVFVPPPWGQPCLCPEVER ALSCQGPVVDSCRPCRGHEGM AYHTQQMRSADEGQTVFYTC TNCKFQEK
24126	54494	A	24264	66	238	
24127	54495	A	24265	2	278	
24128	54496	A	24266	168	565	TENFRALSTGEKFGFYKSSCFH RIIPGFMCCQGGDFIRHNGTGGK SIYGEKFDDENFILKHTGPGML SMANAGPNTNGSQFLICTAKTE WLDGKLVVFGKVNGMNIWEA MECFVSRNGKTGQKIKITA/DCG
24129	54497	B	24267	20	88	
24130	54498	C	24268	183	254	

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24131	54499	A	24269	412	590	KSGLATQG/GRRRGWVFLAPQ KGGEGVETQREGVGVLAPSPE KRDLPLRVKDQGRPCVV
24132	54500	A	24270	550	852	
24133	54501	A	24271	207	381	
24134	54502	A	24272	412	589	KSGLATQG/GRRRGWVFLAPQ KGGEGVETQREGVGVLAPSPE KRDLPLRVKDQGRPCVV
24135	54503	A	24273	191	235	
24136	54504	A	24274	95	375	AEKIWEGVSQRALGQSSRGSGS GCQMNPLSGRPQVVCFFTAHM LTKKREEGASMLNMPCFQ*KE EMIQANLGPADSSHCLGIEGPP WAPLTP
24137	54505	A	24275	144	293	WQVPFLFWQPFPEPELWPKAL* LTPSQIFSD*RLKTDAA SPRKP PAPR
24138	54506	C	24276	1	909	
24139	54507	A	24277	1	1744	MGCLGTQRAPRAFLLLPLPLHF AQLSNLTQLQAAASLSMVTHR SSGGGGERGATAAGTEQGGAC LAASLLRGLWDAGEVTPIRVRV RPYDPFTLAPLHEHSEAQCVAS PSLTVTKFKSLPKSLLAGSREV ARSRALCHGQARPPRPQVTQQ RTQLQGQRLQWRPATEGPHSP RRGSDSAKGTHPPTTGTCPPRR RQGAGYSRYNSGESRRRLGRQ QDLVARSDEQRDPAPATRRRED KMIEELQPFGEHRPRRSPSQGC DTLFQALWFLASPSFQRGGQLQ VLALCKAAAGPGAPQAAS TAG TREHGYAWKLGDTNRHRAK RKSTQWLRRFPAGCPDVCSAL ADLRAFMGLRGEEVCADWSM GGHSGGECRRGTGGQRAVVPK SPVQEKGEPLSLLYFMVDEK ERFLRITSEHEDNDNSNNSSNHS SINETKETCFIHEPKTPAPVTDW EGSLPLVFNHCRDASLIHSCFK GVRPHRDACLG/RTLSGK/FPL SWGGRGKYPSTPSPPLAASPTFL GQGQELVTSARNLTTRPNAC GPGFLLSHVPSVRDPTGNRTVQ LTWQPLPEPELWPKAL
24140	54508	A	24278	2	120	QSSAAKPRTSKGGSVREPWAR VPGALGVAAR*AEQSD FQ

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24141	54509	A	24279	1135	1483	ILTMGTGSLSTPSNAVIEKV*VC CSSLSTG*SKV/QVASNTSLCDG ED*GVVIQKKVKLWVFCIFYVL VQSYYS*R*SQIETVRNGCSHW GRFQDIALITGHCKIWTLIVFIQ YFNV
24142	54510	A	24280	1	860	ATTGCTNLRDDIMRLDDTVHV VIATPGRILDLIKKGAKVDHV QMIVLDEADKLLSQDFVQIMED IILTLKPNRQILLYSATFPLSVQK FMNSHLQKPYEINLMEELTLKG VTQYYAYVTERQKVHCLNTLF SRLQINQSIIFCNSSQRVELLAK KISQLGYSCFYIHAKMRQEHRN RVFHDFRNLGCRNLVCTDLFTR GIDIQAVNVVINFDFPKLAETYL HRIGRSGRFGHLGLAINLITYDD RFNLKSIEAQL*TEIKPIPSNIDK SLYVAEYHSEPEVEDEKP
24143	54511	A	24281	848	1218	PMQRKSMLKISVS/PVSVQKFM NSHLQKPYEINLMEELTLKGV TQYYACITELQKLAETYLHRI GRSGRFGHPLGLAINLITYDDH FNLKSIEQLGTEIKPIPSNIDK SLCGAEYHSEPEVEDEKP
24144	54512	A	24282	241	477	
24145	54513	A	24283	38	208	MTAGAPPPPPPFETPEGV*GNP TCSGG*EDASGSTRSRQHPVGL PVSCALRACHLK
24146	54514	A	24284	794	1455	AQQGGTSKKRRFPQDQQRAG LACSRPPGPGCGFQAPAGERY PNIKPHPTSVAPLVLCICYLM/P MLPWAWSYWRGARRPSRHPG AFPCSAHQCPASAARSPTLRQE DPEKGSQASSFTGPSQSMVD RCLKGQPLDVSRRQLSLPQTGL RPVLVNQLSKKPTGYPTQIQW VLMRDTGKDTDTTEEKEGHAK MEAEIGVMYPQEHLEPPESGRA KGEIPL
24147	54515	A	24285	90	354	QSPGVHQLSRFVS*SYSERP*SL LVSTRYHTRALH**HYADSIQ* ARSSKHTGLIGCTVP*RGFPRT HSFYSRKREPRRTSSFRGIL
24148	54516	A	24286	236	520	TACFLTHVAIKWVMHSSIPSSN GGGIYMIGLKAQVSMRKLWLK SPWSPLLLSPSLRHPHGKFFM IS*QRKRRLLGPGSQMVLHDMQ APPKSQGL

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24149	54517	A	24287	16	278	FAQAMKPHLVQQLQLESPLG* AYDNPLSFSKIHLSDLHKPVL*L GDSNDVLGTLESMSAQSCPV VPMSDHLPPMHSPGKRPEV
24150	54518	A	24288	74	168	LGKCLFLHSCP*APPEAICLQLP LLSSPNGP
24151	54519	C	24289	92	564	
24152	54520	A	24290	1	876	
24153	54521	A	24291	71	282	PLVTQVVFLFPTNSSLDLLQ/S PSP/GSGPHSNWQPFGLDKWA GVKHPNEECAASKIQTGPPCVV PLPWL
24154	54522	A	24292	81	1054	PRLFSDCFPPPTAAWTCRAFSC SGPHSNWQPFGLDKWAGVKH PNEECAASKIQTGPPCVVPLPW L*EEPNAIYPSVPVCFLLLA HWIQA*CHQCNGPVWYLVEV KSNQVLSK*HYDTKPES*YTPY GQEWKRGHLPQWPHTRYQE MY*FAQAMKPHLV*QLQLQSP LG*AYNNPLSFSKIHLPSPHGSH SEPCL*GPTRTLV*L*KQTGM LAVAPEENQHLYAWQLPQGRP SLLPQAVQGLSPQTKVERLMA ASVGEGMLPILGMEKLF/PSGK KD*SGFTSSVSPASSGSHTSF QVAGSHSFPNAFTLTVDTW
24155	54523	A	24293	5	88	
24156	54524	A	24294	779	1041	PPLSSSPGP/DEQSD/LWWQSSIP LHQETVKVLH*MGVPVPCATQL DKIHQQGFSDPYRGAVLLASG WCPKRPEIPEEGATTLLCCFPAS
24157	54525	A	24295	248	3714	
24158	54526	A	24296	4177	7804	TFQESRFEQGFQKAIFILELVDA EDPDEEEEEASSIFSSFFLFLP SSSSCSFSSSSSSLLRSPGDKD MPTAGMPSLLQSSSESPQSYPE GEDSQSPLQIPQSSPESDDTLYP LQSPQRSSEGEDSSDPLQRPPG KDSQSPQLQIPQSSPEGDDTQSP QNSQSSPEGKDSLSPLEISQSPPE GEDVQSPQLQNPASSFFSALLSI FQSSPESIQSPFEGFPQSVLQIPV SAASSSTLVISFQSSPESTQSP
24159	54527	A	24297	145	219	

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24160	54528	A	24298	191	1075	QPKVSRHCQTSPGSYLYSLQSG RWTGKPLQQTKS VYLRSFHH HHFQNHRRHYLHHHLLYHHHH YHPHPSHHLLHCY\SQHHHHH HHHHHHHEHHLCRHHKSTQVE YSVFAERENDLGNCTGDEAL HDNGTTERVSGPPAGYLYRAD YAIQLQPFMPRLGRRTPGAGGP HSRAPELAYLQKLITSPATLPFV YLETGGWSPRDAHRVDNDFDM GPRENMGSVWEKSLFTRNPSK SSYIADKNLIYLYASECIGRQSQ KARASKSGVQAEHPYITGAIKD DTRAIKTRDLANRLK
24161	54529	A	24299	155	381	LICTSFKILSRLLFCPSLL*SSSSQG ACISKLLSVLTIAHLYFALEKE VLTFLSRAIVSSSTLLTHGVAHS LTLFH
24162	54530	A	24300	1052	1338	TGWDGPPANCSSPMEGDSNVH CSCVCCSCFGLLL/CAIHCCCA PPGCSACGAATLLYSAPLGSSA YGIALLSPFHHVRMMLSTKQEV GLHQTLLNP
24163	54531	A	24301	1	723	MLNVQALVVMVMCFMWASL WAPGGHPSAGNISWVSGLVSP PEWSSWELVVS VVGWAGKLW LHESLLTLNLSCGLLVVLVALV FDEWHWPWSGHVAEACSTGYWS TGGIWFHEIAAP*DCSSSPAME QSWMEND\DELIEVGFRRLVIT NFSLEKEDVRTHLKEAKNLEKR LDEWLTRINSIEKTLNDLMELK TMARELRDACTSFSSQFDQVEE RVSVIEDQMNMKREEKFREK RVKRNEQSLQEI
24164	54532	C	24302	295	430	

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24165	54533	A	24303	811	1947	QTERNSINIRNRNGHQHPICRS PSSKTKGSIKPQRSGRNQSRKA ENSKNQSTSSPPKDCSSSLAMK QSWMENDFDELGTAGFRRLVI TDFSELKEDVQTHHIKEAKNLE KKIRQMVTNRINSVEKSLKDL ELKTMARELCDACTSFSSRFDQ VEERVSVIEDQMNMKREKEF REKRVKRNEQSLQVIWVYVKR PNLRLIGIPESDEENGTKLENTL QDIHQENFPNIARQANVQIQEI RTPQRYSSRRATPRHIIIVRFTKV EMKEKMLRAARQKGRVTHKG KPIRLTADLSAETVQARREWGP IFNILKGKNFPRISYPAKLSFIS EGEIKYFTDKQMLKDFVITRPA LQELLKEALNMERNNNWQPLQ
24166	54534	A	24304	1	2394	
24167	54535	A	24305	1902	2413	
24168	54536	A	24306	2	610	WAPPAIHIRCMPAEAYNFRKPL SLIPSAIQSNELIIMNGNRALNIQ LLKRYQCTLDIRYKQTSMLNC YEGTVITPSHIQYPCLSDSYGLY DIGIRNTDFLKGELSMNIRPLHD RVIVKRKEVETKSAGGIVLTGS AAAKSTRGEVLAVGNGRJLEN GEVKPLDVKVGDIVIFNDGYIG VKSEKIDYEEVLIMSESDILAIV
24169	54537	A	24307	1	801	
24170	54538	A	24308	1268	1579	TAIWSPSKSALYAAQTSGCSWI ALPSISTGSNAWIPRCRVGARF SSTGCSRITSSRSQTTASSRSTIF FAALMVVARPRSSSLP*MNGLN SSSAIFFGRPH
24171	54539	A	24309	583	796	IHCIDIRFSATPAGGEFWQYIAS RQSIFHAIVETGHALIQSSVPG LTPAMKAVATTSH*TVESCFRS ASR
24172	54540	A	24310	1	313	MPNVDDVVGEMVNTMSASRSY QANVEVLNTEKAMSIATTTDP TNTGVSTTSSSLTG/SNAADLQ SSFLTLLVAQLKNQDPTNPMEN NELTSQLAQISTTLRAY
24173	54541	A	24311	54	323	SASAQVSALSIHSAAFQNEYLSP CPN*RLVSFAFTNSSRQSG*PEK SVSQTPVITASAF*YADIAASV RNKILRPGTNVFGDTIGFRVQ
24174	54542	A	24312	816	866	
24175	54543	B	24313	1	985	
24176	54544	A	24314	1828	2505	
24177	54545	A	24315	1	1938	

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24178	54546	A	24316	4201	4668	
24179	54547	A	24317	269	503	
24180	54548	B	24318	1	1702	
24181	54549	A	24319	829	1584	
24182	54550	A	24320	1238	1926	IQAAYNRIAPSSSPKFPACGKP CLGERGIRGPGPSFGLINRPST PDPITITGVSTT/SSSSLTGSNAAD VQS/SFLTLLVAQLKNQDPTNP/ MENNELTSLAQISTVS/GIEKL NTTLGSISGQ/DNSQSLQASNLI GHGVM/IPGTTVLAGTGSEEGA V/TTTTPFGEVWDGTL/TDGT APNGSYNVAIS/ASNGGTQLVA QPLQFALAAERFCALSPGAPYR YDTWVRQWVASP
24183	54551	A	24321	487	1509	FYLQGLRQQPQVRQPLNIGVTA QGVNAAACHPHIAEQQLDHRH RTNVLRITNGVLRPAEGIERGS FIVSTGFCDFVADFQERVFWR TDVFNHWRVAGNVLFQQVPH AARMLQRGIAFGEAVFVQFISP GGFIVLAFRRV VAGEQAIFKAVI LTHDQAGGGIGFVFAVEFFIV QQVQQYA*QESNVSTGTNRGIV VSYRRRTKARIDHNQLRAVV NFGFHRPAEPDRVSAHHHDEV GVLDVDPVVGHRKTFDDIWH DQFIDQVRVRRFSGDNRRLQDRE QVGLQSANNPIDKSLFRGINQF QLYAAFTAQDVNIDIFKTRQQF FAVIGQTTGVQVQK
24184	54552	A	24322	377	749	
24185	54553	A	24323	140	298	
24186	54554	A	24324	342	1094	MGAPWLHRPRRALQRWRLGS GFSCGSLGLQENNGRRPVMV LALSTLPRRPTRCGEFYCLIKP GFRLGMKSVKMEIRGLWAGGE DKIAVPAEPRASGPERTLSDLH NESIF/ITGGGSLGLALVERF/IE EGAQVATLELSAAKV/ASLR/Q RFGEHILAVEGN/VTCYADYQR AVDQILT/RSGK/LVNTPAETLE TGFHELFNVNVLGYLLGAKAC APALIASEGSMIFTLSNAAWYP GGGGPLYTASKHAATGR
24187	54555	A	24325	1	1785	
24188	54556	A	24326	2	1760	
24189	54557	A	24327	2437	2679	TFQYIGQPHGDEFPHVAPVKHG DKLGEKGNHDKSRHLFHRFN H*MR*IRLTSNCAGSDAISQRD NKEKNQDQWHDITFNKG

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24190	54558	A	24328	3	415	
24191	54559	A	24329	1	1932	
24192	54560	A	24330	1932	2117	RAISLGRTAAGYLNSDVAQRA ASGADPAGDFVFWH**IRKNLS GGARYAIPHLYQHAWHP
24193	54561	A	24331	1	1017	MRYREPPARGVEPNELHACRSE DKLSEDAFDQCTGANPRYPLI SELKQILLDTYYGRDYVEDRLS FLLAVALNNGERLDGEMSEK LVMPFRHVSDAFEQTRETIGVR GNNAINDMVRQRLNRFRTSEQ AEGNAIYRLTPLGIGITDYIRQ REFSTLRLSMQLSIVAGELKRA ADAAEEGGDEFHWHRNVYAPL KYSVAEIFDSIDLTLQRLMDEQQ QQVKDDIAQLLNKDWRAAISS CELLSETSGTLRELQDTELEA GDKLQANLLRQDATMTTHDDL HFVDRLVFDLQSKLDRISWGQ QSIDLWIGYDRHVHKFIRTGID MDKKPRPSRRCL
24194	54562	A	24332	5	220	GLSWLNYC*ASTLTISLRCA AVPLTRICRPRLLPSRRERTAL PCITYVKIAVTLTATCASCVR WIPA
24195	54563	A	24333	3	180	
24196	54564	A	24334	229	564	PGFKPRHSSWQRLPSLGHPL GSSVFTLLNLATAHSSGPCLLQ LELSFHSPSTTAVCRRHRPTAD HPSESGRVSHVLLIQ/QRCPLLL WIRLKACHCSCTAKCPGSSQLS
24197	54565	A	24335	148	404	
24198	54566	A	24336	213	1306	SEHSVAHGRGIMDLSLLKALS EADAIASSEQEVQRILLEADR LQKEVRV DGLGSVLRLNESTG PKVMICAHMDEVGFMVRSISRE GAIDVLPVGNVRMAARQLQPV RITTREECKIPGLLDGDRQGN VSAMRVDIGARSYDEV MQAGI RPGDRVTFTTFQVLPHQRVM GKAFFDRLGCYLLVTQLRELH DAELPAEVWLVAASSEEVGLR GGQTSITRAVSPDVAIVLDTAC WAKNFDYGAANHRQIGNGPM LVLSDKSLIAPPKLTAWVETVA AEIGVPLQADMFSGGTG DGA VHLTGTVPTVVMGPATRHGH CAASIAADCRDILHMQLLSAFI HKSNELGGLRLRLQICRDGNE
24199	54567	B	24337	1	1075	

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24200	54568	A	24338	438	1462	QIVQCLDVPSYTFIWFVAVLDPIY GDSVSTGLVVAIHSIIVNAITPIG LYLLNPSSGADGKKNSNLSALI SAAKEPVVWAPVLATILVLVG VKIPAAWDPTFNLIKANSOVA VFAAGLTLAAHKFEFSAEIAYN TFLKLILMPLALLVGMACHLN SEHLQMTLASALPPAFSLKLIY CAA/ARLMCYTRTGTSLAITLT ETVTQKL TGSRPRISSYGRNLM WPLAWYKDNKGPHLCSQLETT RIHSTAAQGRSSGSLRRGLGAS PFYRQHDQARSEGQIPITRIPMG LAQRAPKGRAQPRGLTAPFTN GALGQPQGRGTSKQASQTRPR ASAWPHPTT
24201	54569	A	24339	30	177	GSQYQRCNNAAASDRLRSYRK QPAER/WLAPPDITSPPASRRRA LILLY
24202	54570	A	24340	3350	3430	
24203	54571	A	24341	425	824	SISGSENACFNATNHSGRYSQY GACLTSSSCRKGQLARRGLSYQ SPHAPADPAFPAARRSPVFCLS DDGGHKSPRDMSDPKPSRHPD QVALTRRIPPPAVALPSVVKR TVHEGQGDDESNPSPLSPDVH
24204	54572	B	24342	1	2118	
24205	54573	A	24343	1	888	
24206	54574	A	24344	730	1101	
24207	54575	B	24345	1	1992	
24208	54576	A	24346	880	1103	TMMRRLISRQPVLPQKCFSLVI SNPWRVFGGTGGGNQER/CRY AEESVAETRLCP*CRLYAEYDP GSGCAGLSL
24209	54577	A	24347	1	952	MITLRKLPLAVAAAGVMSAQ AMAVDFHGYARSIGWGTSGSG EQQCFTTGAQSKYRLGNECE TYAELKLGQEVWKEGDKSFYF DTNVAYSVAQQNDWEATDPAF REANVQGNLIEWLPGSTIWA GKRIFYQRHDVHMIDFYWDIS GPGAGLENIDVGFGLSLAATR SSEAGSSSFASNHIDYS/NEN AND/VFDVRLARWDSPPGPLTG FPSPALACTSGVSGQKGVGPP EAQVTFATPKKPGKEACSSIQV LNRGYRPPTFSYNTGVRRSARD YYPRRQRSISTNSPSRRWKGL NSRRCTGNRPLVGAVS

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24210	54578	A	24348	805	1274	ASFATIRPVTKLAMRVAIFDSV VGQRYWGSAA SPEHSRFAVLW ILASIFR/DRIASLRVQATVK\$*K MS*A WYWQGC FRNWKSSPA*Y QFFSPARSASSHFAGEPVSLHSP IALGYRSESSSCHTSTASLSVH RDY AHLHGLRFDHSSRRRLCY C
24211	54579	A	24349	275	490	
24212	54580	A	24350	1	696	
24213	54581	A	24351	1	735	MFIPDYRSVSRVLGSGPGYASR MNQPDVMPDIPGKRFYQRHDV HMIDFYYWDISGPGAGLENIDV GFGKLSLAATRSSEAGSSSFA SNNIYDYTNETANDVDFVRLA QMEINPGGTLELGV DYGRANL RDNYRLGKGLSQSGGVAFDNE KFAYNINNNGHMLRILDHGAIS MGDNWDMMYVGM YQDIHWD NDHG\TK\WWTAGIRPMFKWT PIMNTGMKF/GYE/NVESQGGP QNIRTIYLAKP*QPDVMPDIPGK RFYQRHDVHMIDFYYWDISGP GAGLENIDVGFGKLSLAATR EAGSSSFA SNNIYDYTNETAN DVDFVRLAQMEINPGGTLELG VDYGRANLRDNYRLGKGLSQ SGVAFDNEKFAYNINNNGHML RILDHGAISMGDNWDMMYVG MYQDIHWDNDHG HQVGGPAG IRPDVQVDAHHEHRDEIRYEKL NPRARDKTFVQFTSQNPDR
24214	54582	A	24352	1	3414	MIVQPLAIIGSHFDSIAAGNLAR PIAVYGRNEITAIFASLKTMQQ ALRGTVSDVRKGSQEMHIGIAE IVAGNNDLSSRTEQQAASLAQT AASMEQLTATVGQADNARQ ASELAKNAATTAQAGGVQVST MTHTMQEIA TSSQKIGDIISVID GIAFQTNILALNAA VEAARAGE QGRGFVAVAGEVRNLASRSQ AAKEIKGLIEESVNRVQQGSKL VNNAAATMIDIVSSVTRVNDIM GEIASASEEQQRGIE
24215	54583	A	24353	1	2493	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 99/054,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
24216	54584	A	24354	1	1201	MQPALLVLNKNVRQEARRRAR ACRIRRASGIVQFGKVRRLAA VELRQRQTPERFVLLRGTRQQA TGQRIVKTEQRVHIITQRSFRPG EGRRINDHFRFPAHLPSIRPIGK HQTFFGISGHHNFFTVAIGDDI AQLDRIGANQSVLKGFNKFVV QYATDSMTSQGKGLSQSGGVA FDNEKFAYNI/SFNGHMLRILDH GUNWDNDNGTKWWTVGIRPM YKWTPI MSTVMEIGYD NVE SQ RTGDKNNQYKJTLAQQWQAG DSIWSRPAIRVFATYAKWDEK WRYDYTGADNNANFGKAVP ADFNNGSFG/RGDSDEWTFGAQ MEIWGLSRASGTLVTRAWRYK TTPTRHCLLMNHYAGEAAMR WKNYLKSTQKVLQNFANWP KYSLSLTFHFPEFSKSC
24217	54585	A	24355	188	406	FIRSFDPSPFVPSVLD RFFVLSTVF HSSSIFLVVIDRPSVCGEPSLF*V GGSCPTNSLYRCSGLAWYLMR SMD
24218	54586	A	24356	1	1798	
24219	54587	B	24357	1465	7841	
24220	54588	A	24358	174	3762	TLNDAMRREKCLARINRTAKS GVVMPKLVWMMNQVRVGELT KLANGAHTFKYAPEWLASRYA RPLSLSLPLQRGNITSDAVNFF DNLLPDRITVRDRIVKRYHAKS RQPFOLLSEIGRDSVGAVTLIPE DETQHHYESLTITDEGEFVVFV GPSGCGKSTLLRMIAGLETTITG DLFEGEKRMNDTPPAERGVM VFQSYALYPHLSVAENMSFGH ATGLAQHKEVAEVLPSRRICWI ANRRSPVVS SVWRL
24221	54589	A	24359	364	845	RPLLDHGSSPRLNFLRFWYV VVH AHTLMRMTEGWAGFDILRPYR WRRVIAFVVAFYFRHLIALLVV QMHFKLVGKNDVVFVTAQLID STVQLIDSTTTVTQFTHIQQLM IQRAGTKCRKEDFRHWFVHHHP WVL/MSPPSVTLYALFPDRSHR PRRDGSPDA
24222	54590	A	24360	781	1275	

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24223	54591	A	24361	1	1185	MDKFDANRRKLLALGGVALG AAILPTPAFATLSTPRPRILTLNN LHTGESIKAEFFDGRGQYIEELA KLNHFFRDYRANKIKSIDPGLF DQLYRLQGLLGTRKPCSGYVT TAPAARSYRLTSKFIAVGGKAL SSLNIIHIAAPHLEALIIGESDTK NFASHDHAILIYKLEPTTGMLR TRAYIGQHMPLYCSAMGIYIM AFGHDPYVKSYWESHQHEIQPL TRNTITELPAMFDELAHIRESGR TMDREENELGVSCIAVPVFDIH GRVPYAVSISLTSRLKQ/PRQH RFRLRERQAGGTPPAGTNSVT GGASLHHARCQRRK*KPYRPER A/ESFLPARGKICWP*AGTLTVC IMASASRLISGCTPDSTCWSTA HAPICRRRGRAINRCHCSS
24224	54592	A	24362	1	801	
24225	54593	A	24363	1523	1950	LLPA/AQKRRVDFLRATDFNAL MPGVVEIDGKNIYTQIIDLTRE AVVNRPEVHRRYIDIQFLAWGE EKIGIAIDTGNNKVSESLLEQRN IIFYHDSEHESFIEMIPGSYAIFFP QDVHRPGCIMQTASEIRKIVVK VALTALN
24226	54594	A	24364	281	997	LTFARLKGITRKIGRLQSRRRKR CKAMGVDVNRVYSLDELVRG NDILFSATGVTGGELVNGIQQT ANGVRTQTLLIGGADQTPMAT LTEDDVLEQLDAQDNLFSFMK TAHTILLQGIQFLPSLFVDNDE EIVEYAVKPLAQSGQIDDIDV ALRLIYALGKMDKWLYADITH FSQFVWHYLNQDETPGFADDM TWDVFISNVNITRNAMLYDALK AMKFADFVSWSEARFSGMVKT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24227	54595	A	24365	263	1410	AMISRRRFLQATAATATSSGFG YMHY/CLNSDAIALGIEQRPDLI LLGGDYVLFDMSLNSSAYS DV LSPLAECAPTFACFGNHDRPVG TEKNHLIGETLKS AVITGMLNQ ATVIAYANRPPELVGTGDLWS GQCKSASASETNLSRLVLAHNS CSKEVMRDEPCDMLGSHTHR WQLSVPMAGEPFCHVADERYV LGLNAFCERHIYTIPRGGKRIPQ TFAADLPKGITVNPVQSTITEE TFQTLVSRLEKLG YTVNKP EVDYNVGYTSLASGDATFTAV NWTPLHDNMYEAAAGDCKFPY REGVVFVNGAAQGYLIDKKTAD QYKITNIRQLEDPEIAKLVD TNG DGKADLTGCNPG LFGEGAINH QLGAYELTNTVTHN
24228	54596	B	24366	1	2872	
24229	54597	B	24367	1	1704	
24230	54598	B	24368	1	1470	
24231	54599	B	24369	1	2301	
24232	54600	B	24370	1	900	
24233	54601	B	24371	26	856	
24234	54602	B	24372	1	1743	
24235	54603	B	24373	1	1410	
24236	54604	B	24374	1	957	
24237	54605	B	24375	1	2742	
24238	54606	B	24376	755	1816	
24239	54607	B	24377	1	1968	
24240	54608	B	24378	926	6441	

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24241	54609	A	24379	1	1739	MTWTHEAVNRREPLRGCEPNW DVIDVKPAGCMISRRNELPYTLG LRIDMLVDLGTASLMGQSSVY NTTDRHSTHRMDGLEQLMQQA DFAADIAVVAPWDNWSPTAGR FGLIRLLDEQTAPYAWYTSPMH LMDEKCSCHRRQRPVIGLNQPO YQSGTIEVDNVSFAYRDDYLVL KNINLSVPSRNFVALVGTGSG KSTLASLLMGYYPLTEGEIRLD GRPLSSLSHSALRQGVAMVQQ DPVVLADTFLANVTLGRDISEE RVWQALETVQLAELARMSMDG IYTPLGEQGNLSVGQKQLLAL ARVLVETPQILILDEATASIDSG TEQAIGHALRRDCSPLIDHCDA DTILVLHRGQAVEQGT HQQLL AAQGRYWQMYQLQLAGEELA ASVQPLPNSDRRGSMKLVTVII KPFKLEDVREALSSIGIQLTVT EVKGFGRQKGHAELYRGAEYS VNFLPKAA YTGIGDG/KIFVAE LQRVIRIRTGEADEAALYLWHT ATERDGPFRNFTAGAFRASLPH PARHGRRPILAAPFMPVNPRLP PRRRHLASGRSLRFNCCTAGDE TCSARSGERRSLVF
24242	54610	A	24380	547	684	

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24243	54611	A	24381	1	2208	MLLVSAVSVNAMSISGQAGKEY TNIGVGFGTETTGLALSGNWITH NDDDDGDVAGVGLNLPLPLPL MATVGGKGVYTNPNYGDEGY AAAVGGGLQWKIGNSFRLFGE YYSPDSLSSGIQSYEEANAGA RYTICVQVFVVVMLIRNQLFTP VNTAIDGFATNYAIMPAYAVG EGVATHGLQFELMRTTGGNTQ HVFHHPLPLFAMWRYAAEMFP YQQMCQFVRYHFFNKSFTVFQ QQNGIEANFIAFQPRSGGSA LGRNVFGFRYPQCCQDKQYV QSRHPEGVGVTQRVEHGQERC ANDHVQSSGTLMQEGVMSAS LKNQQGFSLPEVMLAMVLMV MIVTALSGFQRTLMNSLASRNO YQQLWRHGWQQTQLRAISPPA NWQSGAAMLRVYHSNRLDVL EALMEFIVERERLDDPFEPMIL VQSTGMAQWLQMTLSQKFGIA ANIDFPLPASFIWDMFVRVLPEI PKESAFNKQSMWSKMLMTLLPQ LLEREDFTLLRHYLTDDSDKRR LFQLSSKAADLFDQYLVYRPD WLAQWETGHLVEGLGEAQAW QAPLWKALVEYTHQLGQPRW HRANLYQRFIETLESATTCPPG YLRASLYAAIQHALASVREHTT LVVIAHRLSTIVDADTILVLHRG QAVEQGTHTQLLAAQGRYWQ MYQLQLAGEELAASKGHAELY
24244	54612	A	24382	2	729	DCSLPIDHCADTILVLHRGQA VEQGTHTQLLAAQGRYWQMY QLQLAGEELAASVQPLPNSDRR GSMKLVTVIHKPFKLEDVREAL SSIGIQLTVTEVKGFGRQKGH AELYRGAEYSVNFLPKAAAYTG KIGDG/KIFVAELQVRVIRRTGEA DEAALYLWHTATERDGPFRNF TAGAFRASLPHPARHGRRPILA APFMPVNPRLPPRRHRLASGR SLRFNCCTAGDETCARSGERR
24245	54613	A	24383	683	1161	RTGHCH/SAFSSTVLTSCSLSRF SFLAHLQYLLRVAEPLPNSDR RGSMLKLVTVIHKPFKLEDVREA LSSIGIQLTVTEVKGFGRQKGH HAELYRGAEYSVNFLPKVKIDV AIADDQLDEVIDIVSKAAAYTGKI GDGKIFVAELQVRVIRRTGEADE

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24246	54614	A	24384	631	1149	FFGIKEQVITANNANSNRNKTD RCCRNWLEDHADNHCHKHSEV MPCLRRHTVGD RDKKHDTHH HQWGQ*FPYIIFWLVSPLAISRS K VSTHGLRQDRDFILLREASQSF RFVLRVYDVADHIAGKFTVHD LQFIGYHGGQAQLVAQVFSKES KAAGGNRHFFAQRQFLEHQLR
24247	54615	A	24385	833	1264	
24248	54616	A	24386	1	1632	
24249	54617	A	24387	2078	2371	
24250	54618	A	24388	1	159	
24251	54619	A	24389	530	811	RPGTGTAQVLNRRIKISRST*L TVVMGYWSHPSVSLKWDRR KSPKCSSALRVNISNTLLSTARR RKRYLIVIPALLVVRRCRPRGPS ACG
24252	54620	A	24390	1806	2115	AAFQEIELAFQDPQCVGLLTAP MLMPLFLDQLILQCFFW/W/TN LERA*TSFSALFIDLQPPGYRTT TSKHKVSSSLIKGHVLLDHSFH DLNTQLWISTNAFRFGN
24253	54621	A	24391	1476	1751	ALLLVSFASQRFISA/TVGNQNA GVDLLNLTLVGGIFVLNNAGN FAVFTGDT SITGRIIQFHRQQTN ATLRF SITQTLECFDRQRHVA VEH
24254	54622	A	24392	606	4519	EEVVRAISAKRNEPEWMLFRL NA YRA WLEMEEPHWLKAHYD KLNYQDYSY SAPSCGNCDDT CASEPGA VQQTGANAFLSKEV EAAFEQLGVPPVREGKEVA VDAI FDSVSVATTYREKLA EQGIIFCS FGEAIHDHPELVRKYLGT VVPG NDNFFAALNAAVASDGTFIYVP KGVRCPELSTYFRINA EKTGG FERTILVADEDSYAAKRLTDYP HQLSGGERQVRMIAMALLTRP ELLIAD EPTTALDVSVQ
24255	54623	A	24393	129	256	

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24256	54624	A	24394	1	1082	MAMSKVKSTITRESWILSTFPEW GSWLNEEIEQEQVAPGTAFAMW WLGCCTGIWLKSEGGTNVCVDF WCGTGKQSHGNPLMKQGHQM QRMAGVKKLQPNLRTTPFVLD PFAIRQIDAVLA THDHNHDIDV NVAAA VMQNCADDVPFIGPKT CVDSWIGWGVKERCIVVKPG DVVQVTALEIHAPDAFDRTAPI TWLADQKRRRTVKGRITRPN RSVTVRPRRRDAVIGRFYRHQS ITQKGLLLMVMPGCAFLWIDS ELNLTIDALFEGVSGITTTGAT VIDDVSSLPRAVLYYRSQNLFIG GLGVIVLAVAVLPLLGGGAKL YQSEMP/AAI*G*QTHSPPGRYV TDTVDNLFIFRCRT
24257	54625	A	24395	49	281	ASDHRYLCSQSVPLRGIPACYL LQAPLTRWR/RIPPSRRICAAIDS AISRSQQRWLTA VCCGCTVNFTN TCLLPDGVCA
24258	54626	A	24396	737	1419	CIWRMYSHRLVA WRRVCRRR/ RYLTRFAKTRGVAIVMVGHVT KDGSLAGPKVLEHCIDCSVLLD GDADSRFRTLRSKRNRFQAVN ELGVFAMTEQGLREVSNFRGR GKRKFISPKKTPALAKFRNLL PPKVPNGTSTVRFRHSRICWMN PLPGAA WNCILTKKPISPGVQ VFPESFTPARLEAFAGRSQACL VPAQNILHQKSQA WLFDFPEQE KELRELSAWMAGA
24259	54627	A	24397	526	1693	STTGIRSIAMSNPILSWRRVRA/ LCVKETRQIVRDPSSWLAIVVIP LLLLFIFGYGINLDSKLRVGIFL EQRSEAAALDFTHMTGTSPYIDA TISDNRQELIAKMQAGKIRGLV VIPVDFAEQMERANATAPIQVI TDGSEPNTANFVQGYVEGIWQI WQMQRAREDNGQTFEPLIDVQT RYWFNPAAISQHFIIIPGAVTIIM TVIGAILTSLVVAREWERTME ALLSTEITRTNELLCKLIPYYFA LGLMLAMLLCMLVSVFILGVP YRGSVLILFFISSLFLSLTGMG LLISTITRNQFNAAQVALNAAF LPSIMLSGFIFQIDSMFAVIRAVT YIIPARYFVSTLQSLFLAGNIPV VLVVNVFLIASAVMFIGLTWL KTKRRLD

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24260	54628	A	24398	655	915	IAVNVTLAFNGGKQLR*STSLI CCQEGLAFAVNLRQHFRVQTIS FFFLPVLRFWRPQIQAKKCHP APRTAKGIPQQVIRAMRLLFK
24261	54629	A	24399	549	827	
24262	54630	A	24400	472	626	WRFFRPRKDNIRRTLFADGHQI AAQPGNLNLSCTRTIF*IKRINTFP GRWRK
24263	54631	A	24401	333	617	SDQSETDYRFADGERHLENQPH AGQTGRGGAGPGCTLYQRFAQ LCEVSEVERSGCRTLSAQHVEQ NLPAAICGGDDADGAVVHLWT TA*RTRIGTLRSGPKMNDISAISI TATDSGWKILLHMLS
24264	54632	A	24402	74	265	
24265	54633	A	24403	1	1005	
24266	54634	A	24404	1068	1185	SVAIRQASTGNRCQCLCPACA WA*VNADVK*SARVSRL
24267	54635	A	24405	1	2292	
24268	54636	A	24406	720	2496	RRAGYRKAADAMTTIVPEKLS REVGSFHFLDRTTAVHRQPV SATTTVHEFLRCHQFPLVVC GRMTTPRAMFLFSSAHLMLPN HNSHINTLFPVAGTLMVEPTES ESKVELDRFIDAMLAIRAIEDQ VKAGVWPLEDNPLVNAPHIQS ELVAEWAHPYSREVAFFPAAL VTGSGRGIGRATALLAQEGYT VAVNYQQLHAAQEVMLNLTQ AGGKAFVLQADISDENQVAM FTAIDQHDEPLAALVNNAGILF TQCTVENLTAERINRVLSTNVT GYFLCCREAVKRMALKNQGGSG GAIIVNVSSVASRLGSPGEYVDY AASKGAIDTLTTGLSLEVAAGQ IRVNCVRPGFIYTEMHASGGEA GRVDRVKSNIPIRQGGQAEFF AVQTFPVWRVAQHCAVRPFRQ RIGQLRDIHFLKGDQFTNPRKT GVTPQPPCSTYPDPSPPPVPAAG HIDRPALAPTFTPIIMCSKATVK PLSPSPPGTPDPASVLPFREQRA AVHRLRTVVTRHLLALRRDPF ANRHRQQDQRNGGFHHRQRHL HTGKTRSLHHHQFAALRQHPK TKQRKQSRHREEDLHIFRHAQ
24269	54637	C	24407	49	186	
24270	54638	A	24408	470	811	
24271	54639	A	24409	1	1006	
24272	54640	B	24410	1	2793	

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24273	54641	A	24411	463	1258	CCRSSWCNDSSETGLQIVASYF EDRNGDSLALRPEGTAGCVRA GIEHGLLYNQERLWYIGPMFR HERPQKGRYRQFHQLGCEVFG LQGPDIDAEILMLTARWWRAL GISEHVTLELNSIGSLEARANYR DALVAFLEQHKELDEDCKRR MYTNPLRVLDKSNPEVQALLN DAPALGDYLDDESRHFAGLC KLESAGIAYTVNQRLNRYLS ANLIENNLSLFDGEGYRFYHPK PTKNAERENRQCRNDLFFRCGF
24274	54642	A	24412	221	832	TMAENQSTVENAKEKLDRLWK DGITTPGGKLPSERELGELLGK RMTLRQALLNLEASKIFRKDR KGWVFTHPRFNYSPELSASFQR AAIEQGREPFWGFTENRTSDI PETLAPLIAVTPSTELYRITGWG ALEGHKVFYHETYINPEVAPGF IEQLENHSFSFSAVWEKCYQKEPV VKKLIFKPVMPGDISKYLGG AGMP
24275	54643	A	24413	158	481	
24276	54644	A	24414	2201	2350	
24277	54645	A	24415	621	1830	AGWKRGGAGEPDQGLQA\EME VLENLQELKDLNQRQAHAESKI FRKDRKGWFTQPRFNYSPELS ASFQRAAIEQGREPSWGFTEN RTSDIPETLAPLIAVTPSTELYRI TGWGALLEGHKVFYHETYINPE VAPGFIEQLENHSFSFSAVWEKCY QKETVVKKLIFKPVMPGDISK YLGGSAGMPAILIEKHRADQGG NIVQIDIEYWRFEAVDLINLCF MVTINNARKILQRVDLPLYLH AYAFHNLNMLRLRVLPADLLDIA SENNLRGVKIHVLDDGERFSLGN MDDKELSAFGDKARRLNLDIHI ETSASDKASIDEAVAIALKTGA SSVRFYPRYESNLRDVLIIAND IAYVRETYQDSRLTFNIEWGKS SCCSPYVHPWAKLAAIYYRLQP HINDAF
24278	54646	A	24416	83	502	
24279	54647	A	24417	15	95	
24280	54648	A	24418	500	786	LTQRFGTVPLLQAYLYSAFFF TPEFLRPAPPLFSAAVLPEQRQR AQGIGGLVIRPTVELHQALQLF FGHQPKIQSLHALLRGSTGFQA SFRLPL

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24281	54649	A	24419	1	2914	MYYSHASCVADQYACGMHRT PSRTGRPRIHAPRQARLKPQVK VASKKRNARDKMQPPNEQQKT RAHACTPSSRFRAVVRTLTCPV VANVTRIFPRYFSNTRVLRRRR KQARGTWWRRLRHLHLYVQPH KHYSYIYRLYRVTYVMSAQV VDTGIYEFTRKKHDIGTIELPNS EIRYHGNPAMSRPRKTPTPPNSP ASERATGPTTLLPPIRQRRYAA RHTSTIAYTNSTSDIFEAPYNKA APIMRYTSVYCSLFSP
24282	54650	A	24420	2	420	CPYPENRWGKILARPLLFRAA *ASRFAGAGMPGRLIPTVRPRN SNSGRLVSASRCAKESLTVTTC TPLPGSAVREASN
24283	54651	A	24421	212	497	
24284	54652	A	24422	1	1149	
24285	54653	A	24423	535	589	
24286	54654	A	24424	1	1458	MFDPETLRTFIAVAETGSFESKA AERLCKTTATISYRIKLEENTG VALFRTRTSVTLTAVEGHELLS QARDWLSWLESMPEAAATVW MFVPTPLSVASGLQRIGRAGHQ VGGVSKGLFFPTRRDLVDSAV IVECMFAGRLENLTTPHNPLDV LAQQTVAAMDALQVDEWY SRVRAAPWKDLPRRVFDTL DMLSGRYPGDFSAFRPKLVW NRETGILTARPAFAADSDIAD GQTORFDFSILQSMADHLSQTA WR/GIQYDAEKSLEWHNVENRQ LDAQFFHMGMGFRFRVRMFSV DPATHLAREIHFRPELFKYND GVDTKQLEGQSDLGAFGRVF KAPELARRDVVSFLGASYFRAV DDTYQYGLSARGLAIDYTDISK EEFPDFTAFWFDTVKPGATTFT VYALLDSASITGAYKFTIHCEKS QVIMDVENHLYARKDIKQLGIA PMTSMFMPRKNASRLSKRCYDI RERDGREERK
24287	54655	A	24425	157	650	PIRASTCLKPLITQCFRQFGSE GVNDHLLGILLIDPARAQIEYLF IINTPHRRVAFAFHICIDFQLRF RIHFQFAHQJIVVGHLTIRFDG VLRDVDQTVKYRAAFVADDSF VQLSAVTKTFIVFQPGTGITHLV FHRHRQAQ*PFKVPFSRRLRNGI HTHC
24288	54656	A	24426	269	2024	

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24289	54657	A	24427	1	3548	MPRSNYFSERCKGEIFLKFNEM QRTGSFKIRGA FNKLSSTLDAE KRKGVVACSAGNHAQGVSLSC AMLGIDGKVVM PKGAPKSKVA ATCDYSAEVVLHGDNFNDTIA KVSEIVEMEARIFIPPYDDPKVI AGQGTIGLEIMEDLYDVNDVIV PIGGGGLIAGIAVAIKSINPTIRVI GVQSENVHGMASFSHSGEITTH RTTGTLADGCDVSRPGLTYEI VRELVDIVLVSEDEIRNSMIAL IQRNKVVTEGA
24290	54658	B	24428	1	2691	
24291	54659	A	24429	2174	3315	NLPKPDWARSAPHASANYKS NTRRLPFAREQ/QDQHTLLAGT LFI AKILIPMQIA SAAYRRRC DAQLHFLPLQLAPRGHRYKRV CQVRYPPHIALIPVV FRLMNDAN GLSQPADAGLAHHEMRNFLDF ASSNVAASRRRCVAALPCATG KGRQANEQAENKCSKDPQTHR TDNKETKTPPARPTTTTQPHTK EEEPLSTPTQTKHPPTHVGTGP HPTPASGQTEKHERKRPQOKS NARQNSKDKRTPNKSCTTKPN RGYNQHPAGEPTMSTHEKVVP HQQNRKIQAPPKRQKTDHRT HNTHPHPPHRAASTTTQAAPPP RRATRSGETSATAHNNTEPHGTR HTQPGDHKRAEEHDRTADEPT PPEHTLPSHTQLGP
24292	54660	A	24430	1	2925	
24293	54661	A	24431	341	689	RPLAFRQRCTFYWR/PGSANC LV*GASGTDPRLYSPCAAAADD CGRRQNA GRRRRATSGD*SPHR RWENALLFDSRHRHCPRRAKN AGGEYRQQRGIAGSDLQQRFTA AEKDHSRS

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24294	54662	A	24432	1	1931	MGTLGLTLVTLVVAELPAET DVAADPAASPTCTAVNQITGRA IVAADFFIIFQLWQNTVRQLVT HFKPHGQSEMSDTPELINRARY LTYLYCRQPAKAIRESQELA WKKQATHEYQVLVTRCKQTL HQVEPLREIEPGRKRLVFDENL RPKQNPPIHLLDTCWPLTVDEH ANRSSIGNNNISFVNVRAVVTN VLNTMRTACNSQATIQIYNADI ARDFGTRGIFSINSFSTVIRGG VVTVDLSAGAAIGDSALAFVID DGLVAVNLDTDGLRIGDGHGA LVIHRCVAGDINTVTAAADM DLEDPRIISARFGVVRTQVRTW VALYKEKHGEKGLIPKPKGVSAD PECVLGRESCDRAAHVPYQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK AAEIPRSTFYHLKALSKPKY ADVKKRISEIYHENRARYGYRR VTLSLHREGKQINHKA VQRLM GPSHLKQRLRSSDTALTEERDF KATRPNEKWVTDVTEFAVNGR KLYLSPVIDLFNNEVISYLSER PVMNMRRSRPGVGYFYALTPV YLANRLQALLGVEQ/HHPDGL FLTGYVADGGYHS
24295	54663	A	24433	3	158	
24296	54664	A	24434	1	3432	

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24297	54665	A	24435	1298	2649	TFITRPTSNGTSTIFKLMNRRRLR GGNVATLR/RLTIGMIFQDHL LMDRTVYDVAIPLIAGASGD DIRRRVSAALDKVGLLDKAKN FPIQLSGGEQQRVGIARA VVNK PAVLLADEPTGNLDDALSEGIL RLFEEFN RVGVTVLMA THDINL ISRRSYRMLTSDGHLHGGFGG RLDRFRKSVGGSGDGRNAPK RAKSSPKPVNRKTNVNEQVR YAFHGALQDLKSKPFATFLTV MVIAISLTLPSVCYMYKNVNO AATQYYPSPQITVYLQKTLDDD AAAGDPDRPSLQLRWRVIPGFS IAVAIYFLNESLGRPLMITGYSA ECSLAWPVRSGLRKAPMKTFF LQSLTIEAQKQFALVDSICRH FPGSEFLTGGDLGLTPA TELKPR RLPSGVEQVLADAFHAQAAL VQGAGTGAIAGLAALLKPGQ RLLVHDAPVYPTTR
24298	54666	A	24436	546	707	
24299	54667	A	24437	428	1464	RNSRSLAEISRLRGQTRSGPLM LLNLQSMGASWYLSPIVDLFN NEVISYLSERPVMNMDHLL MDRTVYDVAIPLIAGASGDD IRRRVSAALDKVGLLDKAKNFP IQLSGACWHCRA VVNKPAVLL ADEPTGNLDDALSEGILRLFEEF NRVGVTVLMA THDINLISRRSY RMLTSDGHLHGGFGGRLDRF RKS VGGSGDGRNAPKRAKSS PKPVNRKTNVNEQVR YAFHG ALQDLKSKPFATFLTMVIAISL TLPTSCYMYNIAKSERISDIST QLNAFPGCEVAVSDAPSGQLIV VVEAEADSETLIQTIESVRNVEGV LAVSLVYHQEEQGEETP
24300	54668	A	24438	1	429	
24301	54669	A	24439	307	424	
24302	54670	A	24440	300	468	
24303	54671	A	24441	946	1558	KGCVSIPFFSFWAVMSNLTYL QGYPEQLLSQVRTLINEQRLGD VLAKRYPGTHDYATDKALWQ YTQDLKNQFLRNAPPINKVMY DNKIHVLKNALGLHTAVSRVQ GGKLLAKVEIRVATVFRNAPE PFLRMIVVHELALHKEKHNK AFYQLCCHMEPQYHQLFEDTR LCNRIRLNGHDHFRRRYALFRV NTGRTASPIVQ

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24304	54672	A	24442	1	774	
24305	54673	A	24443	1	452	MELKKLMEHSHIPDYRQAWKV EHKLSDLLLTICAVISGAEGWE DIEDFGETHPDFLKQYGDFFENG IPVHDTIARVVSCICPAKFHESFI NWMLDYHSSDDKD/DHRN*W KNTPAFL*QESP*GSDSCH*CVL NNAQSGHRTDQDG*EIQ
24306	54674	A	24444	486	572	
24307	54675	A	24445	1	683	MHSLVIGQIKTDKKSNEITAPE LLNMLDIKGGIKITDAMGCQKD IAEKIQQGGAVMNLQRDDST LIRIFALHELHRLKEHGLTRGAL LDYHSRYKLVLAAHPQESRK LGPVADIIHQWQNLDDYSPQY RQRVVVLLSHPANARDHTNVL MHVQGYFRPHIDSTERQQLRAL IDSYRRGEQPLAPLMRIKHYM ALYPDAWLSGQRYFELWPRVI NLRHSGVL
24308	54676	A	24446	896	1066	WRLSPSSR*LMPKVPRIQAYFT T*YCS*VIQRSPC*FHCYSRSIPW AWGAGKQSLT
24309	54677	A	24447	1	3660	
24310	54678	A	24448	1	1530	
24311	54679	A	24449	1	1890	
24312	54680	A	24450	746	1872	KHWRGSLISLSTPARFNGGPFW GANQGGDPKGRGGSQRALFR KNNRGGETVSGAEDACIVNNN AAAVLLMLAATASGKEVVVSR GELVEIGGAFRIPDVMRQAGCT LHEVGTTRNTHANDYRQAVNE NTALLMKVHTSNYSIQGFTKAI DEAELVALGKELDVPVVDLGL SGSLVDLSQYGLPKPEMPHELI AAGVSLVSFSGDKLLGGPQAGI IVGKKEMIA RLQSHPLKRALRA DKMTLAALEATRLVYLHPEALS EKLPTLRLLTRSAEVIQIQARL QDPLAAHYGAFAVQVMPCLS QIGSGSLPVDRLPSAALTYTPH DGRGSOLESLADRWRELPVPVI GRIYDERLWDLRCLDEDEQRFL
24313	54681	A	24451	1358	1419	

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24314	54682	A	24452	1	1568	MKGRNIDAQEIQKRYGMVGD PVIIGVVVLGLIFGLAAGEGFKGC ASLMITVAAIMVLFPRMIRLIVE GLLPISDGARKFFQKYFKGREV YIGLDTAVTLGHPPTIAVGLLLI PIMLILASILPGNKVLPLADLPV APFFICMATVIHRGDLVRLISG VIVMITVLLIATQFAPYFTEMAL KGGFSFAGESAQISALSVGNMF GWSISELSLGIHGRVVAVGIVA SVVLFLRLVLSMSWLKEVIGTEK AVIAMCHLRALPGDPSFDAQLG MNWVIDKAWDDLMAQLQNGG VDVAMFSNEFSLPYLTKVRPET TAAMARIHQLMDSIRIPFGVNV LWDPVASFDLAMAATGAKFIREI FTGAYASDFGVWDTNVGETIR HQHRIGAGEVKTLFNIVPEAAV YLGNRDICSIAKSTVFNNHPDA LCVSGLTAGTRTDSALLKRVKE TVPDTVVLANATGVCLLENVEEQ LSIADGCVTATTFKKDGVFANF VDQARSNNPSAIPAFAFVKSIDG DRYQINPNRHGVNDG
24315	54683	B	24453	1	3352	
24316	54684	B	24454	60	2284	
24317	54685	B	24455	1	2475	
24318	54686	B	24456	1	2890	
24319	54687	A	24457	1065	1139	
24320	54688	A	24458	282	615	
24321	54689	A	24459	2657	2919	
24322	54690	A	24460	1	835	
24323	54691	A	24461	167	338	
24324	54692	A	24462	834	1515	LRWCSMPCCRWSKDRAAPSPA YSRLSSHVIAAGYVGGGVARG HSWVFVALTLVLTAVLFSLAGL LNGVFAKTFDDISLVPTFVLTP TYLGGVFYSLTLLPPFWQGLSH LNPIVYMISGFRYGFPLNHNH PGVAVDINRLLLPRKQEKLGK LDKDLQIAGVQDAFADSKSLK DQEIQTQLQAFEARVKSSAQAK MEKDAADNEAKGKEYREKFR QIPSVSSCQKQ
24325	54693	A	24463	3	557	
24326	54694	A	24464	255	693	
24327	54695	A	24465	3	242	QKAPVLANQRQPRRPTGALLLE /SLPLVAESSDG*EPMNTATEPH SRPLP

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24328	54696	A	24466	1	2636	MKNIIRTPETHPLTWRLRDDKQ PVWLDEYRSKNGYEGARKALT GLSPDEIVNQVKDAGLKGRGG AGFSTGRKWILMPKDESMNIRY LLCNADEMEPGTYKDRLLMEQ LPHLLVEGMLISAFALKAYRGY IFLRGEYIEAAVNLRRRAIAETTE AGLLGKNIMGTGDFDFELFVHTG AGRYICGEETPLLKPQTGVWQ RHSCWKLQELAMNDRDFMRY SRQILLDDIALDQQKLLDSQV LIIGLGLGTPAALYLA
24329	54697	A	24467	506	673	
24330	54698	C	24468	1	3411	
24331	54699	A	24469	2455	2694	
24332	54700	A	24470	1	1081	MGGLRDPWLHKLRSLWGLCR YGHKEQYDHRIELNAPGDDTT LVPTGLAIHIADPSLAAMMLPR SGLGHKHGIVLGNLVGLISDY QGQLMISVWNRGQDSFTIQPGE RIAQMIFVPVQAEFNLVEDFD ATDRGEGGFGHSGRVFCNMAE KQTAKRNRREIQLSLAMLES SDGSQRITTAKLAASVGVSEAA LYRHFPSPKTRMFDLSIEFIEDSLI TRINLILKDEKDTTARLRLIVLL LLGFGERNPGLTRILTGHALMF EQDRLOGRINQLFERIEAQLRQ VLREKRMREGEGYTTDETLLA SQILAFCEGMLSRFVRSEFKYRP TDDFDARWPLIAA/SCSNMTPD
24333	54701	A	24471	93	475	RCKCADAATRGKSRRLPDVQ NSARQYG/W/GCATHARSG*HI VEAVQSG/TPPQPLRPRGTSRKV STDRYWRAASQLPAQYQDLTSI YDVVYTPDPRVAKRAFKSPDD GPVMWRMGHQPHLIPRNVLAQ
24334	54702	A	24472	254	1150	RFLTCRYGPGMAEDMQSLVGG TVTRSG*LSVVVNNNGE/LLAK ELSVQVGIRPEYLDRLHAFSG GQRQRIARALSSQPDVIVLDE PTSALDISVQAQILNLLVTLQEN HGLTYVLISHNVSVIRHMSDRV AVMYLQGQIVELGDAQQEIAQA LRRTPAPMVYIGNLGRSLPA ANLKLESKLAIMEQYVGKKVID AVIVGPKVDVSAVKERIVIEV LEASDIPYRHDRQLLHNALEKA LQALGGLEVIQLYRRDSNLVPG QLLKTSMEGKTRLYAADSRLIA AKGSPQIPTLDSLK

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24335	54703	A	24473	1874	2927	KEDQVKGGMVCPKLLCQGTR *RGGVVGGISQASVTSGVYSA SCQPTPAIMQLHL/ANAASRRL QPDNRPNPGWHRPPIHAFTTP GLVSVSFLGPCSTPTCLPFSES SVGESVNLWPQSNENLRRTL GEGNLLTFIGNGKHEIIASIFFA FSEGISAQSHWQPRYISPAVCT LVTEIDIKANKITFSIFDENAGA WLPFFCKAVVPGWVYKPNLGH EIACVDHWLMPNRLIENLCDIM LPIWVLTKFNDCCAGCVPCCVII VDDALHGAPKRMCCITRGMRL LLKLSVHAATRSTLQQAASHGH CAWSAPGWLDTSGMDGDLW WTLHEVLRDLCTSHGNIVESAR
24336	54704	B	24474	1	672	
24337	54705	B	24475	1	2496	
24338	54706	A	24476	3260	3363	RPDSGGP*RRRYLRCAHRRR AVRNQQLTACA
24339	54707	A	24477	112	224	
24340	54708	A	24478	1614	2326	CTYSRCKRPDKRSASGNFALSS LKSSPLTKNRRYWKVSPTHLLL SKRPKISLNAYFGACSLVRPVL AAASDWTLQGAWSPTRAKALP ICESWRIPYADSLSLAASCDV FVHSSSTASHFDVVSTLLNAGVH ICVDKPLAENLRDAERLVEGIM REWREERGQGVVHKPIPGWQS TLEQRGFVGCARHFIECVQNQT VPQTAGEQAVLAQRIVDKICSS FNVVVRVAPLGDPIQSKPVV
24341	54709	A	24479	19	885	
24342	54710	B	24480	1	1704	
24343	54711	A	24481	974	1156	

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24344	54712	A	24482	162	1602	HRRKRARGTPKATTTTRKPARTI ETLSPLLAILAFAPKLAICTRSPL L/DDMTPTFTQCTNAYSHSGIRNP TAISSAAYPRRITGY/KLGPTE ERTVYGIYGISESNLAECEKGV KSAVALTPALQPIDGVAVSYID AAVALGNTINEMDKYYTQENY KDDAFAGKKTLLHQTFLKNLEA FEPVAESYHAAIQEINDKRQLA ELKNIEEREKGTFFHYYS LAVMI SAKQINNLI SQDKFDAEAAAMKK VSELETLVAQAEADKGGMNF SFINSAGQYQLEAKKYVRRIRD KVPYSDWDKEQLQDANSSWM VEDSFPRALREYNEMLMTRIGG GAGDQDMVNDFSYSPQLVGRG WFNDQVATGCTRDSTFNQQQV ALSVNAYVVVNRFGKIDWKPM YAEADKLLAKPNMRFKSDKLV GDLSIGDQQMVEIAKVLVSYESK VIIMDEPTDALDTAEASLFRVI REMKSQAPRYCLYLPPHENNL
24345	54713	B	24483	1	1263	
24346	54714	B	24484	148	894	
24347	54715	B	24485	1	1071	
24348	54716	B	24486	168	1088	
24349	54717	B	24487	1	1236	
24350	54718	B	24488	1	849	
24351	54719	B	24489	1	1548	
24352	54720	B	24490	1	1372	
24353	54721	B	24491	1	2469	
24354	54722	B	24492	1	1917	
24355	54723	B	24493	1	1159	
24356	54724	B	24494	1	2294	
24357	54725	B	24495	217	2476	
24358	54726	A	24496	477	916	SLPECEDRVQYRRSLFADPSYR YGLARHGDP RRAGRLRDV*PL HE*YRHWHDQS/RLLIASVLPQ VWHGACNAMTSSCIARQVS*N TALIIRMRKGDLSAVMSSQTGL INIVRRGLLSCFRLTAMKISTV SPFRPQMPSIVRSVWC
24359	54727	A	24497	1136	1317	
24360	54728	A	24498	3	317	
24361	54729	A	24499	1	1245	

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24362	54730	A	24500	85	1293	ITVATTQHQAQLTLRRAGIRQP DMAVQRDHLPRFVAGVIRHIM LMLHSQRRTGLLITAKNRLFF QRRSVPKFHSKLNQAYCLJAAT DCPRRLLLICRYPHFHLHQIIL AIGISAVFEPHQIIGVSRCCPR HLGVERVLFLFLNDFIEQVIIRC HVVQCSAPAAAANIQY AHPWF* LQFFTNNHFELRLGRFQIIGIFPV SAGILHEGIKHAAEQVITQIVML FADYPGTFTFL/RD*RDERRQY AACL*NDGGVGSRDRLRVRLC* KTYPVGHIPTSHYPN/CSPNPKE PSCRTRLKKSGFFTRISAGAEPL MAIPARLSNSLACGARDSAAKE VLLWFRFVLLKQTLNWTTK NVTSLWRTLGSVPVGKEVRAW TIPV/VS NRAAGSGQNPY*F*KR
24363	54731	A	24501	2794	3531	SPRDSPTFWTKGGPGGSRGKAL RLVVGTDHFQAADNIPDHMMY KSIRFNIYHHIRTVTRDINMHNV APRGSGLALHRTERGEIILAQQ ALRSPMHPFSVQRFVKMGYPFT QYRRAQPMIVDDVAITASRGA KSGMKIIRYSFNPTSDVTR*IRI YAQGP RR VFAQRCGFEMHNL GTVYPCVSTPGAEDGDGFVRH LGERLFQLLHTADFLPLPAVI LTGGVLNAQRNFNRRLLPYVE
24364	54732	A	24502	1	1767	
24365	54733	A	24503	1	1275	SNPTAIGGRPRRPYQAEDRSLD FVDALNRKILKDSIFHALQTIM VGIKDFLRLTQVFFDLATRIPRH LYHPVDITTHYGRFCRHRRHIF QLLQLCFRFLCFLRHLRRVDF ALQGFFVVRVVHFEFFLNSF HLLVQIVLTGLFLHLLFNAVAN AFLNLQQIDFRFHHCHQIFQTFV NVGHLQNRHRKIGIVFRSDVL EHPHRNNTIKLVVQVTHLQQN GDIQAFATFLSHFLLFGRNGDA HHAYVIIRCHVVCQSAPAAANI QY AHPWF*LQFFTNNHFELRLG RFQIIGIFPVSA GILHEGIKHAAE QVITQIVMLFADYPGTFTFLQIE ETSAGNTQRVFEMMGELVLET RLRSPAGFTQWIPHQGCRWSCL PVPRTGLALLSPWVVDGTGRR GAGGGTPQGGSSCTGAHGGGG
24366	54734	A	24504	1	2052	

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24367	54735	A	24505	1	1060	MNARQQVAALRVPGVEKATIV YRRSLQEMPAWREEVEEALHD GFRFLNNPERFDADGTLTLRV SLGEPDEKGRRRPVETNETVTL LVDSLITAIGEQQDTEALNAMG VPLDKNGWPDVDHNGETRLTD VFMIGDVQRGPSSIVAAVGTAR RATDAILSRNIRSHQNDKYWN NVNPAEIYQRKGDISITLVNSDD RDAFVAQEAARCLECNVCSK CVVDVCPNRAVNSIAVPGFQNR FQTLHLEAIVCNECGNCAQFCP WNGKPKYKDKITVFSLAQDFDN SSNPGLVEDCRWVPHRGLYH RLYREPTWRSEWPRRHICPEGS TFPERHCDHLSANNSRNKLLPL QKPGFIN
24368	54736	A	24506	1316	2678	
24369	54737	A	24507	2172	5242	IYFSERLPALCTPDHYREPCQ YNCTRLDYDSALNIRELKKVAL EKGWDEYKQRWHKPAAGSGSR HPVAVIGAGPAGLAAGYFLAR AGHPVTLFEREANAAGGVVKN VPQFRIPAEIQLHDIDFVAAHGV KFEYGCSPDLTIEQLKNQGFHY VLIAITGTDKNSGVKLAGDNQN VWKSPLFLREYNGTALKLKG HVVVVGAGNTAMDCARAALR VPGVEKATIVYRRSLQEMPAW REEVEEALHDGVEFRFLNNPE
24370	54738	A	24508	192	484	RGLVHRGRYRWRQKWSAGSP ARHPV/SQSTTDPATHALSTKII SPIPNAPISALARTTATRL*RSM NQPPVKRPTVIPRVKPA*ISEPE VGPIILGP
24371	54739	A	24509	1	1713	
24372	54740	A	24510	1	651	
24373	54741	A	24511	3	783	PVLSKTPLTAKAIDAAPQDKP YKLTDSLTPGLFLLVHPNGSKY WRFYWLNRFLQAIGVYPLI TLKEARRRATESRSLIANGINPV EQARKEKAIDALNMAAGFKKV AEDWFATRVGGWSESYAKQV RSALKEDVYPVLGKRISVDITA RDVLLALLQKKERTAPEQARNV AGASVRSSSLPLSPNWGGWLA RAAFPHHITIAARMTKHPPCW WCTILACRQASLAVRGSTHYSL ELLIRRHILSLRSPICASPLTV

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24374	54742	A	24512	746	2387	WTALPARLKKQIRSGRKLPLTVM PALRETDTFDTFMESWYYAR YTCPQYKEGMLDSEAAANYWLP VDIYIGGIEHAIMHLLYFRFFHK LMRDASMTNPSSVPRAGGPAL LFENPKGYSMPLVCLNFGTPKR VAMGMGQEDVSALREVGKLL AFLKEPEPPKGFRLDFDKLPQF KQVLNMPKRLRGAPCQKQIV SGDDVDLNRIPIMTCWPEDAAP LITWGLTVTRGPHKERQNLGIY RQQLIGKNKLIMRWLSHRGGA LDYQEWCAAHGGERFVSVVAL GAVPATILGAVTPVPDTLSEYA FAGLLRGTKTEVVKICISNDLEV PASAEIVLEGYIEQGETAPEGPY GDHTGYINEVDSFPVFTVTHIT QREDAIYHSTYTGPPDEPAVL GVALNEVFVPILQKQFPEIVDFY LPPEGCSYRLAVVTIKKQYAGH AKRVMMGVWSFLRQFMYTKF VIVCDDVDNARDWNDVIWAIT TRMDPARDTVLVENTPIDYLDLF ASPVSGLGSKMGLDATNKWPG ETQREWGRPIKDPDVVAHIDA
24375	54743	A	24513	576	878	NLGSVWHYFRRSPEPATHHDA ANLERSPAA*RLSGARYRILAV *ADQSQTGSGDGSPDLQTGRV GDEARHRKRGLHVPQPRSEPPV GARGFPYRFATRRW
24376	54744	A	24514	2	878	
24377	54745	A	24515	1	735	
24378	54746	A	24516	1	1992	
24379	54747	A	24517	721	1239	

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24380	54748	A	24518	1	1954	RQLNGVQLAFRESFHTVTRVTE QHAAGA VAIHQHRNQLLTGAL GIFAVA VVCLQQRDLILLADHL AEHVQFVIAQFVTCQQHGNV RNRITIIFFLLFNELRKIVETVRVQ QTQTGEVAFHPQLFRGRVVYG PDLNARRNGVINCSTLEDPPQF GLILFVYITIGIQVGPFFASLRV SGLRLNLFVAVLVIIGGLVTAIL HKLFDIPLPVVLGIFSGAVTNP ALGAGQQLRLDLGTPMEMVDQ MGMSYAMAYPFGICGILFTMW MLRVIFRVNVETEAQQHESSRT NGGALIKTINIRVENPNLHDLAI KDVPIIINGDKIICSRLLKREETLK VPSPDTIIQLGDLLHLSRGSPL DTQDIDLQINSSVEKQFGDAIRT TILDVILARYNVRGVQLNVDDK GALDCILRARLEALLARASGLP MISASLQQRKTRTRRSMLFVPG ANAAMVNNFSIYPADALMFDL EDSVALLREKDTARMVYHALQ HPLYRDIETIVRVNLDSEWGV NDLEAVVRGGADVRLTKTDT AQDVLIDIEKILRIEKACGREGP GSTGLLAAIESPLGITRAVEIAH ASERLIGIALGAEDYVRNLRT RSPEGTELLSARCPIWQAARSA GIQAFDVTYSDANNEAGFL/QE
24381	54749	A	24519	5121	5492	
24382	54750	A	24520	2520	3525	
24383	54751	A	24521	1	1263	MAINSPLNIAAQPGKTRLRKSL KLWQVVMVMMGLAYLTPMTVFD TFGIVSGISDGHVPASYLLLAG VLFTAISYGKLVRFQPEAGSAY TYAQKSNPHVGMVGVWSSLL DCLLAVVIIAIIYVGFSLAGFHV YIGMLFVPGANAAAMVSNFSIYP ADALMFDLEDVSALREKDTAR RMVYHALQHPLYRDIETIVRVN ALDSEWGVNDLEAVVRGGAD VVRLPKTDTAQDVLIDIEKILRI EKACGREGPSTGLLAAIESPLGI TRAVEIAHASERLIGIALGAEDY VRNLRTSPEGTELLFARCSIL QAARSAGIQAFDVTYSDANNE AGFLQEAHAIKQLGFDGKSLIN PRQIDLLHNLAYPTQKEVDHAR RVVEAAEAAAREGLGVVSLN GKMVDGPVIDRARLVLSRAELS
24384	54752	B	24522	62	405	

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24385	54753	A	24523	891	3240	RYRKSPGSRW/CMSCILTSWITT MFPI*RLGQWC*NPCVTMAL/L APIDVHLMVKPVDRIVPDFAAA GASITFHPEASEHVDRTLQLIK ENGCKAGLVFNPTPLSYLDY VMDKLDVILLMSVNPFGGGQS FIPQTLDKLREVRRRIDESGFDI RLEV DGGVKNVNNIGIEAAAGA DMFVAGSAIFDQPDYKKVIDE MRSELAKFEDIRGVAFDL DGT VDSAPGLAAAVDMALYALELP VAGEEKVITWIGNGADVLMER ALTWARQERATQRKTMGKPPV DDDIPAEQVRILRLKLFDRYYG EVAEEGTFLFPHVADTLGALQA KGLPLGLVTNKPTFPVAPLLEA LDIAKYFSVVIGGDDVQNKKPH PDPLLLVAERMGIAPQQLFVVG DSRNDIQA AKAAGLDAQARRK NAGYYYYLRLAKRQMRAGVA EALRDDLLAAKLNVLVNA GD YKFKQIASEKLLIVVTSTQGE PPEEVALHKFLFSKKAPKLEN TAFVAFVSLGSSYEFCQSGKD FDSKLAELGGERLLDRVDADV EYQAAA SEWRARVVDALKSRA PVAAPSQSVATGAVNEIHTSPY SKDAPLVAVRPLNVEGRARAG GASSFLADRV EEEGEVRV FIEH NDNFRLPANPETPVMIGPGTGI APFRAF MQQRAADEAPGKNWL FFGNPHFTEDFLYQVEWQRYV
24386	54754	A	24524	950	2124	MSLISSVIAATWLHVKS YRLSC GFYACQSLVLS/IFPTLSCLFA AEQLLIWSASAFITKVLVPLIM TYAARNIPQNIPEKALFGPAMM ALLAALIVLLCAFVVQPVKLP ATGLK PALAVALGHFLLGLLCI VSQRNLRQIFGYCLMENGSHL VLALLAWRAPELVEIGIATDAIF AVIVMVLLARKIWRTHGTLDL TPLLSLLCFACRKRRLSATRTV TVLHSLGITLLILALWVYQTA ADAGEIFAAGLWLHIDGLGGFL LAILGVIGFLTGIYSIGYMRHEV AHGELSPVTLCDYYGFHFLFLF TMLLVVTSNNLIWMWAAIEAT TLSSAFLVGIYQORSLEAAWK YIIICTVRVAFGLFGTVLVYANA ASVMPQAEAMAFWSE

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24387	54755	A	24525	1	757	RWRLPGVPPNFGFSKFLPAP GFALSVEYWILLPAMILLMIESV ASFAWFIRWFGRVVPGKPSEAV ADAAPLPGSMRLVLIIVIMSLI SSVIAATWLHVKSRYRLSCGFYA CQSLVLVSIFATLSCLFAAEQLL IWSASAFITKVLLVPLIMTYAAR NIPQNIPEKALFGPAMMALLA ALIVLLCAFVVQPVKLPMATGL KPAL/AGLATDAIFAVIVMVLL ARHWRTHTGLDVNNLHALK GIMSCSYSS
24388	54756	A	24526	249	3943	
24389	54757	A	24527	1	1278	
24390	54758	B	24528	48	144	
24391	54759	B	24529	27	239	
24392	54760	A	24530	1	551	
24393	54761	A	24531	3	258	MLFDEPTSAlyPEMIN*VLDVM VELANEGMTMMVVTHEMGFA RKEANRVIFMDEGKIVEYSPKD AFFDDPKSDRAKDLAKILH
24394	54762	A	24532	2	979	
24395	54763	A	24533	1	4116	
24396	54764	A	24534	1	1195	MLIAEGLMTAKNITVITNSLPA AFALSENKDITLVCCGGTVRHK TRSMHGSIAERSLQDINADLMF VGADGIDAVNGITTFNEGYSIS GAMVTAANKVIAVLDSKFNRR RGFNQVLPIEKIDIIITDDAVSEV DKLALQKTRDTSLVYVLSLADF FRTASTIGERDGTQVEMILFAGF VYLVISLSASLLVLTDCSTEVK KGEVVVVCGPSGSGKSTLIKTV NGLEPVQQGEITVDGIVVNDKK TDLAKLRSRVGMVFQHFELFPH LSIENLTLAQVKVLKRDKAPA REKALKLLER/VSGFFAHANKF PAQLSGGQQQRVAIARALCMD PIAMLFDEPTSAlyPEMINEVLD VMVELANEGMTMMVVTHEM GFARKVANRKHITRSTIALQSL ATCT
24397	54765	A	24535	383	962	TDNDRPGLGTMKKASAIVTN VAVVLSGRYRRERASGEWAAL SFLRPHTLTVFVPHIQWDDPQ MSRPSGRHLFRCRTVQRKHAL QVVEKFRPFFPSDRYRYGAPGD YAQSFGGQIDDVVKAQITPSKF RRFLRVSF*IRLPILHSGKSPLR RMPNLMRRHSHTARHYPALGT RGQPPTDRQERPAVASGO

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24398	54766	A	24536	1477	2387	
24399	54767	A	24537	1	1560	
24400	54768	A	24538	305	718	
24401	54769	A	24539	1	2161	MNDVDRVGGKNASLGEMITNL SGMGVSVPNGFATTADAFNQF LDQSGVNQRIYELLDKTDIDDV TQLAKAGAQRQWIIDTPFPPEL ENAIREAYAQSLADDENASFAV RSSATAEDMPDASFAACTLVPG QNLSTSNKDVIELPDNQYDLDK MVNIYPVTPGLIDQLRAKPMIS QANPELEQQIANIYERIGIGDV LMVTVDHPELTPAGQYRSA SDTGNWVNADGAIFYPIGRLLK VAGKTLTQVRNEITARLDSVIE SPQVDVSVAAFRSQKAYVITA EVSQSGQQFITNIPLTIMDAINA AGGLTADADWRNVVLTQNGV KTKVNLVYALMQRGDLRQNKLL HPGDILFIPRNDDLKVFVMGEV GKQSTLKMDRSGMTLAEALGN AEGMNQDVADATGIFVIRATQ NKQNGKIANIYQLNAKDASAM ILGTEFQLEPYDIVVTTAPLAR WNRVISLLKKLERLTSIAITLPGI IDTENGIVHRMPFYEDVKEMPL GEALEQHTGVPGGEAKGLVGAP PGARDVIQVVSIPNVGRAVIPN GHLLPGSSSLVEIAHTQGGL MGKRCYCGNHGCLLETIASVDSI LELAQLRLNQSMSSMLHGQPL TVDSLCAALRGDLLAKDIITG VGAHVGRILAIMVNLFPNQKILI GSPLSKAADILFPVISDSIRQQA LPAYSQHSVESTQFSNQGTM
24402	54770	C	24540	1	1389	
24403	54771	A	24541	405	576	CEMGAPPWPGCWLSLFDVDG RFVLAWMLFQGSYLALAGLDQ PVHIHLGQLLALWRPL

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24404	54772	A	24542	1	1127	MARTLAHELIDFGEIKRGLLGIK GTEMSADIKAFLNDVQRGAF VSEVLPGSGSAKAGVKAGDIIT SLNGKPLNSFAELRSRIATTEPG TKVKLGLLRNGKPLEVEVTLDT STSSSASAEITPALEGATLSDG QLKDDGGKGIKIDEVVKGSPAAQ AGLQKDDVIIIGVNRDRVNSIAE MRKVLAAKPAILALQIFPVDHR GAIGGQTTDIPDPSPGINHDRC MKGLSFAGEMVTYTNTHARRA FTNQPRDFMSVAWLKGIAILP SVGEVRSPVAGRIASLFATLHAI GIESDDGVELIHVGIDTVKLDG QIFSAHVNGEAGLKRvVKKKEH AD/VQRHAESV*RRGQAQGTG GIRRDQNRVQPGCERCTHQLLR
24405	54773	A	24543	95	599	QIMRMLNGSSTPNTSLPTPQAF DRSLPINATARPSTSTRHSAE SSISRDVSNVS/HSGG*TGGIK G*CHAHADLTACHEADSRGSP SHAVAAVALHVLD/GWYLGQD TAAAYATGSVSPSSGNQFSRP SAAGRFSAVSPAQGAQRHPGR ARRRRRRRTAGGCRR
24406	54774	A	24544	640	890	LANAQLGSNEISIFQCFAAIQRFI KLHRDASVINHPLAE/TRK*YPV SVYHLRHPPAIR*PAIRDNA**I LPVTGPGYSCSRHQ
24407	54775	A	24545	3	257	ETDIFICDSREFFHHFAKASVHI* PVVSIANFAIQSGKILALGAENI ATTSDRRARQKQAVCKAHDAS SVSFRTLSVRPTNDPC
24408	54776	A	24546	332	1047	RTRPYCPGMGNPEMTGWMAA AVVTLMIRMCFSVYTMLESCE QRMVIVGYGRCFADRQNLMLVC LRSMNPVFTGSCARMRCCLSEN LLYRHRNGHIQAEW*KKAISD VKQYRTSCWERWNAASA TIFR/ LSPVEW/LTDNGSCYRANETRQ FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDYISIMPKPDGLT AAKNLAFAFEHYNEWHPHSAL GYRSPREYLRQACNGLSDNR CLEI
24409	54777	A	24547	1200	1544	LTGVADGNVDKPCYKFARLW YWIYAPFPPIRVVKVAYREYRP PTTPRVQRVDLTFCHRPAPDR MHRV*SSHRALPGCWSKVPAQ KSSRTVSGTD*VDLLSPRAQRA PSPLQG

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24410	54778	A	24548	263	625	
24411	54779	A	24549	742	851	VSAQQRVILNKIAVLNRK*RYG CWRLWICPYISRHLNLSNPLQA RCRRYSRGER
24412	54780	A	24550	1	532	MKTLLIIDANLGLTRLYGEDPAG AAARKAKLEIIDNPNDPAEMAI VGDSIPNDALNGKNVWLGDIS RAVAHPFLFLSERKGHAKPYTA PVAATAPVGASGPKRVVAVTA CPTGVAHTFMALKPLPKPKRN VAGIPDTGQCETVQITSCW/AA VETPLRQRSSVSSGVADG*WF MLPG
24413	54781	B	24551	1	888	
24414	54782	A	24552	1	2283	
24415	54783	A	24553	992	1662	KKAISDGLTGSSSAVITERDC VSRSRWTAIVIRHCTGRSLPAA STVKQYRTSCWERWNAASATI FR/LSPVWELTDNGSCYRANET RQFARMLGLEPKNTAVRSPESN GIAESFVKTIKRDYISIMPKPDG LTAAKNLAEAFEHYNWHPHS ALGYRSPREYLRHGLVSFISLQ KFINDFAFEDGLFSGYDAEKRQ YEKSSWNYQLDENGYAKRDET LTHPRC
24416	54784	A	24554	1	2262	
24417	54785	A	24555	158	410	
24418	54786	B	24556	1	2607	
24419	54787	A	24557	715	1016	KSAAVPRSGASSQSDSAHFAQP EYAAFSRFRGSRFRHPRAA*YF GRLNHHVRSERGINP*YHRFNL HWRYVADAISADGAFRTVSGG GRRSGAGRVDWQ
24420	54788	A	24558	652	1214	RTDHCVSRSRWTAIVIRHCTG RSLPAASTVKQYRTSCWDRWN AASATIFR/LSPVWELTDNGSCY RANETRQFARMLGLEPKNTAV RSPESNGIAESFVKTIKRDYISIM PKPDGLTAAKNLAEAFEHYNE WHPPSALGYRSPREYLGQRACT GHAIKSGPSSAFFGAPVRRVSRT SVTAKACPRGLL
24421	54789	A	24559	647	1976	
24422	54790	A	24560	289	574	ETPASSPTLRTSIPSISWMTGRSL RRVMMLCFFPSESGTVSEKAWP EWSSFSSPPSCRTSASSPPSHLR /NIDVSPKHVVFATIPRNYTMSF LPR
24423	54791	A	24561	816	1375	

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24424	54792	A	24562	1	3993	MSQKLKVVTTIGGGSSYTPELLE GFIKRYHELVPSELWLVDVEGG KPKLDIIFDLQCRMIDNAGVPM KLYKTLDRREALKDADFVTTQ LRVGQLPARELDERIPLSHGYL GQETNGAGGLFKGLRTIPVIFDI VKDVEELCPNAWVINFTNPAG MVTEAVYRHTGFKRFVGVCSN IGMKILKTRITLDTTGSTSTGDTL LTQSLLMELSALCRVEVEEGLA LVALIGNDLSKACGVGKEVFG VLEPFNIRMICYGA
24425	54793	A	24563	1136	3608	KKAISDGALTGSSSAVITERDC VSRSRWTAIVVRHCTGRSLPAA STVKQYRTSCWERWNAASATI FR/LSPVEWLTONGSCYRANET RQFARMLGLEPKNTAVRSPESN GIAESFVKTIKRDYISIMPKPDG LTAANKLAEAFEHYNWEHPHS ALGYRSPREYLRQACNGLSD NRCLEIYGQIQLGTGELNITTGV VVTAARDTHIALNFQKRRTTGLA TQSRQRCQNRVRVMGKIVYRD AIRFTTQLQTATSINKRTRQVSG ICRRYTNMASRCNRHQAIHVIM FAYQRPFFHFAHFFAIQQNFPGS IGGQLFRLPVTLTHQLLLAPA AHRHGLFQVDVIFRPDNTALPR NDTHQMVELFLDRFQVVKDIG VIELKVVEDQRTAVMMNKFRA FVEKGA VILIRFDKKKIDFLQYR FHTRISTGHGVANNHQIRLRLE LAGIVPLNQLNPLNSVPMINI MNGGENADNNVDIQEFMIQPV GAKTVKEAIRMGSEVFHHLAK VLKAKGMNTAVGDEGGYAPN LGSNAEALAVIAEAVKAAGYE LGKDITLAMDCAASEFYKDGK YVLAGEGNKAFSTSEEFTHFLEE LTKQYPIVSIEDGLDESDWDGF AYQTKVLGDKIQLVGGDLFVT NTKILKEGIEKGIANSILJKFAQ HAGLLHMYTCAMLGVGQGQCW RYCMSQAFKEDRFAQDQRVAV
24426	54794	B	24564	83	2851	
24427	54795	B	24565	1	1578	
24428	54796	A	24566	574	753	
24429	54797	A	24567	1	2112	
24430	54798	B	24568	27	969	
24431	54799	A	24569	1	1773	

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24432	54800	A	24570	822	984	PSALCGCHSL*CSNASARFFAA VNPSGAFGCRADHPDGELFLTG YVADGGYHS
24433	54801	A	24571	1	4287	
24434	54802	A	24572	1	2384	
24435	54803	A	24573	3	3682	ACSARPSEAELELIDTLNADN TIDGILVQLPLPAGIDNVKVLER IHPDKDVGDFHPYNNVGRCLQR APRLRPCTPRGIVTLLERYNIDT FGLNAVVGASNIVGRPMSMEL LLAGCTTTVTHRFKTNLRHHVE NADLLIVAVGKPGFIPGDWKE GAIVIDVGINRLENGKVVGDDV FEDAAKRASYITPVPGVGVPMT VATLIENTLQAMSNMATFSLGK HPHVELCDLLKLEGWSESGAQ AKIAIAEGQVKVD
24436	54804	A	24574	1	1382	MLRGVNVLADAVKVTILGPKG RNVVLDKSFAGPATITKDGVSVA REIELEDKFENMGAQMVKEVA SKANDAAGDGTTTATVLAQAI TEGLKAVAAGMNPMDLKRAS RSRKGYPARIRQELNQKGISR EATEKAMRECDIWCA**RF*S DKHHHRT* ^Q /PTRHRYPD ^{ESV} PGSHNHRSAHALSSAQGYILLP RAVLSGWR ^{FENVHPTGYPAG} SGSVFVPPMTSRRLPAPDNFA APHRYRVLKTGLLSPGCHVRN ADTL
24437	54805	A	24575	466	1215	
24438	54806	A	24576	1104	1923	LAIPMKDFITEAWLRANHTLSE GAIEHLPADSRLTPSARELLES HLRIKFIDEQGRLFVDDEQQQP QPVHGLTSSDEHPQACCELCRQ PVAKKPD ^{TL} THLSAEK ^{MVAKS} DPRLGFR ^{AVLDSTIALA} VWLQI ELAE ^{PWQPLADIRSLGNIMR} ADALGEPLGCQ ^{AI} VGLSDEDLH RLSHQPLRYLDH ^{DHLVPEASHG} RDAALLNLLRTK ^{VRET} ETVAA QVFT ^{TRSFEVLR} P ^{DIL} QALNRL SSTVYVMMILSVTKQPLTVKQI QQRLGETQ
24439	54807	A	24577	243	644	HAGSVCP ^{SLYRCQRTAKRSGFY} LLLKRLWSFSGNI* ^{IHSGQQNPG} RNQQLGLPRSRK ^{GESSRAHPSC} QRRPQV ^{WPHPLAGSRPPRPWA} ACARLGP ^{IAPARQIPERWPGQV} PVLADAHVLPCLAGSLR ^{PALYD} F

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24440	54808	A	24578	237	454	RSRLPEGVPVCWCNHSVR* RDFPVGKLHRLWL/LALPGVRLIF RASTKRITGYINARSASIASASA RNRLV
24441	54809	A	24579	377	1155	KAYSFATMKSALISCRWQNA* SVSTFVMVRW/LKGVQFRNHEI IGDIVPLAKRYAEEGADELVFY DITASDGRVYPTLITRLADRF VQCIVVGIDTWYDARNLKDISV VGLLGAQVPSVRAGMPQSRQ TEGAQGMVRNNEEGSLRLSHH QACKATHTQQWTLVTAQSSY NLFPEQWVKLFVGIRQGDPL AFSQKLSRQTQQQTQTTPRI VGQAPKDLQGTGTPTTHAVH SGDHAAGEQSCSKAPIYPI.T AQFSLETRSFWSGEWGYSTHG ELRRRDKGRRFPY
24442	54810	A	24580	1107	1458	RTFWWTTCNSLAPCAGGYPST GAALPVSRKLPGRGLLSGWG EHNARYRAGTFLWALFCAAAY AYWRRQ/WGQYGMWFLRIRRG TLGDGTIRRVFVGLSWAAVVIV EIGVEHIGVFKA
24443	54811	A	24581	171	352	PPAPAESDGLPAHTTRARTTA DDLNRKRRQHVG*YRTRGSP RPNRTWVRVCYRSPHR
24444	54812	A	24582	5	226	
24445	54813	A	24583	476	1939	RPESQHNTAKPAMKVLEQARR FLGIRWLAPASLAN/PVILLVV GNILNIVLDVWLVMLGHMNVQ GAALATVIAEYATLLIGLLMVR KILKLRGISGEMLKTAWRGNFR RLALNRDIMLRSLLLQLCFGAJ TVLGARLGSDIAVNAVLMTLL TFTAYALDGFAYAEHSGQA YGARDGSQLLDVWRAACRQSG IVALLFSVVYLLAGEHIIALLTS LTQIQQLADRYLIWQVILPVVG VWCYLLDGMFIGATRATERNR SMAVAAAGFALTLLTLPWLG HALWLALTVFLALRGLSLAAI WRRHWRNRPGTGCLNTKGS QQQHRHDSITQHIHLQLLIRV KTTTTNNSQQTPOYPQCYQYHT DSRQHRQQRNMVCQRIPHALPS PRFRQISRGSTAKVPCAKARAF LRVKSDPTLITRLADRFVQCV VGIDTWYDAETGKYHVNQYTG DESTRVTVQWETLDWVQEVQK RGAGEIVLAYVSE

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24446	54814	A	24584	1	50	
24447	54815	A	24585	354	456	HLFSEACCSPGVRLRCRPF*SP GTDRLVVMHGH
24448	54816	A	24586	494	835	ITWLPGRFPFQGSSEQFLAGVP GATGGSESVLHTRNSYKMLEV RREVAALISALKVSAKCRNCGS SHALTEP/ASSPCWRETSTRPTG APAPTIPPPAASPSGPMCVQPH GED
24449	54817	A	24587	3	726	
24450	54818	A	24588	1	1635	
24451	54819	A	24589	1614	2454	RTTHAPASTPNTGTMLCRPYPC CWRKRTPMIFRATPQWVFSMD QKGLRAQSLKEIKGVQWIPDW GQARIESMVANRPDWCISRQRT WGVPMSLFVHKDTEELHPRTL ELMEEVAKRVEVDGIQAWWD LDAKEILGDEADQYVVKVPDTL DVWFDGSGTHSSVVDVRPEFA GHAADMYLEGSDQHRGWFM SLMISTAMKGKAPYRQVLTHG FTVDGQGRKMSKSIGNTVSPQD VMNKLGAIDLRLWVASNDYTG EIAGSDENLKRACHYNACSSISL ARRRH
24452	54820	A	24590	362	517	TKSLISSMSSISSPPVLIICRNSS PEV**RKI*LGTELEFVIMVIAVS AWP
24453	54821	A	24591	250	930	
24454	54822	A	24592	1388	1912	VCPAAMTGFAAGSFPCTAVVTFP DITPLLWILMC*LAILMAESEP AISPTTISVVP*YAAESLLRVRI VPFSVTSPLPLILCVIAQLRSVE MVSRLPLITEASPRFFCSLTLSA LPVSMMLNCPTRKLLSPSNTSVL AVALTIPFPLMLLRSSPVTFVS NRPSWAIFPLPNP
24455	54823	B	24593	1	6018	
24456	54824	A	24594	510	1003	VALQADQKHKHERLPPPIPTM FQLAQPGVQLHAKPVYQVPV MMQATEPTGI*VRIPVLSISTNA PSITSIWPLFVRKISVLTLSVV AASHAASSPRQCAIRCKIWGRW AGSLRRDDGFGVRSRGSRYGA SVSISNFSAGINGKSSRSSPRRS SQTQVPVMP

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24457	54825	A	24595	197	4314	RASTELSLRCCAPSLQ/ALLHFLYLACFTWMLLEGHLFLTVRNLKVNANYTSTGRFKKRFMPVPGYGIPAVIIAIVSAIVGPQNYGTFTHCWLKLDKGFWSFMGPVAVIILINLVFYFQVLWILRSKLSSLNKEVSTIQDTRVMTFKAISQLFILGCSWGLGFFMVVEVGKTIIGSIIAYSFTIINTLQGVLLFVVHCLLNRIQINSLLLTWTLWILRQRLSSVNAEVSTLKDTRLITFKAFALFILGCSWVLGIF
24458	54826	A	24596	1409	1573	
24459	54827	A	24597	1283	1563	
24460	54828	A	24598	281	839	CVPTTDLVVQSQI*PRWRNWPRLCSCSHVSMKAASSPERTFTYCSGIYWLISGSGIGVSVPLLIISIGESVINLAVRPVIAHAIRVAITTRQTRVAVTVVVALPVFRAVEHHVFQHLTQTRTGFRWHQFFFNRRQREQSFTQGEQQRWANFQNGKVNNHQLAQLRLRLIIGRVRFENQRFVVFDHLA
24461	54829	B	24599	I	5652	
24462	54830	A	24600	559	1665	RVERKATIEMKSQRTTSDSWLII LAKQTGIIRAACKGKKTIFILHDGPPYANGSIHIGHSVNKILKDII VKSKGLSGYDSPYVPGWDCHG LPIELKVEQEYGKPGKEFTAAE FRAKCREYAATQVDGQRKDFI RLGVLGDWSHPYLTMDFKTEA NIIRALGKIINGNHLHKGAKPV HWCVDCRSALAEAEVEYYDK TSPSIDV/AHPFMGFDVPAILGD HVTLDAGTGA VHTAPGHGPDD YVIGQKYGLETANVPVPGDGT YLPPTYPTLDGVNVFKANDIVVAL LQEKGALLHVEKMQHSYPCC WRHKTPIIFRATPQWVFMSMDQK GCDIGFHASSNGKRRADDSDN HVRRLCARQGRQPHPHQFQRT

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24463	54831	A	24601	1	1190	MTDFRESDTMSLFDKKHLVSP ADALPGRNTMPVATLHAVNG HSMTNVPDGMEIAIFAMGCFW GVERLFWQLPGVYSTAAGYTG GYTPNPTYREVCSGDTGHAEA VRIVYDPSVISYEQLLRKYRCV AVALLGYFKCKPILLNPSYKSM QDDLAFIARFIHKDLKFRRFSL KADQKSRIYERVLSIAGVNSWK DKQHQPRLVEHLLVCAESWVA PRALFDAIEYLAHQKIAIPAYL VAFLVLGPLVLSLIPSQLPSLT WSSITYSIVVIVEAGYQYHSRLR RFRGRVEVNEQIEYLIHNPIRTRA RAVNFVDNNNRLQAPRILRQDS WWITRPLPGLTWAIGSPGILPQ VVK SARVMKQAVAYLEPFIEA SKEQKKTNGKMVIATVKGDVH DIGKNIVGVVLQCNNYIEVDLG VMVPAEKILR*KLGGTPRTL*R SNRVPGPPEDRHSCFLGCV/YW FLVP*CLSSLRRCRR*RGQAS RIQ*LSSKLAISTIL/GLRRFGR VEVNEQIEYLIHNPIR/IAQGG QLC**QQSASGPTDITAGFMVD HQTFTGADVGDNRVARNPATG GQIGARHETGGGLPRTVY*SQQ RAGQNQRQDGRHREGRRPRH

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24464	54832	A	24602	1	1591	MGILVSPLLAPLIGLLDTMWN WRACYFLFLVLCAGVTFSMAR WMPETRPVDAPRTRLLTSYKTL FGNSGFNCYLLMLIGGLAGIAA FEACSGVLMGAVLGLSMTVSI LFILPIPAFFGAWFAGRPNKRF STLMWQSVICCLLAGLLMWIP DWFVGMNVWTLVPAALFFFG AGMLFPLATSGAMEPFPFLAGT AGALVGGIQQNIGSGVLASLSA MLPQTGGSLGLLMTLMGLLI VLCWLPLARGYRLSSWTSTTAS EDIDCEEGDGEGRNETHGLQLAV EPEGLQPNYMGRGKIRFRDTC LFCTQSRGSQWGFARTELVAL PPFLSGAADYRAGLALWLARG ADCDVDERHRADQSNLARSS GGFIALAAGAKSDRRRLRELNQS LQKELARNQHIAERLLEETESV RRDVARELHDDIGQTITAIRTO AGIVQRLAADNASVKQSGQLIE QLSLGVYDAVRRLGRLRPRQ LDDLTLAQAIRSLMREMELEGR GIVSHLEWQSMNQR*AKTSA* RCFVSARKG
24465	54833	A	24603	1	1752	
24466	54834	A	24604	1	699	
24467	54835	A	24605	965	5516	
24468	54836	A	24606	84	3760	
24469	54837	A	24607	27	278	

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24470	54838	A	24608	311	2529	REWGSTRRCERRISLSRNIAW RTIWRITRPCRCVFRFIATL LHLHLIMNDLPLEEYPCVRDLV PGRFLKFL/HRDPKGTTLVLASD LPGRIIPVDPRSIIIVMLFLAVRWL QRQLAGQELLETRATRLINGER GSNVLTGIYEWPPRTSSALDTL LREIQNAREQHSRLDLIRSYA AQDVKTGLNNRLFFDNQLATL LEDQEKVGTGHGIVMMIRLPDFN MLSDTWGHSQVEEQFFTLTNL LSTFMRYPGALLARYHRSDF AALLPHRTLKEAESIAVFRALS RLPDLWHRSIGTLTEALPQTDK RQEQIAVALTSYGLYGLGYGS KEIQLTYSGTAGDLISPLSAIH GRCILNTLVFIVKLRWMENTLH RFGTHHGCSAVRSSHLDGSPR RSSWHMARARNHIHVEENMA LLMEQAIANEGLFYRLLYLQRS LTAASSLDDMLMRFHWARDL GLAELLVVLPEAKAVGVSAMS MLGSDADWGVVLTFSRDASHY QQGQGTQLLHEIALMLPELLER WIERGWEEQQVWRYGFLRYVAF LTGWSAQNELKANPAKGVSAP KAPRHLPKNIDVDDMNRLDID INDPLAVRDLMYGAGRLSELV GLDIKHLDESGEVWVMGKGS KERRLPIGNAVA WIEHWLDL RDLFGSERERRQHAGTNVLQT ADQRASRARQGERLHRAAGR
24471	54839	A	24609	1	1749	
24472	54840	A	24610	1	2911	MNIDAKILNKILANRIQQHIKLL IHNNQVSFIPGMQGWFIHKS KVIQHINRTKDKNYMIISDAEK AFDKIQQPFLKTLKLLVAGM MAVAAPDDPPPSVSSSKPSTV APPGRISPSGRALCTSLPSALSSS SKFSLRLRFQVPAKLGVMVAVAA AAGVNAMLKRVAVAAASKPH VEIRQDGDQFYIKTSTTVRTTEI NFKVGEFEEETVDGRKCRVR PQSHYSVPVSLGAHGPLLLEE PVSPFAACGAPS
24473	54841	A	24611	249	609	QIEVCVRIKPKAGTVLAYS*RSR QERPPAPGMTSLSLAAVSSDNP VSGDEHILARASGRFIGRVA QPKRIQRSSTPRAATDLGNPG HRPCTVRKSALLVVSVCRRHSS RSLRFRSC

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24474	54842	A	24612	942	1121	
24475	54843	A	24613	1010	1658	EISSKRSRTVCKRRAPMFVSVD FTCHAASAMRLIPESVNSIFTPS VAISALYCTVIEAFGSVRIRSKS LVVSACSSSTRIGDDLAVPGSGQ TVSQSGTRQKR*TECGQF*PSR VWWKRCNLLPAAAGHAERLH EKHPDRKTRRVRLVWLAGPPT RLGTMTMGAGTLVLGACCLPWP REGAHNVATAACGGWRARCD LRFLRSCKLGLSRQFFGWN
24476	54844	A	24614	1	1995	
24477	54845	A	24615	1	2853	
24478	54846	A	24616	1	1755	
24479	54847	A	24617	2942	3454	SVPDWLMCTAFLSLSRINSRL LKAELLTSSIPVLLPSLLPRFQ VPSLFATAVPVSAAPLIAPSV*L LKTTPADIIRPVTLPLLLNTPAFC TILLMVPVLFTELNSAPAFMVIC AVISPALLRIPPLTSTLFVITPAF LMTAPLSSFTKLLMMPLVFSR RPLDTVI
24480	54848	A	24618	1	2959	MKRYRPREILPWKVPVPGNYTPK IFKIKGTGHNPMASJENFDAHTP MMQQYLRKLAQHPEILLFYRM GDFYELFYDDAKRASQLLDISL TKRGASAGEPPMAGIPYHAVE NYLAKLVNQGESVAICEQIGDP ATSKGCCRSNGRNGGRKIVAVS LKKVSGAAKPCGHFRSTRYRV AYSTIINNKAGIWSAFEGVSAT RPNPTPRASPAVRTLSRGTPPEPR KISTDADNLAQGSCLKERLPAWL WGKKENSKWEVLD
24481	54849	A	24619	441	1425	
24482	54850	A	24620	1	2574	
24483	54851	B	24621	1	1725	
24484	54852	A	24622	160	390	
24485	54853	A	24623	892	1183	
24486	54854	A	24624	1	2493	
24487	54855	A	24625	435	829	ASDVLVSEGCYR/GASALTST SVICINTDKALRKIRLPLNGLR KPLNAMTLPGLITWPLCITTEKE DLSISDRLSTCIVKFSHPPEMS VRKFVPPAILLCSVCLRFSCPTR HQKAPAKWILKSCSAWMR
24488	54856	A	24626	763	1863	
24489	54857	A	24627	1423	1712	

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24490	54858	A	24628	1	2792	MTYLSAQDHELIQVVQNGHLQ MCGKSETGNEASPVKCIVLQVL RGLQYLHRNFIIHSQEQTIPDPSI SDQQETPLLAGDMAQRGRGG FYYVTAYIYVDKKAPVHMRTA AQGLITLCCQGFSGLLGYRLGG VMMEKMFAYQEPVNGLTFNW SGMWTFGAVMIAIIVLFMIF RESDNEITAIVMEDSMSSATT LTPPEQVDSLIMQIAEENGLE VLDQLSQLPEGASAVGESSVRS QEDQLSRSFICLMAMM
24491	54859	C	24629	213	345	
24492	54860	A	24630	1	474	MHQTTAKTPHTSYPNNYEEHN RRANRSKNYDRIRHTTILKRTN PAQTITNLLKSFRNRYNYVQPR SCRSIFIHIPGERDLNLCIAPNPP AIFPISIGYLGPDNLNLPYAPFI TINLTGPAPTTTHPVGNLGTTG NPEPGGCGILIVWCCVNWACL WDSVVAAPREPYMPAGLLRHR RHYRHRREDLIAPPAARQTDE NRRPALCHEYAVGHRKIKTNV EHTEPYILPLITHSQPLNRGAFF CPGVRFVVSVDLFEKRL**RR WRRSPAGI*GSRGAATTLQRQ AQLTQHQTIRIPPPGSGLPVVP KFPTGCVVVGAGPVRFFVING
24493	54861	A	24631	1	924	
24494	54862	B	24632	177	468	
24495	54863	B	24633	592	883	

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24496	54864	A	24634	1	1926	MATAKANQEIQEWLGKYGTAR VKLNVDKDFSLKDSSLEMLYPI YDTPTNMLFTQGAIRHTDDRTQ SNIGFGWRHFSGNDWMAAVIT FIDHDLRSRSHTRIGVGAEYWRD YKLKSANGYIRASGWKSPDIE DYQERPANGWDIRAEGYLPAP PQLGASL.MYEQYYGDEVGLFG KDKRQKDPHAISAEHSPEFRSE ALKLVNASVLLPQPVNSACMN HNSSTGAVNSKISRLLNVNW RCLPRLHVSNSASWQNGMKS WL SSKRPRHTSEAPEMKYVFIEKH QAEFSIKAMCRVLRVARSGWY TWCQRRTRINIAVVRADGSRT SFVYTSYLAKVNEEWKNNVGT GSTVKWPIGLGGKNDGIAAF VQRLPGAIGYVEYAYAKQNNL AYTKLISA*NEVCLY*KTSG*V QHQS NVPR/RSQWPAAAGIRGV SGGQG*TL*YAAQMAPELPSS TPATWRK*TKSGKTLV/HGST VKWPIGLGGKNDGIAAFVQR LPGAIGYVEYAYAKQNNLAYT KLISADGKPVSPTEENFANAAK GADWSKTFAQDLTNQKGEDA WPITSTTFILIHKQKKPEQGTE VLKFFDWAYKTGAKQANDLD YASLPDSVVEQVRAAWKTNK DSSVNFDMANVFFRVTPGNFL VNREASHQRRVFAVRAGVDFI YRASSDGLRRCRDRRTFRKRIN
24497	54865	A	24635	1387	1639	ESKPLNLGRSGFLLTRALSAQ PLWQSPDQHLTPQAGLRSRL*A QRQA*QKTASRVV*PKPLWAL VKATSEDISVVL*ESACQC
24498	54866	A	24636	1570	2516	IEVAMSI VVKNNIHVVGQRDW EVRDFHGTGYEYKTLRGSSYSYF IREEKNVLIDTVDHKFSREFVQ NLRNEIDLADIDYIVINHAEDH AGALTEMAQIPDTPICYTANAI DSINGHHHPPEWNFNVVKTGD TLDIGNGKQLIFVETPMLHWP SMMTYLTGDAVLFN YDAFGQH YCDHLFNDEVDQTELF EQCQ RYYANILTPFSRLVTPKITEILGF NLPVDMIA TSHGVVWRDNPQT IVELYLKWAADYQEDRITIFYD TMVNNTPMMAAIAQGIA/ETG PRLAGENFNVARNDKHEDPDL LSFRSERGA

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24499	54867	A	24637	24	363	
24500	54868	A	24638	2	366	RATPRHIIVRFTKVEMKEKMLR AAREKGRVTLKGKPIRLTADLS AETLQARREW*QNLSAFACL*R ILFLLHL*SLVWLDMKCWVENS FL*EC*ILAPTLFWLVGFLPRDP LLV*WASL*G*PDLSLWLPLAF FPSQLW*I*QLCVLELL
24501	54869	A	24639	232	292	
24502	54870	A	24640	4	911	
24503	54871	A	24641	2795	3226	SWWISFLMCCWIWFASILLRIFA SMFIKDGLKFPFLVVS LPGFGI RMMLAS*NELGRIPFSIGWNSF RRNGTSSSLYLW*NSAVNPSGP GLFLVGKLLVIASISEPVIGLFTD STSSWFSLGRVYVSRNLSISSRF SSLFA
24504	54872	A	24642	1	3285	
24505	54873	A	24643	1	4368	
24506	54874	A	24644	200	335	YALLNKDSSPWYPFSVPVLASN TRYLWPLSST**GSLSVWLSPD V
24507	54875	A	24645	174	263	
24508	54876	A	24646	1244	1354	

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24509	54877	A	24647	194	2481	GMFRMNLMEPLTQCINAGHEM TKAIAIAQFNDDSPARKITRR WRIGEAADLVGVSSQAIRDAEK AGRLPHPDMEIRGRVEQVRGY TIEQINHMRDVFGLRRAEDV FPPVIGVAAHKGGVYKTSVSVH LAQDLALKGLRVLLVEGNPDQ GTASMYHGWVPLHIAAEDTL LPFYLGEKDDVTYAIPKTCWPG LDIIPSCALHRIETELMGKFDE GKLPTDPLMLRLAIETVAHDY DVIVDSAPNLGIGTINVCAA DVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEFDPVRILL TKYSNSNGSQSPWMEEQIRDA WGSVMVKNVVRVETNEVGKAA PMVDSLIARVGMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWVSGNERDQELLTEDALDDLI PSFLLTGQQTAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDQMAALSRLLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSPHGELSARSGDALQ KAFTDKEELLKQASNLHEQK KAGVIFEAEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMVLNLDSPQSFSPGAGDHA NSPQSSSPSTGVHINSPLSSLS AGVHTISPOSSNPSVGVLTALSHP DLVWVFTLTAHSRPLVWVFT
24510	54878	A	24648	1361	1694	
24511	54879	A	24649	1	3852	MKLMETLNHCINAGHEMTKAV AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRGYTIEQI NHMRDVFGLRRAEDVFPVVI GVAHKGGVYKTSVSVHRAQ DLALKGLRVLLVEGNAPQGT SVYHGWVPLHIAEAALLPF YLGEKDDVTYAIPKTCWPLDI IPSCALPRIPELMGK/FDEGRS FMPGPP/HHHPLGRSSQ*QVSNS LDRAAKGN*KPLCHC

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24512	54880	A	24650	1	1720	MEKLLLENDLSKDVSRLETVF VPPEKHEKEIALKSNIVELKKQ LSELKKKCGEDQEKIHALTSEN TNLKKMMSNQYVPVKTHEEV KMTLNDTLAKTNRELLDVKKK FEDINQEFVKIKDKNEILKRNLE NTQNQIKAEYISLAEHEAKMSS LSQSMRKVQDSNAEILANYRK GQEEIVTLHAEIKAQKKELDTIQ ECIKIMKRAPVIPKHTLNTQPV DTSLSTPAAPMVDSLIARVGV MARGNATLTPVCGRDVKFTLE VLRGDSVEKTSRVVWSGNERDQ EQLTEDALDDLPSFLLTGQQT PAFGRRVSGVIEIADGSRRRKA AALTESDYRVIVGELDDEQMAA LSRLGNDYRPTSAYERGQRYAT RPQNEFAGNISAMADAENISRK IITRCINTAKLPKSVVALFSHP GPELSARSVIDSAPNLGIGTIN VVCADVLI VPTPAELFDYTSAL QFFDMLRDLLKNVDLKGFE PVDRIILTKYTNINASQSPW MREKFGMAWESMVLKNV VRETDEVGKGQIRMRAD FVQAIQSRSTGAWRNAL SIWEPCNEIFDRLIKPRSEIT
24513	54881	A	24651	1094	2271	APFHRPHTKQSLQEQT DVVSIN EFLKQMAF* AQKLKE/WRTSAA SDITPAGFCSCRAIKDAEK PGRLLPHPD/MEFRDRV DQ/RVVSFPGQIIVHMR NVFGPRLPRAKDVFP PVIGVAAHKGQVYKTSV SVHLAQDLALKGLRV LLVEGNDPQGT ASMVSREGDPALH IYQEAPFLPFYLGEK DDVYIAIKPTCCP GLNIIPSCLALPRIET ELMGKFDEGL LPTDPHLMLRLAIET VAHAHDYDVIVIDS APNLGIGTIN VCAADVLI VLTPEIMFDYTSAR QFFDMLRDLLKNA DLKGFEPEVRIL LTKYSNSNGSQ FPWMEEQIRDAWGS MVLKNVVRETG VEVGKGQIIRMRT VFEQAIQSRST DTSLSSTPAAPMVDS LIARVGVMA SR
24514	54882	A	24652	1	1415	

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24515	54883	A	24653	3008	8165	ILIPFFIGLQNRFTQRLSETKEIT NPYAMRLYESLFQSSKTNGSGI VSLKIDWIIERYQLPQSYQRMP DFRRRLQVCVNEINSRTPMRL SYIEKKKGRQTTHIAIRDAEKA GRLPHFDPMEIRGRVEQRVGYTI EQINHMRDVFGLRLRAEDVFP PVIGVAAHKGGVYKTSVSVHL AQDLALKGLRVLLVEGNDPQG TASMYHEWVQNLHIHAEDTLL PFYLGKKDDVTYAIKPTCWPG DIIPSCALHRI
24516	54884	A	24654	1	848	
24517	54885	A	24655	2354	3640	NVICNQELVYSSRHQFAPGATV LYKGDGMVLNLDNRVRPTEYR YGVFLNVLLPATKYFQLHDP RNMELNYSLASEDI.VLKGLRV LLVEGNDPQGTASMYHGWWP DLHIHAEDTLLPFYLGKDDVT YAIKPTCWPGDIIPSCALHRI ETHLMGKFDEGKLPTDPLML RLAIETVAHDYDVIVIDSAPNL GIGTINVVCAADVLIPTPVE/L FDYASARQFFHMLRPLLKNVD LKGFEPDVRILLTKYSNSNGSQ SPWMEEQIRDAWGSMLKNV KEFAGNISALADAENISRKIITR CINTAKLPKSVVFFLTPVNYL PGDALQKAFTDKELLKQQAS NLHEQKKAGVIFEAEEVITLLTS VLKTSSASRTSLSSRHQFAPGA TVLYKGDGMVLNLDNRVRPTE CIEKIEAILKELEKPA
24518	54886	A	24656	667	870	QIVSSEPKYTDFLSKIPFEQVR DVQRNGDHTEGAVR*LSIAFFS ALLKLLAFFTEEVRAAAVVRFV
24519	54887	B	24657	1	1086	
24520	54888	A	24658	2	250	WRTKSLDIPPLIYPNGIVKNILR HLSQLLNPVTRPFSWILRFP*RP *RKISTSFIRPLFTFLPA**MLIRS SVWQ*KTVSW

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24521	54889	A	24659	1	1608	MAETA VINIHKRKNSPRIVQSN DLTEAA YSLSRDQKRMLYLFV DQIRKSDGTLTYMYTRKPDGS GIVSLKIDWIERYQLPQSYQRM PDFRRRFLQCINAGHEMTKAIAI AQFNDDSPARKITRRWRIGEA ADLLGVSSQAIRDAEKAGPLPH PDMENRRGRVEQRGGYTIEPNN HMRDGVGTRWRRADVFPLI GIVAGHKGGRYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWWPDLHIHAEDTLLPF YLGEKDDVTYA IKPTCWPLDI IPSCALHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLPD LVKNRDLKGVPEPDMRKQRHR KAKDLLAQDPTAMTTDELLKE ATRCPICTAYLEKPMSECECV FCLSCTNSLQKEPQGGVLC PF CLEASQKNNIRLNRLGLRVSH IKELEPKLKKILKMNFKDAEVP RFSSPKPCSSFFSTCYLSKNC SN HPCYSPYPGSGWG
24522	54890	A	24660	1	1128	
24523	54891	A	24661	1035	1208	SLIDRIEALGIFRAAV*GSAAY HG V*YERRRTFLCMLFGYFLSR RLESLLLPEVQS
24524	54892	A	24662	1	1316	MEIRGRVEQRVGYTIEQINHMR DVFGTRLRRAEDVFPPVIGVAA HKGGVYKTSVSVHLAQDLALK GLRVLLVEGNDPQGTASMYHG WVPDLHIHAEDTLLPFYLGEKD DVTYA IKPTCWPLDIIPSCAL HRIETELMGKFDEGKLPTDPH MLRLAIETVAHDYDVIVIDSAP NLGIGTINVALQNFQRYTGQH VHRIGMAERMWCDNRNERHT VSSSGGNRLPNPGPDRSDLALK GLRVLLVEGNDPQGTASMYHG WVPDLHIHAEDTLLPFYLGEKD DVTYA IKPTCWPLDIIPSCAL HRIETELMGKFDEGKLPTDPH MLRLAIETVAHDYDVIVIDSAP NLVFRICFVIWAQERIDIKGFEP DVRILLTKYSNSNGSQSPWMEE QIRHAWGSMVLKN/VVRETDE VGKDTGVRKSIWCHRN SRWE

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24525	54893	A	24663	504	1254	SYVKYFPHPQAQKYFQQIHSAI GLHNADHVHKLHLLGDNRYPIW IMQPSAHHPARQPEHDIAFGKC SSSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWWPDLHI HAEDTLLPFYDPLMLRLAIET VAHDYDVVIDSAPNLGIGTINV VCAADVLIVPTPAELFDYTSAL QFFDMLRDLKKNVDLKGFEFD VRILVVRVSQRMVVAGCIIAFID KLLNVLICFPFSVKNRFVIFHSV DFECVIRF
24526	54894	A	24664	1	3216	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPFG FGDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLPNTQTASPRALA DSLMLQARQVSRL/VKRAPTC WPGLDIIPSCIALPRIETELMGK FDEGKLPTDPLMLRLAIETVA HDYDVVIDSAPNLG
24527	54895	A	24665	1	419	MSSSDKDFDFSVANVMVNFAP VFPMGKYYYTQADKVLPLAIQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE/ VGCCR*KRL*IFSLVYQCAQSI QRALQCTYQPISSHLLYRVTEP VYAVSA
24528	54896	A	24666	1	2598	

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24529	54897	A	24667	1	2027	MRGHREKAAACKPRTRASEGT TPASTFILDFQPPNCNYTSGDNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQSQAKKRDA ELANGALGHELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWLFTDSRGSMTIDGINSN DIYMLGYVSNSLTGPYKPLNKT GLVLQMGDPNDVFTYSHFA VPQAKGILCEEDNYTAGDNHM MRAPHCEEDRAHKFVVFDANA GTESGHQGEESLFNRACGGGGT FFFSKESQKLQSQAKKRDCINA GHEMTKAIAIAQFNDDSPARK ITRRWRIGEADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHM RDVFGTRLKR AEDVFPFVIGVAAHKGGVYKT SVSVHLAQDLALKGSLLPKND FLFKLGLEGLPLGKIHSPTGA DVARGSSGLPKSEFLPERNTQ ELQQDSEEGPLALQVLQSNLM DFADFGTTIKQDFRLLGQTSVD RLLQLSQQGA VKGNQLLPVSL VKRKTTLPNTQTASPRALADS LMQLARQVSRLESGQNNNDGIC EIHVAKYVEIFGLTSAEASKDIR QALKSFAGKLVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQAL QCTYQPIHSLLYRVTEPVYAV
24530	54898	A	24668	1	989	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRRERVIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQH HRIGMAERMWCDNRNRERTVS SSGGRNLPNPGPDRSCDNLKTC HTSHGSVMAETA VINHKKRKN SPRIVQSNDLTEAAYLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPE/V GCRR*KRL*IFSLVYQTCAQSIQ RALQCTYQPIHSLLYRVTEPV

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24531	54899	A	24669	350	1203	LLTARLTWVSARLMSDFADFG TTIKQDFRLLGQTSVDRLLQLS QGQAVKGNQLLPVSLVKRKT LAPNTQTASPRALADSLMQLA RQD/LALKGLRVLLVEGNDPQG TASMYHGWWPDLHIHAEDTLL PFYLGKDDVTYAIKPTCWPL DIIPSCALHRIETELMGKFDEG KLPTDPHMLRLAIETVAHDYD VIVIDSAPNLGIGTINVVCAADV LIVPTPAELFDYTSALQFFDMLR DLLKNVDLKGFEVDVRIILTKY SNSNGSQSPWMEEQIRDAEGSR
24532	54900	A	24670	1	936	
24533	54901	A	24671	1070	1324	LGTPGGCSRMTALVPLINDD TPTRRTRLPLGQGVFSVRS*TV ADQSTSGDGDSTCNVRGSCPCR IAITILITPATPAACV
24534	54902	A	24672	1	1212	
24535	54903	A	24673	2373	3381	FKRGQYQGLLRPRFHGQILYA RRQGADAAGDSGIW/HGIWTEP MTM*KKDER*PSPQTAS*DNW KSIRGSCWQALSITRN/CKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHGDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR KPDGSGIVSLKIDWIERYQLPQ SYQRMPPDFRRRLQHFIVLRER PETVLIDLIRTKDAVRELDNL QYRKMKKLLFQEAHNGPAVEA QEEEEED
24536	54904	A	24674	31	811	RRGLLGTRLRLEDVFPPLVGV AAHKGGVDKTSVSVHLAQDLA LKGLRVLLVEGNDPQGTASMY HGWVPELHIHAEDTLLPFYLG KDDVTYAIKPTCWPLDIIPSC ALHRIETELMGKFDEGKLPDTP HLMLRLAIETVAHDYDVIVIDS APNLGIGTINVVCAADVIVPTP AELFDYTSALQFFDMLRDLK VDLKGFEVDVRIILTKYSNSNG SQSPWMEEQIRDAWG/SMVLK NVVAFQNLFLFILLRIWL
24537	54905	A	24675	1004	1105	

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24538	54906	A	24676	1	1139	MEKKITGYTTVDISQWHRKEHF EAFQSVACQCTYNQTVQLDIKK KLKTVKKNKKHFPAPIHILAR LMNAHPEFRMAMKDVAEYNG YHVVFALAGSPKDADDTSIYM FYQKVGDNIDSWSKNAGR VFK DSDKFDANDPILKDQTQEWSGS ATFTSDGKIRLFYTDYSGKHYG KQSLTTAQVNVSKSDDTLKING VEDHKTIFDGGDKTYQNVQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENG YQGE ESLFNKAYYGGGTASSIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPE/VGCRR*KRL*IFSLVYQT CAQSIQRALQCTYQPISSHLLYR VTEPVYAVSA
24539	54907	A	24677	1	930	
24540	54908	A	24678	1	2486	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DKWPLANADGTVAEYNGYNV VDKFDANDPILKDQTQEWSGS ATFTCDGKIRLFYTDYSGKHYG KQSLTTAQVNVLSDDTLKING VEDHKAIFDGGDKTYQNVQQ IDEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENG YQGE ESLFNKAYYGGGTNFRKESQK LQQSACKRDAELANGALGIIEL NNDYTLKKVMKPLITSNTVTDE IERANVFKMNGKWYLFDTDSRG SKMTIDGINSNDIYMLGYVSNS LTGPYKPLNKTGLVLQMG LDP NDVTFTYSHFAVPQAKGNV V ITSYMTNRGFFEDKKA TFAPSF LMNIKGNKTSVVKNSILEQQQL TWLQVAKRAGLGGGQSGRTVL RERLPNYKNFKGTIQLGQNQY AVSGEIFVVD RNTVEITELPVRT WTQVYKEQVLEPMLNGTDKTP ALISDYKEYHTDITVKFVVKM TEEKLAQAEAAGLHKVFKLQT TLTCNSMVLFDHMGCLKKYET VQDILKEFFDLRLSY YGLRKEW LVGMLGAESTKLNNQARFILEK IQGKITIENRSKDLIQLVQRG YESDPVKA WKEAQEKCDNLKT CHTSHGVSMAETA VINHKRRK

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24541	54909	A	24679	5	253	SAPKVVWRGLRQQGAGISVLP*V CAQP/VQVAKAPELILNFDLPK KYFDKL/R/DTHFFSPHTGKFPT VKILMAPFANSASRGVALC
24542	54910	A	24680	334	842	PDKEGNEJWVDMYTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFISFNMDLADTVMLVVG GHKIFVFHCHTELMSIHQAGK NVNKGRIKLVILFYGL*/QR* YPAERSGYRYIEQLTEMPQNVL YDAIGYQRWYIQ
24543	54911	A	24681	676	1169	DNLKTCHTSHGVSMAETAVIN HKRKRKNSPRIVQSNLDEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPE/VGCRR*KRL*IFSLVYQTC AQSIQALQCTYQPIHSLLYRV TEPVYAVSA
24544	54912	A	24682	1	783	
24545	54913	A	24683	1	1884	
24546	54914	A	24684	1	1131	
24547	54915	A	24685	1	2856	
24548	54916	A	24686	528	725	
24549	54917	A	24687	1	898	
24550	54918	A	24688	1879	2343	
24551	54919	A	24689	1	1254	
24552	54920	A	24690	1	1113	
24553	54921	B	24691	1	1156	
24554	54922	B	24692	1	1980	
24555	54923	B	24693	1	1932	
24556	54924	A	24694	1	663	
24557	54925	A	24695	1123	1764	
24558	54926	A	24696	2	1772	
24559	54927	A	24697	1	1040	MELKTKARELREECRLSRRCN QLEERVSAEMEENEMKREG KFREKRIKRNEQLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLRQANVQIQE IQRTPQRYSSGRETPRHIVRFT KVEMKEKMLRAAEKCDNLK TCHTSHGVSMAETA VINHKKR KNSPRIVQSNLDEAAYSLSRD QKRMLYLFDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDEKSYEQPSKDIRQALKS FAGKEVVFYRPE/VGCRR*KRL *IFSLVYQTCASIQRALQCTYQ PIHSLLYRVTEPVYAVSA

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24560	54928	A	24698	1683	4289	RVFKDSDFKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTFIDGDKTYQN VQQFIDEAGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFR KESQKLQSQAKKRDAELANGA LGIIELNNDYTLKKVMKPLTSN TVTDEIERANVFKMNGKWHK ILVSGTHRARTVEVTDPIHQ RMGCCFTVGAGEICEKPTGCF TLPNCNCQWTSAILDRRSHS IIPSPASGSWVKVVTGSYQLT HSPGIGLRDFADFGTPHQTGFSP AGANQRGPLVATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGPTGKR AVSATQLMHFKILVSRARHART ELEVTDPGSSAENGLFPVLL LRKARKTLMPPHSTCFIKRSAP TQSTAGKTRPRVLKDSDFKDA NDPILKDQTQEWSGSAPFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKTI FDGDKTYQNVQQFIDEAGNYT SGDNHTLRDPHYVEDKGHKYL VFEANTGTENG YQGEESLFNKS VLRRRHLLPDAFDFGPTIKQD FRLLGQTSVDRLLQLSQGQAV KGNQLLPVSLVKRKTTLAPNTQ TASPRALADSLMQLARQVSRLE
24561	54929	B	24699	1	2034	
24562	54930	A	24700	1	1038	
24563	54931	A	24701	1	1149	
24564	54932	A	24702	2	823	WPLQNADGTVAEYNGYHVVF ALAGSPKADDDTSIMFYQKV GDNSIDSWKNAGRVPKDSDFK DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQCDNLKTCHTSHGVSMAET AVINHKKRKNPRIVQNSDLTE AAYSLSRDQKRLMLYFVDQIR KSDGTLQEHGIGICEHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVYFRPEEDAGDEK/ML*IFSL VYQTCAQSIQRALQCTYQPIH SLLYRVTEPGYAVSA
24565	54933	B	24703	1	1206	
24566	54934	A	24704	2	1037	
24567	54935	B	24705	1	1389	

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24568	54936	A	24706	1	602	MGTDGDFICISMTGGAPWGFRI.Q GGKEQKQPLQVAKWANLKP PSHGSVMAETAVINHKRRKNSP RIVQSNLDLEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPE/VGCR R*KRL*IFSLVYQTCASIQRAL QCTYQPISHSLLYRVTEPVYAV
24569	54937	A	24707	1	774	
24570	54938	A	24708	1479	1947	
24571	54939	A	24709	1	696	
24572	54940	A	24710	1	1773	
24573	54941	A	24711	1	1509	
24574	54942	A	24712	1	891	
24575	54943	A	24713	156	242	VAGRGIGYRLSPNKGL*TWSA LCKPIAE
24576	54944	A	24714	1441	1866	
24577	54945	A	24715	1	1098	
24578	54946	A	24716	1	1989	
24579	54947	B	24717	126	848	
24580	54948	B	24718	58	688	
24581	54949	A	24719	1	542	
24582	54950	A	24720	1	675	
24583	54951	A	24721	1	1209	MKMPKHDLLAAILAAKEQGI GAILAFAMAYLRGRYNGVLEA RSLKSRCQQSHALAEGRGGPP VTGRFKSTFTADSWNRYSLPSL TGGGNILHSRTHRTVSRLG RWQELLRDVFGTRLRAEDVF PPVIGVAAHKGGVYKTSVSVH LAQDLALKGLRVLLVEGNDPQ GTASMYHGVVWPDLLHHAEDTL LPFYLGEKDDVTYAIKPTCWPA LDIIPSCALHRIETELMGKFDE GKLPDTPHMLRLAIETVAHDY DVIVIDSAPNLGIGTINVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEPPDVRILLT/ KYSNSNGSQSPWMEQIRDAW GSMGLKNV/VRETDEIGKGGIR MRTVFETAMDKRLLTGAWEK AFFFLEPGFEKSNR

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24584	54952	A	24722	1	743	MIGMELPGLEGTELEGCHEREV VYDRVRVFEKRGAEARHVEARS PGGSGSEKRGWGGARHQRMCR KGADNGGAGRARRVARLRQL ASRAIGRRKGAVLYQTPVINHK KKRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTL WREASKDIRQALKSFAGKEVV FYRPE/VGCRR*KRL*IFSLVYQ TCAQSIQRALQCTYQPISHSLLY RVTEPVYAVSA
24585	54953	A	24723	1157	1471	
24586	54954	A	24724	1	824	MEENERDLEINMINMSKELKVE NIKKHIGMLEKDEIEIIVTKSILI EIEIPTQCLRNLTLLHLAASAGN HMSNTACWYGCEDFTSVSTFA HQGVGSWDAYPEAASLLSCLD NLKTCHTSHGSMVAETA VINH KKRKNSPRIVQSNDLTEAAYSLS SRDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVANYAEIYGLTS AEASKDIRQALKSFAGKEVVYF RPE/VGCRR*KRL*IFSLVYQTC AQSQRALQCTYQPISHSLLYRV TEPVYAVSA
24587	54955	A	24725	996	1169	SLIDRIEALGIFRFAAV*GSAAY HGV*YERRRTFLCMLFGYFLSR RLESLLLPEVQS

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24588	54956	A	24726	3	1743	DSPEARKITRRWRIGEAADLV GVSSQAIRDAEKAGRLPHPDME IRGRVEQRVGYTIEQINMRDV FGTRLRRAEDVFPPIGVAAHK GNDPQGTASMYHGWWPDLHIH AEDTLLPFYLGKDDVTYAIKP TCWPGLDIIPSCALHRIETELM GKFDEAQPNLGIGTINVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEVDVRIILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTDTSLSTP AAPMVDSLIRVGV MARGNAI TLPVCGRDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTAPFGRVSG VIEIADGSRRRKAAALTESDYR VLVGLDDEQMAALSRLGNDY RPTSAVERGQRYASRLQNEFAG KYFLRWLMRKIFHIITRCINTAK LPKSVVALFSPHGELSARSGDA LQKAFTDKELLKQASNLHE QKKAGVIFEAEVITLLTSVLKT SSASRTLSRRHQFAPGATVLY KGDKMVLNLD RSRVPTECIEKI EAILKELEKPAP
24589	54957	A	24727	1	1623	
24590	54958	A	24728	1	1863	
24591	54959	A	24729	1	2622	
24592	54960	A	24730	1	1338	

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24593	54961	A	24731	1	1823	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWGSA TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL VFEANTGTENG YQGEESLF NKAYYGGGTNFFRKESQKLQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYTK VFALDVAARHRCNLTCTHTS HGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQ RALQCTYQPISSHLLYRVTEPV YAVS
24594	54962	A	24732	1476	2221	

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24595	54963	A	24733	1	815	MRVGRKAVGAIWWSSKQELFQ QLFLRTELEDIGPGIVKRELGRE GSKDTGSSDDWEQLPDWKT VGNERDQELLIEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAALTESDYRVLVGEL DDEQMAALSRLGNDYRPTSAY ERGQRYASRLQNEFAGNISALA DAENISRKIITRCINTAKLPKSV VALFSPGELSARSGDALQKAF TDKEELLKQQASNLHEQKKAG VIFEAEVITLLTSVLKTVQSKN LSHFTWICHAEAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKHVVTISP QTSAYERGQRYASRCKNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSPGELSARSGDA LQKAFTDKEELLKQQASNLHE QKKAGVIFEAEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMVLNLDNRVPTCECKRK LRPF*SGQRTDTAYVFDPRDGY

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24596	54964	A	24734	2	1249	DFADFGTTIKQDFRLLGQTSVD RLQLSQGQAVKGNQLLPVSL VKRKTTLPNTQTASPRALADS LMQLARQVSRLESGQLAISGRI LFLPMLNSINKLAAPSQCTEPF FRRDPTLHPKSEVRLPPKVTIT VISNPILITPQEKSVACQTYNQT VQLDITAFKKTVMKKNHKFPYA FIHILARLMNAHPFRMAMKD GELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIYSQD VACYGENLAYFPKGFENMFFV SANPWVSFTSFDLNVANMDNF FAPVFTMGKYYTQGDKVLMP AIQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVYRPEEDAGDEKGY ESFPWFIKRAHSPRGLYSVHIN PYLIPFFIGLQNRFTQRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLPIDWIIERYQLPQSYQRM PDFRRRLQVCVNEINSRTPMR LSYIEKKKGRQTTIIRISDGL QEHGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVYR PEEDAGDERGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQ NRFTQRLSETKEITNPYAMRLY ESLCQYHLCGTLRNSRFCEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVYRPE/VGCRK*K RL*IFSLVYQTCASIQIRALQCT

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24597	54965	A	24735	1	2286	MLTLILLDLQFMAQLAGYQMS FNSTKSKQTKNNFAVGYRTGD FQLHTNVNDGAEFGGSVYQKV CEELDALINLAWTSSTSTRFG LAAKFQLKPIAFISTKVNHWLT GVSYPPLLEAGVKLNLSALCDN LKTCHTSHGSVMAETA VINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPNYAMRLY EIPVVSIRKPGMGSGIVSLKIDW IIFRYQLPQSYQRMPDFRRRLQ CINAGHEMTKAIAIAQFNDDSP EARKITRRWRIGEAADLLGVSS QAIRDAEKAGPLPHPD MENRG RVEORGGYTIEPNNHMRDGVG TRWRAEDVPPLIGIVAGHKG GRVYKTSVSHLAQDLALKGLR VLLVEGNDPQGTASMYHGWV PDLHIHAEDTLFPYLGEKDDV TYAIKPTCWPGLDIIPSCALHR IETELMGKFDEGKLPTDPLML RLAIETVAHDYDVIVIDSAPNL GIGTINVCAADVLIVPTPAELF DYTSALQFFDMLPDLVKNRDL KGVEPDVFIRDKLMERRNRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSPVTPHTF

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24598	54966	A	24736	1	1400	MDAKMHSGGTAPPGTLSQRQP SSNSKNTNGSKLNPLKDTLLSTPS CPEGELVNAARRSNGSGNAITL PVWGRDVKFTLEVLRGDSVEK TSRVWSGNERDQELLTEDALD DLIPSFLLTGQQTPAFGRRVSGV IEIADGSRRRKAAALTESDYRV LVGELDDQEQAALSRLGNDYR PTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKELLKQQAQNLHE QKKAGCDNLKTCHTSHGVSMA ETAVINHKKRKNSPRIVQSNL TEAAAYSLSRDQKRMLYLFVDQI RKSDGTQLQEHGICEIHVAKYA EIFGLTSAEASKDIRQALKSFAG KEVVFYRPEEDAGDEKSYEQPS KDIRQALKSFAGKEVVFYRPE/ VGCRR*KRL*IFSLVYQCAQSI QRALQCTYQPIHSLLYRVTEP
24599	54967	A	24737	1	1628	MLHITNDQGNASQNHAMPPY SCKNGHNLKTVDDGMDAVNG EHFYTAGLSQGPKGSELLFFNI LILVCPPIFRVSGNEVFIRDKLM ERRNRRTGRTEKARIWEVTDRT VRTWIGEA VAPLLLTCDNLKTC HTSHGVSMAETAVINHKKRKF SPRIVQSNDLTEAAAYSLRDQK RMLYLFVDQIRKSDGTQLQEHID GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDSGIVSLKIDWIIERY QLPQSYQRMPDFRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THICDNLKTCHTSHGVSMAETA VINHKKRKNSPRIVQSNDLTEA AYSLSRDQKRMLYLFVDQIRKS DGTQLQEHGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPE/VGCRR*KRL*IFSLV YQCAQSIQRALQCTYQPIHSL LYRVTEPVYTISAY

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24600	54968	A	24738	1295	1675	SVTSLCKVTSVCLTSGRRFLQIR ISDGLTQEHGICEIHVAKYAEI FGLTSAEASKDIRQALKSFAGK EVVYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYLI PFFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIAWVIERYQLPQSYQRMPDF RRRFLQVSDFLMAPYRNDIGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLCQY RKPDGSGIVSLKIDWIIERYQLP QSYQRMPDFRRRFLQVCVNEIN SRTPMRLSYIEKKKGRQTTHIE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVYRPE EDAGDERGYESFPWFIKRAHSP SRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYQS LCQYRKPDGSGIVSLKIDWIIER YQLPQSYQRMPDFRRRFLQIRK SDGLTQEHGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVYRPEEDAGDEEGYESFPWF IKRAHSPSRGLYSVHINPYLIPFF IGLQNRFTQFRLSETKEITNPYA MRLYESLCQYRKPDGSCIVSLK IDWIIERYQLPPRYQRMPDFRRR FLRVVWQENSRTPMPPLLPWE
24601	54969	A	24739	1	1986	

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24602	54970	A	24740	1	398	MVDSLIRVGVGMARGNAITLP VCGRDVKFTLQVLRGDSVEKT SRVPPGNERDQEMLTEDALDD LIPSFLLTGQQTAFGRRVSGVI HTADGSRRRKAAALTEKFCIVD NPPGEIRKRACLFIPHTALNLNR FEDICYAHQLPDGGLLSARVGV MARGNPILSPVCGRNVKFTLKV LRGDSVENPSRVWSGNERAQE LLEHALDDLTLFLLTGQQT AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGLDELDEQMAA LSRLGNDYRPTSPYERQGRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSPHGE LSARSGNERDQELLTEDALDDL IPSFLLTGQQTAFGRRVSGVIH TADGSRRRKAA/DTYRKILYR** PPGD*KKSVPFYSNTCAQSQP
24603	54971	A	24741	1450	3699	RNPLQIPKQQQNEKYQVPQFDQ STIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFQYKVGDSIDS WKNAGRVPKDSDKFDANDPIL KDQTEWWSGSATFTSDGKIRLF YTDYSGKHGKQSLTTAQIFQ MITVFITSLCNTTSSHICLHISWV TTMHGAMPHPGHIPTAPASLPA KVKGSGKVCWLAFLSELTPPS ALQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQHFIDEGN YTCGDNHTLRDPHYVEDKGHK YLVEANTGTENGYYQGEESLFN KAYYGGGTNFFRKESQKLQQS AKKRDAELANGALGIIELNNDY TLKKVMKPLITSNTVTEIERA NVFKMNGKWLFTDSRGSKM TIDVPOAKSTNVVITSYMTNRG FFEPEGSKGSITAAVMAKGLSV ASGNSTPERRRATANENVQPR IRDAEKAGRLPHPDMEIRGRVE QRVGYTIEQINHMIRDVFGTRLR RAEDVFPPIGVAAHKGGVYK TSVSVHLAQDLAKGLRVLLV EGNDPQGTASMYHGWPDLHI HAEDTLLPFYLGKDDVITYAIK PTCWPLDIIPSCALAHRIETEL MRKFDEGNLPTDPHMLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAEQLDISISS RQFFDILRDLKKNVDLKGFEFD

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24604	54972	A	24742	1	3899	MVDSLIAPIVGVMMARGNAITLPV RATNVKFTLELRGDSVEKTSR VWSEKKDRGGQAEVSGEGSS QTKSLQKRQHNSGSDFTARGF HTGQALVRSKGTYYNPTGLGL SHGTEDPNLIGEELDAGEWDK NTRKELAVLNVRDFADFGTTI KQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQFVVFEGGLRVLVR ERVTPKGTASMYQGWWVPD
24605	54973	A	24743	268	2617	RMFRMKLMETUSQICINAGHE MTKAIAIAQFNDDSPARKITR RWRIGEADLVGVSSQAIRDAE KAGRLPHPDMEISGRVVKHGVG YTIEQIYLTRDVFGTRLRAEDA VFPPVIGVAAHKGGVYKTSVS HLAQDLALKGLRVLLVEGNPD QGTASMYHGVWVPDLHIHAEDT LLPFYLGEKDDVTYAIKPTCWP GLDIIPSCALHRIETELMGKFD EGKLPTDPHLMRLAIETVAHD YDVIVIDSAPNLGIGTINVVCAA DVLIVPTPAELFDYTSALQFFD MLRDLLKTVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSVMVLKNVRETDEVGKGQI RMRTVFEQAIDQRSSTDTSLSTP AAPMVDLSLIARVGVMMARGNAI TLPVCGRDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQTPAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSR LGNDY RPTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARS GDA LQKAFTDKEELLKQQASNLHE QKKAGVIFEAEVITLLTSVLKT SSASRSLSSRHQFAPGATVLY KGDKMALNLD RSRVPAYIIRSY IRCGRKGFASAGVGGCRGWLN YAASEQIVLRVHHMRCEIPHRC

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24606	54974	A	24744	1	2624	MTPQKRGYLCKAGARNLDVLL EGCEIFLLIPMGMRSESGVSDA DTVSAPRKKHSLEQGIFRAQVE ASKPSSVPACIVVGNVSGYQFP PGTSYGPDSSELGYREKFMSF VGTMEAGNPPFSANYSKAKK PKPRMFLIERMSPSRVGSQSV QSSCFRDIPEQDQMFPHPSLV RSKEQQPLL.TQSIGVNSARKAM AKRRRHRRRRVSGVLPVIAVG VPS*SVHLPKVLSCSGASWI*QS CISRLGRLSPTRLMNVAIGNDP QGTASMYHGWVQILHIHAEDT LL/PFY/LGEKDDVTYAIAKPTCW PGLDIHPSCLAHRIETELMGKF DEGKLPTDPLMLRLAIETVAH DYDVIVIDSAPNLGIGTINVVCA ADVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEPPDVRILL TKYSNSNGSQSPWMEEQIRDA WASMV*KINNVNRNANEVGKDT LKGFYSLKERPLGNHFLGPNNR PFGKIMKHKTAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDEQMAALSR LGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAFTDKEELLKQASNLHEQK KAGGFCFRNHHQTGFSPAGA NQRGPLAATLSGPGGEGQSAV ARLTGEKKNHPGAQYANRLSP
24607	54975	A	24745	1	385	MWQAISRLLSEQLGEGEIELRN ELPGGEVHAAWHLRYAGHDFF VKCDERELLPGFTAEDQLELL SRSKTVTVPKAFILGQQIARLH QWSDHAVLKIIVTTGVL*GAYV GAPSIWKCPERITLPGYHQ
24608	54976	A	24746	1	1209	

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24609	54977	A	24747	1	857	MHACRSELLGEGEIELRNELPG GEVHAAWHLRYAGHDFVKK DERELLPGFTAEADQLELLSRS KTVNRALKVWA\VGADRELTV FLV\MDYLPPRPLDAHSFILGQ QIARLHQWSDQPFGLDFDNA LSTTPQNPNTWQRRWSTFFAEQR IGWQLELAAEKGIAFGNDAIVE HIQQRLLASHQPPSLLHGDLWS GNCALGPDGPYIFDPACYWGD RECDLAMLPLHTEQPPQIYDGY QSVSPLPADFLERQPVYQLYTL LNRARLFGGQHLVIAQQSLDRL
24610	54978	A	24748	1	2094	
24611	54979	A	24749	1	1209	MVREDLYTYSCNTSREQQQL ENPMESPLCSKEINQGGVFMLA GKASDTLLAGGTMNNLGGEDS DTIVENGSIYRLGTDGLQLYSS GKTQNLVSVNVGGRAEVHAGTL ENAVIQGGTVILLSPTSADENFV VEEDRAPVELTGSVALLDGAS MIIGYGAELOQSTITVQQGAPP VKLRFALYGRPGFTKCGWMLG YKPAHDKTLLRITRGHDFACYQ RTTQLARQGLKVCSSHLIVGLP GEGQAECLQTLERVVETGVDDGI KLHPLHIVKGSIMAKAWEAGR LNGIELEDYTLTAGEMIRHTPPE VIYHRISASARRPTLLAPLWCE NRWTGMVELDRYLNHEHVQGG SALGRPWLPPTENSLMKQIRLL AQYYVDLMMKLGLVRFSMLL A\WSSFLPLWYKWR
24612	54980	A	24750	200	310	
24613	54981	A	24751	1	4398	MCIPVPPIATGDRHFIAVAHIHQ NSRRSPVDSDESSTRSAVAHP ATRDFNVRALYTVTSSVSPTKP PLPATFRQGRYRPAEPCVGSIG VIPQSSCVLANGSTGAQSAFGDI IRAGPPSAGLVPVAQATVIETFL RYQTINERDFWAARNRLKQP YGSRLRFEAYIAIERAAQSV LRISLADAFNVDPRAEDSIFR LLRMPPGSAVQRPDRRHNRRQY YRPAMAFPAGSKANKRQYNG GRQFYRKRICWL

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24614	54982	A	24752	939	2169	RPASPPARDGARWSTGLHSSYS AMCRNASTCAEDS Q L S /DPLA R/PSVASGPYRVTSWKLGGQNI YCRVKDYWPATLTVNRGRWN FDTIRSDYYLDDNVAFAEFKAG AFDLRMENDAKINWATRYT/G DRRVREAITLAFDFEWMNKAL FYNAWSRTNSYFQNTTEYAARN SPPPPELAVLLPPIKKVLPSEVFP QIYQPPVSKGDGYDRDNLLKA DKLLNEAGWVLKGQQRVNAT TGQPLSFELLPLASSNSQWVLPF QHS L QRLGINMDIRKVDNSQIT NRMRSRDYDMMPRVWRAMP WPSSDLQISWSSEYINSTYNAP GVQSPVIDSLINQIIAAQGNKEK FLPLGRALDRVLTNWYYMLPM WYMAEDRLAWWDKFSQPAVR PIYSLGIDTWYDVNKTAKLPS ASKQGE
24615	54983	A	24753	3	450	
24616	54984	A	24754	2	203	PLPDAARYLRRQCQKPARVHDI FAAMHTAHRSPDRPSLPDDAF SSLRL*FFQPEHYPRQYQHRHL CS*ERYQHQUALSRTRFRSG*PTP SVPETSTGSR Y FCGNAHSAPKP PRPPIITGRRVFTTLPILPTRL PASISTPASL
24617	54985	A	24755	1016	1219	
24618	54986	A	24756	1695	2021	PDTFSMLPATRFLPPLQFPDLQH PEAAQYAHWLPASGCFLFLPPP GSGTVFLLPYPSRLCRSTSETP LPAITR*HFPVTD R VQK*ITRRR KPRHKPFYPDDLQ R DAR
24619	54987	A	24757	1671	1911	
24620	54988	A	24758	513	1104	CWRNCARCERNLVFRCQYGIY WCDNAANRSCRTKRDQ P RLVE W*KSACSHHR*LHPCGHC R QF MNELNSGLDLRIHLPGREAHAL RDYLPDAFGPKDLEIKTLLMDE QDHGYALTGDALSQAIAAAN RSHMPYSKSPSGVALECKDGRIL LVAATLKTPH/INPTQICGQPWS MHRRALTSKFGAHGDRRTSAG FRRN
24621	54989	A	24759	131	759	
24622	54990	A	24760	662	889	LPIKCRAARGVPARCLRWTRW ALRRILPPLNR S RAASRWAS PGARK*WMPSLQAVWAAMP VTRLPAWL R WKC

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24623	54991	A	24761	1	1518	MQRRDGDIALIYRSKIGPRTSIT FTARRANPVQRIIAARILLRDHLI CRMSCTAARHANTFDLIQSGS ADNFAAIYGGANDRITRADA VAGAGNWHRFGISNGKLSPRSI TRTSSPARAMTKMPYNPQASG GSNLAVSNPELDKLIARVAAL RAANPDASASVPVELVTASASY PRSLMRCNRILSPGSARGQMIIIT ALFIYAGNPIACVALEVLKVF EQENLLQKANDLGQKLKDGLL AISFWRAKWLIKIFVVCGEAIFV EYVLKNKVIWLLCFANIFYVYV RIGIDQWSTVYAFQELKLSKAV AIQGFTEAGALVGTLLWGW LSDLANGRRGLVACIALALIIAT LVIPFHMVFHPNEQYAYCVNEL NSSVDVWELKDPHGNECVQT LDMMPENFSDTRWAADIHITPD GRVHLYACDRTASLITVFSVSED GSVLSKEGFQPTETQPRGFNV HSGKYLIAAGQKSHHISVVEIV GEQGLLHEKGRYAVGGQPMW
24624	54992	A	24762	3	486	ACRRALKDIAGVEADEVLEVV MVGGSSTRVPLVRERVGEFFGRF PLTSIDPKVVAIGAAIQADILV GNKPDSEMLLLDVIPLSLGLET MGGLVEKVIIPRNTTIPVARAQD FTTFKDGQTAMSAGGAHIRVTF QVDADGLLSVTAMEKSTGVEA SIQVKPSYG
24625	54993	B	24763	1	2469	
24626	54994	A	24764	1255	1761	ESFQVTRTHGTGEPVNKTRTSQA VSHHNQSCQVDQCVPCAVIAG NVFPRHNVQGGH*RNCCQQTNR SSINDFTKLSNTRPISVHSLGIKQ SRPDRHAKASPVVTAVKACEQ VIAAVNQIADHDHQPDRTKQRN AIVVADDLPDLFPVHFFGVVDHQ QHNHRDKKQPGEDLLCC
24627	54995	A	24765	1	3141	
24628	54996	B	24766	1	3969	

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24629	54997	A	24767	643	2082	GAHAMDKHFSTTPAEKNLPVL LALIGIWYNNFFDKNDALVMV DDFPRRSGLSWKIVVVPHEYW VGGSTRVPLVRERVGEFFGRPP LTSIDPKVVAIGAIAIQADILVG NKPDSMLLLDVIPLSLGLETM GGLVEKVIPRNTTIPVARAQDF TTFKDGQTAMSIHVMQGEREL VQDCRSLARFAICVVFRRYRL/A GAHIRVTFQVDADGLLSVTAM EKSTGVEASIQVKPSYGLTDSEI ASMIKDSMSYAEQDVKARMLA EQKPGQGEAKLALKTFHWQQA IADKRVIAGITGVTAGTDHRA DVTVEASDFRVQTTNADSAF HVRSAQQHIHQLLHFTTHLLCQ LAGLDHVVFQGIATNPADQVQ AVGFTRTGKDLCHFHHGGFTHA EELHKAGVEAGKVTGQAKVEQ MRVQAFYLQQNGADHLRTFW HLNTHRVFHRRGVGGAVGKA ADPAHTVREEGHFVITHTGFRQ FFHAAMDVEQ
24630	54998	A	24768	1	502	

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24631	54999	A	24769	1	2345	MFMIGALVLAIVMTLITFMVL RRVIRPLQHAAQRIEKIASGDL TMNDEPAGRNEIGRLSRHLQQ MQHSLGMTVGTVRQGAEEIYR GTSEISAGNADLSSRTTEQAAAI EQTAASMEQLTATVKQNADNA HHASKLAQEASIKASEGGQTVN GVVKTMGAMSTSSKKISEITGR HQQGIRTPVTAVKGRCPGLDE GDTDTAYYALRDIFALTPNRKR LAIPVSTDNPCKPCKDPSLSKD VSNRVQRVPCYDSPRSSVNG NRLPGKDFHDDERSMGRSGSY VLALAYPPKIALSDADSVTVNV AGWQGEISREQFNELIAPLVKR TLLACRRALKDAGVEADEVLE VVMVGGSTRVPLVRERVGEFF GRPPLTSIDPKVVAIGAAIQAD ILVGNKPDSEMLLLDVIPLSLGL ETMGGLEVKEVIPRNTTIPVARA QDFTTFKDGQTAMSIHVMQGE RELVDQCRSLARFACVFFRRYR LAGPVDLFLRPWEVDISRRTSL DSPLPVQVLEASPKGHYTQLVV QPLGWYNEPLTVVMHGGDDAP QRGERLFVGLQHARLYNGDER ASRDPGFLMAREVTCRDPDKTRK LRIRQHHVWIEIVSTLEQTIGNT PLVKLQRMGPDNGSEVWLKLE GNNPAGSVKDRAALSMIVEAE KRGEIKPGDVLIEATSGNTGIAL AMIAALKSYRMKLLMPDNMSQ
24632	55000	A	24770	313	676	DCQPRSSAFTKPDATTAGHYLA GSGGRMTQLAIGKPAISLAHLE REGGENFTFFSLNADGEKL/CVF DANGQ/EHRYDLPGHSGDIWH/ G/YLPDARPALRMVSRH/GP/WQ PAGGMLTPAVVMILPRK
24633	55001	A	24771	1760	2053	FRVHGKNAFSH*IKPAAMLLPS SPVTRS VKPTCCGSAPS KRPNL TLLPSITLMPPLPVTDLKLGCIA PCSSDCFSFITFSISCATRLSVNW LPAAGQ
24634	55002	A	24772	296	732	
24635	55003	A	24773	606	695	
24636	55004	A	24774	1520	1737	PVHGLCGTRRDAGS\PAIYPFHS LML/RFWLR/TCTVPGWPLDDS SLAGEAFSAFTTDAAVWSLISA TAMLAVQAG
24637	55005	A	24775	1	1049	

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24638	55006	A	24776	248	933	RTTMRVSRPKYCSRRERWL/HY DFTVARFDENASCGTFAATS AVLFIHSHCLRLCRVVVLVTRVN FQFTEHSTTQRAFWQHAFNRDF NHTLRTASNHLFGRLFDTTDV AGVVIVHFVSTLVAGYSNFVS QNDDEVITGIYVRSVFRFVLTAQ ATSQSFSSQTAQSFTGRVNNIPV AFYGFWFSCAKYYRHGARWCS NGRKIDQRHTHCFPCIRCTDFA VEIGKEEFIT
24639	55007	A	24777	219	3441	DCQPRSSATKPDATTAGHYLA GHSGLDIWHGYLPDARPLGRYG YRVHGPWPQAEHGRFNPAAKLL IDPCARQIDGFEKDNPLHAGH NEPDYRDNAAIAPKCVVVDH YDWEDDAPPRTWPWGSTIIYEAH VKGLTYLHPEIPVEIRGTYKAL GHPVMINYLKQLGITALELLPV AQFASEPRLQRMGLSNYWGYN PVAMFALHPAYACSPETALDEF RDAIKALHKAGIEVLIDIVLNHS AELDLGDLFSLRGI
24640	55008	A	24778	454	586	
24641	55009	B	24779	130	1557	
24642	55010	B	24780	92	2808	
24643	55011	A	24781	2	1051	WRLRPITPLWRWQKIFFPDA/R YGIRFRNLETGNWYPELLDNVE PSFVWANDSWIFYVVRKHPIFI DLTTEELAASSYHESWVLEDRII KDGSYNIDQGVGVRAISGEKGTG FAYADQISLLALEQSAQAARTI VRDSGDGKVQTLGAVEHSPLY TSGRSGWQSMSREEKLDILRRV DKVAREADKRVQEVTAASLGSV YELILVAATDGTLAADVRLPGK VLLVGQSPNAELSAKQIAM GVDGANEVYNEIRQGQPIGLGE ASNDTWITTKVRSQLLTSDLVK SSNVKVTTENGEVFLMGLVTE REAKAAADIASRVSGVKRVNR TLFLGYAVMFSELILAPVTPSNS
24644	55012	B	24782	1	2079	

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24645	55013	A	24783	1	3214	MGAEKQLIPDGCYVSYIPSSGP LDKWRALLFIQPDYRADPVVR QHITITDLRLIYDYTENFVLP DEVVHGKKSILDRMPGDAWQK FANLRAYYGWMWAFPGKLL FMGNEFAQGREWNHDASLDW HLLGGDNWHHGVRQLVRDL NLTYRHHKAMHEDFDYGFGE WLVVDDKERSVLIFVRRDKEG NEIIVASNFTVPRHDYRFGINQ PGKWRILNTDSMHYHGSNAG NGGTVHSDEIASHGQRHLSL
24646	55014	A	24784	1	1079	MKQIKELQRLGKKTWKMNSS KKPLNMDGPKVDSARALIGRG WGTHKFYRCDIKPTIKTNTSS RGNEKNPDGSHNNHNSWFRL LTSQNMCKVPESPAILVDVGQS AETVQSVLTVKVEHPILRIAVA GYACQRQSCLLAMRHPQYAIN SSKVVKPCSTARQPFQKAYAYP PVVRAFPAINVGISGNKLTNDR RYGRTSNKAWGSGDGHITLSEC GWAPLAAGDNVGVKVSQTLG YYQRILGYIFYPIAWVMGVPS EALQVGSIMA/TKLVSNFVAM MDLQK/IASLSPRAEGIISVFL/ VSFANFSSIGIIAAAECRDWFG ILAAQTLAVRAALRVVQAERD CVLSMEQHQCARGRQR
24647	55015	A	24785	121	258	LTEPRHYCRSIOFFGLTNMGQN CYQLS*E*FIGTLNHIRRIQPLS
24648	55016	A	24786	1	470	WGSQDGHITLSECGWAPLAAG DNVGVKVSQTLGYQYRILGYIF YPLAWVMGVPSSEALQVGSIM A/TKLVSNFVAMMDLQK/IAS TLSPRAEGIISVFL/VSFANFSSIG IIAAAECRDWFGILAAQTLAV RAALRVVQAERDCVLSMEQHQC CARGRQR
24649	55017	A	24787	1324	1539	GWCGCEVPFKITDGLACLQSP QGHQTFCTF*HNLGLQPFWIPM CLCSNVNFKTRLILTQVEEGCR AVSMTQ
24650	55018	A	24788	71	403	RTTFIDLSSGWPFILWQVLSNP *RCLQVGLFAQIFTRMGCLHR FLTCRMGVCTDSSPAGWAVTLI RMSPPIFPASSKSTLSAALLNTSC LHSRDLEPPGAFRSGGPVLL

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24651	55019	A	24789	309	1653	SVLMDESDIYRNNRFFCVFL LVGVPPARGACLGGGGGCLCV RYLRSAWGCGRRFPCVGDN WSAILAHIGKPEELDTARNAG ALTRRREIRDAATLLRLGLAYG PGGMSLREVTAWAQLHDVATL SDVALLKRLPKCRHWFGLAG QTLAHIRVLPVIIRAIGFLLSKV NGMGKLESFNAVSSILGQSEN FIAYKDILGKISRNRMYTMAAT AMSTVSMISIVGAYMTMLEPKY VVAALVLNMFSTFIVLSLINPYR VDASEENIQMSNLFEGQSFFEM LGEYILAGFKVAIIVAAMLIGFI ALIAALNALFATVTGWFGYSIS FQILGYIFYPIAWVMGVPSSE ALQVGSIMATKLVSNEFVAMM DLQKIASTLSPCAEGIISVLLDSF ANFSSIGHARAVKGLNEEQNE GSRFGLKLVYRSTLVS/VLSASI AALVLSDHT
24652	55020	A	24790	754	957	
24653	55021	B	24791	75	3707	
24654	55022	B	24792	75	264	
24655	55023	B	24793	344	461	
24656	55024	A	24794	1	2203	
24657	55025	A	24795	20	198	
24658	55026	A	24796	1239	1409	RGPPTFFHVVWEWQQRPLSVW EADHV*RRDEGACPRMVARAR NCRPKLLELRAESQ
24659	55027	A	24797	1325	1564	
24660	55028	A	24798	323	694	TGYARQKPPVPALGWWTNVSAS TAPPIILPSITGSRLAVIKWLTVS AGKLSALLCASCQKGGGAKWR MAMANGITNKLAIQCSPPHSTI EKFTSQSQHVLA*GVSAVRSM VSSG*GRRRLPALG
24661	55029	A	24799	4708	4878	
24662	55030	A	24800	20	199	
24663	55031	A	24801	743	1186	

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24664	55032	A	24802	1394	2651	KLMTCRHEGSLGDDPGINGQL WDVNRIDVTAHEGTWERWTV RADEPQAFHIEGVFMFQIRNVNG AMPFPEDRGWKDTVWVDGQV ELLVYFGQPSWAHFFPYFNSQT LFSWPQYWAACFGPAPFLPMS REEMDQLGWDSCDILVTGDA YVDHPSFGMAICGRMLEAQGF RVGHIAQPDWSSKDDFMRLGKP NLFFGVTAGNMDSMINRYTAD RRLRHDDAYTPDNVAGKRPDR ATLVYTQRCKEAWKDVVPVILG GIEASLRRTAHYDYSWSDTVRRS VLVDSKADMLMFGNGERPLVE VAHRLAMGEPISEIRDVRNTAII VKEALPGWSGVDSRDLTPGKI DPIHPYGEDLPCADNKPVAPK KQEA KAVTVQPPRPKPWEKTY VLLPSFEKVKGDKVLYAHASRI LHHETNPVAPAH

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24665	55033	A	24803	1	2126	MQEKQVLAAVYVQPSSEGGQSR RRARRVSQCHQHSAAASLAR TAASATADSAHPPCPSRAARAG ATMHVKKYLLKGLHRLQKGGP YTYKELLVWYCDNTNTHGPKR IICEGPKKKAMWFLTLFAAL VCWQWGFIRTYLSWEVSLS VGFKTMDFFPAVTICNASPFKYS KIKHLLKDLDELMEAVLERILA PELSHANATRNLSFSIVNPTPL VLIDERNPHHPMVLDFGDNH NGLTSSSASEKICNAHGCKMA MRLCSLNRQTCTFRNFTSATQA LTEWYILQATNIFAQVPQQLV EMSYPGEQMILACLFGEPCNY RNFTSIFYPHYGNCYIFNWGMT EKALPSANPGTEFGLKLIDIGQ EDYVPFLASTAGVRLMLHEQR SYPFIRDEGIYPMSTGTSIGVL VDKLQRMGEPYSPCTVNGSEV PVQNFYSYDNTTYSIQAQLRSC FQDHIMIRNCNGHYLYPLPRG EKYCNRRDFPDWAHCYSDLQ MSVAQRETICGMCKESCNDTQ YKMTISMADWPSEASEDWIFH VLSQERDQSTNITLSRKGIVKLN IFFQEFNYRTIEESAANNIVWLL SNLGGQFGFWMGGSVLCLEIFG EIIIDFVWITIILVALAKSLRQR RAQASYAGPPPTVAELVEAHT NFGFQPDATAPRSPNIGPYGEG ALPNPG/TPAPPNYDSWRLQPL
24666	55034	A	24804	905	1051	
24667	55035	A	24805	1	1257	
24668	55036	A	24806	1	3116	MPITLPDGSQRSFDPVSVAEV AQSIGAGLAKATLAGKVDGRLI ITPKDEEGLEIRIISCAHLVGHA VKQLYPTAKMVIGPVIEEGFYY DIFFERFPTPEDMAAIQQRMR LIDKDYDVIKKMTPEAEVIELF KLQAAPDRRHAGREGHGLYFH EEYVDMCRGPHVPNTRFLKAF QLTKISGAYWRGDSKNEQLQRI YGTAWADKKQLAAIYQRIIEA EKRDHRRIGKQLDLFHLQEAPE GMVFWHPNGWSVYQ
24669	55037	A	24807	1924	2790	
24670	55038	A	24808	1	1185	

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24671	55039	A	24809	823	5990	MARPVPLWSSWGLRTSYL PKP LSVNP SRNDGSA/FAGTHPLGV TRGTLAGPAFVRLSLVFLRRV LAGSSLLPLLMG*QK/PEVLLPD GASEHDYSLRPSDVKRLQNA LVVVWGPMEAFMQETGKQIT RSEVSPLCRRVAFNKFNRDPQP RYDWGRSLTVLYSGSSLSGGRY VVIIECHCQLSKPLRLQNEIR SLLPEASEPIDQAAQEDEAIPQD ELDDKIAGEAGVHEYVVSTGD TLSSILNQYGIDMGD
24672	55040	A	24810	2305	2550	
24673	55041	A	24811	665	844	ISFNNEVISYRLSGKNQ*LNLG* EIWLESGAFKKALSPQKHPGLE PSVCTPTPTLV PDR
24674	55042	A	24812	1	2031	
24675	55043	A	24813	106	912	HFETVIDQRDFHPVFSHKGIRAT PEGNEEKQQRVADVTEQCGRC RCQPPAATLTQAVKNVHVEDL PQRVGHETGGGDTGDKQVEVG ECAESHTLDALGLRCPPEVMM VRKTVRNMQPGETLLIADDP TTRDIPGFCTFMEHELVAKETD GLPYRYLIRKGG**GLIGFDAAF SPHPNPLPRGARGPIALNV AIGL PYLLRNNLNAFAVTSTVAPVSA STASHNPVIQRGDEEDPFQPOR NSDVLADIGVSGACQFNHLHQ AAQVVMG

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24676	55044	A	24814	1	1495	MQKLTLTYAETRRLYGKEVYH RPSRFIGELPEECVEEVRLRATV SRPVSHQRMGTPMVENDSGYK LGQVRVHAKFEGGTIVNMEGS GIAALCHCRVLIATAALMDPDD AVELSVTTMMFALCNTRNPRV AWDTAPCVPATTAAASMAKRAP DMSQSAPEAGSQKPPRLSCGE SLHPLPATKRAYNYCRPVGRIR HLCRIRQSMPTATLSRLIRPTTV ADPPDKALAPHAVFTRGDSKF LSHKPARSPAIRYLLASVWGPV GMMAMMLAMTGFVVATRKL RRFGFKSCKNGVLYRISSSSITT SPASPIATCRPVLPCWMRMDPM LDMMGQMQLMEKYGDQAMA GMDHSQMMGHMFLGHKVIRA NHVGDWGTQFGMLFRIAVETF KEDWEAVWDQLDDLNLGKIV A*GRDPAAFHIDNGAFTKLSVA YALAEVAAVVLDHRRTHPLM ADRAAYRGAQHLFHTLFRQL ADKARRAMVNLFTIQTAGFRV GQRQLH
24677	55045	A	24815	3	707	GCTLGPVKSFSRLVAVLSWPQ YFYIIERACSPCCGLAPGEAPH VNLFHSTHSEKQKPHNSPYHN DIQPTLNYLPTNQKKQTQEQS HNITKQGSQQLHDVTQVPYQAY RSAIVVGLIRRDVSA SGIDCRM RRERLIRPTGRASDNTEFTGTQ NMQNITHSWFVQVMIKATTTDA WLKGWA*AQRQRPDTPG*RR YRTISRQFPATSVLYPAQPAHA FTGKYTVYCHRLGQILP
24678	55046	A	24816	2	1340	
24679	55047	A	24817	1	2457	

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24680	55048	A	24818	41	1053	QRNQQAHLSP/QHSRDIYDNQV HLVRNCNLEMPDQEFIVLYGPS DCGKSTTLRMIAGLEEISGGDL LIDGKRMNDVPAKARNIAMVF QNYALYPHMTVYDNMAFGLK MQKIAKEVIDERVNWAQILG LREYLKRKPGALSGGQRQ RVA LGRAIVREAGVFLMDEPLSNLD AKLRVQMRAEISKLHQKLNTT MIYVTHDQTEAMTRIVIM KDGIVQQVGAPKTVYNQPANM FVSGFIGSPAMNFIRGTIDGDKF VTETLKLTIPEEKLA VLKTQEV CPDHTLDALGLRCPVP/HDGA QNRAQYAAWRNVADYRRRSG HYPRYSWVLYLYGTRTGC
24681	55049	A	24819	3	131	
24682	55050	A	24820	247	492	
24683	55051	A	24821	2	241	YFFQKSSKTVIGGRRLCSVFRY QFSIVLATC*GTFPPSR*STILS* VTQSA TSSGREGRSSSRSLNGRF MFSIASMMWS
24684	55052	A	24822	1	1143	

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24685	55053	A	24823	242	2151	FSRQHVVKMKHCCKNVVILMP EPVAEPALNGLRLNLRIVSIVMF NFASYLTIGLPLAVLPGYVHDV MGFSAFWAGLVISLQYFATLLS RPHAGRYADSLGPKKIVVFGLC GCFLSGLGYLTAGLTA VCLSSA VILCRGVQLHPVSDLRIPRGEK AGRRNSVDGCCEKAMSVIIVG GGMAGATLALAISSLHSHGALPV HLIEATAPESHAHPGFDGRAIAL AAGTCQQLARIGVWQSLADCA TAITIVHVELHNVGQRLFAL LRKAPGVTLHCPDRVANVART QSHVEVTLESGETLGRVLVAA DGTHSALATACGVDWQQEPYE QLAVIANVATSAHEGRAFERF TQHGPLAMLPMSDGRCSLVWC HPLERREEVLSWDEKFCRELQ SAFGWRLGKITHAGKRSAYPL ALTHAARSITHRTVLIQSERLNH KALEKRTLTVWDNSFLIYRQSD VSEIRLASLFASFIRKSKQQA KHTNRRSKDKEKRTQKRTT SRQRRRRQRMVRVGDQIAGC HCLYSTGSPNRQLREAGIELSDF VRGNEKARERMKAQYSIAGMT SGVVVGTDHAAEAITGFFTKYG DGGTDINPLYRLNKRQKQLL AALACPEHLYKKAPTADLEDD
24686	55054	A	24824	2	91	
24687	55055	B	24825	1	2346	
24688	55056	A	24826	1	1713	
24689	55057	A	24827	1	918	
24690	55058	A	24828	415	816	
24691	55059	A	24829	72	296	FCSATFGRPSDQYQNGE*LRWR GLGSFACQSPAHEPNQWKFVL ARRGFARGTAEAHPSQYRHW KIHRLNPGLR
24692	55060	A	24830	1	620	

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24693	55061	A	24831	1625	2460	GVVNPRQGRVLSMLPAMLLYL LFLLIQTSLKSNNGKGLDPTL WMWTVNLIYLALAIVLNLWDT VPVRRRLASFRRKGARIPFVGC RETCELQIQLVKMMLGRELDT HALQRAGRITLLSDKPVAAFKN YGKKGITAPFDLEVRPGEIVGL AGLLGSGRTETA EVIFGIKPADS GTALIKGKPNLRSPHQASVLG IGFCPEDRKTDGIIAAASVRENII LALQAQRGVCYVFPFAKNSKRL PNALSASLAFALQLNRLNFS PAAISKKCCFYVGY
24694	55062	A	24832	1	2034	
24695	55063	A	24833	3839	3970	
24696	55064	B	24834	694	765	
24697	55065	A	24835	1778	1982	
24698	55066	A	24836	1	268	MTCRLRLRLPGQAGVGKRVSG VPDELSPFLSVSGSRYLQGGVGL VSPTSGANVGLPVISTNVLVKE CRDQKWKWTEKGCLNMFHFK
24699	55067	A	24837	568	713	
24700	55068	A	24838	217	1910	AFTFQESVMAFSQAVSGLNAA ATNLDVIGNNIANSATYGFKSG TASFADMFAGSKVGLGVKVVAG ITQDFDTGTTTNTGRGLDVAIS QNGFFRLVDSNGSVFYSRNGQF KLDENRNLVNMQGLQLTGYP TGTPTTIQQGANPTNISIPNTLM AAKTTTTASMQINLNSDPLPT VTPFSASNADSYNKKGSVTVFD SQGNAHDMSVYFVKTGDNW QVYTQDSSDPNIAKATTLLEF NANGTLVDGAM/ANNIATGAIN /GLSFLNSMQQNTGANNIVATT QNGYKPGDLVSYQINDDGTVV GNYSNEQTQLLGQIVLANFAN NEGLASEGDNV\WSATQSSGVA LLGTAGTGNFGLTN/GSIESGI AFLVNVPLNPKLKRNVVAGAR WHPYGPWPAFAERACLIEPEGD RRTTHIRPNQRTYSRKTKQRQG GHKTRQDNWEQKGDGGRPEP TDPHQHDANRPTVATKKRRKS TQSQRNHRNPKGTHPTTEHGT AGTTKPPDTPQTDNWT HKGSL REGKANRKNPLRGAEVAGGG KQRAKAERQTQRGERREDVDE GEEDRSKKTEK
24701	55069	A	24839	500	653	

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24702	55070	A	24840	445	849	GSPGTAGTEVAVVLKIGGVHD KVIGHYRCSTNTGRVLDVAI/S QNGFFRLVDSNGSVFY/SRNGQ FKLDENRNPAITGTPPT/IQGAN PTNISIPNTLMQRKPTAQIVLA NFANHEGLASEATTSLGRRLNL AWRCM
24703	55071	A	24841	1	453	MKQMDTRGKVINCAFAVSAAF ALGDHLGFAAANNMAMIFPMI VGKLIGGVTAIGVAMMLVPRY EFIKREISWQSPVFTFVVKQGG LKEAELKTLILEQYHAAGIEPES VDSGAIITGESAKTRNAR*TGR FKRSGTENL/KLEQYHAAGIEPE SVDSGAIITGESAKTRNARPTV MALSQLGDFVVASAGPHLE
24704	55072	A	24842	370	670	YSSNIMLRVLSRKALILVPSSSP VKARKPAMLARRGWRSLSRW AILSLPGPR*TGRFKRSGTENL KLEQYHAAGIEPESVDSGAIIT GESAKTRNARNPAGMALSQLG DFVVARAGPHLESVNAGYRTRI RNHGHSWFPGEIGIRSQFHTLR TGSINGKAWGA
24705	55073	A	24843	1	1623	
24706	55074	B	24844	1	4986	
24707	55075	B	24845	65	726	
24708	55076	A	24846	4107	4460	FMSTCGYGGGLSRFPARCLSYQ PLRSWRETVAASG*RRITGSARA NCFCSGLTRDFSIRWPEK*SA QTFVVGTVRCGGMGR*IAA VL SRYSTVESGVSSSTHHLPLQPD PSGRRL
24709	55077	A	24847	624	895	PLVPAYKQSQRQKPHDYLNRC RKSL*QNSTTLHAKNSQ*IRY* WD/SISE**ELSMNTNPQISY*MG KNWKHSL*KLAQDRDALSHRS YST
24710	55078	A	24848	1434	1594	
24711	55079	A	24849	1294	1488	PAGKQTQQRQQFANDGRGEI WRKLKPNPRRQKS*CTSDPRQ KSTLISQREAVIRRFSEAGNFH
24712	55080	A	24850	595	879	RRCTTNIKKIQDQKGNRKA VHRSRFVHGRPITLLFFQLSGRI QSHRLPGRAALFAGIPAACDQS PSLRQPISSEWSDGR*HRRIFRS* SEEF

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24713	55081	A	24851	1009	1478	YSLSVSVWAGATVMESPVWM PIASKFSIEQTMMLSLFSLRSTSI SYSFQPIDSSISNSLVGERSRPR AQISSNSSRL*AIPPLPPMVKD GRIMHGKPTSAATASASSIVCAI PERAVSRPIFFIATSKRRRSSALS IASAVAPIMVTPNSSNT
24714	55082	A	24852	48	209	GLFQVGVAENCRDNNHFSFLH SVVIGSSSERVVAK*PDADHF SASFVPVILK
24715	55083	A	24853	1358	3194	PTASFAATLAIGKPVAFDASAE ERDTRGFISITIRRPFGFTANVT RLETERGGICRSVPWEVVSKE AWAEAPDPGVTLGLKTQHAT /VSEVTSRFRSHYRQFDLDQ AFSAKIFDRYLNLLDYSHKRKT ELGDEAAFSAKLDVFDLYNL AQKRRFRERYQYALSVLEKPM FTGNDTYNDRSKAPWPWNEA ELNALWDNVESLAMTAFAREI DPHTNYLSPRNTEQFNTEMSLS LEGIGAVLQMDDDYTVINSMV AGGPAAKSKAISVGDKIVGVG QTGKPMVDVIGWRLLDDVVALI KGPKGSKVRLEILPAGKGTCTR TVTLTRERIRLEDRAVKMSVKT VGKEKVGVLDPGFYVGLTDD VKVQLQKLEKQNVSSVIDLRS NGGGALTEAVSLSGLFIPAGPIV QVRDNNKGVRSDTDGQVIFY KGPLVVLVDRFSASASEIFARD VVVGLICLSSLDVWLCGLFCR CSVDAERTKRQGGKGEESRKR RRKGVELSYLLFGWSAVVLLF VSDAEQHRASRHGGNACQQHP DVRHDEADGYPRQSHQLRLRR FRCFRPGRPLRLRRCOHERHDL PDDCRQVDRRRNGDWRGDGA
24716	55084	A	24854	100	671	YFCFWTYPLLPVCMCDKRGK HGAPAGDLYVQVQFNHPIFE REGNTLYCEVPINFAMALGGE IEVPTLDGRVKLKVPGETQTGK LFRMRGKGKSVRGGAQGDLL CRVVVETPVGLNERQKQLLQE LQESFGGPTGEHNSPRSKSFFD GVKKFFDDLTR
24717	55085	A	24855	852	1335	
24718	55086	A	24856	326	471	PLQTHPAQQRGHPYQHGGTV S*SCRRRGWSSSRPVIHADAQ LMP

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24719	55087	A	24857	1095	1283	SCRRRGWSSISRPVIHHADAQL MP*PQIVYQHLPFGIYRQDR L*IPD*RPVLTIQDVRGP
24720	55088	A	24858	1	1159	
24721	55089	A	24859	1744	3019	KISPRRPOET/CFQKSTNIAREKT LEQEFVQLFEKIGRRMCLTRE GKKLLPHIYELTRVMDTLREAA KKESDPDGLRVVSGETLSYR MPQVLRFRQRAKPVRLSLQSL NCYVIRDALLNDEADVGVFYR VGNDDALNRRELGEQSLVLVA SPQIADVDFTTEPGRHNACSFII EPQCVFRQIFESTLRQRRITVEN TIELISIESIKRCVAANIGVSYLP RFAVAKELECGELIELPFGEQSQ TITAMCAHHAGKAVSPAMHTFI HALYSCMRMRRLIRATRSCQF NILHEPRRADKRSASGSLRLQE FNYQDKPCMEIRITYEKTPIR MDKGLTNFGSRWILPELAHKE KDEETQQRKSKRDSRREETDT KKKTRDKATKREKDKEIEMA SISITSRCEDKLENFSSMKYYTEI
24722	55090	A	24860	321	575	SYRRYVFPAQ*NRHLQFAVKPP APVIVHPTLVDSEHHSLHDKR RQHRPHHSVAHHGSRNSSATA TINALLGRVAQNAATRGT
24723	55091	A	24861	935	1637	PQPPPLRREGAGLEKELGRR VRVKGSGCQWPICGVVPFIPV ITEQESFQEL/RRITTAESLGK EYEILMIDGSSDNSAHMLVEA SQAENSHIVSILLNRNYGQHS MAGFSHVTGDLITLADLQNP PEEIPRLVAKADEGYDVVGTVR QNRQDSWFRKTASKMINRLIQR TTGKAMGDYGCMLRAYRRHI VDAMLHCHERSTFIPILANIFAR RAIEIPVHHAHS
24724	55092	A	24862	1020	1229	

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24725	55093	A	24863	98	1242	MDKFRVQGPTKLQGEVTSIGA KNAALPNLFAALLAEEPVEIQN VPKLLKDVDTSMKLLSQLGAKV ERNGSVHIDARDVNVFCAPYD LVKTMRASIWALGPLVARFGQ GQVSLPGGCTIGAHVMDKVS GATVTIMCAAILTEGATIEVFY FLPLAIGKFNELYPNIKVRJIEQ GTNNCMESVLCNVEDSFGINM NNVTNSSIDFTPLVQRRPFVL ACRRDHPLAKKQLVEWQELVG YKMIGVRSSSGNRLLIEQQLAD KPWKLDWFYEVRIHLSTSLGLV EAGLGISALPGLAMPAPHYSSII GIPLVEPVIRRTLGIIRKDAVLS PAAERFFTLSDFCGPVPSEDNI FESPASQHQHEYIGSRQCFLMPSE TTGTMHV
24726	55094	A	24864	1	833	MAELGRKSSVAVSWGKVKTT AQMVALAWLLWRPPIWVEYA GIALFFVAAVLTLSWMLQYLT RVQICLISDRFGVIFSRSKSVVK NIVDSSRQEYLEEFYARYNVEL RAPEGFFYLPRSTTLIPRSVLS ELDMVMVGKILCYLYLSPERLA NEGIFTQQELYDELLTDAEAK LLKLVNRRSTGSDVDRQKLOE KVRSSLNRLRLGMVWFMGH DSSKFRITESVFRFGADVVRAGD DPREARRLIRDGD/AMPIENHL QLNDETEENQPDSGEEE
24727	55095	A	24865	819	1428	SPRGISRGGRCPISGDGRIFA GILHGLDNELPLQEEVEGNLE QEGLPPIRQSDALDLCSFSDILV SPNMYIDDGMKRDWPVMKQC ALQRRWRILPDHYGTPEAEKRP GFAPHYCFSYALLVHMQQC DLEVGDVFWTGGDTHLYSNH MDQTHLQLSREPRPLKLIIRK PESIFDYRFEDFEJEGYDHPGK
24728	55096	A	24866	2	1445	
24729	55097	A	24867	1	1785	

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24730	55098	A	24868	3	654	VRFKGRGSSWHMV/SQWDYV ADRFGTADLLPFTISDMDFATA PCIEALNQRLMHGVFGYSRWK NDEFLAAIAHWFSTQHYTAIDS QTVVYGPSVYVMSELIRQWSE TGEVVIHTPAYDAFYKAIEGN QRTVMPPVALEKQADGWFCDM GKLEAVLAKPECKIMLLCSPQN PTGKVVTCDLEIMADLCERH GVRVISDEIHMDMVWGEQPHIS LE
24731	55099	A	24869	955	1278	TLTPDFL*QGHFFRAGIAYQIV KQTTVGTTVEITLRRYVVDGNR IPPRQDRQGDFAFFGATHQW HQVFKRQDIQVTANTATTVT QQAGFTIETRPLRPHQQQ
24732	55100	A	24870	1	1707	
24733	55101	A	24871	1	3615	
24734	55102	A	24872	1	1931	MLLLREHTDTRHDHPRTTRAT RRRRHTEKKRKKRPPATHVL MTATLIPVSRLA TDQPQLFHE SASKPAPHLVSSLGCHCGDASC SGRAVADAMQFKTVFPVFAA AMNPEHMAESGHRITRPEFPDY REL FRES DIKSAVVDISICQCNTP FNYLFRCFELQCLSRHGHSAVG VMQRRHSPMQETRIASPLQRY RWHEDSVNRNWFVSMVGPVSVR VNEWFSAYAMAGMAYSRVST FSGDYLRQPLVSGFHEA
24735	55103	A	24873	1281	2234	ISTNSILRIFSGFRKLMEV/TLR DTPILTFMKNLDR/DIRDPMELL DEVENELK/IGCAPITWPIGCGK LFK/GVYHLYKDETYLIQEVRI KGLNNP/DLDAVGEDLAQQL RDE/LELVKGASNEFDKELF/LA GEITPVFFGTALGNF/GVDHML DGVFMAGDRSHVEEAY/PGDIL GQGEEMMKFTGIPNF/APELFRR IRLKDPLKQK/QLKGLVQLSEE GAVQV/FRPISNNDLIVGAVGV LQFDVVVARLKSEYNVEAVYE SVNVATARWVECADAKKFEFF KRKNESQLALDGGDNLAYIATS MVNRLRAQERYPGRQFHQTRE

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24736	55104	A	24874	2	760	AKFEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIFVA NIESKDPQOI/DRIQALAGWIAE QIGADVNHATRAGLLSKCDLM TNMVFEFTDTQGVGMGMHYAR HDGEADVAVALNEQYQPRFA GDDLPSNPVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRHIVEKNLNLDLQTLT EEAVRLYGDKLTNANVDDVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPRPADFDDWHA
24737	55105	A	24875	2	391	
24738	55106	A	24876	2	1785	WLLYRAHVKG/STEALLPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLLLGDKVIPATIL GIQSDRVIRGHRFMGEPEFTIDN ADQYPEILRDSGKVIADYEERK AKIKADAEAAARKIGGNADLSE TLLEEASLVVEWPVVL/TAKF/E EKF/LAISRTALVPYSADNMYQ LVNDVQSYQPFLPGCTGSRILES TPGQMTAAVDVSKAGISKTFTT RNQLTSNQSILMNLVDGPFKKL IGGWKFTPLSQEACRIEFHLDPE FTNKLIELAFGRVFKELAAANMV QAFTVRAKEVYSASMRYIYVIV YISYRPPNLLDSHIIGFSSITHC AVTSHHYNSCDMTMTIHSYVT PYISVRVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDDTRIHTI ESRCRVCGAHSRDAERLDRF AQTADEIRIADRGFSSRPECIRS LAFGEADYIVRVHWRGLRWLT AEGMRFDMMGFLRGDLCALIS KTRLISENRRKGRVVQAETLE AAGHVLLLTSLPEDEYSAEQVA DCYRLRWQIELAFKRLKSLHL DALRAKEPELAKVGIFANLLAA FLIDDIQPSLDFPPRSGSEKKN
24739	55107	A	24877	1	2022	
24740	55108	A	24878	2344	2523	
24741	55109	A	24879	82	732	

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24742	55110	A	24880	828	2184	SGCILPPESLRLWASVARRPRT NQPRQPGPKIGGISPAGSALALA CGKRTVLFASLCTRTGGSQLGE VPALVLLADQMLALDDQYTFLO RIPRSPYGLAFGPVPHLHYLHQ MRLLDIAPIAFRAMSLAFFVNY LDAVRTGSICSNQNSNDSSAM GISMNVSTLMRVRAIWVYAAAY MERVLNLLNNALRYCHSTVE TSLLLSGNRATLIVEDDGPGLAP ENREHIFEPFVRLDPSRDRSTGG CGLGLAIVHSIARGNWATSDHR SLTGTQPYARIVVFLVRLIFAFR VTQTLTQISFVRVQVQNAFPQ CPLGIGIDVHFYAYAVYGVDF LSSRTGTTVFDDLNTPDFDRC FAFMQAVGKGYTDAYLPIVER RKAMAYGERERNFQYRRGRY VEFNLPSELAATVYQSDPNFAT GCFRLYTSCNTFNMHKAATML VRAEFSQGYQHCV
24743	55111	A	24881	679	1628	PDADAKRVDITLCLAFGCDAQF IEITFTRLPEVRIHHLQSPASALS SCNHLLIRJTQFNADITIGHHL VNRRVVTVLRDMRHHGDIVHP GVRRGVEHYAAMDGPVKEIM EVRLFLAVFVGNHHSRRDSL VQFVVHTNGDITYTFPGNNIRRD IGFKWRIAALMLHHFLIIDPHFA VMSDRIETQHDTLACPNFRYKD FALIPERCRII/SEYLDRTDRLK WCYAAFQGGDQSQASNPMYA KAPV*VRWVHGKALSEKGLH VYQRLYQIFQHAIEYQTGTNDA EISTKLCLFSSSLSSSLQHSI PPNACL
24744	55112	A	24882	1	1515	
24745	55113	A	24883	1954	2859	
24746	55114	A	24884	121	393	SLARWIICNTSEELAANIKRLGD VTVRLNAFAHGVYGEAQSM GERHAGRR*AVG*CVKGARGE PVDISGAQLRGCGVNALSGLR FGTDL

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24747	55115	A	24885	1	3706	MDLGANGWQTFRYVVLNLS ALLAGGMLAFALSFDEIIVTFTT AEQVDAAVRAADAAFAEWGQ TTPKVRAECLLKADVIEENGQ VFAELESSNNTAFARASSNGDL PTKADLQAQLDSLKNQKDLA QDKLVQQDLTDLATLDKIDRI KEETVQLRQKVAAEPEKMRQA TAALTALSDVDNDEETRKILST LSLRQLETRVAQALDDLQNAQ NDLASYNSQLVSLQTQPERVQ NAMYNASQQQQIRSLDG
24748	55116	A	24886	2842	5034	NVRLSPAMRCRWRRGSPMPAM FEVGVKTRIIQSRREVILMADHS KFDAVEPHAVATLSICKTIISDS GLPETIAQRYQRAGSSLEAQP DREIEKRGPAIAQAFDAEGKPS KASEGWARGCGITVDQAERLT TDKGEWLLYRAHVKGESTEAL LPNMVATSLAKLPIPKLMRWG ASDVHFWVPVHTVTLLLGDK VIPATILGIQSDRVIRGHRFMGE PEFTIDNADQYPEILRERGK VIA DYEERKAKIKADAEAAARKIGG NADLSESLLEEVASLVVEWPVVL TAKFEEKFLAVPAEALVYTMK GDQKYFPVYANDGKLLPNFIFV ANIESKDPQQIISGNEKVVRPRL ADAEFFFNTRKKRLEDNLPR QTVLFQQQGLTDRDKTDRIQAL AGWIAEQSGTDAGDQTGYSDE RWVPDAHSEAPSPVSDMLSAL LLLTLVLAGMVRMAARLLMA KPPQAVNRGDIGWLTSPMVIL LVMMMLAMGTHIPQVIRIPGGR FHYSPPHGRGRTDLPAQRSTWHD FCLQAPHLFRNTVNVNSSNR GEAILAALKTQFPGAVLDEERQ TPEQVTTIVKINLLPDVVQYLY YQHDGWLPVLFNDERTLNHG YAVVYALSMGEAEKCVWVK ALVDADSREFPSVTPRPAAV WGEREIRDMYGLIPVGLPDQRR LVLPDDWPEDMHPLRKDAMD
24749	55117	A	24887	49	531	
24750	55118	A	24888	1619	1968	
24751	55119	A	24889	1	553	
24752	55120	A	24890	744	970	LAVISEASNQKRGDPVDHAD*1 AVANMLLNQFQQSYTPMLHDL IVRYDGDIIHQKQSFQVQLPGKL RIVKLIQPVE

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24753	55121	A	24891	52	455	
24754	55122	A	24892	2988	3614	PVSVLTQKRLSPATSHRSTCRVI LNQAYVTPSKCWPDPVEISFNF FHSEDEVVRHPVVARIVNAYEA WEEAEQKTMTPANQHAGGLV QCDKMLLQRRSREVIELSEQNA AQMRHVRGADAMAMIFQEPMT SLNPVFTVGEQIAESIRLHQNAS REEAMVEAKRMLDQVRPEAQ TILSRYPHQLSGGMRQRMIA MALSCRPAVLIADEPTTALDVT IQAQILQLIKVLQKEMSGVIFI THDMGVVAEIAIDRVLMYQG EAVETGTVEQIFHAPQHPYTRA LLAAVPQLGAMKGLDYPRRFP LISLEHPAKQAPPIEQKTVDGE PVLVRVNLVTRPLRSGLLNVR TREVHAEKVSFSLWPGETLSL VGESGSGKSTTGRRLLRLVESQ GGEIIFNGQRIDTLSPGKLQALR RDIQIFQDPYASLDPRQTIGDSI IEPLRVHGLLPKGDAARVAW LLERVGLLPEHAWRYPHEFSGG QRQRICARALALNPKVIIADEA VSALDVSIRGQIINLLDLQRDF GIA YLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVFENPOH PYTRKLLAEDPVAEPSRQRQR VLLSDDLPSNIHLRGEAAVVALI KPGAQIGR/PQSWT
24755	55123	A	24893	134	595	IRTGRENESYKGDISR YKFVSAR ALRNEVRGGRGCHKTRRVSVG KKVIGLKFHRHLPVVPVTPESIVIP PAPVANDTLVAEVSADAPQAND PTFNEDLA*FAVLSTPTTAILISC PGRWGPAAGSECGVRGAHAHR ELALRAFSCCCFSSNAISIPN
24756	55124	A	24894	708	1444	TDAPGDEEASLQRAAQAGVGK IIVPATEAENFARVLALAE NYQ PLYAALGLHPGMLEKHS DVS EQLQALERRPAKVAVVAVGEIGL DLFGDDPQFERQQWLLDEQLIL VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERFVQLGYKIGVGGTITYPR ASKTRDVI AKLPASLLLETD PDMP LNGFQGPNNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP
24757	55125	A	24895	1460	1777	

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24758	55126	A	24896	381	482	IPGPQSPQSSPDGLWLC*NP*RLLWKAPRSDK
24759	55127	A	24897	977	1144	
24760	55128	A	24898	2	280	CTFALRDEYPRMLNVDNKGRLR DHIELQPLAV/DASYPGGDFRK NAVYVPMW*SAHCEPEGRFAE TGSRRYGEDFASTAPGFRRAAT RKRVRKR
24761	55129	B	24899	1	1665	
24762	55130	A	24900	296	495	
24763	55131	A	24901	1	5352	
24764	55132	A	24902	187	280	AVDTGLADIIRDIEPNMVARLP LSFTASLSIS
24765	55133	A	24903	1775	1981	HIWQNSLIVLFRGCRSAHAKVH RWKN*LPLNLAPLLPRSGSSAPI RPPPSAQAQRQPMKSTYGVDRR HS
24766	55134	A	24904	760	1473	
24767	55135	A	24905	1	2124	MNRMSGGYWQLFAESGETCR ARELEQCLEDYDQRKESVRW HLDLHTAIRGSLHPQFGLPQR DIPWDEKFLTWLGAAGLEALV FHQEPGGTFTHFSARHFGALAC TLELGKALPFGQNDLRQFAVTA SAIAALLSGESVGIVRTPLRYR VVSQITRHSPSFEMHMASDTLN FMPFEKGTLLAQDGEERTVTTH DVEVAKNAITEIKTQFEKEKLA QDRIKRNQ/LDANIQLNYSI.DI ANAAGIKKPVYSN/DGIERKLEI EKAIVTDVAELNGELRNRYLV EQLTKAHVNDVNFTPFKYQLSP SLPVKKDGGPKAIIVLSALIG MLYCRVCIKRNADSPFVSGFS DPNVVLLAAVFIIGDGLVRTGV ATVMGTWLKVGAGNSEIKML VLLMLTVAGLGAFFMSSTGVVA IFIPVVLVAMRMQTSRSLMM PLSFAGLISGMMTLVATPPNLV VNSELLREGYHGFSSFSVTPIGL VVLVLGILYMLVMRFMLKGD QTPQREGWTRRTFRDLIREYRL TGRARRLAIRPGSPMIGQLDD LKLRLERYGANVIGVERWRRFR RVIVNVGVSEFRARDVSLIAM SAADVLRQFCSERLLEPDGIA RFSLLPESELJGESVREIGLRTRY GLNVVGLTRTGVALDGLADE PLLLGDISWLWALES DRYAAM LGRSRLTYRRGDEHCRASRSP

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24768	55136	A	24906	834	993	EEIEVARLRDQKSAEGGIQNRE YWPGRSGHR*SPHAPIIGTQFLQ ALFQTWDQFVFALSACGRRHP TDGRRQNPAVSGHVSVAARQPA HSQTDEASG
24769	55137	A	24907	3519	5161	
24770	55138	A	24908	374	1891	KWKLKRPDSNIDHRRVPNLET WFSRHDKTRPTSKNPSDYQAG DIVSWRLDNGLAHIGVVSDGFA RDGTPLVIHNIGAGAQEEDVLF NWRMRQCQHQNHTATFNGP RILAEQPPGKEYAANGNGQLYP MSSLNKQGSDAHFPDYPLASP SNNEIDLLNLISVLWRAKKTVM AVVFAFACAGLLISFILPQKWTS AAVVTPEPVQWQELEKSFTKL RVLDLDIKIDRTEAFNLFIKKFQ SVSLLLEYLRSSPYVMDQLEKA KIDELDLHRAIVALSEKMKAVD DNASKKKDEPSLYTSWTLSFTA PTSEEAQTVLSGYIDYISTLVVK ESLENVRNKLKLTQFEKEKLA QDRIKTKNQLDANIQRINYSLD IANAAGIKKPVYSNGQAVKDD PDFSISLGADGIERKLEIEKAVT DVAELNGELRNRRQYLVPEPITK AHVNDVNFTPFKYQLSPSLPVK KDGPGKAIIVILSALIGGMVAC GGVLLRYAMASRKQDAMMAD
24771	55139	A	24909	1111	1895	PLVNFNSSSHVPVSNPSIQLSSITL PLVENESRARA/VKDQMDAIDH QTGVRLPVFYSIVLPEIRAILQS EGFCQDIVQALVAPLQQEMKL DPTPIAHRTHGLNPNLNKYDA RIAAIDYTLAHDGIGSLRNLDQ AQVILLGVSRGCKTPTSLYLAM QFGIRAAANYPFIADDMDNLVLP ASLKPLQHKLFGLTIDPERLAAI REERRENSRYASLRQCRMEVA EVEALYRKNQIPWINSTNYSVE EIAITKILDIMGLSRRMV
24772	55140	A	24910	77	434	EKKRGREDKPGTMATTFPPATSA PQQPPGPEDESSLDESPLYSL AHSYLGPLIMPMTSPLPALV TGGGGRKGRTKREAAANTNRP SPGGHR/ERKLVTKLQNSERKK RGARRLRQSWR
24773	55141	A	24911	31	295	

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24774	55142	A	24912	75	426	EKKRGREDKPGTMAFFPPATSA PQIQPPGPGGRDSQPWMDLL /YSLAHSYLG/GGGRKGHTKRE TAANTQPPQPLAGHERKTVDP KLQ\NSERKKRGARALRQELM RRRPWLTTPSQ
24775	55143	A	24913	1	1107	
24776	55144	A	24914	1	1468	
24777	55145	A	24915	1	2463	
24778	55146	A	24916	1	603	
24779	55147	A	24917	118	1087	IRSKMTTQTVSGRRYFTKAW LMEQKSLIALLVIAIVSTLSPN FFTINNLFNILQQTSVNAIMAVG MTLVILTSGIDLS/VAASIVGIEV NALVAVAAALALGAAIGAVTG VIVAKGRVQAFIATLVNMLLL RGVTMVYTNGPSVNTGTFENA DLFGWFGIGRPLGVTPVWIMG IVFLAAWYMLHHTRLGRYIYA LGGNEAATRFSGINVNKIIIVY SLCGQLASLAGIHKVARLSSAQ HTAGTGYELDAIAAVVLADDR QSGGDFAGGAGRQKAVITTT GHLEYEHEKTGYPGFRCCAAR HRQCECDGKRHHRAGGLHA
24780	55148	A	24918	1	1286	MHEREPGLRAALAGQLEFRVG LGLGVWTLRLMELLRQRLV VYTASDGQYEMVSRNLNWVN YLVLEDVHIILPDQMRGITGCV ATHPHERRLHAGTVHRQINIVN NPPDCVPRDAGEAEVAPDPSLA SLQLQTPPELGLISCHNSIQVSN EARLFELLICQWRDFRKRIVAA KSMQGRELEGGQGGQDKATNP FRVLALKSGSDPDPHGAGRQG SDLLHPVSDAQVLQHFFQRRRA LLSSPDYHDVVGLCAQEPG YIMELFIHKHCSLAQTAGSLAP EQKKELEMTVRYIYSSADLTAE KFATAIRN/HWHVENKLHWRL DV*RQFDKHCSTADSTRILASF VRHVNAALDVRVVFASGSETT HGDGARRYLRCDVDWRRRT AVAQADKSARACHFYAGYH HHEHFADPVSVGAKYHTVFST

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
24781	55149	A	24919	417	861	AKGPCPDRNHSSDDKDVIADG KTLRHSYDKSRRRGAIHVISAF STMHSLVIGQIKTDEKSNEITAI PELLNMLDIKGIITTDAMGCQ KDIAEKIQKQGVIFSLCPASIID KKVTDLAVAVQGTLTGSGGI LPPGGALKKISEKL
24782	55150	A	24920	3	1767	HISHPDYR*AWKVEHKLSGILL LTIFAVISGAESWKDIEDFGKTH LDFWKQYQDFENGIPVHDTIAR VVSCISPAKFHECFINWMRDCH SSNDKDVIADGKTLRHSYDKS RRRGAIHVISAFSTMHSLVIGQI KTDKKSNEITAIPELLNMLDIKG KIITTDAMGCQKDIAEKIQKQG GDYLFVVKQRNGAVENRAKTQ TRIAFGDHFRRQVSQRIRLFCH RLATQFAARLRMFATGQPMN GLRLLFIIVNKQAALLVNKLDA QMAAFQQLPGRGRQATVRRRE MDLCAFAERMGLPVSRPGDIQE FHAGCRTKFDAGAFRDKHHVA CFGDHGLAFVANMQLPFQHVV DFVVVQGPREECVLP.LHKTGG HAAAVVSGHKISQAHAMRLCA VETTKLDATGINHFDAAAFAGHR FESSVDCACSATVSFIFPSVCD RFGNWLRSGRCSHAARKNEITL TNTRSLRPKRNTERHDMQTR ATVIAAGEKLLPYAETLMSTW QAARKEVAHTSRHNEFSIGASA SLWDMVMTSAGAVVTTVVVA VRPSSFYILCSHKKKRTLHTR EKTVDRRKEYETRKRSETDT

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24783	55151	A	24921	110	1282	SNTPIIKENKMKLKLGMHISI IPDYRQAWKMEHKLSILLTI CAVISGAEGWEDIQDFGETHLD FLKQYGFENGIPVHDTIARVV SCISPAKFHECFINWMRDCHSS DDKDVIADGKTLRHSYDKST/ RRRGAIHVNNAFSTMHSLVIG QIKTDKKSNEITAIPLENNMLDI KGKIITDAMGCQKDIAEKIQK QGGDYLFVKGNGRLNKAFAE EKFPKLKNNPEHDSYAMSEKS HGREEIRLHIVCDVPDELIDFTF EWKGLKKLCVAVSFRSHAEQK KEPEMTVRYYYISSADLTAEKFA TAIRNHWHVENKLHWRLDVV MNEDDDCKIRRGNAELFSGIRH IATNLTNDKVKAGLRRKMRK AAMDRNYLASVLGAGLS
24784	55152	B	24922	258	507	
24785	55153	A	24923	1	3060	MTEIEENMLLPISGQELPIRWLA QHIGSEKPVTHVSRDGLQALHIA RAEELPAVTAALAVSHKTSLLDP LEIRELHKLVRDTRDKVFPNPGN SNLGLITAFPEAYLNADYTDGR LLTKWEMKGNRVSHITRTASG ANACGGNLTDGRGDSFVHDLTS MARYVATGVLARSMGLVIYSFI QHTLTLEEYREITAFLEFETHA AAARYTGEQETLPLSPQWILRQ CKEVALCDGDTFSGEQLNLM LQOREWREGFLAER
24786	55154	B	24924	56	967	
24787	55155	B	24925	1	1776	
24788	55156	A	24926	1	864	
24789	55157	A	24927	424	513	
24790	55158	A	24928	1	5049	
24791	55159	B	24929	1	939	
24792	55160	A	24930	1	1837	

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24793	55161	A	24931	1	2249	MLPDIARFLPRLANDQIEFTW YVNHFTYSNAIKIFCYQMFLAS TQARASGAPLQRLFRAIGGNA WERPFRMVFCSAAFSEESSPFR ETNYEPQLFLGFATDYRFAGW TLRDVEMGYNHDSNGRSDPTS RSWNRLYTRLMAENGWNLVE VKPWYVVGNTDDNPDIKYM GYYQLKIGYHLGDAVLSAKGQ YNNWNTGYGGAELGLSPITKH VRLYTQVYSGYGESLIDYNFNQ TRVGVGAGVNVQAQAEVLNLE SGAKQVLQETFGYQQFRPGQE EIIDTVLSGRDCLVMPPTGGGK SLCYQIPALLNGLTVVVSPLNS LKEKSANPFEFTFAFAHAHFW VIQAIMINTPADGSTHKQART SWLPYSSLPVLSVSTQDEKAKK KMRFMQRSKDSLAKWLSAILP VVIVGLVGLFAVTVIRDYGRAS EADRQALLEKGNVLIRALESGS RVGMGMRMHVQQQALLEEM AGQPGVLWFVATDAQGIIILHS DPDKVGRALYSPDEMQLKPE ENSRWRLLGKTETTPALEVYRL FQPM SAPWRHGMHNMPRCNG KAVPQVDAQQAIFIAVDASDLV ATQSGEKRNTHIILYALATVLL ASVLSFFWYRRYLRSRQLQDE MKRKEKLVALGHLLAA/GVAHE IRNPLSSIKGLAKYFAERAPAGG EAHQLAQHVVQIRRFHAHPAS

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24794	55162	A	24932	261	2115	TLVFCWHAKLLSHGVFMDIISV ALKRHSTKAFDASKKL TPEQAE QIKTL LQYSPSTNSQPWHFIVA STEEGKARVAKSAAGNYVFNE RKMLDASHVVVFCAKTAMDD VWLKLVVDQEDADGRFATPEA KAANDKGRKFADMRKDLH DDAEWMAKQVYLVN VGNFLLG VAALGLDAVPIEGFDAAILDAE FGLKEKGYTSLVVVPVEDLAGI EIDHTTSMVMIFGIIFLTAVVVH IILHWVVLRTFEKRAIASRLWL QITQNKLFHRLAFTLQGHVNIQ AVFWLQKGTEAADILTTCACL WIMMYALLSVFSLDVLILGQV KFPAAVQLPLKGVIFQGIKMGF ILVGLMISLLIGQSPAILISGLGA MAAVLMLVFKDPILGLVAGIQ LSANDMLKLGDWLEMPKYGA DGAVIDIGLPTVKVRNWDNTIT TIPTWSLVSDSKNWSGMSASG GRRKRSISIDVTSIRFLDEDEM QRLNKAHLLKPYLTSRHOEINE WNRQGSRESVRNLRMPNIG VTFCAYLNKYLGTHPRKRDM TLMVVRQLAPGDNGLPFEIYAF NTVVWLEYESIQAIDFHIFAIV EEFGLRLHQSPGTGDIRSLAGA FKQ
24795	55163	A	24933	1	757	
24796	55164	A	24934	8	343	
24797	55165	A	24935	1423	1761	
24798	55166	A	24936	1	851	MKGDTKVINYLNKLLGNELVA INQYFLHARMFKNWGLKRLND VEYHESIDEMKHADRYIERILFL EGLPNLQDLGKLNIGEDVEEML RSDLALELDGAKNLEAIGYAD SVHDYVSRDMMIEILRDEEGHI DWLETELDLIQKMLQNYLQA QIREEGKSIYQEQTTAMKRPDY RTLQALDAVIRERGFEARGTK AVHYTISRLETAH*ATGKYVRAA AVGAYRTAAPDGTAKTAGTA APGGVAGRRVAGR*TNRFDSA AAFTGGQRRQSGDVAASCTGS CVG

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24799	55167	A	24937	1645	2009	PVFIQFVEGMCGTANEPACLLV NQSPAIFYPGKJAAIWQNPRHV ESGSM*TLIDSD*VSPTECLSPR HHYMPFEEAARGYEIEFEKREEE CRKVILVPGAQSAEAAQKAVS GLVNAMPGGTI
24800	55168	A	24938	1	3936	
24801	55169	A	24939	1	2240	MRSPTMTRNSRNGKHDYKPPPR KRRQPPHDHTAPNSTPARNQRG RPHRPNRQAGQREQRANNPTP NTPSPPTNDPAEPHQTRHDSR QPHNTPPAYAEVLAAALLTTDT NVTRRRRLRYMQPDTKLCHSAG KSIYQEQTAMKRDPDYRTLQAL DAVIRERGFERAAQKLCITQSA VSQRIKQLENMFGQPLLVEDET RTQERLRRGEVVGAVSIQHQA PSCLVDKLGALDYLFVSSKPPFA EKYFPNGVTRSALLKAPVVAFD HLDMDHQAFLQQNFDLPGPSV PCHIVNSSEAFVQLARQGTTC MIPHQLIEKELASGELIDLTPGL FQRRMLYWHRFAPESRMMRK VTDALLDYGHKADDIILRITAT AICGSDLHLYRGKIPQVKHGD FGHEFMGEVVEVGKDVKNLQK GDRVVIPIACGDCFCRLQQ YAAACENTNAGKGAALNKKQIP APAALFGYSHLYGGVPGQAE YVRVPKGNVPGFKVPLLSDD KALFLSDILPTAWQAANKAQIQ QGSSVAVYGAGPVGLLTACAR LLGAEQIFVVDHHPYRLHFAAD RYGAIPINFEDESDPAQSIIEQTA GHRGVDAVIDAVGFEAKGSTT ETVLTNLKLEGSSGKALRQCIA AVKRCGIVSVPGVYAGFIHGFL FGDAFDKGLSFKMGQTHVHA WLCELLPLIEKGLLKPEEIVTHY
24802	55170	A	24940	687	792	TPTLTRLRHPVAYRATLK*NR PAKVSQLCCTNA
24803	55171	A	24941	3	510	AGDMVWLCVTRTQISY*IPRTHP AVGIPRERPLRGADTPQRGASH RIRGEGRK*KRWALLCCPGCN I*RHFCFHN*ERYFWIYVVEST GAVKHLQNTGHWLNAGALPV RRPRKSVTGSIAQVSVPIASAR ALLACPCGQCAGYATQFVMSK ITQRFNVACRTRMYAVG
24804	55172	A	24942	189	563	

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24805	55173	A	24943	1224	1772	GPSVSLATSSCSIKVQNPGISR VVAGSSAIISNVSPGCILRTVLR TIITGSGQRRPSASSVWSGHTSC VVRTANFSSGMVNLVS SVTNLS PSIVPRIKFIAGDPINPETNIFAG WL/VNGFRRTYLLNNPVFHNH NPRRHGHRFGLVGHVDHGGV QFLMQLADLCAHLHAQLGIKV
24806	55174	A	24944	1541	3675	LEIIKRKISMRRNWMHSITRY WRFLDFPTLRGGRWMR*SGEK LNPISTPLRANCLALAQTRTL APMSFTWGMPTSQPDCAVPGR RALPELLCLQRSSQSRFAGTAI T
24807	55175	B	24945	1	1497	
24808	55176	A	24946	650	739	
24809	55177	A	24947	4447	4804	RQNDRYSGRERHEITPLCW*IPR IAWALWLRSLRRGPQEKSLHN RVARTISWPYQARHPCKRTLLGG HGFFLHIVLSQLPCLSYPLSSFA GLLARSSMFLKLAARFLCCRRS YAASPLSI
24810	55178	A	24948	1	3774	
24811	55179	A	24949	431	949	NYAIYHQNHGVNISPLGKTHN YRQHQHCITYYWRDLMPANK NYKQRWITPGSASFYRSSHKAL IRLLATRLPAFPWGRRSAWRWP VRY*IRVPSSGSYHLEISMRAWI FPQPKALTPSNLHWKTA*LWS* KTLSFVCWIATVLPARFWKLT D PWLAILPCANITYWQASAPD
24812	55180	A	24950	337	648	

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24813	55181	A	24951	1	1430	MFTYPHSKFRVNRFGVQVLLIE FSILLDGGRTGLGHSLSVWCISG DCSSFLQKPTSLPLRKPSAIIIS DSLSGSADLLRNHNFCVCTAADI FTTDITPEAGDARLIGIAQTVRH LEDPMPRAWKSIHKSCILDPPIHR APVKENTHPARKINISDPAAGA VARIRYEGVLSVCRASASAYVS RSRTITVACWYVSNTGVTGATI GVKRQHRHARLFSGDGAPGFG TGKRDIRQLRRLVKIQRTFFA AVLHVPTPWSRAIDAAALLTVI DVKVLTACACQACRTLALRVA QVIDRCSNPGDIMSSVARRYWF ISRWSAKRDCAVSYDQDPGQA QRSRCSCLVAVDRGLWLSAYC RSLMTQTLLPDDVPRILPNASSP SRLRCLHIWVITACWICANSSG FIARNLGLCGWEKRLVKDLTRI QDTGRAKEILGATATLEFRIR*T PTLTRPLRHPVAYRATLK*NRP AKVSQLCCTNA
24814	55182	B	24952	1	1295	
24815	55183	A	24953	3151	3207	LQWLID*WCL**TFDLRFA
24816	55184	A	24954	2740	3917	NGRSVWAVKLELFRVKPLDIPQ QRVGQQHVLLKAFNRRLAMQF IQLIATDVTEILPLHVVEDGTD LYCLALSHLRCGRSLRWREL PRGLGVNVSWCYPFKAQQQCA AEITDKAGQREIFGFARVKENA GYVIECYQPDGDKLIRELPF SSLIFARQWVVGELLQHLPE DRITPIVGMQLQGVVEKGGLRV EVADTNESKELLKFCRKFTVPL RAALRDAGVLANYETPKRPVV HVFHFIAPGCCYTGYSYNNNSP FYMGIPLRKFPADAPSRSTLKLE EAFHVFIPEWDERLANGMW AVDLGACPGGWTFQLVKRNM WVYSVDHGSVMQ/SLWTTGT CWGTRFHSARGQKFPEVLQGS QTLPAATDPPGMQWLASGVLE
24817	55185	A	24955	1	519	
24818	55186	A	24956	510	731	

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24819	55187	A	24957	1	1055	MRLCPEKTTKAKRVKAVLAWS KEEPWLSEWSEFVLEMGYKKL GDFSTAGAILTEIRPSPASAFTL DSQPPENNLSEAKYAPNNIESI AKYFAPKSPMFSESPPSGTALDS FNRNERRRWPWPKNKSGFGSD LTLKIGISSPDIALERLYEQAR KLKSGKFRALSELDESARSGVLK VLCAFAQQDYRSASASTRKCD CCDGGGFTEAQVFTNKVSYPW GKPPYWSKMSRAVRPSDWESW TQAREVVRVKCKPCNGKGVIS NSCRCHGKGVKLVAKHESDRRG VPVMKACDRCGGRGYARLKFS SVMMRALILLRRLKKTAAEQQL QPLFEELVAECHKQESMADSIL SKVTR
24820	55188	A	24958	361	725	
24821	55189	A	24959	1100	1738	WQRSTLPLLFESAMQTGVNAG NPVAW*KSAGYGHKLYDAKN RLVLVQSTALWASQLVQYLSTF FRKNLKRPFVTLADEIEHVN AYLQIEKARFQSRQLQVNIAIPQE LSQQQLPAFTLQPIVENAIKHGT SQLLDTRVVAISARREGQHLML EIEDNAGLYQPVTNASGLGMN LVDKRLRERFGDDYGISVACEP DSYTRITRLRLPWRDEA
24822	55190	A	24960	1	2043	
24823	55191	A	24961	2164	2487	KLKRJARHNFHGIRDHLHFQQV NRFSSGFPTTYWLMADHVHH LKTYSTCRIEGGHRLKDHRRHS CAAPLTKLFFPRVKNIFSQQGN LPPMYAITARR*QTHNQHCGD

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24824	55192	A	24962	128	2574	QVVVVMAMVAKVVIDIVVVV GVEMIRVKVVAIVVEVVVEV VVVMVAWWWW*/*DMG EARWWVEYGVWEVEHILNA PQQYLLAGIGDTLAKWYEA LAPQPETPLPLTVRLGINNAQ AIRDVLNLSSEQALSDQNNQ LTQSFCDVVDALAGGGMVGG LGDRTFTRVAAAHAVHNGLT VLPQTEKFLHGTKVAYGILV QSALLGQDDVLAQLTGAYQ RFHLPPTLAELEVDINNQA EIDKVIHAHLRPV ESIHVLPVTLTPDTLRAAFK KYSQSCFVIRLGGDFIIHQLA ENIIVIFVNNHNGTRCQTFQ WAI SNCHTVSLQKFSVRKFL SDLFAIGGRRGVVRPPTEA PGHQSNDQAHVSVSFDGLDL VFFV VNWAGVVFCDLFSR KRGRFSVWRNKGFGRYCQRL ANFRDRQAFQLLNQIH FTRCKQVDNNGGTEFKATH FLAFQQCHRTVVFPGRPAIK TRVERLDYRNRNMEKSNQ GANLRVHGGTWEKLVQLDS AGMVNRVSSVGAPLREPI TEGKGAKEDTWGNLSSNDP LLEAFGGQFGIAISMHQ TLATRGGKRNARPTTRP RFHRTGNPRGIAPHIGTAN ARYSTGHCVPVALPFGLRG PPLARENVATATKGHESA SRETVVA VAKLTSLVLLI CDATHALPIQVLRNDIR VIAAGNGCTDDLQLEHLP ANTDIR
24825	55193	A	24963	117	335	PGLAPATRRSTPGRFNADAGAD *RRAAGTGAGRAKRRGVGIHR CLADPFLADCRNAGLRGAALC GTAAASGK

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24826	55194	A	24964	208	1903	YLAIKTFRCLHDFFTDEQLSRA VWYIGKRAIAAAQTKLPAPFGL PGAKHILFRGHCSDESVDQLAA ESGDDRSVIGVGGGALLDTA KALARRLLGLPFVAVPTIAATCA AWTPLSVWYNDAGQALHYEIF DDANFMVLVDPEIILNAPQOYL LAGIGDTLAKWYEA VVLA PQP ETLPLTVRLGINNAQAIRDVL NSSEQALSDQQNQQLTQSFCDV GDAAHAGGMVWGLGDRFTRV EAAHAGPNGLTGLPQTEKFLH GTKVAYGILVQSALLGQDDVL AQLTGAYQRFLPTTLAELEVD INNQAIEDKVIAHTLRPVESIH LPVTLTPDTRLAAFKKLIQGLIS AEQLAQALAEQNGVAWESIDA WQIPSSLIAEMPASVALHYAVL PLRLNDELIVGSEDIDPVSLA ALTRKVGKRVYVIVLRGQIVT GLRHWYARRRGHDPRAMLYN AVQHQLWTEQQAQGEIWRQYVP HQFLFAEILTTLGHINRSAINVL LLRHERSSLPLGKFLVTEGVISQ ETLDRVLTIQRELQVSMQSLLL KAGLNTQVQAQLESENEGE
24827	55195	B	24965	31	205	
24828	55196	B	24966	69	402	
24829	55197	B	24967	1	721	
24830	55198	A	24968	1	1703	
24831	55199	A	24969	2853	2889	LIIGLDLPAVSAIFQALRFTHV GIADGGAYVVQR/HRPDEPRRR CCSE
24832	55200	A	24970	297	473	
24833	55201	A	24971	1179	2148	CQVLRPRTKRLNVFLHRMQH QWRQREL VHNMC FVIACAKRK RAPFVQAAEEVVRPGQHDDEFP LAIWQTGGSTQSNMNMNEVLA NRASELLGGVRGMRKVHPND DVNKSQSSNDVFPTAMHVAAL LALRKQLIPQLKTLTQTLNEKS RAFADIVKIGRTHLQDATPLTL GQEISGWPA SRSGTGSWRYS GG YWTKYPSGVCASRSKMNWYST RASDGGHASDAVRTAQAADRE LRAPVRDELNASITSKTRLAEST SLAEWVKASPHDDDKPILLPGE WEVNTRRERQKQGIPLDAGSW QAICDAARQIGMPEETLQAFCC Q

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24834	55202	A	24972	166	365	NPFSNSPWETYPVAFITPLALFM GIYLRYL RPRGRIGEVSVIGLV/SP DFRHYLWRLGGKSDLGTVL
24835	55203	A	24973	83	362	KPPCFLQASVTCWLRLPFASMI LPPCACS*ST*ESIRPAVVGPREP EGITFRFRGRTRVVNRMFIDVL RHLFTVIHPLFQFGVTYITDDN
24836	55204	A	24974	584	853	
24837	55205	A	24975	1	3017	MSQDPFQERAEKYANPIPSRE FILEHLTKREKPARDELADEL HIEGEELEGYAPVLAPESGILI MRPTLTMPALTKFVDGTPGVW TGNLFPFLFITIACGAVSGFHAI SSGTTPKMLANEGQACFIFYGG MLMESFVAIMALVSACHDPGV YFAMNSPMAVLAPAGTADV ASAAQVYVSSWGSITPDTLNQI ASEVGEQSIISRAGGAPTLAVG MAYILHGALGGMMDVAFWYH FAILFEALFILTAVD
24838	55206	A	24976	3	206	EPDFLPL**RRNHEQNYRDGKC TGSYRSLRTGR*SGQYDHLRL DPGKSENGRSTGRRCTGTSVA G
24839	55207	A	24977	3	982	GDAEPFVFLPRIRKCDHEYSLDH YQHRFYLRNHRHGKNFGLYRT RMRDEQQWELIPPRENIMLEG FTLFTDWLVVEERQGLTSLRQ INRKTREVIAGAFDDPAYVTWIA YNPEPETARLRYGYSSMTTPDT LFELDMDTGERRVLKQTEVPGF YAANYRSEHLWIVARDGVEVP VSLVYHRKHFRKGHNPLLVYG YGSYGASIDADFSSRLSLDR GFVYAIHVVRGGCKINLVVD NGKIVRAEAAQGKTNQGTCLC KGYYGWDFINDTQILTPRLKTP MIRRRQGGKLEPVSWDEALNY VAERLSAIKEKYGPDIAQTGSS

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24840	55208	A	24978	1339	3640	SPLSTAGISICGPLLIITDVLDT TVAGIKGMATGEGTTEWNSV MVAMLLTLIPPVIVIVLMQRAF VRGLVDMRNKMAGLKLQAVT KSWDGKTQVIKPLTLDVADGE FIVMVGPSGCGKSTLLRMVAG LERVTEGDIWINEQVSELRLIG YMSRKMGGGKNRRREPHIDVKK GIFGLSITPEFSEPLAEDFLSRRQ YGIRFRNLETGNWYPELLDNVE PSFVWANDSWIFYVVRKHPTV LLPYQVWRHAIGTPASQDKLIY EEKDDTYVYVSLHKTTSKHVVI HLASATTSEVRLDAEMADAE PFVFLPRRKDHEYSLDHYQHRF YLRNHRHGKNFGLYRTRMRDE QQWEELIPPRENIMLEGFTLFTD WLVVVEERQRLTSLRQINRKT EVIGIAFDPPAYVTWIAYNPEPE TARLRVGYSSMTTPTDLFDLDI DTGERRVFKPPEV/PGFYAA/SY RREPRW/IVSADGVKYSFV/APR QHFRDAPVLSFLLFSDRAPFR NNGPRVLLLYYHPELLGVT YSQLSVHEARPKPLPIPHSRHRH VPTRNEMAEQEKRPAGSQSLFR GLMLIELSNYPNGCPLAHLSEL AGLNKSTVHRLQLGQSCGYV TTAPAAGSYRLTTKFAVQKA LSSLNIIHIAAPHLEALNIATGET INFSSREDDHAILIYKLEPTTGM LRTAYIGQHMPLYCSAMGKI
24841	55209	A	24979	1	248	
24842	55210	A	24980	839	1625	PDAFILTTKPAGAIPTSTSTRIP FCPSFAPCENATPAAET/HQRNT RPEWRFTFAFFLFAIFRNAVNT VTMSIRKIGVHHNAANLVPW MTKFFQRFQIAFQSRGAVFHQH HHAGYAGQGRKTALEQRLVFL GFGINKQMRVPLIGEVYQFSG *CQRQSFTADGFTDSNAFNIS GNSTARDKLFIAGYGNRYFHC GVNAQIIFMQELGDFRHFVIF/A QKGNEYHGDTRISPGFRFRGHH PLGALRLAASVERSGNGHRA
24843	55211	A	24981	2538	2864	GSSLINSKVMPS/SF*QQNRKFAY KRAQVATDEFHAESFVRGRAP MKRKL*LFMQLGGDVIOFPDGF IAGNTVYRCQQLAVGDAVGKI LHNRYAFRQSTVIQQQCRHLP
24844	55212	A	24982	1	1281	

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24845	55213	A	24983	1	2180	METLNLVADLRSVTGEALLL DEPGVGVDPISRRELWQMVHE LAGEGMLILWSTSYLDEAEQCR DVLLMNEGELLYQGEPKALTQ TMAGRSFLMTSPHEGNNRLLQ RALKLQVSDGMIQKSNIVGI KDTIDSVGHRLTMTINTKSVRP SFSVFCGYDDHLLNTMLGGD GAITASANFAPELSVGIRAWR EGDLATAATLNKLLQLPAIYA LETPEVSLIKYSMQCVGLPVET YCLPPILEASEEAKDKNRPLVD LEHAALQVGKGIIPPLREYGAS EVRSVTRAFNHMAAGVKQLAD DRTLTMAGVSHDLRTPLTRIRL ATEMMSEQDGYLAESINKDIEE CNAIEQFIDYLRGTQEMPME ADLNAVLEGVIAAESGYEREIE TALYPGSIEVKMHPLSIKRAVA NMVVNAARYGNGWIKVSSGTE PNRAWFQVEDDGPGLAPEQRK HLFPQFVRGDSARTISGTGLGL AIVQRIGDNHNGMLELGTSE GLSIRAWLPVPGTRAQGTKE GAREDAVEFFAKLGFVNQGEIT TPTTPIRHFMLIKPVATLDDIL HRGDWCAQLQQAWEHIPLSE KMGVRIQYTGQKFITMPETG NQNPHTLFAAGSLFSLATLTGW GLIWLMLRERHLGGTILADAH RYSKPISGKPHAVADLGALSGD LDRLARGRKARVQMQVEIFGD
24846	55214	A	24984	875	1150	
24847	55215	A	24985	1507	1974	
24848	55216	A	24986	1	1006	
24849	55217	A	24987	1491	1703	RECRYATNGKNNGCCRSAGSD FSSRLRYVR*PFIYTQ*SCGIGH CPGTDIRAKIRRTARFIKNYGT CPS
24850	55218	A	24988	1	1758	
24851	55219	A	24989	1773	2165	PSRGVEVNSGWNWQATNRRVI RNFDDLDQLIPTGARNATQICFI NFVTVTMTLNNCRRIVQLANQ/ DYRQPTGTAVAETHGTAEIALL ATNFNVAVFIAPLGNQRHNRVL TVWHKFRRVGVLVHVGNNMASVI N
24852	55220	A	24990	1	141	SPGKIRPVIAAAMKQIKEFMSP DSDFFRYMKTPTSATR*YNDGCG TGQ

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24853	55221	A	24991	1430	1933	PIHVCMSGLTMPDSACMAFPFPS AVRRWNSFPPTFSAHTSSPCA CYPRCYRTVKGVL**HHR*W/V LISTPGRGAYAASKYALEAWS ALRMELRHSIGIKVSLIEPGPIRT RFTDNVNQTQSDKPVENPGIAA RFTLGPEAVVDKVRHAFISEKP KMRYPVTHGDI.WR
24854	55222	A	24992	1318	4265	LAIVAFDLQNHIFSKGFWPS DKFYAAKVEEQNRQRHYHGT SYNLEPDIKSSPGGLRDIHTLQ WVARRHFGATSLDEMVGFGFL TSAERAELNECLHILWRIRFAL HLVVSRYDNRLLCVHPTLLTTL DIHGEAQIWRREVSSRYGGYPK AQAAQPDQLMSDYFFRVSLAM QNKTLFLSLDDTLVNNAQLTLN KTRPAMVDVITDGIPLVINPQ GIAKLLRNETLTLKPNLEPVFY NAAQTLLMPKLDAL
24855	55223	A	24993	1	454	MGFDDTRDRALFEDSAMSQQP TVPDRLRWLLQTFKYQKNIRI* STPRKKPMRHSIWNWGSRRRC WSNPKRTFMSISVRGNMAAIM SFHTSAVMRSHCSILTTIKSRW ATLNTLILR
24856	55224	A	24994	65	330	
24857	55225	B	24995	1	1998	
24858	55226	A	24996	1175	1877	QQVPQKGPGRAKRHLHAAGW HWHQDRCPPEKNVRQ*RRYR AVRFIII
24859	55227	B	24997	1	3117	
24860	55228	A	24998	1888	2412	ARFKHVGDDTVTHRLFRRAAQ IVRVV*RAVSHRQHFTGVDIHQ HGATRFSLVKGHRIVQFAINQR LQAFINTQRQVVRSLAVSRRI FNYATIAVFTHNALTRLPGKPFJ ETLLNALNPLTEHAARDLEDSP VRITAYIEDVDALAQAGADIIAI DGTDRPRVPVETLLARIHH
24861	55229	A	24999	1	2457	

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24862	55230	A	25000	1	3019	MAALRQSFWSQLFDRVHIGLD FFDASINRIA AWVIGTRNMKKA LLRALLEPTAELRNWKRRAITL RVWHCWKSRNRCRGRSSGKCI ANVTIRQQDHQIETVFINQRLH ERMFPFVFLFAERLSGDEDLGL KAPILEALNDLGYEKPSPQAEC IPHELLNGRDVLGMAQTGSGKT AAFSPLLLQNLDPELKAQQLVL APTRELAVQVAEAMTDFSKHM RGVNVVALYGGQRYDVQLRA LRQGPQIVVGTPGRLLD
24863	55231	A	25001	60	545	PSPFTAGASMAVERSTGVHEGE LVLETLVIDGDENT/CAGTRRSL RANA*CLFHPFRAGAELAEV WFCRYPHCGCEQNTTTEQRR TEWMVTESLADFLDPHPGKT VEGYAPKRRARNRRAEDHRQ RLRHRTRKKQTHGQRRRHRPE PAQRQPQTGTTD
24864	55232	A	25002	1410	1575	
24865	55233	A	25003	200	691	
24866	55234	A	25004	1336	2028	
24867	55235	A	25005	1	345	
24868	55236	A	25006	671	1204	RTSDKLPFCRRSRMENLARFLS TTLKQLRQQRGWSLSRLAEAT GVSKAMLGQIERNESSPTVATL WKIATGLNVFPSTFISPPQSAT/P SLFPYDPQLCFEHLAIQMASGAI SESTPHEKGVIHVVIDGQLD LCVDGEWHTLNCGEVGRFAAD VTHIYRNGGEQTVHFHSLIHYP RS
24869	55237	A	25007	2251	2466	
24870	55238	A	25008	181	626	WQNFDTCGGMDLKDLAALR FQQEALNLRAQRQEVLAANIA NADTPGYQARDIDFASLKKV MQRGRDATSVVALTMTSTQHI PAQALTPSTAEQYRIPANPSL DGNTVDMDRERTQFADNSLQY QMSLSALSGQIKGMMNVLSQ N
24871	55239	A	25009	57	278	
24872	55240	A	25010	171	532	KPVQFAIADGNNQPLALLNIHL PVMMLAIAHGPLLPAPPELLV LFDD/PLSSRVLLINAFSGGSDT AMRRAGKGAPALLPELPIITV VSPFLPQSSPRRKPIMSKRIPSAV NQRNPRQ
24873	55241	A	25011	1	648	

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24874	55242	A	25012	158	514	VLQLIKAVWQTQKPSWLHP VDSAPGLQMELPASPVPTCTP QPLGGRWDWALWSRGWRLLR RLGPHRSPRRS*GSLWPWPAQ KGAPIVQRWAKGLLKCHQSGS PGRGGAESERGL
24875	55243	A	25013	1	693	
24876	55244	A	25014	119	304	DRRRCACHKITVIPKRMITAGIRL PPQTVNI*LGNFLRALIASTAGI MTAQMVASHSPAPP
24877	55245	A	25015	361	540	
24878	55246	A	25016	191	446	AKRRLGVYDADCCSIDKTQSL ACTTRNCGAYSCKLCGKYAKP VGGIPQPLQESHVR*CCN'VMEL SPCSDFT**HPPGAVSQPQT
24879	55247	A	25017	1	2259	
24880	55248	A	25018	1	1170	
24881	55249	A	25019	3	1240	
24882	55250	A	25020	1	1259	MAGPRYPVSVQGAALVQIKRL QTFAFSVRWSDGSDTFVRRSW DEFRLQKKTLKETFPVEAGLLR RSDRVLPKLLGQASLDAPLLGR VGRTSRGLARIQLLETYSRRL ATAERVARSPTITGFFAPQPLDL EPALPPGSRVILPTPEEQPLSRA AGRLSIHSLEAQLRCLQPFCTQ DTRDRPFQAQAESLDVLLRHP SGWWLVENEDRQTAWFPAPYL EEAAPQGREGGSLGSSGPQF CASRAYESSRADELSPAGARV RVLETSDRGWWLCRYAGAGPE ELDTSARNAGALTRRREIRDA TLRLGLAYGPGGMSLREVTA WAQLHDVATLSVDVALLKRLRN AADWFGILAAQTLAVRAAVTG CTSGK/QIASCWRWNSNQCARG QR*MATTYGI*SSYLSVH*F*AN RQQR

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24883	55251	A	25021	803	2061	AKPAARGGILAAPVRDTLFLYF RLKKNQRQEGFINTYWPWKKP GIFYMCVPIKGANAQDVA AFC VTARGRQNCLESIARGPALIN NRGAARGRCNDRVVEVDHGFA VLTFNFQGVSPGEFTQTVDHFD FAAFRHTSQTTGLIDHFLFPGT NLVDIGFRFAEDDTVFSQRFGF FDNFCYVQQCFRRDTADVQAN TAKGVVTFYDYGFTYWVKV LDPGSEVVAEAGDGASIDLAH RLDIDVILLDLNMKGMSGLDTL NALRRDGVTAQHILTVSDASSD VFALIDAGAAGYLLKSDPEVL LEAIRAGAKGSKVFSERVNQYL REREMFGAEEDPFSVLTERFLAD VLHELAQGLSNKQIASVLNISE QTVKVHIRNLLRKLNVRSRVA ATILFQSAAFRSFRFRATSDNV
24884	55252	A	25022	1	1569	
24885	55253	A	25023	2151	2709	YLREASETARRQFTLPVILYNF RDLTGQDLTPETVTRLALQNE IVGIKDTIDSVGHRLTMTINTVKS VRPSFVFCGYDDHLLNTMLLG GDGAITASANFAPELSVGIYRA WREGDLATAATLNKKLLQLPA IYALETFPVSLIKYSMQCVGLPV ETCYCLPPILEASEEAKDKVHVH LTAQGILPV
24886	55254	B	25024	1	1201	

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24887	55255	A	25025	I	2209	MIGEIRDGETAEIAIKAAQTGHI. VLSTLHTNSTCETLVRLQQMG VARWMLSSALTLVIAQRLVRK LCPHCRRQQGEPIHIPDNVWPSP LPHWQAPGCVCYHGFYGRTA LFEVLPTVPVIRQLISANTDVESL ETHARQAGMRTLFENGCLAVE QGLTTFEELIRVLGMPHGDGAA MDREENELGVSCIAVPVFDIHG RVPYAVSISLSTRLKQLYAGLP VWCDGSRFFAQKARAICKQKW GYVGAKSRQRWLFYAYDRLRK TVVAHVFGERTMATLGRMLSL LSPFDVVIWMTDGWPLYESRL KGKLVISKRYTQRIERYNLNL RQHLARLGRKLSFSKSVELHD KAAGGVPVLVRELLKAGLLHE DVNTVAGFGLSRYTLEPWLNN GELDWREGAEKSLDSNVIASFE QPFSHHGGTKVLSGNLGRAVM KTSAPVVENQVIEAPAVVFESQ HDVMPAFEAGLLDRDCVVVVR HQGPKANGMPELHKLMPPLGV LLDRCFKIALVTDGRLSGASGK VPSAIHVTPAYDGGLLAKVRD GDIIRVNGQTGELTLLVDEAEL AAREPHISELSAFTFGTGRGYS AFGVKCPFRKRALSDPCYAMR EVADFLINKGVDGLFYLGTTGGE FSQMNTAQRMALAEEAVTIVD GRVPVLIGVGSPSTDEAVKLAQ HAQYAGDGIVAINPYWKVA
24888	55256	A	25026	I	3395	MSELPTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKYIPCSWLGRNIVKMAILAK VIYRFNAIPIKLPMTTFKELEKT TLKFIWNQKGAASRSNPEPKNK LEDHITNSTIYRLSTKSCSVSGL KQTLLEAESEALTSYSHRVFSAW DFGLCGDVHVRRLRQRILYELK GOVPALLLDGDTLLTEGVAIM QYLADSVPDRQLLAPVNSISRY KTIEWLNYIATELHKELKFSFH WSTTSHKGLGM

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24889	55257	A	25027	145	681	FNGATQRJFDARGKPSYIGSIQ HVNADV DQRATTLQFFIGKDT AGNAAAATQAGGGNVNLSQN AVGHLFTQLLRIERKTMVKVV GQHLAQFARGIDISRACYHMA ARFQCHQGMFVMKTVR*ADA NHIRFHCQQHGLRIVPHGCIPV FCQRLPLGKAAVTD SYQFQIRC GCSSTKH
24890	55258	A	25028	696	953	LSGLCSVRRAYPGGRSCPGVP* FVGLVARRPPGG*GSCFVLLPH QRS GTG GCL*QPPFPAGAGARK IRECIRVGRSAGHAAGGET
24891	55259	A	25029	3	506	RGKPSYIGSIQHVNADV DQRA TTLQFFIGKDTAPAGNAAATQGA GGGNVNL SQNAVGH LFTQLLR ERKTMVKVV GQHLAQFARGID ISRACYHMAARFQCHQGMFVM KTVR*ADANHIRFHCQQHGLR VPHGCIPVFFCQRLPLGKAAVT DSYQFQIRCGCSSTKH
24892	55260	A	25030	291	560	
24893	55261	A	25031	63	404	
24894	55262	A	25032	660	1073	LSHECSFWLTNQLVSPRAQTVS GELQPAYAHGVLRCRQYPSAFE KASETPQSSNPCSSYTIHPTVE NFQTCRNQHL SKGCLINAGRA GPSPTGGWGELEVA AAAARLQ GAWKRHLQSSRPPGQALFASPP *WTGSVQ
24895	55263	A	25033	272	511	GSDTALPSAIAAPLLAAMAWLP PRERGT LAH/QVLEHYQLAQLP VSA/LQ/MPLHCPPQAIAHHQQL/ EQQALASLQNWGVFHV
24896	55264	A	25034	1	3300	
24897	55265	A	25035	1117	1376	PPPIGLTYSSASPLSFLCTVRKP FSRSCW*QTN SNPISSCP ELVTP SE*L*PRRSIRLDSLAVRGFAS RIWLSAITFP SGSLA
24898	55266	A	25036	207	427	DEHLQQRKKPLFLNYGRTEQA SVK*RI SWVQNPERSSLC*GILA A*NPMSVSL*LT*HCL SARRY ELVCQPK

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24899	55267	A	25037	2012	2547	LKFARPKLWGIFRNRQYHHMLERRSQAIDAPALDRGAALGALMRLEHPNASAEAAALTMLAQLSPAQSGEALHGLLALARHQLACQPAFIAGFSSHLNQLSEADFINALPDRAAMAWLPPRERGTLAHQVLEHYQLAQLPVSAALQMPLHCPPQAIAHHQLEQQALASLQNWGVFHV
24900	55268	A	25038	1	150	DKASRGRSRQQS/CAVLQPLLVI PRQT/VVWSGPPANSSRPGEEDC*KEN
24901	55269	A	25039	1	150	DEASRGRNRQQS/CAVLQPLLVI IPRQT/VVWSGPPANSSRPAAEEEDC*KEN
24902	55270	A	25040	96	389	PCLSP*LYPSGVHKSTFIYGFYNT*PCTSQLFWQHSC*GSITSSSYFYLLPEEGTGSNLCCSAASAGDTQANRVWSGPPANSSRPAAEGHDCWKEN
24903	55271	A	25041	1181	1364	VSLGNIKFRQTGAPLQGSFQRKEQSAIFAVLQPLLVI PRQI/VVWSGTPADSSRPAAEGPDC*KEN* RVNRQPTWEKIFPIYPYDKGLISRIYKELKQIYKKKIKPPHQKVGKGYVFSKEDIYAANRHMKKCSSSLAIREMQIKTTMRYHLTPANRGIINCPFLDDAASCIDPTYS SNIFPPVNLWSGLPMKPKEVKIKRQKKEHLLKDRDFSQEPIMALRTVILEILMEKEMDNSQRECIKDILTKHLVELSILARTFKNTQLPERAIFQIKQYNSVSCGVSEWQLEEAQVFWAKKEQSLALSILKQMIKKLDASCAANNPSKLTYTECLRVCGNWLAETCLENPAVIMQTYLEKAVEVAGNYDGESSDELRNGKMKAFSLARFSDTQYQRIENYMKSSFEFNKQALLKRAKEEVGLLREHKIQTNRCPSGTKLPEEGTVSNLCCSAASTGDTQANRVWSGTPADSSRPAAEGPDC

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24904	55272	A	25042	42	963	VQEGCVRPFCRSAGVCWRST PDSVCLGITSGGCRTAKTAACS FLWKLCPRGTPARCQVECSYTR CLSLSLGGVSQAGGTRVRDPL EEEVCPAELERCAGRSVAVFR ASRQEHRLRLKLTSPPLPPGA LSQGDGFSIYKPLTGVA AFLSD ALPKRRNLERQSGYSTFEELCF QKRTWGRDAVRISDLLLDGHS HFGKCPISRLEAENMPVSEL SAAAGCSTEVNHFVFGIHWQKGK CSKYTAPSKSSVPVSSTRGHVHI TVQNPTLVFVFGKLNIDSPIGDR NIPVLTAGNCKTLGDLRSFPHN
24905	55273	A	25043	98	352	
24906	55274	A	25044	3	414	PEEALCALAELERCAGRAAALF RAERQKRLRLKLHPQPLPPG ALSQRDGSLSISP*LG/LRLSFR DALPREQFYRLFTDRSDRVEN SVTDVCHIESKMEPLRLGP/SNV SIMRPSLVCSFTTLVFISSNAQSS LVA
24907	55275	A	25045	2	1544	STTRGSPQEARQYRHNQAYVA YSIQGDGAEDDDERIVRFHTRL PVFMLPPTPRKTSWIVAPVLEV LARAIRHETEIQGIHTGTEDVPV SLFADDMIIYLDNLKDSRKL EVIRDFSKVSGYKINVHESVAL LYTNNDY AENHIKNSPTFTIGY VLAFFVVMVIAVSCVRLLYAHN CTQHTSLKHKCQAWVVTVDVA AAFMTQATREERRIAYSAPGGY FFHILEVLARTIRQEKEIQIGTG KEEVKVSFLADDMIIYLENLKD SSRKLLEVIKEFSKVSGYKINV SRGSPDTLVYKEEIVFLVPA KKSKIKVLADPLCYAATTWR MTIIAGLPVEYNDRFIRGIAVFA PWRKTPGIYHQSHDPLCYAATT WRMTIIAGLPVEYNDRFIRGIA VFAPWRKTPGIYHQSHGACLG RRSRTITVVDAPQVMDMDPT CSLFTTGQCLGEPDLLASARRL QFFSHQYSIAVLMANARGNSA\ LWDNYGGILVRADRGSLLVG

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24908	55276	A	25046	1	1228	MLQSNRTAASHSPSIQPAIQPAI QPASQLSIHNLWTQFRHSTKIPV EWWNGE WLNGRMPEDHHEWQ CNYQNVQQFIDEGNY TSGDNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTRETVDNFKHIVR GAKLLFPAIQPYPPLYFGSSD VAQELAAEQVDLYLTWGPEPE LVKDFIEQVRKAAAHGRKIRF GIRLHVIVRETND EAWQAAERL ISHLDDETIKAAQAFARTDSV GQQRMAALHNGKRDNL EISPN LWAGVGLVRGGAGTALVGDG PTVAARINEYAALGIDSFVLSG YPHLEAYRVGELLVPLLDVAI PEIPOQPLNPQGEALRKK
24909	55277	A	25047	1	1075	MTIKGEQAKKQLIAAALAQFGE YGMNATTREIAAQAGQNIAAIT YYFGSKEDLYLACAQWIADFIG EQFRPHAEAEERLFAQPPDRA AIRELILRACRNMIKLLTQDDT VNLSKFISREQLSPTAAHYLVH EQEAEHRFAMGELPDEVLEICQ RLAKLTEMLRGLAELFLNDLSE KTGSHDIVRLHRLIQMNRALG MFEAQSKLWRLASLAQSSGAP VTKWATREEREGQLHLWFHCV GIRVSDQLERLLWRSIPHIVTS ATLRSLNSFSRLQEMSGLKEKA GDRFVA/SGFP/HLTTANRAKLL FPGCALSLPSTTKSSILPKWRPF SVSRWRAKNISVCWYCLPADG RCSAFSTM
24910	55278	A	25048	530	642	LKTLW/PAVQEPVPHRYHGATV FRIMQTIFIKQICRLLL*GTAGHF VCGITACHAAEAHRLTVQPV RILDQRRPAQLHSRQVTAIRQ PLHRRQA VRDDAVCQPLLVVC VFRMLPQQFPRRLRVLHRLAFA GQAAFTVIAIVDGNTVFAFAQVA DVCQPAVAJILPLLCEFSGQVI MITLRPPVKAALLYQPVQRIVT EDAVAAVQEPVPHRYHGATVF RIMQTIFIKQICRLLL
24911	55279	A	25049	1075	1479	

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24912	55280	A	25050	2	588	RWSSLTSSRYGFCRCPEADKE CLHVKSAAAGKKATNVGHYAG WLRTYSPHLAAHRVNFFFGINA HMDQRGPGRLMISCNEACGSA CYSNHSYMRNDKHAVRRADSG RAEGGGPRVKSIVKAPVITPKK KPVVSTLKHVVLMLAWVTCSP LTVLSPDGEMFDVMEKYAFSA WKWKRLRLAISQATFHALLPE KIG
24913	55281	A	25051	912	1169	
24914	55282	B	25052	1	1665	
24915	55283	A	25053	43	302	
24916	55284	B	25054	116	1534	
24917	55285	A	25055	1	1017	NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQSAKKRDAELANG ALGIHELNDYTLKKVMKPLITS NTRETVDENGKHIHVRGAKLLF PAIQPPYPPLYFGGSSDVAQEL AAEQVDLYLTWGDPA DLVNEI VEQVRAKAAAHGRKIRFGIRLH VIVRETND EAWQAAERLISHLD DETIAKAQAAFARTDSVGQQR MAALHNGKRDNL EISPNLWAG VGLVRGGAGTALVGDGPTVAA RINEYAALGIDSVL SGYPHLEE AYRVGELLVPLLDVAIP/EIPQP QPLNPQGEALRKK

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24918	55286	A	25056	1	2677	MVLNRLLTGLFFGSTPPRCHYD LIGADPDRITRSVRLYWRHSLN ELISMLPKFNKELTRKLFKLQE MLPFLNLHMSPERMLQRMDSE KVVTFTTALMTGLSGAMASVL LLVMTVVFMLEFVRHVYPYKMR FALNNPQIHIAGLHRAIKGVSH YLALKTLLSLWTGVIVWLGLEL MGVQFALMWAVLAFLLNYVP NIGAVISAVPPMIQVLLFNGVY ECILVGALFLVHVHVMIGNILEPR MMGHRLGMSTMVDGVRVLKD GTDLNQTGSFYLAARPYAEKN GAFIQGVLATFSEADALTRSQR EQSIALLAKTMGLPAPVIASLLE ISQPVSNHPITRLTAEEAALQQ QTADLFYENRLVPPKVDIRQRI WQPTIRLEGKQFMSLNMFWFLP THGDGHYLGTEGSRPVDHGY LQQIAQAADRLGYTGVLPTGR SCEDAWLVAASMIPVTQRLKF LVALRPSVTSPTVAARQAATLD RLSNGRALFNLVTGSDPQELAG DGVFLDHSERYEASAEFTQVW RRLQLRETVDENGKIHVRGA KLLFPAIQQYPALYFGGSSDV AQELAAEQVDLYLTWGEPEL VKEKIEQVRAKAAAHGRKIRFG IRLHVIVRETNDQWQAAERFV LSGYPHLEEA/YRVGELLFPLLD VAIPE/IPQPQLNPQGEAVAND LSPRTVAASGDQLLAGAVGFS
24919	55287	A	25057	114	372	
24920	55288	A	25058	2270	2760	TSPISQIRQYSIA/VGSTGNLGL SIGIMSARIGFKVTVMHMSADAR AWKAKALRSHGVTVVYEYEQD YGVAVEEGRKAAQSDPNCFID DENSRTLFLGYSV/AGQRLKAQ FAQQGRIVDADNPLFVYLPCEV GGGPGGVAFGLKLAFGDHVHC FFAEPHTSPCMLL
24921	55289	B	25059	1	2460	
24922	55290	A	25060	1	993	

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24923	55291	A	25061	332	1349	ILYDSDIYRFSCRSGGHIPAVIY HLSAKRRTMENAKMNSLIAQY PLVKDLVALKETT/WGFIPATL HGKGLPYVGLTEQDVQDAH/ ARLSRFAPYLAKAFPGKWLP TG GHIESLGA/LPAMQKRLAEKEY QQPISGQLLLKKDSHLPISGSIK ARGGIYEVLAHAEKLALAEAGLL TLDDDYSKLLSPEFKQFFSQYSI AVGSTGNLGLSIGMSARIGFKV TVHMSADARAWKKAALRSHG VTVVEYEQDYGVAVEEGRKAA QSDPNCFFIDDENSRTLFLGYSV AGQRLKLAQFAQQGRIVDADNP LFVYLP CGVGGGPGGVAFLGK LAFGDRVHGLQA
24924	55292	A	25062	284	1494	RLSLPDMFPPVQQFPVSLHRAF YRYDKSAYYALRIAGIASRLNP RRFSPSILTPERRCVVTLRNDIR RDVLRHNQPRSTASTRQARRR MKSSCWHMPTTSKPQALSHTS NSPTTSSIRPNWSYSNVCNRSRT MANLSGYNFAYLDEQTKRMIR RAILKAVAIPGYQVPFGGREMP MPYGIWGTGGIQLTASVIGESD VLKVIDQGADDTTNAVSI RNFF KRVTVGNTTERTDDATVIQTRH RIPETPLTEDQHIFQVPIPEPLRFI EPRETETRTMHALLEEYGV MQV KLYEDIARFGHIATTYAYPVKV NGRYVMDPSPIPKFDNPKMDM MPALQLFGAGREKRIYAVPPFT RVESLDFDDHPFTVQQWDEPC AICGSTHSYLDDEVVLLDAGNR MFVCSDTDY
24925	55293	A	25063	1	333	

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24926	55294	A	25064	1368	2451	PAHAAPGGGC/VRSALACRFLWN MRVTGKSYSTLRRVLSAIWNW RMMRCALTRALVAFRVR/SSVP LAAVLAIFYARENGAGTMFEPE AAYDEDTSIMNDEEASADNET VMSVIDGDKPDHDDDDTHPDDE PPQPPRGGRPGLRGLTLRWFSV AAQRSDILDVATLSLKVAAALAT LIALVLGTAAAAALWRRDFFG KNAISLLLLLPALPGIVTGLALL TAFKTINLEPGFFITVVGHA/TFC VVVVFNNVIAFRRTSWSLVEA SMDLGANGWQTFRYVVLPLNS SALLAGGMLAFALS/FDEIIVTTF TAGHERTLPLWLLNQLGRPRD VPVTNVVALLVMLVTTLPI/LGA WWLTAKATYLEKLKV
24927	55295	A	25065	1	2072	MSEQLTDQVLVERVQKGDQKA FNLLVVRYQHVASLVSRYVP SGDVPDVVQEAFLKAYRELTPR RPYLLRAFYEWLLDNQLTPHL VVDVTLPGVQVPMFYARDGQI VLNIAPRAVGNLELANDEVRFN ARFGGIPRQVSVPAAVLAIFYA RENGAGTMFEPEAA/YDEDTSI MNDEEASADNETVMSVIDGDK PDHDDDDTHPDDEPPQPPRGGRP ALRVNVNIVAIIFTTKPTAMGIA VRFTTAKGETPAIPDVTTTTAVI GETARASVVAKCIGIITTA/VPV VKPFANISPATTSVPRFFGLPAS SSHTLIGAIIGLNTNALLTGSSV MDALNLREVTKIFSSLI/SPVIG LVIAAGLIFLLRRYWSGTTKRD RIHRIPEDRKKKKGKRKPPFWT RIALIVSAAAGVAFSHGANDGQK GIGLVMLVLVGIAPAGFVVNM NASGYEITRTRDAVTNFAARES EASVIRHSNRFIETNGGRRCSR GITLTLHKL/SAQPLLA/VLNR LEQKKPVGLRYPDQAQSLVCLP TQTRTGWNLNGFEVGFRCV LMIYGRSLEAQATASLAAATG YDSHIFDLFPASASQIDTDTAV ILLCHDLNRELPLVLAAREAKP FYLALGSYRTHTLRLQKLHEL GWSVRQETTQIRAPVGIFPKARD AHTLALSVLAEVASVRLHQEE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
24928	55296	A	25066	2	332	AGYSTRALAIIVNKPSSAIPPT SGLASRKRNPA SNDFNGCSRGCGGGNAGRLNNGSKRSASTPP TIRPTNIA PPAASPKAPPARWN VSSGSAPAPRRRANPETQLR
24929	55297	A	25067	1	3192	MNKKFKYKKSLLAAILSATLLA GCDGGGSGSSDTPPVDSGTGS LPEVKPDPPTNPEPTPEPTDPE PTPEPIDPEPTPE/PEPTPEPTD PEPTPEPIDPEPNQNGAELSYN TEKTLTIRDSVFITYTENADGTIS LQDSNGRKATINLWQIDEANNT VALEGVSADGATKWQYNIING ELVITGDNATVNNNGKTTVDG KDSTGTEINGNNGKVIQDGDLD VSGGGHGDITGDSATVDNKG MTVTDPEM
24930	55298	A	25068	1078	1317	
24931	55299	A	25069	135	361	SCSMLAGLCG*GSSSSVSITTCF ALSASTIA*PREPQALPV*PLA LPNSSQDGTMPKATSIFFSSPLCT RCTRPP
24932	55300	A	25070	469	841	RWWKQYAAAGFQCMCATAVS NLTRPVAA*TAAPESKSPVLPN SPASTVRRS*PVSTMPIRPGDG DHDPRFKAPSGTPHQPPRAGHS LRRHG*TENCTAA*GQLRTPG DNGTVMSADTITFP
24933	55301	B	25071	1	2922	
24934	55302	A	25072	1	3849	
24935	55303	A	25073	1	2280	
24936	55304	A	25074	672	1045	GAVLSINCRTLSAASGENVA TPP/VTSNNNTPIINKPKPLALAE ATGVIIAPKPPSSAAPMASPVTF CAVHKPLIRPNIASGVCVCSIVY CSNELTALNQPN SARQTTPKIH GIRPNRPMARN
24937	55305	A	25075	650	1465	RKPCAADICQLSASAGYSTRT ALAI VSGLASRKRNPA SNDFNG CSRGCGGGNAGRLNNGSKVI NVPAAASP*FQATPPVASNKPP MGEITDPRRTVNMVIA PACIKF SRPTSAGVAANS AVTPSDAKKP SHKPSK*IASNDGSGSSALRHSP MKPMPPQVPRASKITFLRS*RSA STPTTIRPTNIA PPSVSVTESPTCQ VECVI IWICTGTATPSKPRDTIE MKRARNTARNAGCVSAGSSGS SAEVGSSNSKTS GSIASARA IET RCC

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24938	55306	A	25076	156	3092	LNRRWIANIAKLEAEQARKLK KTEKDSLKDEVLHSLLPRAFSR FSQTMMWIDTVNGLIMVDCAS AKKAEDTLAVLRKSLGSLPVVP LSMENPIELTLTEWVRSGSAAQ GFQLLDEAEKSLLEDGGVIRA KKQDLTSEEITNHIEAGKVVTK LALDWQQRQIFVMCDDGSLKR LKFCDELDRQNEIDREDFAQR FDADFILMTGELAAALQNLEGL GGEAQHSGTGSLEPVKPDPTPN PEPTPEPTPDPEPTP
24939	55307	B	25077	61	2118	
24940	55308	A	25078	132	280	RRRAALPERSGPGLDHRRVRH/ GCHVLPVPTLVKRRKVSVD AQWKSSV
24941	55309	A	25079	1	1449	
24942	55310	B	25080	110	550	
24943	55311	A	25081	657	805	RRRAALPERSGPGLDHRRVRH/ GCHVLPVPTLVKRRKVSVD AQWKSSV
24944	55312	A	25082	756	938	
24945	55313	A	25083	781	1257	
24946	55314	B	25084	1	2727	
24947	55315	A	25085	1	2286	
24948	55316	A	25086	1161	2024	VRSVAVWPCLOQDPDCHHNRCG TGGTSRPGPARNPRIEPTCVG\ RJRNLGVLLYDADAMERAAS ENEKDLYQRQLDVFLDPNDPK VIEQAIKDGIPLSVIEAAQQSPV YKMAMEWKALPLHPEYRTLP MVWYVPPLSPIQSAADAGELGS NGILPDVESLRIPVQYLANLLTA GDTKPVLRAKRLAMRHYK RAETVDGKVDTRALEEVGLTE AQAQEMYRYLAIANYEDRFVV PSSHRELAREAFPEKNGCGLPF GDGCHGSDTKFNLNFSRRIDAI DKTEPHF
24949	55317	A	25087	664	1065	VAPEPHHGKQLCREGLGVFH PTHHTHHLGVLSLLITIFDAQS VHGPDDGCGQLDSVAVDNRLV LFHVFSGEAFMDDDLHLLHNGA FS*FSSPEQE*F/PRLWRR*CHPL *GFSQSPCSARGRLSPLRSEYIP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
24950	55318	A	25088	434	1663	PAGAFDPDIANDFGEKSLMPGG AVINGDFNNVLPVDLVDPQQV QEFVDHAWYRYPNDQVGRHPF DGITDPWYNPGDVKGSDTNIQ QLNEQERYSWIKAPRWGRNAM EVGPLARTLIAHYHKGDAATVES VDRMMSALNPLSGIQSTLGR LCRAHEAQWAADAIENNYSRN PSQGYSTVPRSPHPKVDPIITKP SGPAGPEMTRKQTQREDRPRSR PSMTTSPTSNLKPSVPAFKGVG YLDSDLRIGAADYQPTQDILR TRVKTGIVETHFTFKNLHFT EQASVHACYCRFLDFVEGQRSE RKKWIHCEDVTAIIFCVALS YDQVLHEDETTVLSTRIVDGH YSDHSTIACPAFGTYTLLLEKEL ALSCSTLLHIPHQRSFAGSFLAD NLNCTQAAVIPEFGGF
24951	55319	A	25089	1	1247	MTFGGDQIFESLVYRSFRHVV SRGSPWYLHTNSDLSPVESKKE LIAEHILETFPWNLKGLTEIPWG DASGESGAVGLVLA AVHYHP QRQSLMEKLALNKDAVVLVIS TEGDDQVIERLESDAVLYRGI EDVVTNLDVLERMQPSESLLRA VLHTKHLMNPEVLAAARRIVC QVVEIMARLAKEVRQAFSGV RDRRRRSFIPLARNFDFKSTLRA NLQHWHPQHGLYIESPRFNSR IKRQSEQWQLVLLVDQSGSMV DSVIHSAVMAACLWQLPGIRT HLVAFDTSVVDLTADVADPVE LLMKVQLGGGTNIASAGEYGR QLIEQPAKSVIILVSDFYEGGSS LLTHQVKCKVQSGIKVLGLGA LDSTATPCYDRDQAQALGNVG AQIAALMPGELGSLAWENLLA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hnd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
24952	55320	A	25090	1	1691	MGAYLIRLLLLVIPTLWAIITNF FIVQIAPGGPVDQIAAIEFGNA GVLPGAGGEGVRASHAQTGVG NISDSNYRGGRLDPEVIAEITH RYGFDKPIHERYFKMLWDYIRF DFGDSLFRSASVLTLIKDSL PVS ITLGLCWYFVCRCACVVTHA.SL WQSASIEVPRTSATAKARKTEP GRQTKRKVRSSQTVAAARQRIAT LPHSMTVCNPGLFHSQMADAL AHRYYGFNIAEPWDNGSEAML QRDIGLKSESRLMAGKRCSC KGECGWSLDMQARVSTCFYVR LTCGTELEDHRICIIDTCNCKG PQRRYVIKFRELCLVNSTVTLV DQYELTVTDELYDGSSQALA GISDLSSYATCDPGYCTDRVT LVDVRKRQSKTGPYKEIGRYGI DRNRSPNPNPGRGKPDLMPSQC IACGACACACAPANALTIQTDDQ QNSRTWQLYMGRCIY/CDGRCE EVCPTRAIQLTNNFVLVTNKA DLYTRATFHLQRCRCRPFAP QKTIALAAELLAQQNQAPQNR EMLWAQASVCPCKQRA TLIN DDTDVLLVAKEQL
24953	55321	A	25091	1	866	

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24954	55322	A	25092	338	2388	CVQEPLITVSWRLFAIPAGMKF SLFLRCLFCFHLAARYLVLLCQ LH/SQGIKVLDFTVQSGPSCQ MLAWFGADVIKIERPGVGDVT RHQLRDPIDIDALYFTMLNSNK RSIELNTKTAEGKEVMEKLIRE ADILVENFHPGAIDHMGFTWEH IQEINPRLIFGSIKGFDECSPLYV VKAYENVAQAAGGAATTGF WDGPPLVSAAALGDSNTGMHL LIGLLAALLHRELNMTVAEIVE REEWAGFRARETAALAEAVTAP STVIATGGGIILTEFNHRHFMQNN GIVVYLCAPIVSLVEDFRQRTME VLRLAFLSSGILEFFTSLSIALVA VYFGFSYLGELDFGHYDTGVTL AAGFLALILAPEFFQPLRDLGTF YHAKAQAVGAADSLKTFMETP LAHPQRGEAELASTDPVTIEAE ELFITSPEGKTLAPLNFTLPAG QRAVLVGRSGSGSRYPYINHR NVRLGPVITDVPWENSGDKSLP EATAQVISSSGGATKVEDGLGD LNKPVSNQNLVTGIDTPVYNAP SAGSAPFVGLADNMRYPIHLHL KDRLNQTYWYQIRIGDRLAYISA LDAQPDNGLSVLTYHHILRDEE NTRFRHTSTTSVRAFNNQMA WLRDRGYATLSMVQLEGYVK NKINLPARAVVITFDDGLKSVS RYAYPVLKQYGMKATAFIVTT
24955	55323	A	25093	1810	2399	STFRNSDDEPYIVRPVAVAWRD YVPQPARNLNSFTNGNLEEPV MVNYFLQGDYQGMVHFTRF HQHPSGLS*WVAGNIFQILCAN QPVRKRTRDNVQLLHSRQQRG VFRCSRRVL.TGLVDRFGRQT HREAAGEFSGEITGVTDGAWR HFRLVLTQAQRAEEARQQAIS GGTEPSAFPDLPVDTEYVMNF
24956	55324	A	25094	1	577	MPVSTAVATVIKTKQVEFLQ VGVPVLYFLRANPIKTLDNQK RLDSKGNIKRCRVPLIKAEQIA WLQRKLGNAAARVEDVHPISER PQYFSGDGKSGKIQTVCFEVIG CREEPDAEECHGDREQRRVFIR EDGFFVTKLDLYPNRRA/GHISTT AVISPSQPPHAPRVAQSSEPRSA AHALARAIQSTTV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
24957	55325	A	25095	51	407	TCPIRAQRVETLYDRAYREVFG WNPGRPTGRPNARHTG*SKEG GRTEADETDAADSGQRGMEQR SEMDRKP GTTGQRSEKPRRTL ECLALHETRIFLPQRKETHSSDA HDMGPPML
24958	55326	A	25096	3047	4131	AHSGQMYMPLSSCIRSCILGSV VMTGFPQKSAGQKROKTADC RKRPLQYTKSLSL/AVKAILAK GYDPVKWRKKDKVLDV LKE LESGKYSDGDKHAFDQMLHSI GKQGGDPYLVMA DFAAYVEA QKQVDVLYRDQEA WTRAAILN TARCGSSMESKRLDNAALAGI SPNYINAHGKPOSIAETKRRL DAMIHQRTATKVAVTPVPNV VYTSGKKMPMVVEGSGEYSW LLTTEEGTQYKGHVTGGKAFN LPTKLPEGYHTLTLTQDDQRAH CRVIVAPKRCYEPQALLNKP WGCYQLYTLRSEKNWGIGDF GDLKAMLV DVAKRGGSFGLN PIHALYPAJRRAPAHTARLLAV
24959	55327	A	25097	524	697	AANWWWKSRRNR*KMTAM LDRIISHIIRTVRMSGSVAVTRA AVPGLLLLLLIATA
24960	55328	A	25098	1	1938	
24961	55329	A	25099	33	226	

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24962	55330	A	25100	1	2314	MDRAGDGPRIPLSGPTDVYGD VYL RDPGNHGGKT TNGPLRFPV LLPFGQQVFPRTVPNFVNVPSS AALPARYMQTIENA AVWAQIG DKMVTVGNI RAGQII AVEPTAA SYAFNCGFGKAFIDKGHLEPV QGRQKVEDGLGDLYKPLSNQN LVTWKDTPVYNAPSAGSAPFG VLADNLRYPI LHKLDRLNQT WYQIRIGDRLAYISALDAQPDN GLSVLTYHHILRDEENTFRFHT STTTSVRAFNQMAWARVDRG YATLSMVQLEGYVKNKINNRA TEREELRVSKITVILGVIAIILG VLFENQIAFMVGLAFAIAASC NFPILLSMYWSKLTTRGAMMG GWLGLITAVVLMILGPTIVVQI LGHEKAIFPYEYPALFSITVAF GIWFFSATDNSAEGAHLRPIRR KKVYRFNYLRSDGPYQGWVSE RLILRAISPGSKLVHFPFLFDS LYRTL VKAGEKSGLLAPVLEKL ADYNENRQKIRSKLIQSLIYPC MLTTVAIGVVI LLTAVVPKITE QFVHMKQLPLSTRILLGLSDT LQRTGPTLLATVFIVAVGFWL WLKRGNNRRHFHALLRVALI GPLICAINSARYLRTLILQSSG VPLLDGMNLSTESLNNLEIRQR LANAAENVROGNSIHLSE/QT/ AIFPPMMLYMVASGEKSGQLG TLMGAQSHWECA TVNAASRIR
24963	55331	A	25101	20	825	GFPRSRSCYASCTACRTHYTA EK/QLTRALAKLARATSNEKLS QAFHAHLEETHGQIERIDQVVE SESNLKIKRMKCVAMEGLIEEA NEVIESTEKNEVRDAAALIAAAQ KVEHYEIASYGTALAEQLGY RKA AKLLKETLEEEKATDIKLT DLAINNSFYKEDIFMNRIEHYH DWLRDAHAMEKQAESMLESM ASRIDNYP ELRARI EQHLSETKN QIVQLETILDRNDISRSVIKDSM SKMAALGQSTADTTKNSTHRQ SNTRQGN
24964	55332	A	25102	2	269	GIIGLHLQQQEAVAVAIVRGAT RMLFATLVAAVAGERHYQRW ADC*CAAAG*NVVTVESRTAA ASSHYVGVSRSQSHITAVISAPV DVPW

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24965	55333	A	25103	607	727	RQAVYRG**TAGQRANLLLLR RHSACALAAAGESQSSCPAG
24966	55334	A	25104	465	574	
24967	55335	A	25105	3	636	AHTSGFGDKSEKVSPOKRLHA MSRTFFWENL RCHGNLGSPTY AFQISAIDRVNFALV VGLHLRH DYRNEKLGRSGRHYQAPVGNR SSADGMHRDPCQLDICCILLG AGSIYGLYRIEQLPDVATLK DVRLQIPMQIYSADGELIAQYG EKRRJPVTDGPVMWFPFMIITTC VKGNFALNNQFREDMLNNTYE GIYGNVNFENNKQT
24968	55336	A	25106	434	1205	
24969	55337	A	25107	368	532	
24970	55338	A	25108	722	934	
24971	55339	A	25109	82	420	ARADPHRAHTAGVNGVNARLR IFNADTCLRRHAQPTGGEKDF RVRFVFKLGSIRAEGEKLAQL QRR*NRRRIQDRSQPNRD/RA VPEDLPSEKMPGRTALT VNSR SEWT
24972	55340	A	25110	618	788	WYPCCRNWRYLAGGDSQFCR GERA*R*IASQSGVT*AVATVV FPSVLAGLRITGHS
24973	55341	A	25111	186	1198	QKTAVSTITALTRWGS/SRA/G KRGAVLRSRVTRGKYHYPPSSW RETSSSVQNAPLMRQIKEVFLAI RIEQLLTKEILELYLNKIYLG RAYGVGAAAQVYFGKTVDQL TLNEMAVIAGLPKAPSTFNPLY SMDRAVARRNVLSRMLDEG YITQQQFDQTRTEAINANYHAP EIAFSAPYLSEMVREMYNRY GESAYEDGYRIYTTITRKVQQA AQQA VRNNVLDYDMRHAIAA RHYVLWKPTANIRARYKAQGI ELPAVVPAGDPNPMGHHAIRL AAYGGVYLLHGTNADFGIGMR VSSGCIRLRDDDIKTLFSQVTPG TKVNIINTPIKVSAPEN

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24974	55342	A	25112	1087	3289	RLRSCGAQKNTPCNAAGCRW RTTL SKMGGLLIAADLQDPVQ DMEMWQHPTGIAC/AGVLT E/GCRGEGGYLLNKHGERFMER YAPNAKDLAGR DVVARSIMIEI REGRGCDGPWGPHAKL KLDHL GKEVLESRLPGILELSRTFAHVD PVKEPIPIPTCHYMMGGIPTKV TGQALTVNEKGEDVVVPGLFA VGEIACVSVHGANRLGGNSLL DLVVFGSARQVLHLQESIAEQG ALRDASESDVEASLDRLNRWN NNRNGEDPVAIRKALQECMQH NFSVFREGDAMAKGLEQLKVI RERLKNARLDATSEFNTRQVE CLELHNL METAYATAVYATFR TERRGAHSR/FDPPDRDDENWL CHSLYLPESESMTRRS DYTLEA DEGRDMMLLDALIQLKEKDPS LSFRRS CREGVCSDGLNMNG KNGLACITPISALNQP GK KIVIR PLPGLPVIRDLV VDMGQFYAQ YEKIKPYLLNNGQNPAREHLQ MPEQREKLDGLYECILCAC CST SCPSFWWNPDKFIGPGSLLAGY RSLGIAGIPKCSARYLSGEKRSV AWQQIAAEIGISIDAQFNESLKG ISRDESLRRILQHGKGEDFNSQ ERAQLAYRKNLLYVHSLRELT VNAVLPGIRSLADLRAQQISV GLASVSLNAPTILAALREFFT FCADASQLKNSKPGPGIFLAGC
24975	55343	A	25113	47	630	VGWETSFAQIRSRFLRIRFCRAY SSTL FVSAANPTT*G/QMV F*CG NGAQHKNILLYRSIHGGFHQ RGHHINTFNKRWR**NRT*YQ RDVRATTGSGGDRKTHLAGA VIRDITHRIERFTRRAGGNHNV QMFQVVDGRKCATAISTVLDM FGDHFGRQKIASQRWLAKTIR TVQQPICKNIVRKPGCHSLA
24976	55344	A	25114	731	829	

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24977	55345	A	25115	2	3744	RLPFKYPVKVKPLPAFPSKILLN SPAIPQLPITMNGSDFSLPEGPM NRWENIQLTPETRLAPRAYFFS YDSVAQARTFARETSSLFLPLS GQWNHFFDHPLQVPEAFTSE LMADWGHITVPAMWQMEGHG KLQYTDGEGFPIDVPFVPSDNP TGAYQRIFTLSDGWQGGKQTLIK FDGVETYFEVYVNGQYVGFSSK GSRLTAEFDISAMVKTGDNLLC VRVMQWADSTYEKDDQDMW.W SAGIFRDVYLVGKHLT
24978	55346	A	25116	1	2643	
24979	55347	A	25117	2499	2935	RSGGVACNCAVSASCMVLVTVL PWL.SL.PV/SVFGLDGFFASLG VTALLAATPAW*GVKT*CRPG RSP/SLTVRLGSVISP MIGGLLA TGGVALLPLLSLALPPPQPRE HPLKSLLAGFRLLASPLVGGIA LLGGLLTMAAVRV
24980	55348	A	25118	676	1035	
24981	55349	A	25119	1	1842	
24982	55350	A	25120	1	1341	
24983	55351	A	25121	563	1360	PSVLRCRNWVI*SPYCISLPSRV SSLPFLVWIPVAR/CTAIGASRE AMLGVLVEPMLLLGLWVAAQ VAGSTNISNITDTVYHWP LSQSI PLVLALCACAFATFIEMGKLPLF DLAEAEQELQEGPLSEYSGSGF GVMKWGSLKQLVVLQMFVG VFIPWGQMETTAGGLLALVI AIVKLVVGVVLIALFENS MARL RLDITPRDMIRIELDSWEQNGE AIKRTGQPLLLSLVRNLLDNA VRYSPQGSVVDVTLNADNFVR
24984	55352	A	25122	382	1424	VLENLEPPNQHDIEILTVQR KEEETALSCLVLRLKLTETEPVI IFEGIEAPATLPADVEVPVGKDEN DNVEVSRWGT/PREFDFEVRDH VTLGEMHSGLDFAAAVKLTGS RFVVMKGQIARMHRALSQFML DLHTEQHGYSENYVPYLVNQD TLYGTGQLPKFAGDLFHTRPRH ECFRHIGSLGLATPLVTECMQW LFGIPH TLQLDIIITCWIILNAIC VACGLQKGVRIASDVRSYLSFL MLGWVVFVVGASFIMNYFTDS VGMLLMYLPRMLFYTDPIAKG GFPQGWTVFYWAWVVIYA IQ MSIFLARISRGRTVRELCFGMV QEFGCKSSSTKIDNADNFQA

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24985	55353	A	25123	416	610	
24986	55354	A	25124	662	811	AQQLPGMSDWQNSQEQHQMK N*VRLFMRTSRKLMRLNVLIK LWSPNRT
24987	55355	B	25125	1	3264	
24988	55356	A	25126	489	3256	PRVFSSATRSVLAMRRWVYRV RRIQYRRTTQTAVFHSTHGNYS EGQPVGTLDIDRYKANENVEL VHYAQPLLNEADSLAKVMPSDI PLKQRRWGLQMLEGDIYSRA YAGEASQHLDAALARLRNEMD DPALHIADARYQCAIACDVVS NTLTAEPSRFTTAVDKIVLNRFL GLPIFLFVMYLMFLAINIGGAL QPLFDVGSVALFVHGIQWIGYT LHFPDWLTIFLAQGLGGGINTV LPLVPQIGMMYLF
24989	55357	A	25127	779	910	
24990	55358	A	25128	2203	2665	ACWARISAAVIQRSGMPGVRV CGRIKSCSKAVRCQRHVFATCV WNGRQVTSAGTWSTIAWYSG VMSSAISWSRPAIPFSAEA* ^T IG KSSC ^Y VGRVEVNEQIEYLHNP IRTRARAVNFVDNNRLQAVS KRFFGYEARLRHRAKVCNVHQ QH
24991	55359	A	25129	241	918	
24992	55360	A	25130	2142	2646	KGVC GTTNPAKITQAILQAFHEI FGE GSCHIASVAVESGVPEQPF GSEETRAGARNRVANARLLP EADFWVAIEAGIDGSTFSWVV IENASQRGEARSATLPLPAVILE KVREGEALGPVMSRYTGIDEIG RKEGAIGVFTAGKLTRASYVH QAVILALSPFHNAVY

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24993	55361	A	25131	473	1765	KAWLMTGIVRHWKGRAVPPA EQLLEHLGNGKSFDSVAQAWD AAMADAKAEDTVLWGVFAFRI NAAVAKDDTQIHTMCYCEFT DIMDSIAALDADVITIETSRSDM ELLESFEEFDYPNEIGPGVYDIH SPNVPSVEWIEALLKKAARIP AERLWVNPDCGLKTRGWPETR AALANMVQAAQNLRRGARAG CAADFAASARLAVGEALTNIA ATQIGDIKRIKLSANWMAAAG HPGEDAGLYEAVKAVGEELCP ALGLTIPVGKDSMSMKTRWQE GNEEREMTSPLSLVISAFARVE DVRHTITPQLSTEDNALLIDL KGNNALGATALAQVYRQLGD KPADVRDVAQLKGFYDAIQAL VAQRKLLAYHRSDDGGLLVT AEMAVLSSLGGQGGYFGHMII/D SQQYPGKSKTGQSTPDVAAQA RQSWIP
24994	55362	A	25132	602	2563	VVTTLTLVLTAVGSVLLFLV MKARMHAFALMVVSMGAGL FSGMPLDKIAATMEKGMGGTL GFLAVVVALGAMFGEILHETG AVDQIAVKMLKSFSGHSAHYA IGLAGLVCALPLFFEVAIVLLIS VAFSMARHTGTNLVKLVPLFA GVAAAAAFLVPGPAPMLLASQ MNADFGWMILIGLCAIIPGMII AGPLWGNFISRYVELHIPDDISE PHLGEGKMPSGFSLSLILLPLV LVGLKTIAARFVPEGSTAYEWF EFIGHPTAILVACLVAIYGLAM RQGMPKDKVMEICGHAIQPA GIILLVIGAGGVFKQVLVDSGV GPALGEALTGMGLPIATCFVL AAAVRIIQGSATVACLTAVGLV MPVIEQLNYSKRRGFTGRVEEN FGVCKGPSKYHSQHDAINRQG REASDAHGTLENLPLVPQPN AATALAALRASGLEVSNAIRD GASAILPGRFQIVSESPRVFDV AHNPHAAEYLTGRMKALPKNG RVLAVIGMLHDKDIAGTLAWL KSVVDDWYCAPLEGPRGATAE QLLEHLGNGKSFDSVAQAWDA AMADAKAEDTVLWGSFHTVA HVMIVIDARRSGGKLCQMHVN VQDKIDEENQVHICLCLVLVIV SGCKYVGYSCLKSEHYSLVR

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24995	55363	A	25133	518	1079	TQKETNKRCSPLVGWYPAFRM AHFLASERSCYQKLSNRKSH AVAGMVSGMTVANLL/EHSAG NVFKSGI*LALHLFIDRCF*YCG DGIGLFLGARYSRRGERKSART ISLFAQPGPVVNFRRHIDVWQRR CVCLVQLRKAIDVYFRFFGNG DDLYYDVSWARDGAGKYAKW QDFRTLFTTAHCSSD
24996	55364	A	25134	322	798	AQRAHVVGTVGKFDEDDADIL HHRHNLAKVFGRLFLIAELE FIKFRHPLYQLGDAFTKKLFHIL ILVVGGSIFNHVMQRRRHQRFI VEFHLGQNAGNATGCVI*GSPL ERVCP*ASRATRYACRRRLIW SIARPAKVSAACSAIATSK*RS KGQRVLLGNCHVEVAIREFT
24997	55365	A	25135	440	906	CGFSSRLPHSSYSAHHA VAPS VLMASGRPRWSQWYRWIFRA GVYTGSIWFFICSTVRPHDASQ RRLSSLT/QVSQDFTFQPVNHQL WAGGKPTAGITVGKQ*W*PFIK FTVPGDDSGDGRGQFLQIAAG KCRAQTFFSFCRAGKHDPCCRRT VS
24998	55366	A	25136	1059	1541	TAPLLRPGCRLS*SAHPAAPA QSTNQCPGDRYAATLPAHHRH TNHG*IADVHQHISATPASAAS YAPGFLKDGAPASERHRETGC GRDRPH*PSLYKLSGILRPYQPA SFPG*QQRALVSAR*LLPVQCSL HSQRCRRRPHRLHRSAPAPGIR ERRSR

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24999	55367	A	25137	236	2211	QGALMSEDIFDAHVAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLLYAHSLHIIPG FADSAVERLITHEKLAEMTEK SAMTMDYCNGDETPSPQRSYS VLRSKFDAWLMEQAEAEAGAQL ITGIRVDNLVQRDGKVVGV DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVAVGVKELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNT LSLGLVCGLHHLDAAKSSVPQ MLEDKQHPAVVAPLIAGGKLV EYSAHVPEAGINMLPELVGDL HERSLIFVASGPAGNSKETASD KLEELPTKNWEVPGANWNT NGGIPSPVEKLKGMLAPNYRR MVLPAQLQLLLQNAKGGELLG AAGGQIAFNLGSVAVGAYCGGM MLTLGLAYNYVALPAALLSFA AMSSLLLYGRYKRQQAADTPV LAKPLQLDNAPFRCEVNLIR EEIGFNALDKFKRTTGALLQLQ QALHPALGADLCGSTGFAVLFI SPVRGNTHLRHLVHIFGTDLDL NRHSVRADHRGVORLLAVRFW NGDIVFHAARTLVQAVHLAQ HAITGVRIIDHAEVSDVHDRV KTLLEHFFAVNRKMLLPTTD AARYSRFLQTPDFRKNLLDHL
25000	55368	A	25138	1	1932	

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25001	55369	A	25139	1	1200	MAIPAFGLGTFRLKDDVVISSVI TALELGYRAIDTAQIYDNEAAV GQAIAESGVPRHELYITTKIWIE NLSKDKLIPSLKESLQKLR TDY VDLTLIHWPSPNDEVSVVEEFMQ ALLEAKKQGLTREIGISNFTIPL MEKAIAAVGAENIATNQIELSP YLQNRKVVAWAKQHGIHITSY MTLAYGKALKDEGIARIAAKH NATPAQVILAWAMGGGPVEW RR*QIWRGFSSAS*RHELYITTK IWENLSKDKLIPSLKESLQKLR TDYVDLTLIHWPSPNDEVSVVEE FMQALLEAKKQGLTREIGISNF TIPLMEKAIAAVGAENIATNQIE LSPYLQNRKVVAWAKQHGIHI TSYMTLAYGKALKDEGIARIAA KH NATPAQVILAWAMGGGPVE MAKVADMAGIFVSKLKTFNAG VKGSTLGASGPQYVMVPKKHA DQLRESLASGEIAAVQSTLVAD NTPLNSRYVTVRSGLTSSIASR LGVSTKDLQQWNKLRGSKLKP GQSLTIGAGSSAQLANNSDSIT YRVKKGDSLSSIAKRHGVNIKD VMRWNSDTANLQPGDKLTLFV KNNNMPDS
25002	55370	A	25140	2237	2404	
25003	55371	A	25141	307	642	
25004	55372	A	25142	1449	2084	NAPRCAYYVDVIAVTMPTTCC TLKISPLCRELILTLANRTTTQR AEPMTRRLIQVLFDELPPQPPQ QLHLVPVSSHPIRTMVEMMAK GPVEWGALQGWAGFFAMSER NLARLIVKETGLSFRQWRQQLQ LIMALQGLVKGDTVQKVAHTL GYDSTTAFITMLRKPDKTAGTS LYHRRYGVSLSSAWQGVGPP RYCRQANSVLSDFRCVLI
25005	55373	A	25143	981	1103	
25006	55374	A	25144	222	379	
25007	55375	A	25145	1	1452	
25008	55376	A	25146	500	854	
25009	55377	A	25147	1	1374	
25010	55378	A	25148	2	167	
25011	55379	A	25149	781	1047	
25012	55380	A	25150	1	783	

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25013	55381	A	25151	442	857	L VKNPVKRMEIQQKNLTLFEYL DWWDVLFLLSELLFANTWL AATSESVDDCSGVKPPSGKNGT *AMPSWAKASIIASSARCAMLY SFCTQTISAILRASATCVGVTL RPICFTRPCCISASTVRLASIDP SAGP
25014	55382	A	25152	3	4105	
25015	55383	A	25153	2	269	YKNPYIAAIQPKTHDTLTPINP GRIKLWLMTRKPMWVVPERSN *IAARSLG*VGRM**P*QA GAE ATMYAGSTPIASATGTIAASAA A
25016	55384	A	25154	1	1370	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAVYGIAWMA ETMFAPACYGYIILPTYPDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPQSVKAD IATNPFKRPGGAFIRITQTRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSLLTDFS TAVGSI VMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVIAAAGVICPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTEGAIPFAAADPLRVIPSI MVGSVGGAVTAALVGAQCYA GWGGLIVLPVVEGKLG YIAAV AVGAVVTAVCVNVLSLARKN GSSTDEKEDDLLDFEIN
25017	55385	A	25155	1	789	MKIIAGITPADSGTLEIEGNYY RLTPVHAHQIGIYLPQEPPLFP LSIKENILFGLAKKQLSMQKM KNLLAALGCQFDLHSLAGSLD VADRQMV EILRGLMRDSRILIL DEPTASLTPAETERLFSRLQELL ATGVGVIFISHKLPEIRQIADRIS VMRDGTIALSGKTSELSTDIIHQ AITPAVREKSLASQKLWLELP GNRPQHAAGTPVLTLENLTGE GFRNVSLTLNAGEILGLAG/TEL AETLYGLRTLRRGRIML
25018	55386	A	25156	1	1332	

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25019	55387	A	25157	1594	2220	MWVNPGRGRAENTIIGGNATGI GTLNVQDQDSVITVRRLS* KPGILVFKLTPAETERLFSRLQE LLATGVGIVFISHKLP EIRQIAD RISVMRDGTIAGTGFDDFGFT HPLRQQRLPQHLVSMRAAVQ QIFTEIQRGVRPGCNVLAFGQ RGWTPGIVFQQVVELSLKFRIFL RTDKSFFQLAQRHQDLVWHVH AAKLTKIGVK
25020	55388	A	25158	14	237	KTTSPAKLFNACRISLLASAE/ CQSEYFISFNMDLADTMVFL* GAIRFSDLVNEQIQHTFLIPGETI CRLSEVV
25021	55389	A	25159	1	1506	
25022	55390	A	25160	158	639	SGC*PGRPSLN/GRLDVLSAWS VSILRLGGMALEGSIAIYVINF DVKPPQRFRLSVPAASITVLIQ QFVHLRRELRRKLALPAHHLV FTWGNVSAVDETRQWMVIKPS GVEYDVTMADDRWWLR*PAV RWKKAANKPLPIHQIRWSTV AMPKLA VLC
25023	55391	A	25161	2	2886	SVPTIIFFFLPVLRFWRPQIQQA KKCHLFATGTQSRNRTLQR AKGIPQQRMTAKREEISIGILHV TPQQRRECRGDNRFARFRTP WRLGHCVSAAVTGVLPAVAG SPLAYSDTDEFYPVAGGTMSQ HLPLVAAQPGIWMAEKLSLPS AWSVAHYVELTGEVDSPLLAR AVVAGLAQADTLRMRFTE EVVQWVDDALTFELPEIIDLRT NIDPHGTAQALMQADLPQDLR VDSGEPLVFHQTTLGFI
25024	55392	A	25162	1	1659	
25025	55393	B	25163	200	646	
25026	55394	A	25164	1	3197	MPHRQHGPQMTPSHQRTTINR DQREQQIPGTAAPQTRPQSAPY CEPHTRRRRTLQPHNRGFTAKY TSTQARKYHMARPERSNDS PVHTRSRWNATQTERHTQH SPSSRLTLRTNCTSHAHHR RHAQWHRVGLLDVKPTGVPSN TVFSPKKNALWADRVDTSRGR TTVEQDNHPNGGNVVGTPSDN NFWLETGGDPNKEYYHHHHY NEDYCRYYP LIAEPLLP KENSILFGLAKKQLSMQKMK
25027	55395	B	25165	1	2505	

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25028	55396	A	25166	159	1744	NSRISGLQQRRLMHIMVTQGG MSLSIVHTRAAALGVNAPPITVE VHISKGLPGLTMVGLPETTVKE ARDRV/RSAINSGYEYPAKKITI NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEYELVGL ALTGALRGVPGAISATEAIKSG RKIIIVAKDNEDEVGLINGEGLI ADHLQAVCAFLGKHALERP PTDAVSRAHQHDLSDVIGQIEQ GKRVLEITAAGHNNLLIGPPG TGKTMASRLNGLLPDLSNEEA LESAAIILSLVNAESVQKLWRQR PFRSPHHSASLTAMVGGGAIPG PGEISLAHNGVLFDELPEFERR TLDALREPIESGQIHLSTRAKI TYPARFQLVAAMNPSPTGHYQ GNHNRCTPEQTLRYLNRLSGPF LDRFDLSLEIPLPPGILSKTVVP GESSATVKQRMMAARERQFQR QNKLNWLDSPFIRQFCKLESE DAMWLEGLTILHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR
25029	55397	A	25167	127	503	NRCLLLTLRCKGRNREEENDA EAESEKLKKNFNRPSGRLSYGD RMFDIGVNLTSQFAKTVMMML *RRLGLR*TTGLELRELLPLIP AEKL*/YETDAPYLLPRDLAKP STSRVHCVIEARAWFK
25030	55398	A	25168	3	406	

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25031	55399	A	25169	1	1252	MFDIGVNLTSQFAKDRDDVV ACAFDAGVNGLLITGTNLRESQ QAQKLARQYSSCWSTAGVHSH DSSQWQAATEEAIIELAAQPEV VAIGECGLDFNRNFTPEEQER AFVAQLRIGADLNMPVFMHCR DAHERFMTLLEPQMVENYETLI FEAHSTDYQTPQSLRQLVIDHF AIIKVGPAITFALREALFLAAI EEELVPAKACSGLRQVLEDVM LDRPEYWQSHYHGDGNARRLA RGYSYSDRVRYWPDSQIDDA FAHLVRNLADSPILPLISQYLP LQYVKVRSGELQPTPRELINHII QDILAHTTQPVKANKQKKEEH AMPNIVLSRIDERLIHGQVGVQ WVGFAGANLVVANDEVAED PVQQNLMEMVLAEGIAVRFWT LQKVIDNIHRAADRQKILLVCK T*WKWYWQKGSPPYVSGRCKK LSTTFIAPPIDRKSCWFVKHPPIIS
25032	55400	A	25170	2	319	YSSVFSLSASAFSSSRFRPLPT* KREKKTPISNRQYIGIANSVCEK TSGGVSNIPTTNAPTSTYGRFLR KSSGEVPIQHSSTIATGTSKETP NAINSAITKLK
25033	55401	A	25171	1	1011	MIPHPKLEGDRSTQALPPTPVIR VTERRNLNWVGTTIGFVHTGK PLSFVYDMADIIFDFTVVPKAF EIARRNPGEPRDREVLACRDIR SSKTLAKLIPIEDVLAAGEIQPP APPEDAQPVAIPLPVSLGDAGH RRRRSGRVSESVWRSGVMFSR RASGDKPQPKPKVMPEHAECPP AARRGQMMSICPCFALKIDIAD NKFFNGETSPLSFSQSQAQLARQ FHQKIAGYRPTPLCALDDLNL FGVKKILVKDESKRFLNFAK MLGAPEKCHRRKNDF*RRSDRI VLIRL*REFSSHQKGLRDRPAH KAVLGDNQLFSGGTGAPVWPG FAKRAVMF/TP/LKNLLSAISIFN AKHGHILIIWPRLAAGGHSACS GITFGFGCGLSPLARRKLMTP RQLTSDTRPDRLLRWPASPSET GSGMATGCASSGGAGGCISPA ASTSSISGINLANVLLLRKISLH AKRTSRSGSPGLRRRAISKAFGTT VSNLMMMSAIS
25034	55402	A	25172	1	510	
25035	55403	B	25173	1	1482	

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25036	55404	A	25174	704	1069	RLWQADCKENAGIGDYYWTF PQPTFVSTQKYCHVDNSCYM NFDFAPEYHAHWRYGLLMVG ESQHGLGANAIQASQCFAAN QPLGADATFLQKIGETICFGLFI TGVFSIDSAFCEDIT
25037	55405	A	25175	1	639	MARVWLCDFIPYGYLPTLNA PESTRKQIMPWTRLSGSLHTWN RTPNRRIGRYPSGLPPDSANRPR REPDACRSLHSPAKYRGPNPRD RLDHQQNGLPARGKDTPRSNK PSISQWNTTKPQRHQPRGKKG HKSPAPEMPKPPQATSSREQT KYGADELWRSPWKTRYIELKA RGPMACTVITSLNVCCAHVRL VMVTLKQTDPIRNLGEMPSKSQ TKKAREVHLHLHLQELAQEQ EPPARKRKQTQWAVSERK
25038	55406	A	25176	82	356	AQCEEYRVPQTLKRNPKQCFDI SIRGSGQPCGIFSTPVRNTLQNM GQMGWLVA PG*WLWREIRKH NRWCACPRKPGRAGISMALRW GSGHA

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25039	55407	A	25177	1	2635	MNKSQKYL VWT VLSIMGA FAL GYIALNRGEQINALWVIVASVC IYLIAYRFYGLYIAKNVLA VDP TRMTPA VRHNDGLDYVPTDKK VLFQHHFAA IAGAGPLVGPVLA AQMGYLPGMIWLLAGVVLG AVQDFMVL FVSTRDRGSLGE LVKEEMGPTAGVIALVACFMI MVILAVLAMIVVKAL THSPWG TYTVAF TIPLALFMGIYLR YLRP GRIGEVSVIGLVFLIFAIHSGGWV AESPTWAPYDFDTGVQLTWML RLINRSIMMDFSLTEEQELLAS IRELITTNFPEEYFR TCDQNGTY PREFMRALADNGISMLGVPEEF GGIPADYVTQMLALMEVSKCG APAF LITNGQCIHSMRRFGSAE QLRKTAESTLETGDPAYALALT EPGAGSDNNSATTYTRKNGK VYINGQKTFITGAKEYPYMLVL ARDPQKDPKKAFTLWVVDSS KPGIKINPLHKIGWHMLSTCEV YLDNV*TSVWR TCACPALRRA TQRYRRQSRAGNLRTSGEAI RR DMEWTS LRSEDWEGD TIKQC ISAATSCVYGV TGE GILEGGDA QILREPLPGTKLGLLNWPV FDA LESRSTRERD GKPGEICGETA NILIRGPENRPLRRDPPGKP

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25040	55408	A	25178	216	1829	TVCRCHFVTTKHIGRERNQAR QCLVGKTTDTQQHNCDIRVGE QADHTRANHQHCTQRVDHLTG NDQVHKPTLEQRRQVTTEDT TEVSKQHRHPGEHRDLFQRTL ISADDQRRLLLELQNDNLNHN IWLRLAAQPEDHIYGCGEQFSY FDLRGKPFPLWTSEQGVGRNK QTYVTWQADCKENAGGDYYW TFFPQPTFFVSTQKYYCHVDNS YMNDFSAPEYHELALWEDKA TLRFECADTYSLEKL TALLGR QPELDPWYDGVTLGIQGGTEV CQKKLDTMRNAGVKVNGIWA QDWSGIRMTSFGKRVMMWNWK WNSENYPQLDSRIKQWNQEGV QFLAYINPYVASDKDLCEAAQ HGYLAKDASGGDYLVEFGEFY GGVVDLTNPEAYAFKEVIKK NMIELGCGGWMA DFGEYLPD TYLHNGVSAEIMHNAWPAW AKCNYALEETGKLGELFFMR AGST/GDIGGYTTLFEMKRSKE LVLRWCDFSAFTPMMRTHEGN RPGHEWAF/DGDAKHRHLAVY
25041	55409	A	25179	277	488	
25042	55410	B	25180	260	1500	
25043	55411	A	25181	1	764	MQEWGRYTILSGCCNSALKGD VCLLYGFRVAGRRQASE*TPGA YNRVPSSKK*GFQLVLLPFSAN GKSPA Y*RFKSFAEDGEKDAG FPHPYAEAGYDNGGRRSGAGT LLSR*ITAGARGAWRV*RLTG E*MAGKRT*VTASGSQR*IMV FLWSLYRSYRL/GRVROHNGPR YLPVLARNWKMSAWVA AAW QGLTDMKRKTMKIRSGSIVILA SGYAATAA*PLSGDRIFLP*PGK TG*RHGGTPSCAGFTGDY
25044	55412	B	25182	1	3117	
25045	55413	B	25183	270	388	
25046	55414	A	25184	2154	2279	
25047	55415	A	25185	614	623	RPNSGAR*GRGDKRSTQSVPET VRLLCAGTFDQPGGNARWDD QYRCIRSGIVGVRAVLLGGDIL DTQPLPVELAETLGKSAE

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25048	55416	A	25186	1208	2813	CYGVAVWPFDPDLKFEFWRYFT HALMHFSLMHILFNLLWWVY LGGAVEKRLGSGKLIVITLISAL LSGYVQQKFGSPWFGGLSGVV YALMGYVWLRGERDPQSGIYL RRGVIIFAPIWIVRRWFEMTPTQ WSNYFFENLFKYEWVQTRSPA GAIQFEAVDAPEIIPDFDPSKK RKPTMLVTDLTFRDPEFEKISR RFLNDPQAFNEAFARAFWKLT HRDMGPKSRYIGPEVPKEDLIW QDPLPQIYNPTEQDIIDLKFAI ADSGLSVSELVSAVASASTFR GGDKRGGANGARLALMPQTR TGDVTRRQPIRALPVLEKIQKE SGKASLADIIVLPGLFVVEKSA SAAGLSIHVPFAPGRVДАРQDQ TAIGMFELLEPIADGFRNYRAR LDVSTTESLLIDKAQQLTLTAPE MTALVGGMRVLGANFDGSKN GVFTDRVGVLNDFFVNLLDM RYEWKATDESKELEFGRDRET GEVKFTASRADLVGSSNSVLRA VAEYVASSDAHEKFKDFVAA WVKVMNLDLDRFDLL
25049	55417	A	25187	1520	1960	PVPLNFGWQRSTEVLIHVNPS STAAMTISPWRR**RRRTKQLS APLLLGVSAGW/LTIILVAFMA WLLAKT/AFGRSFYATGDNLQG AR/QLGVRTEAIRIVAFSLNAER DFDDL RDSGLIAMILFIMPTLS SISSRRLLNPGVPSEI
25050	55418	A	25188	1155	1778	SASGGVMLKFIQNNREITALLA VVLLFVLPGFLDRQYLSVQTLT MVYSSAQIILLAMGATLVMLT RNIDVSVGSITGMCAVLLGMLL NAGYSLPVACVATLLGLLAGF FNGVLVAWLK/IPAIVATLGT/L YRGLMSLWTGGHWFEGYPRIE KPSPPVAGVHHWCVTQIGGLRP AVAKRVGPDLPDGNKGAAGV NTLDNYGVGDKVCV

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25051	55419	A	25189	1	2227	MVTIAGIILGGLALVGLITYFGK WTVLWKEWLTSVDHKLRLGIM YIIVAVMLLRGFADAIMMRSQ QALASAGEAGFLPPHHYDQIFT AHGVIMIFFVAMPFVIGLMNLV VPLQIGARDVAFPLNLSFWF TVVGVLVNVSLGVGEFAQTG WLA YPPLSGIEYSPGVGVYDWI WSLQLSGIAVAHIAAQNVAVLL ISSDLEEIELMADRVYVMHQGE ITHSALTERDINVETIMRVAFGD SQRGVMLKFQNNREITALLAV VLLFVLPGLDRQYLSVQTLTM VYSSAQIILLAMGATLVMLTR NIDVSVGSITGMCVLLGMLLN AGYSLPVACVATLLGLLAGFF NGVLVAWLKIPAI VATLGTLG LYRSIMLLWTGGQWIEGLPAEL KQLSAPLLGVSAIGWLTILVA FMAWLLAKTAFGRSFYATGDN LQGARQLGVRTEAIRIVAFSLN GCMAAALAGIVFASQIGFIPNQT GTGLEMKAIACVLLGGISLLGG SGAIIGAVLGAWFLTQIDSVLV LLRIPAWWNDFIAGLVLLAVLV FDGRLRCALERNLRRQKYARF MTPPPSVKPASSATSDFICIGIVA LPLTMVIVSGGIDISFGSTIGLCA IALGVLFQSGVPMPLAILLTLL GALCGLINAGLIITYTKVNPVIT LGTLYLFAQSALMSEEQKNTK KTRQREDKKKKQKQKREEK
25052	55420	A	25190	1055	1206	SFALFSSSSPRSRP*FASTKS*TL TTGQVLPSTNVRFLTGNWGPPV VATG
25053	55421	B	25191	1	1386	
25054	55422	A	25192	1	449	MQDPILLALLEDYNGDLEKQV PPAQSGPQPGKAGRDRPIVIML DPGHGGEDSGAVGKYKTREKD VVLQIARRLSLIEKEGNMKVY MTRNEDIPIQVVRV/AKAQKQ RADLFVSIHADAFSTRQPSGSSV FALSTKGGMCSYRGSGCLQ
25055	55423	A	25193	1536	1941	STSNQNSTALCRRRGLVHCIDG ANDDDSVVMVWPSGSGRPWSAE PGAPQR/YAQLVVEDVELDLH FIVFGDDVMLNVVLQGGAFML ALGLVTNVGVLAAHHHVALVS GVPNDGGGTWVGGRVCVQSQ LCTCWSHCQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25056	55424	A	25194	240	855	SRAGYAPAAQKVASPYVRRE R*NQSDPAVLTGIGERGK*LLS RDFFIAPLAGMIVEKRGAVHLA RWSVPVERKGQWOPAGLWAQ FFLADIVCPAATALPDJTTAEDQ HIDHPAVVHVHVIPVNTCAED NHRAPMRFMGGIGKFTGDGFNI LARHPGNLLTPGWGVRFDVSVI FRTVFIFQPAIEAVIRQYQINAD HRTGVAID
25057	55425	A	25195	840	1157	QYAPTQAPARPADPFALPTVQA RLTPFCYLVAKGDWCVYRRSY SLWHSVASPRVRQSPRLGY*GY TANSPGILLAPLSLRGEMFLPQD APKSVPPYKRGKSVAIN
25058	55426	A	25196	1076	1339	LVCVASMPVEISTDASASSGVI VISSAMSGSWAETKRRLAMV* PEPLHLWAISIPTTSGRFTSSLIS PPPAR*YSPARYIPRVWRV
25059	55427	A	25197	2	118	
25060	55428	A	25198	1809	3145	ARHKQHAYGYRYRQSPRCYGV SGKKRGLRYYGSLAISGSSRI TR/LLCMYLRFFIGVIGADIAN MGISAGAMWLLSVSQVSLAAV SQVVAVRVWPASSYTRVTVES NRQLKYKQFALSNPERVVVDIE DVNLNSVLKGMAAQIRADDPI KSARVGQFDPQTVRMVFELKP NVKQPQLFALAPVAGFKERLVM DLYPANAQMDQDPLLALLEDY NKGDLEKQVPPAQSGPQPGKA GRDRPIVIMLDPGHGGEDSGAV GKYKTREKDVVLQIARRLRSLI EKEGNMKVYMTRNEDIFIPLQV RVAKAQKQRADLFVSIHADAF TSRQPSGSSVFALSIQRGARPVG DRYVDHTMDFMVQSLTIADSL KFGKAVLNKLGKINKLHKNQV EQAGFAVLKAPDIPSILVETAFI SNVEEERPNGQPGHPLDPATTM GTLIDCAHADSVQ
25061	55429	A	25199	1	277	
25062	55430	A	25200	902	1006	
25063	55431	A	25201	2	1265	
25064	55432	A	25202	409	525	
25065	55433	A	25203	91	431	NHKPGNIDVARRIQRGFGADQI GHLRPVERQCSPPDKRRFIAADG REIRGKQRAGHIFQLLSRCLLQI LNHCQRRAAHFRQLSNQRHQ QLLPV/IYHAAEREYPAGACLV RWLL

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25066	55434	A	25204	3	71	
25067	55435	A	25205	1	1212	
25068	55436	A	25206	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVDIVVNATAAFIAVIII SLLLDSEGGFEWAALHVLRWG YGPGRLLPFNRIGLIRIRTRIRQR LLFGLVTFILLNRSQNP AQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQQGCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSLKRVYHSPG APDIREFT RDAIP
25069	55437	A	25207	5	402	EIFS VVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLKSEGDWLPETVISAF NMPSSLSLISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVF TLFHRI
25070	55438	A	25208	48	219	PETCGHLWAYVWPSCAAVIGL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25071	55439	A	25209	1	912	

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25072	55440	A	25210	1	1857	MRVCARACVTRTRMVCVYAH TCVVCVRTYAYVVRVVRVHVRA RVRVCAYARTRVRNSLSLPFIQ LTLATPIHHIQEEFNIRGIVPVL RRVKPDLAIGDITPSCDTPDLH DYSEVRINQGVGIICTLNHYHGRG TLAGLITPRLIRMLEQTALEHN IPVQREVAFGVITETGYIQLFLP GWEIGFSPALLLAFLCSTSPGF GDPDLGVIA YQD TVRPNAAT AISELNALAVKGVILTGDNPRA AAAIAAGELGLEFKAGLLPEDKY KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTLDDR VVAGSAGRYGGDGA GDSECVKIVAQEIRQTDNRNIE DRSPRPSGERVVRGKGGIEAN QPLSTAFNTQITIRQSIRLFSNQF VFHKGISRVVAGSSAHSNVS PG CILRTPNCRRGFPISTCGEGKAA YGVQRDGGHAEYLLAEKDLI LLPDALSYEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY* LPDVYV*IGVARVSWMNGRID SELRTVRVAYAHTRTRARTCTR TRTRTYAVVRTHTHVCA YTHM RVRVRTHARAHTR
25073	55441	A	25211	3	1180	SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFDL LPAQQRMKGENWYRGTA DAV TQNLDIIRRYKAEYVVL AGDHI YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIEFVEKANPPSPMPNDPSKS LASMGIVFDADYLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHFPFLSCVQSDPAEPYLAR CGYAGNFMESEPRSGLIRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRPVDPVELVLV AAEFITPGDPTRLHSGSFIDIR QIIHQTRSHLEGVKTGIRFLNH FSGNPQGGIAHVNGVARFQVK QCHQAWGQQAARLRFAQRG SLQIAIHRVDIIHRFDRVRL
25074	55442	A	25212	16	543	
25075	55443	A	25213	1	3387	

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25076	55444	A	25214	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTPFGVC TSASMNVPVLTLRIRTRVTGVEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*ITTCANR*STSARGSL ERLIMATLL/VVAGTFD*SVWF GHDTDVVTLRYFHEALCYSVT LRTPHRRVLRFKSQLHPGELACFI SPVA
25077	55445	A	25215	905	4761	PPHNWMPSNATPGIAFVWCAY GAI/LPGDAPVPVDDYRKVVVR KDTKGLIARWKYFWMVSIALG VAFALYLAGKDPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTGDLGLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGS ALGGALGIIAALLRQEFLLVIM GGVFVVELSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25078	55446	A	25216	269	1219	QTRTRRVQLQDLIEYVAIHQW/ FSDKHPVPFYSCIFDDSIITNCYS WSISKDGYFIFGGAYPMKDGQT RFLTMKDKMSAFQFQFGKTVK SEKCTVLFPARGQDFVCGKDNA FLIGEAAFGISASSLEGIIYALYS TDIPRSVLLKQPKLNPAYWRA TRLVCITLFGQIVNTICMAAPDL RKWIMLSPVAHKGHHLEWVLH DMQILPVRPSPGCICSGSTFFC NWGCPYDRPQWQLYPSMCLC VHIGPAPVRSEKVESKRAISKV DQDSAFRGCCRSNGNRNGGRKI VASLKKVSGAAKPCGHFRST RYRVAYSTIIN
25079	55447	A	25217	1	1158	
25080	55448	A	25218	1156	1899	LKLGIRYPQCQRLVTHSLDGISL PLHTAH*SQNSAENTHRAISLK AVPPFFTAERRGVNAEEHRNGR LINGECRQRFNVLRVANGVRN VQFAKARDNRDIA SFRQIGFDT FQTEVAQHFTDFRVAGFAFAD DSDLLVRLHFTALDAANADNA NIAVVIELRNLHLERTVKVNVR RRNVVNNRLVQRGHVFRHIFV VQTRDTVQRSSVNDREVQLLV GRVEVNEQIEYYADAFVIMLER LCKVLCCR
25081	55449	A	25219	1	2583	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25082	55450	A	25220	278	787	TLLSATRQVYALLSTKPAFFSS HSSFSTSSRLISSRAASSMDVAF PIAFSASKTVSIKFFSR*KLLRNS HRPPFMVMRSIIIRSPSNVFMAS* FRFVSIPTLRIDAVRRSTIWCSTT ARFSSRADAKFIKNVFQQAIPDS AAKWFFFPVPGFPLNAKFVHPVI SSSAMDFA
25083	55451	A	25221	866	1144	
25084	55452	A	25222	19	1203	NWNLTPTYASLTGFTADNPEYH LSNGMKSXSVDTRSIYRELGAT LSYNMRLGNGMEVEPWKAA VRKEFVDDNRVKVNSDGNFVN YLSGRRGIYQAGKDLDRFKNL VLVHAARYAADLSYPLMQEL EKRYEGKLRIQTVVSRETAAGS LTGRIPALIESGELESTIGLPMN KETSHVMLCGNPQMTRRLLIPAS VEVYHDSLCKRKIWHGWEQHIT ARYLVGADGANSMVRRHLYP DHQIRKYVAIQQWFAEKHPVPF YSCIFDNSITNCYSWSISKDGYF IFCGAYPMKDGQTRFTTLKEK MSAFQFQFGKTVKSEKCTVLFP SRWQDFVCGKDN AFLIGEAAAG FISASSLEGISYALDSTDILRSAL RKPIRTEQGANGAIRELEKFRPA
25085	55453	B	25223	58	359	
25086	55454	A	25224	4	329	
25087	55455	A	25225	1	1008	
25088	55456	A	25226	1	1335	

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25089	55457	A	25227	3	1886	HRLNITAENDCRRLHCSLRDLS SLLQAVGRLEAYFIGDVFAARF NDALT VVERLVKVTLYGSQIKL YNIETAVPSVLKPDLDVHAQS LAGGCRLSAHWLAQYCSEIHR QNTQQFVTLISTMDAITPLIST KVQDKLLLSACHLLVSLATTVR PVFLISIPAVQKVFNRITDASAL RLVDKAQVLCRALSNILLPW PNL PENEQQWPVRSINHASLISA LSRDYRNLKPSAGAPQRKMPL DDTKLIHQTLQRLRKILWENIS GVESTKSSTDFAYQFGCRESVQ VSLGLFPFIHQSDVTDEMLSF FLTLFRGLRVQMGVPFTEQIIQT FLNMFTRQLAESILHEGSTGC RVVEKFLKILQVVVQEPGQVFK PFLPSIIALCMEQVYPIAERPSP DVKAELFELLFRTLHHNWRYYF KSTVLASVQRGIAEEQ MENEP QFSAIMQAFGQSFLQPDHILFK QNL FYL\ETLNTKQKLYHKKI FR\TAMLFQFVNVLLQV\LVH KSHDLLQ\QEIGHRHSYNMASV DF\DGFFA\AFLPEFL\TSC\DGV\ DANQKSVLGRNF\KMDRLCPCL PGPAPHSPRMCTGWS\TTCGLLT DSGNDSLAPWGLWKLLGPCLL PGGTRDFLLVAT

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25090	55458	A	25228	689	3053	VDCRMS/FSYIEKFTDFLRRLFVS VHLRRIESYQFPVVEFLTLLFK YTFHQPTHEGYFSCLDIWLTLFL DYLTSKIKSRLGDKEAVLNRYE DALVLLLTEVLNRIQFRYNQAQ LEEL\DDETLDDDDQTEWQRY LRHSLEVVAKVMEELLPTAFST LFPVLQDNL\IEVYLGQQFIVTS GSGHRLNITAEENDCRRLHCSLR DLSSLLQAVGR\LAEYFIGDVFA AR\FNDALTVVERLVKVTLYGS QIKLYNIETAVPSVLKPDLDIVH AQSLAALQAYSHWLAQYCSEV HRQNTQQFVTLISTTMDAITPLI STKVQDKLLLSACHLLVSLATT VRPVFLISIPAVQKVFNRTDAS ALRLVDKAQVLVCRALSNILL PWPNLPENEQQWPPRSINHASL ISALSRDYRNLPKPSAVAPQRKM PLDDTKLIHQTLVLEDIVENIS GESTKSQICYQSLQESVQVSL ALFPAFIHQSDVTDEMLSFLLTL FRGLRVQMGPVFTEQIIQFTLN MFTREQLAESILHEGSTGCRVV EKFLKILQVVVQEPGQVFKPFL PSIHALCMEQVYPIIAERPSPDVK AELFELLFRTLHHNWRVYFFKST VLASVQRGIAEEQMENEPQFSA IMQAFQSQSFLQPDHILFKQNL YLETNTKQKLYHKKIFRTAML FQFVNVLLQVLVHKSHDLLQE EIGIAIYNMASVDFDGFFAAFLP
25091	55459	A	25229	1	853	MISVANEIAEAGFDPOQRTSED LLDLAESRVFKIAESRANKDEG PKNIADVLDATVARIQLFQQP HDGVTGVNTGYDDLKKTAG LQPSDLIIVAARPSPMGKTTFAM TLVENAGR/MLQDKP/VLIFSLE MPSEQIMMRSLASLSRVDTKI RTGQLDDEWDWARISGTMILLE KRNIYIDSSGLTPTEVRSRARR IAREHGGIGLIMIDYLPLMRVP ALFDNRITLIEAIEISRLKALAKE LNVPPVALSHLNRSLERAEER PGNSDLGESGIEQDADLIL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
25092	55460	A	25230	206	1073	VKITSWLMSNSAI.PGTLKLLAL ILKCSTCVRVLPSELRLER/Q GQLDSVGGFA/YLAEL/SKNTPS AANISA/YADIVRERAVVREMIS V/ANEIAEAGFDPQGRTS/EDLL DLAESRVFKIAES/RANKDEGR NPMFDDRGRGKRGEPDLIIVAAR PS/MGKTTFAMNLVENAAML/Q DKPVLFISQTKI/RTGQLDDEDW ARISGT/MGILLEKRNIIYIDSSG L/TPTEVRSRARRIAREH/GGIGL IMIDYQLQMRVP/ALSDNRNTLEI AEISRLKHFEKLALICGCRNNG TTRYCKSLLA
25093	55461	B	25231	1	483	
25094	55462	B	25232	287	635	
25095	55463	A	25233	1	2469	MPSDISLASCLRLATSRIFTDHR RQSDCMATAINRIPVDDDEDNVR RFETHCANNVRTALHLFADIHP DVLMDIRMPMDGKALKEM RSHETRTPVILMTAYAEVETAV EALRCGAFDYVIKPFOLDDELNI VQRALQLQSMKKEIRHLHQAL STSWQWGHILTNSPAMMDICK DTAKIALSQASVLISGESGTGKE LIARAIHYNSSRAKGAFIKVNC AALRESLLESELFGEHKGFLER ANEGTLLLDEIGRM/PLVLQAIL RILQEREFERIG/GHQTIK/VDIAS LLAPTRLQAMVKEGTFREDLFY RLNVIHLILPPLRDRREDISLLA NHFLQKFSSNQRDIIIDIPMA MSLLTAWSWPGNIRELSNVIER AVVMNSGPIIFSEDLPPQIRQPV CNAGEVKTAPVGERNLKEEIKR VEKRIIMEVLEQQEGNRTAL MLGISRRALMYKLQEYDATGF FRDGMTIMVGGFMGIGTPSRLV EALLESQVRDLTLIANDTAFVD TGIGPLIVNGRVKVIASHIGTN PETGRRMISGEMDVVLVPQGT IEQIRCGGAGLGGFLNPTGVGT VVEERQTSIDTSRKRPFELGRP SRNNDKIRPRSGAGSEEPRT LHDSLKRLQTDYLDLYQVHWP LRPFYCFGKLGYSWTDSPAPVS QLDTLDALAEYQRAGKIRYIGV SNETAFGVMRYLHLADKHDL
25096	55464	A	25234	1	891	
25097	55465	A	25235	1	1614	
25098	55466	A	25236	1	946	

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25099	55467	A	25237	1055	1474	NGVKSPPPPNHQTGSAPGFSAI KNRTFAWPTLPNTSCWANTML IGSRELGIRSSQSGPLLGVRVWC /CRCRGTQG/HSQGGKG/TPENGI RAYKFTSS*ASFRNSACFRQPSR IKPLRKATWLLCGLSTRHLITK RLSSPDWA
25100	55468	A	25238	2036	2743	DLLIRQMPLLSRRVIPVIRVPVT GVLWKSFTPRITIFGH/ALIDQH SMIVAAQGLTPDHQLLQIYDR ARVSASRIVHQAQIYGDAVVR YAFIEHRAEVDFASIEGNEENN VWLCDCAKVYGHAQVKAGIEE DAIPTIHYSSQVAEYAIVEGNCV LKHHVLVGGNAVVRGGPILLD EHVVIQGESRITGAVIENHVEL TDHAVVEAFDGDTHVVRGPKV INGEERITRTPLAGLL
25101	55469	A	25239	2234	2571	IMSSVDSSLVPLKAMVPSRITL IRSAIWRISG/RLMRDKNNTHAS SKQLLQATKQAFGRFRGRKGG RFIEDQNPRVAHQPAEDFIHILA IGDIQRSCQTMQIKLAAQRRQQ VLH
25102	55470	A	25240	659	1206	WKSTSNATAKAPGSVMAVDLR IPIRFGVMLSAA/FGDDVVDLIA QVDLVTAVAGPVVLERIAPAIA KGQVVRKEQGHEsplNHAACEN MVRGTTQLKGHVMMNALPEDA KAWVEEHVGFVDSAVDRIVPP SASATNDPLEVTVETFEWIVD KTQFKGALPNIPGMELTDNLM AFVERKFLTLKH
25103	55471	A	25241	332	683	ALPGR*RHVHLPGSAYEWNDA EPAQESDELSKMLTAICWLTA TA/STSLKI*R*KVALRCLVGRIR RLRRIRQQCQLMRRSRVL.SGR LSSV
25104	55472	A	25242	1	841	MVKVAGECRVRSASHLPLNLR STKNTEDRGANNQEGTNTQKT RGETNERLKKNEHRDLRLARY PAKENNKQGDKNKPRTYEKL GTVTHQEPHHADQSPGLCLFR TSRAQVERGPTVLLLSIQENQIE RYDSNHSQNLCLRVPTVTQT RRDYDIAERYRQKGIKLPARKE RLMTIAERLRQEGHQIGWQEG KLEGLHEQAIAKIALRMLEQGF RDQGIARRASCQRQRQSSLP P/EHCCAISGATARKPAALPAAR IRRILVSIIRCTSGCPALSG

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25105	55473	A	25243	240	651	RCPPQSCLLAEGRWCG*K/CRK VSV*SNRYR*SRLSLGELLRAYS RNRDLPGF/SSGSARVLVATDV AARGLDIKSLVLVNFELAWEP EVNVHRIGRTARAGNSGLAISF CAPEEAQRANISRPPHAPHAS DHQSTP
25106	55474	A	25244	1455	1643	RDPHQICVAESVYLAAFVLLCA GLCVRRRSTTGARNAAAAC*N GLW*AEAQCPAYYVCPVVG
25107	55475	A	25245	549	641	
25108	55476	A	25246	1378	2084	PNFGYSPPASSCGQVSQNSS*LQ CSVSGRDKMLRTGPCARTVSSS YLMGVSFSDA**DAR*VCACH NTIAALSASAEFTSCERASHSE ARSGCCNSVRVMSNPNCCPRSL IGVDILFFQESTAKRCKRSLSG SGSACGKSRVRFTPYRPARRTP LRSTTSPISAAFPSPGWECNAAS TCSAALRSTAITSLPSLAKFRAS SPSNSQTPRTAGLTGSAASESSI PQPQAAANS
25109	55477	A	25247	1134	1428	GPCGCCSSNVARCASQTSSRFA AV/WHGAIGAR*LNADNRPLWI EITREHAELPGKTGRRMETKQR RAITFTQRQNGFESHPTGAVFFS INNRCQFGDR
25110	55478	A	25248	96	535	RPQTTVQPALYVVAEQSICSQP* *FSTKCDRKPAAVLAPAGYAAL PVLFFSAKLDSWLRWNSASG RRQNGSFSCAALASKRPSASS KLNSA**SLPSAVFAAPVRVAA SMHISGFCALASIRPSASTRRPSA SVFITSTFLPLR

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25111	55479	A	25249	1471	3026	SPLRSSVACRGWHRKNNRRGW CPRRGDPARPVRDSLQIHATAIII VATPGRLLDHLQKGTVSLDAL NTLVMDEADRLMDGFSDAID DVIRFAPASRQTLFSATWPEAI AAISGRVQRDPLAIEDSTDALP PIEQQFYETSSKGKIPLLQRTL RFANGSARVVLVATDVAARGLD IKSLELVNVELAWDPEVHVHR IGRTARAGNSGLAISFCAPEEAQ RANIISDMLQIKLNWQTPPANS SIATLEAEMATLIDGGKKAKM RPGDVLGALTGDIGLDGADIGK IAVHPAHVYVAVRQAVAHKA WKQLQGGKIKGKTCRRRCYPLA APYVRHCSLVGRAASHQALWH VAGFGLYALFRRTGGCRLRCR YSGGLRLIRPTVAAGICRPDKT RKRRIHRAPFPDAARAPYPAY RSQYNQFFFTNSDFSFIGPKPSM LQSMCLCAPCNQADVFHFGANV SASKSYLFTFRSLMMVTLSPCS QQIAVSIFNDQLVAFLCRCFCV PLRRHIHQMYMPLSS
25112	55480	A	25250	196	330	
25113	55481	A	25251	62	617	NRRLPSGGDEMSAQVSLH RISQFLVQESSCWDWVKFRD GVAQLRPKEVRFVIMRTTVNGQ TRVPRKGVQPPTTWIFNDKQD LERRIARLETGMAWAEPPSRT RHLISNCQISETDIPNVFAVRVN YLLYRAQKERDETFYVGTFRD KVPPSEDTTWRLCKRDIVLDQ AVITSHNLSLVF
25114	55482	A	25252	1	318	
25115	55483	A	25253	1	510	
25116	55484	A	25254	9	79	
25117	55485	A	25255	1	361	
25118	55486	A	25256	863	1245	FSQIYLARSALSSAHSRSPWQH SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEERGKIVRMSSGNFI
25119	55487	A	25257	909	1069	GILSPFLVFVRVVKDQIVVDVW YYF*GLCSVPLVDISVLVPVPC FGYCSSLVV
25120	55488	B	25258	1	1878	
25121	55489	A	25259	778	990	
25122	55490	A	25260	312	635	
25123	55491	A	25261	4047	4276	

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25124	55492	A	25262	1599	1776	WFPASSMSQPKKAQDQDTSQP NSTRGTERS WYHSF*NGSKQ*K KSNSSPTHFMRPASS
25125	55493	A	25263	1	162	
25126	55494	A	25264	1	3370	MNRAPIPKQSKDKTSRETKNTS RSKTRERTDELEGLSTDNHAET QHAETNTDMTHERYTQIRNHT YKTTHQMEDKRTKPKREKEIH NRPDMAKAGIPRSILNTGHPG KLMQTEVHHVRTL.KIMLKVYS RALQEEQFSSKAIGRLFPCAD DLLETHSHFLAQTHERSGYVPL CVCAHTKIFYEFMEDVNTAYT KRHTMFRSLSMVSECLFSLING DDMFVTFAAMQAQQGRSSLV WLFSQLYLYSFISLIYMYV
25127	55495	B	25265	44	238	
25128	55496	A	25266	1	444	MPAEFITGERSSEGGFRIHAGI EQAISRGLAYAPYADLKNLDD KTIASFQQQLSDMGYKFQFITL AGIHSMWFNMFDLANAYAQG EGMKHYVEKVQQPEFAAKKD GYTFVSHQQEVGTGYFDKVTI IQGGTSSVTALTGSTEESEQ
25129	55497	A	25267	710	1395	DLPGISSKWVIAVIFGHLIVGFI PPAIIVRAGIT*RQVR/WIAAHE GKAPQQIIMAHLDYAPLSDA DADANLGLTLQGMDDNAAG LGVTLLQLAERLKNTPTEYGIRF VATSGEEGKLGAEENLLK RMS DTEKKNLTLVNLNDNLIVGDKL YFNSGVQTLERHQRFSNTVKP WPDQSVISNRPFAGNTGSVDND EIQRNLNDTNYNRMWEYNNRG VGSKVVAEAKK
25130	55498	A	25268	2	2105	
25131	55499	A	25269	754	1133	RAANQHQTVDLTRLQTRIAQR LFNRHSQAIEQRQPIQFVLVK FAFPFRFLIPANVQWRLIATFC RFHTGVQCQFTLVKRGPGDIR DYQQTNLDWYNSRNTTKLDES VNRV/HAAIQS*RQNGNL
25132	55500	B	25270	1	1275	
25133	55501	C	25271	1	1167	

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25134	55502	A	25272	275	2424	SPAMHFAQSF7/WQNNLDDNTIA SFQQLSDMGYKFFQFITLAGIH SMWFNMFDLANAYAQGEGMK HYVEKVQPEFAAAKDGTYFV SHQQEVGTGVYAASGNSLLM RALNAAWPGIIDCSNHFARLRC SVWSIPRSDLRCAAFFRTGRLA CCPAGDEKPYPSLRSSRWSGRG ATALHYTAKRCRDPKTRQRRJ RQPARALDVGCGVTALSDLP CRTSQRCRFPDKTRQRRIRQPAR ALDVGCGVTALSDLRGAALHG SLANYRVVNFLFRLPDAMILSV LLRSCPFVPLLRRLRAGAPVGP YCTGTPITPLPSTRLFAPLPNRC SMAGMYGGLQPVPHPAIGARC LMRCLTHLRPTMGTSMAEE ALGTSFKRLCAHYSRMRCWRIL SGLRGARPNKIVCRIRRLRIRPI LRLRFPFRHSRVVFIQGGNPRR AKQRTGEEVEKCHQFQHGK CCARGGAACLVFEYVVFVFWT SLPDSFCRKSFPTRIRGSMVPSL WDFPPGV DGRKGKTSWNGVPG PCVTCGLGLTCPESPCCPLSLG DGYPEKVS VGPPIPLKFQAILQA FHEIFEGSCHIASVAVESGVPE QPFGEETRAGARNRVANARR LLPEADFWVAIEAGIDGDTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS
25135	55503	A	25273	1	441	
25136	55504	A	25274	3	2919	AVSNCSEGLSKEWGP RPRCHR GMEKLPLGGKFWPTQ/EAVRT VRARLQAD/VTGVPTVLVARTD ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRLAY APYADLVWCETSTPDLEARRF AQAIHAKYPKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFFQFITLAGIHSWFMFDLA NAYAQGEGMKHYVEKVQPE FAAAKDGTYFVSHQQEVGTGY FDKVTTIQGGTDPDKAFT
25137	55505	A	25275	432	549	

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25138	55506	A	25276	652	2689	KFSVGYAVQNFNATVSTKQFQ VFSEQNTSSYFAEPQLDVNYYQ NDVVHFVTTTRDDMPEATRVHL EPTINLPLSNNWGSINTEAKLLA THYQQTNLDWYNSRNTTKLDE SVNRVMPQFKVDGRMVFERD MEMLAPGYTQTLEPRAQYLYV PYRDQSDIYNVDSSLLQSDYSG LFRDRTYGGLDRIASANQVTTG VTSRIYDDAAVERFNISVGQIY YFTESRTGDDNITWENDDKTGS LVWAGDTYWRISERWGLRGGI QYDTRLDNVATSNSSIEYRRDE DRLVQLNRYASPEYIQA TLPN VNHHTITMEHLHMKTRTQIEEL QKEWTQPRWEGITRPYSAEDV VKLRGSVNPECTLAQLGA AKM WRL LHGESKKGYINSLGALTG GQALQQA KAGIEAVYLSGWQV AADANLAASMPDQSLYPANS VP AVVERINNTFRADQIQWSA GIEPGDPRYVDYFLPIVADAEA GFGGVLN A FELMKAMIEAGAA AVHFEDQLASVKMRHMGRT ASDQPWLAYAPYADLVWCEPP PPDLELARRFAQAIHAKYPGKL LAYNCSPSFNWQKNLDDKTIAS FQQQLSDMGYKFQFITLAGIHS MWFNMFDLANAYA QGEGMK HYVEKVQQPEFAAAKDGYTFV SHQQEVGTGYFDKVTTHIIGGT SSVTALTGSTEE SQF

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25139	55507	A	25277	134	1695	FPDPA RLPPVSVNHHITMEHLH MKTRTQIEELQKEWTQPRWE GITRPSAEDGGKLRGSVNPEC TLAQLGA AKMWRL LHGESKK GYINSLGALTGGQALQQA KAGI EAVYLSGWQVAADANLAASM YPDQSLYPANSVPAVVERINNT FRRADQI/QWSAGIEPGDPRVY DYFLPIVADAEAGFGGVLNAFE LMKAMIEAGAAAVHFEDQLAS VKKCGHMGKVLVPTQEA IQK LVAARLAADVTGVPTLLVART DADAADLITSDCDPYDSEFITGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDELARRF AQAIHAKYPGKLLAYNCSPSPFN WQKNLDDKTIA SFQQQLSDMG YKFQFITLAGIHSWFMNFDLA KAYA QGEGMKHYVEKVQ QPE FAAAKDG YTFVSHQQENRSSK QQQPLLTVGRIRRSRRIRQSVPR TGIGCASRRFNTAKPWADAVIS NRPFAGNTGSDVDNDEIQRLN DTNYNRMWEYNRRGVGSKV AEAKK
25140	55508	A	25278	230	380	
25141	55509	A	25279	432	1247	PSQEPSVHGRWMA*KGHSRIV* WRAYD*THFNPVLKKS VSLGS NIRHMLAEATTELDGTGPV LV*PNRH*PAYWMRAYLNLKK MSCRSFRKA*RW* CETQT VV HRDRVDQGNHFDVVARHYH LYAFLRKERQLIFFKFKYARIQY AG
25142	55510	A	25280	243	430	RRPSYSVLQRLPSAVLLPYY*R DWYHRTAGRRRDGNAGRQHQ NGCYPPDPDRDGRSAFRNP
25143	55511	A	25281	10	638	SSVPTAGSRYNHLRAPRYSPLF ANYSMSDRCCKPG/LDSSTG* WFQ*RSVPLPILLPDTSRHQL*C SDPTRNGPA/QACQRFHIVERV ARVHHARFAATVTVDHVIDQ RFFQICRT/PWCRLHRHHWRSS GTR*TF*SPARHFCLLHNDSSYR STARPTCSGTDVDRRCSDAHL CDHWSGSRAHADTDAECWCL NPQPAPSL LQCRR
25144	55512	A	25282	803	1622	
25145	55513	A	25283	498	686	RRPSYSVLQRLPSAVLLPYY*R DWYHRTAGRRRDGNAGRQHQ NGCYPPDPDRDGRSAFRNP

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25146	55514	A	25284	1	2063	MKNFMENVLRYLSDDKWKPD AKASMTVGTNLDTVYFKRHGQ VTGNSAAFDHFPDFAGISVEHL SSYGDLDQEMPLLILNGFEYV TQVGNDPYAIPLRADTSKPKLT QQDVTDLIAIYLNKGGSVLIMEN VMSNLKEESASGFVRLDAAAG LSMALNKSVVNNDPQGYPNRV RQQRATGIWVYERYPAVDGAL PYTIDSKTGEVKWKYHVENKP DDKPKLEVASWLEDVDGNRKR NFSNDARANGTAAFTDCEQTQ VVHRDRVDQGHNFHDLVARH YHLYAFRQFDGTSHSVSTVEL RTVAFEERSMTAAFIWSWTECTL QIRTCQNPTGKVWTCDELEIM ADLCERHGVVISDEIHMDMV WGEQPHIPWSNVARGDWALLT SGSKSFNIPALTGAYGIIENSSSR DAYLSALKGRDGLSSPSVLALT AHIAAYQQGAPWLDALRIYLK DNLTYYIADKMNAAPFELNWQIP QSTYLAWLDRPLNIDNALQ KALADQEKVAIMPGYTYGEEG RGFVRLNAGCPRSKLEKGVAG LINAIRAKKSATMIDTTLPLTDI HRHLDGNIRPQTILELGRQYNIS LPAQSLETLPHVQVIANEPDLV SFLTCLDWGVKVLASLDACRR VAFENIEDAARHGLHYVELRFS PGYMAMAHQLPVAGVVEAVID GVREGCRTFGVQAKLIGIM
25147	55515	A	25285	3	371	
25148	55516	A	25286	63	180	
25149	55517	A	25287	2	205	
25150	55518	A	25288	495	707	REFSSHQKGLRDRPAHKAVLG DNQLFSGGTGAPVWP/HSENV VPVDPMTMKRLPDDVNHPLADY YWRLSFA

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25151	55519	A	25289	1	1713	MTWAYSPSYGKPLSVPGHIGL MTRFGMDVTLAHPEGYDLIPD VVEVAKNNAKASGGSFQVTS MEEAFKDADIVYPKSWAPYKV MEERTELLRANDHEGVKVAPEK HCLAQNAQHK/DWH/SIEEMM EPATREGEAQNKHGRPAEINGA SCKEGRSDQKAYDEKSRPDEM PIDDNVVLNKGDLVQVSGDAR RVKTIADRIGFISHSQVTDLLAF CAFFVIGLMIGMITFQFSTFSFG MGNAAGLLFAGIMLGFMRRANH PTFGYIPQGALSMVKEFGLMVF MAGEIQVDGNTIYPHIWKSCDG GVLFQKQYLLRLGIILYGFRLTF SQIADVIGISGIIDVLTLSSTFLL ACFLGQKVFGLDKHTSWLIGA GSSICGAAAVLATEPVVKAES KVTVAVATVVIFGTVAIFLYPAI YPLMSQWFSPETFGIYIGSVIEV GVDVNPNASLMIIENPERLGQAQ LHQLRGRVGRGAGLLTACCST KRRFLKAAPEVTRTGLADDRSS GLPLQTGYELASMQGLVDVVR LSPQGTDTFAMLDAFRANENG AAPLPLTANSDCNGYWRRLAG
25152	55520	A	25290	629	1054	ASGRFREVTG/MEEAFKDADI/V YPQSWAPYKVMEEERTVLLRAN DHEGLKA/LEKQCLAQNAQHK DWHCTEEMMELTRDGEALYM HCWPADISGVSCKEGEVTEGVF EKYRIATYKEASWKPYIAAMI/ CPVNTPNQVHCSSNC
25153	55521	A	25291	235	780	
25154	55522	A	25292	1	2783	MTYRNNHQIGVAFLFQTKFCIE DGGVKTFDGYRVQTQSRHAEQ EVTDV EINFCHPLCIHQIFTV HISEELATFIVGRFRFRGKAAI GIFLVNNQLQPDIVHRGFCTEH HDVRGIKHFTLVEHVITGSGFG NTRFTFRAGNNKMPRLGVGA GWAVLQGVPPRVFGVWPLPEYP AYACGKFNGAIRAGDAAQLAA YAQAFIQLHGPIDAGDGVNRA DHRAGDFFFEIVFQNLFAIADV LAINHAVNAQLRLRNP

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25155	55523	A	25293	365	722	TSCLSALAIK/QQHLDEKKELG HL SAGARRLLGIIVTF/CADSG VNLRYSAV*PAGAVVLPDAAV GGSDARTADAGALLGANVDCA VADRFLPLYLVALHLYAELGRS GQPGVRAVSALR
25156	55524	A	25294	798	1094	
25157	55525	A	25295	1	2780	MGIVASASVQAAEINYNDGKN LDVYGKVKAMHYMSDNASKD GDQSYIRFGFKGETQINDQLTG YGRWEAEFAAWTDMFPEFGG DSSAQTDNFMFKRASGLATYR KITSSAYRWPELNLQYHRCIS AARAMLLSGRPVMQINERTAV RRQMTVYLRVERIHEIDPLVSL SHSMSVIPIDVERPIAAAPCTPG LWRKTPLRVPSTYPLRLPGRA RVVCHRTFRLHLCKDWVFMFS GLLIILVPLIVGYLIPLRQQA
25158	55526	A	25296	66	300	QSTYCDNPPVPVSRGL*P*RRSS STSSAGYQK*RYCQHRHDPASR IRTVQRTDSQRTVKRKFMLLP EASVPASEIC
25159	55527	A	25297	240	424	RCSRDEHDFQLIANLRIVITFA TFA*CTA*LPLGNHVSVAAH*A G*GGAPVTAQVVFVQHG
25160	55528	A	25298	1	1425	
25161	55529	A	25299	1	471	
25162	55530	A	25300	1269	1390	
25163	55531	A	25301	601	1119	VAAGAV*RGH*NVQLGKLFV ASDLRINAIGGVVVFS*FIQGL TNAIGSGFNNAARCRKPTGQVA ADGGRDAGFFTIANNQCTYAA GIFFQCSGEFVGIFQFQFAIAGIR DTNLRQRFIAGRTDGTQHRFQ LRLNRPQRGVAEQCTIARTLAIS SRMAVYLVRLKVSISEL
25164	55532	A	25302	1666	1769	RLKRHPPLRPSWPPY*GTAHVW HFSPANWKPGL
25165	55533	A	25303	1	1970	MKDDIFFRTSGGGVTLSGGEVL MQAEFATRLFLRLWGVS IETAGDAPASKLLPLAKLCDE V LFDLKIMDATQARDVVKMNL P RVLENLRLLVSEGVNVIPLPLI PGFTLSRENMQALDVLPLNIR QIHLPPHFQYGEKPYRLLGK TW SMKEVPAPSSADVATMRMAE RAGLQVTVGKEGWVSIE TQGA LGTENRLADEDIRRADVALLIT DIELAGAERFEHCYVQC SIYA FLREPQVMSAVREV

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25166	55534	A	25304	2804	3494	LSLAEWKCLNPSQRALYREVM LENYRNLEAVGQLQPQSTQRIP *GRICNGDRLTSQKGLDLVLEA LPGLLEGGQLALLGAGDPVL QEGFLAAAAYPGQVGVQIGY HEAFSHRIMGADVILVPNRFE PCGLTQLYGLKYGTLPLVRRTG GLADTVSDCSLENLADGVASG VFVEDSNAWSLLRAIRRAFVLW SRPSLWRFVQRQAMAMDFSW QVAAKSYRELYYRLK
25167	55535	A	25305	1	1306	
25168	55536	A	25306	818	1658	
25169	55537	A	25307	2611	2826	
25170	55538	A	25308	609	2359	PPPKIAPVWGCRKKSIPARSKSI FCFALFFPFFLNGEILPESPCPF WTLFRNDGGKKRDPLAPVYLL GKLTISPGPICPDMIGVLFDSV RREVAHIGNVQHRFCGPLFLKL VEFIDFILTIDIAAIIQYLVVICE VDQRINQIAIATRIFRTGYTAAD LRQIILMQLLIFLVVTRFVALT TQFFHFFRCVTKNKDIVSDMI QHLDIRTVQRTDSQRTVKRKLH VTGAGSFRPCQRNLFQICRRN DQLRQANAVVRDEHDFQLIAN LRIVVDHFRYVIDQMNNVLRH VIGRSRLTAKNIHARYPLRIRVG LDAVIAEMASGLDPFWRPDVV HAHDWHAGLAPAYLAARGRP AKSEFTVHNLAYQGMFYAHH MNDIQLPWSFFNIHGLEFNGQIS FLKAGLYYADHITAVSPTYARE ITEPQFAYGMEGLLQQRHRERR LFGVLNGVDEKIWSPETDLLLA SRYTRDTLEDKAENKRLQNA\ MGLKVDDKVPLFAVVSRLTSQ KGLDLVLEALPGLLEGGQQLA LLGAGDPVLQEGFLAAAAYP GQVGVQIGYHEAFSHRIMGGA DVILVPSRFPCGLTQLYGLKY GTLPLVRRTGGLADTVSDCSLE NLADGVASGFVEDSNAWSLL RAIRRAFVL/WSRAGSWRYSAR AIRCCRKVSLLRRQNRTPVRWAF RLAITKHFRIALWAARTSFVWCP

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25171	55539	A	25309	1028	1632	TSASAGTARNFSSNFAVRTTGH STSEATSSSRI.SLK.SAL.PPIL.RAA SSASALMFFVIGDDFP.TSRRISG Y*SALSMVNSGSPIKRWPRITRS D*MPRMVAGMTLSP/MQQGHG VHRTHEVHV.VAPQRISFGIGSF AREVATIFGSSASV.FRR*YRNH APNLLTCLSCVCLQRRTPGQSPG RVFRFHD.PVAFRQVS.YFQRQTP IA
25172	55540	A	25310	1	336	
25173	55541	A	25311	1889	2257	SAMTFFPRSSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTCTGRTKCTSL APQRISFGIGSFAREVATRRPYR DIKEGFSQREAA.LPQSLRVVPQ TGTWSAAGAQA
25174	55542	B	25312	1	735	
25175	55543	A	25313	1439	1744	SAMTFFPRSSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPMQGHVPWQLMVVL WNTRQRWKPPSSPD.RYVNRAMS LPSRKGEMLK.PAPCRK
25176	55544	A	25314	1209	1972	SAMTFFPRSSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTCTGRTKCTSL APQRISFGIGSFAREVATIFGSSA SV/HFALHMGAIQPPAFIGSQT LSL.VNGNTATT.PQPSAALLGLP SASNAWAIAGPRFSISRSGCASA RLATFSARRRGASKPLNGCLLR ATLSSPD.KFQQGSTG.GMLWGV LRHSPKFSITADGREFTL.HWPN TGAMTGCATPGEYV.WYSTFDN TQRKYPPHWEL

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25177	55545	A	25315	1	1521	METQHRLMRTFQPRQQDWTY ALWGGVKKLRWLFFFLLWGLFLF AGEEELGIRQTRTNDFLVTGDN LLRIFRFDVGNEDKVRQQFAVV RIHREVLVTFHGVNQFRSRHR EEFLFEFCVTPKLNEGTTQRTN NRGIAVLNTGHRHPDLVAAVE QQLQQFTHTAYQIVPYESYVTL AEKINALAPVSGQAKTAFFHP GSETGENGVKMVRHTGTGP VIAFRGGVHGRTYMTMALTG KVAPYKIGFGFPFSGSVYHVPYP SDLHGISTQDSLDAIERLFKSDI EAKQVAAIIFEPVQGEFFNVA PKELVAAIRRLCDEHGIVMIAD EVQSGFARTGKLFAMDHYADK PDLMTMAKSLAGGMPLSGVVG NANIMDAPAPGGLGGTYAGNP LAVAAHAVALNIIDKESLCERA NQLGQRLKNTLIDAKESVPAIA AVRGLGSMIAVEFNDPQTGEPS AAIAQKIQQRALAQGLLLTCTG AYGNVIRFLYPLTIPDAQFDAA
25178	55546	A	25316	114	187	RSTISSVRYGDDAFKP* RQAWN VL
25179	55547	A	25317	105	317	YLFLLSRFNHWISMEKKLGLSA LTALVLSISWARVFSVCRKIW RQLPARQHCSSAGVLLALAFYC WPLPC
25180	55548	A	25318	1	593	
25181	55549	A	25319	1	729	
25182	55550	A	25320	1	1005	
25183	55551	A	25321	1	1361	
25184	55552	B	25322	1	2793	
25185	55553	A	25323	27	255	

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25186	55554	A	25324	225	1408	RIIYMHMESQKIWFALSTPMEIR NECCLPSSHSPKMYLGACLFPL SSSWGIDDRDDLRTIHRMIDN GHAARLAGFYHRWFRYSPECW RDYLAELNEQQQAYAQFVAST AECCGEGGIKAWDYVRMGFLS RMGVLNWNLSEESLWQSRH LRALRYYSNWRQYFAGYTFGR QYWQSPEDDHLPLREFLAQET TDVDIIRRAYLALLPSFHTETDP QGFKQLRHAYDDALPIAQSPAK SVLQPEEYEWALLVEMGLL HRIAMVQLSPAALGNDMAAIE LRMRELARTIPTDIQLYYQTL IGRKELPYRTCQLHACTSADTP LRKIPRFSGLHFYAFCPNIYSS YHSAAKYGGSCQPGSTAHLRG YYWRWHFIAGLCHADPHAHSS
25187	55555	A	25325	230	380	
25188	55556	A	25326	432	1247	PSQEPSVHGRWMA*KGHSRIV* WRAYD*THFNPVLKKSVSLSGS NIRHMLAEAEATTELDGTGPV LV*PNRH*PAYWMRAYLNLKK MSCRSFRKA*RW*CETQTIVV HRDRVDQGNHFDVVARHYH LYAFLRKERQLIFFKFYARIQY AG
25189	55557	A	25327	10	638	SSVPTAGSRYNHLRAPRYSPLF ANYSMSDRCKKFPF/LDSSGT* WFQ*RSVPLPILPDTSRHQL*C SDPTRNGPAIQACQRFHIVERV ARVHHARFAATVTVDHVVIDQ RFFQICRT/PWCRLHRHHWRSSS GTR*TF*SPARHFCLLHNDSSYR STARPTCSGTDVPDRRCSDAHL CDHWSGSRAHADTDAECWCL NPQPAPSLQLQCR
25190	55558	A	25328	803	1622	
25191	55559	A	25329	498	686	RPSYSVLQRLPSAVLLPY* RDWYHRTAGRRRDGNAGRQHQ NGCYPDPDRDGRSRAFRNP

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25192	55560	A	25330	1	2063	MKNFMENVLRYLSDDKWKPD AKASMTVGTNLDTVYFKRHGQ VTGNSAAFDHFDFAGISVEHL SSYGDLDPQEMPLILNGFEYV TQVGNDPYAIPLRADTSKPKLT QQDVTDLIAYLNKGGSVLIMEN VMSNLKEESASGFVRLDDAAG LSMALNKSVMNDPQGYPNRV RQQRATGIWVYERYPAVDGAL PYTIDSKTGEVKWKYHVENKP DDKPKLEVASWLEDVDGNRRR NFSNDARANGTAAFTDCETQT VVHRDRVDQGHNHFDLVARH YHLYAFRQFDGTSVSSTEVEL RTVAFEERSMTAAFSWTECTL QIRTCQNPTGKVTWCDELEIM ADLCERHGVVISDEIHMDMV WGEQPHIPWSNVARGDWALLT SGSKSFNIPALTGAYGHIENSSSR DAYLSALKGRDGLSSPSVLALT AHIAAYQQGAPWLDALRIYLK DNLTYYADKMNAAPFELNWQIP QSTYLAWLDRPLNIDDNALQ KALMDQEKVAIMPGYTYGEEG RGFVRLNAGCPRSKLEKGVAG LINAIRAKKSATMIDTTLPLTDI HRHLDGNIRPQTILELGRQYNIS LPAQSLTLIPHVQVIANEPDLV SFLTCLDWGVKVLASLDACRR VAFENIEDAARHGLHYVELRFS PGYMAMAHQLPVAGVVEAVID GVREGRCTFGVQAKLIGIM
25193	55561	A	25331	2	696	FLLLLWEIRKSSQQTPTPTMNA AEMAQLVAGVDEVGRGPLVG AVVTAAVILDPARPIAGLNDK KLSEKRRLLALYEEIKEKALSWS LGRAEPPEIDELNILHATMLAM QRAVVGLHIAPEYVLIDGNRCP KLPMAMAVVKGDSRVPEISA ASILAKVTRDAEMAALDIVFPQ YGFAQHKGYPTAFHLEKLAEH GATEHHRSSFGPVKRA/LGTCV LILVSRLSKPESEDVL
25194	55562	A	25332	2	63	
25195	55563	B	25333	138	182	
25196	55564	A	25334	356	706	ISDICAPNMVSAIHAIPYTATMA IIPERKTSFFEIDAGLVLVRIIISA PVSSINI*ITSIDSGLPKDGRRS ESAPRRATTAIAPRKIHIAISQLL VVIIIRSLVGCRRMRWRVLSLD
25197	55565	A	25335	1746	1873	

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25198	55566	A	25336	1998	3626	PKAARMANVPNNNTTGTAMVGI SVA/RHILQEIQHHQEHQHNGFE QRFYHFVNRKLDEWGRVIRVE NLHS/AAGRMAVIPPVLP*WLS RYREHSRRLPA*SPKGEAASNP EVIARTLRKLKNQPELSEDTIKK AVESLSLELVLTAHPTEITRRTL IHKMVEVNACLKQLDNKDIA YEHNQLMRRLRLQIAQSWHTD EIRKL RSPVDEAKWGLCRNGK TACGKAYQITWALNKQLEEK PRLQTCPSKFGSGPFYF
25199	55567	A	25337	243	604	PRFPFPLPPATSSVQTAMTDG*N ECERICVGYLRYSSHSAPDARR QARHTHPVVGKHALPALTKAT HPSWWWQCAAMAEDSTDARQ LKA*WGVNGFLDRSATMDGR LYPVAMCLLPATK
25200	55568	A	25338	1	3287	MPITLRRSVEKEQLIEIANTIMPF GKYKGRRLIDLPEEYLLWFARK DEFPAEARYTHIDLHVPAPLLV MFTLDTRQSACDRNPHLPIHVC SSWTSKCAPRLWTRALLPRTR TPPYATGTTIGSRASWVFTPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLHKM VEVNACLKQLDNKDIADEYHN QLMRRLRLQIAQSWHTDEIRKL RPSPEAIMTEQEKTSVVEETR EAVDTTSQPVAT
25201	55569	A	25339	1	1425	
25202	55570	A	25340	534	1391	RQKRRLYQTYWYKQPRYLPP EHRQRHRHQSAQVSRPYSYG EVRPLSQYQPEWQCWEPDVEW VRQPPQDAITDPDFCFYQPM TFEQFVREFAEWSQKRPAAM MIGIRADESYNRFVAIASLNKQ RFADDKPWTGGHSWYIYPIYD WKVADIWTWYANHQSLCNPL YNLMYQAGVPLRHMRIPEFG PEQRQGLWLHYHIEPDRWAA MCARVSYGYTTGGLYPGQARG AAV*TEALKPSGLPQVCALNQC LLSVHRYAGHVRQERCDGADG RPAVHERRQLL
25203	55571	A	25341	786	1009	HHSHEQQFQWPVGASGVDRW AVYLHQICPLTQFQY/WCRARQ EGIMSSPGQQVGFIA*VTSSFS R*KGRRVSSA
25204	55572	A	25342	2446	2970	
25205	55573	A	25343	1	2184	

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25206	55574	A	25344	706	1293	IHRLLRRIHQIIDLRIWQRTVEI HGAPVRFIQMAAWTHIAVLLT* QLRQLRAGFQRNSWAIFYFFHH RKQYIFHFDLRRFPVIMHALFC AVQRCADLMAHRRQKRRFCLA GFFCFRPLSVFYHQFLQFSCTR FDLRRQLFAVAIQCMNIAFAAA LVDFDLDPIDGITLARQLAQQY PSLVLIGFAHVHIDETLQ
25207	55575	A	25345	1	3291	
25208	55576	A	25346	882	1019	
25209	55577	A	25347	1	2265	
25210	55578	A	25348	284	535	CVAASVTGTRVLPIPLLNRRSR RSPVRYVSKGNWWGVSVCNCAS NNSNSVSR*SLPPMRSHAWRKV RRIMRQLPLERPRPGFTI
25211	55579	A	25349	131	208	LVRWLLSPGW*WKISPIISICLFP V
25212	55580	A	25350	1	3108	MDSQDKYFEATQTVYEWCGV ATQLLAA YILLFDEYNEKKASA QKDILIKVLDDGITKLNEAQKS LLVSSQSFNASGKLLALDSQL TNDSEKSSYFQSQVDKIRKEA YAGAAAGVVAGPFGLIISYIA AGVVEGKLIPELKNKLKSVQNF FTTLSNTYKQANKDIDAACKLKL TTEIAAIGEIKTETETTRFYVDY DDLMLSLLEAKKMKMINTCNE YQKRHGKKTLETYLTDPVTF RERLQMSIYKIPLPL
25213	55581	A	25351	1	296	
25214	55582	A	25352	3	164	VGD/NVGTARWGIFALIIVETL AWFTVVASLFAQHKQRAENLI QRLHLLWSFNP
25215	55583	B	25353	91	990	
25216	55584	A	25354	1146	1881	RCGVQWMTYIRAVFVNLTNP KSIVFLAALFPQFIMPQQQLM QYIVLGVTTIVVDIIVMIGYATL AQRIALWIKGPKQMKALNKIFG SLFMLHNAFAWFLGAFLLTVI AWFLLGNAQKMPQTTLQWGIL VFLGVVASGIGYFMWNYGATQ VDAGTLGIMNNMHVSAGLLVN LAIWHQPHWPTFITGALVILA SLWVHPNKRFRNWLTLIAIAH GGVQSAPQAFQAQGFHHQTALA LKTLYYPMR
25217	55585	A	25355	1943	2287	
25218	55586	A	25356	44	274	

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25219	55587	A	25357	876	1400	YRHRVDRSPGNDRLFETWRSAG CAARLLRQSGETRLLSRVVRDY GGRWPVSLLDGLPDATWCTEK RGGFCTCATGRAGEKWAQFPE\
25220	55588	A	25358	1	1428	SLLTNLANPKAIIFYGSVFSLFV GDNVGTTRAWGIFALIIVETLA WFTVVASLFALPQMRGRYQRL AKWIDGFAGALFAGFGIHLISR
25221	55589	A	25359	421	797	IIFPFLLFHLCNQLSHLLQYAVV NAPVRRILPIQLLWQQLIQGGEK LKSIRRAIQHIGQTIIGMFQIMP IMIAIYETDRATGDGI/WAAH*T HEYPCHVRSQSFHENHDDVQE NPPHPWKIQTPGH
25222	55590	A	25360	1	1320	
25223	55591	A	25361	1	1251	MLLSIITVAFRNLEGIVKTHASL AHLAQVEDISFEWIVVDGGSND GTREYLENLNGIFNLFVSEPD NGIYDAMNKGIAAQQGKFALF LNSGDIHFHQAANFVRKLKMQ KDNVMITGDALLDFGDGHKIK RSANRAGLFLIGYAGFRIIVEFF RQPDQAFTGAWVQYISMGQILS IPMIVAGTMKQYLELMQKVLD EGTQKNDRTGTGTLISIFGHQMR FNLQDGFPLVTTKRCHLSRIHE LLWFLQGDGTNIAYLHENNVTI WDEWADENGDLGPVYITTVL NQLKNPDPSRRIIVSAWNVGE/ LDKMAIAPCHAFFQFYVPDGG LSCQLYQRSCDVLGLPFNIAS YALLVHMMAQQCDLEVGDFV WTGGDTHLYSNHMDQTHLQLS REPRPLPKLIIRKPESIFDYRFE
25224	55592	A	25362	3	1327	

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25225	55593	A	25363	1	2443	MGLIGFVLTALWIKLIHNPTDH PRMSAEELKFISENGAVVDDMD HKKPGSAAASGPKLHYIKQLLS NRMMLGVFFGQYFINTITWFFL TWFPYILVQEKGMSILKVGLVA SIPALCGFAGGVLGGVFS DYLI KRGLSLTLARKLPVLGMLLAS TIILCNYTNNTTLVVMLMALAF FGKGFALGWPVISDTAPKEIV GLCGGVFN VFGNVASIVTPLVI GYLVSELHSFNAA LVFVGCSAL MTMSARSATGHECVFWCNGKP RRLAMRLIYWCAAAPTGDVVQ KLTGKWALIANSHRAGQPTRN VNEEVGQRLLEEMEWYDNYL NMGKTDRSANPSGKKGGLA NVVEKALGSIKSGKSAIVEVL SPGQRPTKRGLIYAATPASDFV CGTQQVASGITVQVFTTGRGTP YGLMAVP/SH*NGNWKITASVT SIQPNTNELPNCCMNGVSTANT TSKSSLVICALR

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25226	55594	A	25364	1	2701	TFFLPAGEILPPRLEPQITLPVGS RRIISIAVTDLPEPESPHLRSGLG WASLCCFMVICKFFPAEGLIL AAVCDSSRGSRVWCNGNRRYG YASDLLVRCGATVMFSEVTEV RDAIHLLTPRAVNEEVGKRLLE EMEWYDNYLNMGKTDRSANP SPGNKKGGLGKRGSSKALWLP LLQIQARKQVGLRVYTVACVL RTGTWYDRNGPDWRVPGQLN MGNPAPETGRYLAHPATPHD PRITPDHPHSIKPHAPTNNQPPDT LTPTHHHHTDTRDPPPPRTRT PRQSTHTTTPHPTTTTRHTDIHP PTHITNPPPTRVLTQLHHTNRI IPHRTHTTTTCRRNHHNQMNNTT PPPPHTPQITHRHNTTLREQTQ KHRQHIHGTQHHTTRKPTPTT RQYNTSIVGTIGGIMVERKVIE ESLQALQERKPRLFHGRMARN GADAVGSDCGGAMS FSVIHG MRPRLVLIGAGHVNRAIQSAA LLGFDIAVADIYRESLNPELFPP STLLHAESFGAAVEALDIRPD NFVLIATNNQDREALDKLIEQPI A WLGLLASRRKVQLFLRQLRE KGVAAEEHIALHPVGYNIGAE TPQEIARVLAELQVKNNAPGG LMMKPSHPSGHQM VVIRGAGD IASGVALRLYHAGFNVMILEVE KPTVIRCTVAFQAQAVFDGEMT VEGVTARLATSSAEAMKLTERR

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25227	55595	A	25365	1	1262	MGNWHLSPCPAPAPGHSCFLFL VGTSRILAVPGHTGSKAINKA ALLLESYMSQALKNLLTLLNLE KIEEGLFRGQSEDLGLRQVFAG QVGGIQLYAAKEPVPEERLVH SFHSYFLRPGDSKKPIHYDVETL RDVAPVLDVAGATPPTIRHQRV TALVAPKNGSRDVRSCAGKMP TDGSIKAVLLPFQVSTIGGVITYE RVGTDQGPQCPHVQRSSAVR PGPEAAPGDNSYPPYEDRSTCG MQAPDASYSANPDLSFTWSPCL SEDALHTSPLYCTTPTSGGEAF KGLASDLVPHEDKMVLQNGKC FTSPRHTEWAVLRAGHALARG RNLLDLAAGGMAWVMSQEC PGPGTICSRDLQGTCLRMQIL PPKDPVTRGSGTHCNAGTKRELE EFSSQVTLTALIQPLMQVSAQF RAADGAP
25228	55596	A	25366	2	176	
25229	55597	A	25367	1	1395	MRESLEPRDLLNCCDQANANS DMDMKSRLRGYQMEIMNLLG AGVKDFELESDDLVLVEEISK QQSIHDVAWLLLVAFVYICEQR NDLKSLEIFTREAEHKSLENLEP DHVPEELDTSARNAGALTRRRE IRDAATLLRLGLAYGPGGMSLR EVTAWAQLHDVATLSDVALLK RLRNAADWFGILAAQTLAVRA AVTGCTSGKRLRLVDGTAISAP GGGSAEWRLHMGYDPHTCQFT DFELTDSRDAERLDRFAQTAE IRIADRGFGSRPECIRSLAFGEA DYIVRVHWRGLRWLTAEGMRF DMMGFLRLGLDCGKNGETTVMI GNSGNKKAGAPPARLIAVSLP PEKALISKTRLLSENRRKGRVV QAETLEAAAGHVLLTSLPEDEY SAEQVADCYRLRWQIELAFKR LKSLHLDALRAKEPELAKAWI FANLLAAFLIDDIISHRWISPPPE
25230	55598	A	25368	482	765	

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25231	55599	A	25369	1	1575	MGSVTKSRGPTDSSAFFQINRD YSFLDYILGGCQIMFTPWARLL QSTCCEQCSKKAHQDLADLA SILPSNTTPLIVSDAGFKVPWYK SVEKLGWYWL SRVRGKVQYA DLGAENWKPISNLHDMSSSHSK TLGYKSLTISNPISGQILLYKSRS KGRKNQRSTRTHCHHPSPKIYS ASAKEPWILATNI.PVEIRTPKQL VNIYSKRMQIEETFRDLKSPAY GLGLRHSRTSSSERFDMILLIAL MLQLTCWLAGVHAQKQAFRF MRLVDGTAISAPGGGSAEWRL HMGYDPHTCQFTDFELTDSRD AERLDRFAQTAD EIRIADRGFG SRPECIRSLAFGEADYIVRVHW RGLRWLTAEGRFDMMGFLR GLDCGKNGETTVMIGNSGNKK AGAPFPARLIAVSLPPEKALISK TRLLSENRRKGRVVQAE TLEA AGHVLLTSLPEDEYSAEQVAD CYRLRWQIELAFKRLKSLHLHD ALRAKEPELAKAWIFANLLAAF LIDDIISHRWISPEVPDPKRRT
25232	55600	A	25370	1	1341	MAGGRKFPDGGDRITLCLGSQ PGVLAPRSPEKRRAINQRYPSK TGQLPASITDMMRTARHHLG NGISVPKGAELAHPTVLELFAI SAKPIHPEELDTSARNAGALTR RREIRDAATLLRLGLAYGGG MSLREVTAWAQLHDVATLSDV ALLKRLRNAADWFGILAAQTL AVRAAVTGCTSGKRLRLVDGT AISAPGGGSAEWRLHMGYDPH TCQFTDFELTDSRDAERLDRFA QTAD EIRIADRGFGSRPECIRSL AFGEADYIVRVHWRGLRWLTA EGMRFDMMGFLRGLDCGKNG ETTVMIGNSGNKKAGAPFPARL IAVSLPPEKALISKTRLLSENRR KGRVVQAE TLEAAGHVLLTSL LPEDEYSAEQVADCYRLRWQIE LAFKRLKSLHLDALRAKEPEL AKAWIFANLLAFLIDDIISHR WISPEVPDPKRRT
25233	55601	B	25371	1	1233	

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25234	55602	A	25372	1	2197	SHSRGSPGKAVDFTLVSHA AW FGLPHFSTPAFNGQAMMLIAPV AVILVAENLGHLLKAVAGMTGR NMDPYMGRAFVGDLATMLS GSVGGSGVTTYAENIGVMAVT KVYSTLVFVAAAIAVAMLLGFSP KFGALIHITIPAAVIGGASIVVFG LIAVAGARIWVQNRVDLSQNG CNPAYAEHHQHPGYSCLKTR VSFSLRIISTNLRRRECRAQFRF HVDASARHGFRLLWQIQGVAQP VFHITIREVEAAMRATAFGTEVG RNSRCIRRFHQVIQFQALNALG VELAGIDSRDRLKVLLEEMKRT FHWGRQTISKHIIWGLMLGR AMTPLMLDATSGKLTVDGA HAGAAMGILAVTADQNSAELA YYKSGSFRIEDVLWPSAVTDDN IKRNAFAADGSVNSYSVPFSSV PLLQRQGRIKYAVTLAKYRTNS NEQQESKFAQATLQWGGPWGT TWYGGGQYAEYRAAMFGLG FNLGDFGAISFDATQAKSTLAD QSEHKGSYRFLYAKTLNHLG TNFQLMGYRYSTSGFYTLSDT MYKHMDGYEFNDGDEDTPM WSRYYNLLYTKRGKQLSLISK RLLESENRRKGRVVQAEETLEA GHVLLLTSLPEDEYSAEQVADC YRLRWQIELAFKRLKSLHLDA LRAKEPELAKAWIFANLLAAFL IDDIINSHRWISPPERIPSARKWT
25235	55603	A	25373	1	2754	
25236	55604	A	25374	1	652	
25237	55605	A	25375	1	1800	

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25238	55606	A	25376	1	2187	MAGPRYPVSVQGAALVQIKRL QTFAFSVRWSDGSDTFVRRSW DEFRLQKKTLKETFPVEAGLLR RSDRVLPKLLGQASLDAPLLGR VGRTSRGLARLQLLETYSRRL ATAERVARSPTITGFPAQPLDL EPALPPGSRVILPTPEEQPLSRA AGRLSIHSLEAQLRCLQPFCTQ DTRDRPFQAQAESLDVLLRHP SGWWLVENEDRQTAWFPAPYL EEAAPGGGREGGPGSLGSSGPQF CASRAYESSRADELSVPAGARV RVLETSDRGWVLCRYAGAGPE ELDTSARNAGALTRRREIRDA TLLRLGLAYGPGGMSLREVTA WAQLHDVATLSDVALLKRLRN AADWFGILAAQTAVRAAVTG CTSGKRLRLVDGTAISAPGGGS AEWRLHMGYDPHTCQFTDFEL TDVRDGERLARFAQPPDEIRIA DGEFVWRPKIRSLAFGEADYI VGVHWRGLRWLTAEGMRFDM MGFLRGLDCGKNGETTVMIGN SGNKKSPGPPFRARFIAVSLPPE KALISKTRL/LSENRRKGRVVQ AETLEAAGHVLLTSLPEDEYS AEQVADCYRLRWQIELAFKRL KSLHLDALRAKEPELAKAWIF ANLLAFLIDDIINSHRWISPPPEV PDPKRRTNSLWRITKMVIVSLQ VAIRGTVSLTAPSLCNSACCCC VSTNSATTLNDFAFARSVIDLTI
25239	55607	A	25377	2	333	RLGVWQDILSRASCYHGMV WDKDSFGHISFDDQSMGYSHL GHIVENSVIHYA/ARLVIGADGV DSWLRNKADIPLTFWDYQHHA LVATIRTEEPHDAVARQVFHGE AFW
25240	55608	A	25378	3	235	VAVLEQRVHEPLAANAPPQLR VS/ARLGVWQDILSRASCYHGMV WDKDSFGHISFDDQSMGYSHL GHIVENSVIHYA
25241	55609	A	25379	1	774	
25242	55610	A	25380	1	1076	

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25243	55611	A	25381	1138	1737	SVSTEPSVA AFSSIKLRQDPH/ DNLHHQYN*GDIAFC\FTPYFH NCLCQS*WARAFQ* RANEF* R MNCTQLARTSGSHHLLPLTLRF* QICISSGQLIQYVVCRFIHPPEH RLTIHPLAGQGVNLGFMDAE LIAELKRLHRQGKDIGQYIYLR RYERSRKHS AALMLAGMQGFR DI.FSGTNP AKKLLRDIGLKLAD
25244	55612	B	25382	1	735	
25245	55613	B	25383	1	1941	
25246	55614	B	25384	847	849	
25247	55615	A	25385	1	1227	
25248	55616	A	25386	324	1533	EGFMEHQ RKL FQORG YSEDLL PKTQS QRTWKTFNYFTLWMGS VHNVPNYVMVG GFFILGLSTFS IMLAII LS AFFIAAVMVLNGAAG SKYGV PPFAMILRAS YGVRGAL VPGLLRGGIAALMWFLQ RGS PFYDLIQTALSSPHKV TIEQFYR EVGVFLGIALIAVVISVLNNFFV SHYVFRWRTAMNEYMANWQ QLRHIKGR TAFINAIMTLIAFLP VLVTLSAHVPELPIIGHIPYGLVI AAIVWSL MGTGLLAVVG IKL P GLEFKNQ RVEAA YRKELVYGE DDATRATPPTVRELFS AVRKNY FRLYFHYMYFN IARILYLQVDN VFGLFLLPFSIVAGTITLGLMTQ ITNVFGQVRGA FQYLINSWTTL VELMSIYKRLRSFEHLDGDKI QEVTH TLS
25249	55617	A	25387	1526	1683	
25250	55618	A	25388	2709	2918	CWCFWHR RSCCGSVRYALS AV PGCCQPET*RRRFPHSAF*RFRS SETGQTGA YVSGPDLQPERLQR LWC
25251	55619	A	25389	1	1812	
25252	55620	A	25390	134	386	RLKPSAAIRRRVSSSRISTPLNPA STTAFVGTDC AIPRLRATSGLA GSPLIQNRFCRARQPRWSAPVA RHA AVYARHWRNQII

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25253	55621	A	25391	181	1630	RIRQFCFYHHCVLTLAICAFIVIT LTIWVSFRVSVLVFAMADDIKV AVVGAMSGPIAQWGDMEFNG ARQAIKDINAKGGIKGDKLVGV EYDDACDPKQAVAVANKIVND GIKYVIGHLCSSSTQPASDIYED EGILMISPGATNPFLTQRGYQHI MRTAGLDSSQGPTAAKYIETV KPQRIAIHDKQQYGEGLARSV QDGLKAANANGVFFDGITAGE KDFSALIARLKKENIDFVYYGG YYPEMGQMLRQARSVGLKTQF MGPEGVGNASLSNIAAGDAAIEG MLAPVLITVDQPFVQAGFQPLR RLLPAHETGRRTRAYGVGRLT RQIRRIQIATTFRHNAQAAESKD FQWYRCDPQLFHLMNROHAR QHHSNVKAMIKVNRFLFIGR RSLHRYVALNMRITLGGVLLHH GEVGEDQRVGTQLRRHIHGAL PTGVTVMRKS VN RDVKFAA MLMDKTHRFLQFFLGKVKAGE
25254	55622	A	25392	2	505	
25255	55623	A	25393	1	2038	
25256	55624	A	25394	188	1771	GKQTSTSPAGWENSLRMRYT MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDDMMNWP VLLKSVSR LGNSEQQGR LF GFF ETGRGIVDTTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKD KTIWLI AFN VFFVYAVYCGLTF FIFLKN IYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVSVRVKGTASQ GQKIPEEFKQFFGDDL PDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQ LNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLN FIQT DASINRGNSGGALLNLNG ENPIDQLKVVG RPHDRIDGPLK TTGTARYAYEWHEEAPNAA YG YIVGSAIAKGRLTALDTDA AQK APGVLA VITASNAGALDKGDK NTARLLGGPTIEHYHQAIALVV AETFEQARAAASLVQAHYRRN KGAYSLADEKQTVNQPPEDTP

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25257	55625	A	25395	356	849	GSACRVREIPRPASQMP/HTLPA GSRPPGSEAEPPGEAAAPPARRE AHQIPRRRGHLPSSPGPRTHVA AHNIRVVTEAHADSHALLSDLG AAPFVMSRILRVDGEDPPHV DESIQPTTENAVVFRPVQLTSAI ETGGKEEPYGLSAASLGRAESS AASLAGRR
25258	55626	A	25396	154	379	LVPRLLKGLDLPSEINPLSSCSLV REKDPPTTSCHTT/NPRNISPIS NPDSTGNRTVQLTW*PLPEPLE LWPKAL
25259	55627	A	25397	4761	5127	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQT/TSPRNISPISNPHTR TSKRLNRSQGAFQLNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL
25260	55628	A	25398	1	753	MGSWLQGLRAMVFALNYMVT RVRNKKDPPITSGPQT/TSPRNI SPISNPR/PKETRFICGPKTPAPL MDWEGSLPLMFNHCRDTSIIH PCFQGVPRCDACLSPSPLAASP AFLGKGQVPLNPFFTLGKSRF SGGGASTPTPSFHVSTPSLLFW GRGKYPTSPSPLVASPAFLGK GQVPLNPFFTLGKSRFSGEGA KAPETITDAELRVTLTVEAAVC STIALSLGWEILPRHWGKEEVT KTIYYVIP

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25261	55629	A	25399	174	2238	LRSGLDPWEINPLSSCSLLHEKD PPTTSGPQTVTSRNPISPNRQR RHILSMDPKLRRRSWTWVGSPL LVFNHCRDASLIHPGFRGVRPR RDVCLGPSPLATTIDAEYVTL TVEGKSIPFLIDTEATHSTLPSFK GPVALASIHVQNVQIKRDKEGH YIMVKGSIQQEELTILNMYAPN TGAPRFIKQVLNDLQRDLDSHT IIMGDFNTPLSLDRSTRQKVN KDIQDLSALHQADLIDIYRTL HTKSTECTFFSAPHRYSKIDHI VGSKALLSKCKRTEIINCLSDH SAIKLELRKIKLTQNHSTTWKL NNLLNDYVWHKEMKAEIKM FFEINENKNTTYQNLWDTFKAV CRGKFIALNAYKRKQERSKIDT LTSQLEELEKQEQTRSKASRRE EITKIRAELEIETQKTLQKINES RSWFPEKINKIDILARLIKRR EKNQIDAIAKNDKGDIATDPTEIQ TTIREYYKHLCPNKLLENLEMD KFLDTYTLPRLNQEEDESNNRPI TGSEIVAIINSLPTKSPGPDGFT AKFYQRYKEELVPFLQKYKEEL VPFLKLFQSEKEGILPNSFSEA SILIPKPGRDITTKENFRPISLM NIDAKILNKILANQIQQHIKKLI HHQDQVGFIPGMQGWFNIRKSN VIQHINRTKDKNHIISIDA EKA FDKIQQPSC
25262	55630	A	25400	3	267	EKDP LTTSGPQTVTSRNPISPN LRLFAFTWTDPDTHQAQQITW AVLPQGF TDS PRYFSQAQISSLS VTYL IILIKTHVLSPIMSD
25263	55631	A	25401	167	408	LGSRTFPWEINPPSSCSLLREKD PPTTSGPQTVTRPNISPNLVS GLFLLSSPTSLTIPQLPSSFNDD TLQSLPSLNF
25264	55632	A	25402	142	441	LRLGDL PWEINPLSSCSLLCEKD PPTTSGP/PRNPISPNVSGFLFL SSPTCLTIPQLSPFNLGATLQSL PSLNFNSFHLVETKETRFIRGP KITAP
25265	55633	A	25403	79	381	LGSGLDPWEINPLSSCSLLREKE PPTTSGPQTVTRPNISPNPELA TLAGNLATGPRNARSPGFLLSH VLSVWDPTENQTVQLTWQPLP QPLELWPKAL

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25266	55634	A	25404	1	511	MWKGPKGLDMYGYKSSVSPKTS DILGRDTLLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLPWEINPLSSCSLLHE KDPPTASGPQTTSRNPISPLNR VSEVSDHAGTPALVLHP
25267	55635	A	25405	570	1182	LGSDDL PWEINPLSSCSLLHEK DPPTTSGPQTTSRNPISPLNH ALKGLKPAITRLQHGLLKPNIS PYNSPILPVLKPKPKYKLVQDL CLINQIVFPIHPVVPNPYTLSS PPSTIHYSVLDLKLAFITPLHAS SQPLSAFTWADPDTHQVQQT WAVLPQSFTDSPHYFSQAQISS LSVTYLSIILKTHVLSLPIVSD
25268	55636	A	25406	489	615	LRNTWNSPRLMACALHSGSPSC TWGPYS*SGLSENLASQRVCP YQENNVGRVRDTEIKEHCYEES SYRAATQIQVRKVGIIPEYPPFM ASLRTHCICETCYEMKISFSKS LNPLEKNKKSQPANCAVKEVS EQLRRRQAFSVAAGLKGGKSP AQSIKRNKQKPYQHFQTLQQLL PLQWAPCYGSPNFATHGTHQG LWLVLSTVAAQAVPGALIAEA TALLAWIQGAVS
25269	55637	A	25407	579	715	LGSDDL PWEISPLSCSLLHEKD PPMTSGPQTTSRNPISPLNLR
25270	55638	A	25408	1553	1896	
25271	55639	A	25409	964	1332	SCRFIIRYQACCNLHPGEINSH VAHTKPVWWSLHTDTHENCHL NTAVFFYHWWLAEFFLNPLRR/ CSC*HSLPGQFPVSLCLRVLSVD CAHPWGKPEAPS*HPGPWFQS SLPSPLWPLYQHP
25272	55640	B	25410	1	717	
25273	55641	A	25411	590	1142	PNSSWMRGEPKKDPPTSGPQT TSPRNISPISNRP/KETRFIGP KTPAPLMDWEGSLPLMFNHCR DTSIIHPFCQGVPRDACLSP SPLAASPAFLGKQVPLNPFFTL SGKSRFSGGGASTPTPSFHVSTP SLLFWGRGKYPSTPSSPLVASP AFLGKGQVPLNPFFTLSGKSRF SGEGA

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25274	55642	A	25412	1	790	MGLVHLQRQSYWTVQRSSINH FLGCNPHTGKDKTLYMRWTKS FRKVEDPPTTSGPQTDQPKKHL TKFKSETKETRFIHGPKTPAPV MDWEGSLPLVFNHCRDASLIH SHFKGVRPRDACLGPSPLAAS PAFLGKGQVPQPLISLCPDPLFP HPNLISLRPNLCPHPDLVSLCP DPFPAFLAHKNFQTPPEPQQGI PPEPPPPGACYKC/HEI*PPGQG MPAAQDSS*AMS/LSVRDPTGN QTVQLTWQPLPEPLELWPKAL
25275	55643	A	25413	1	736	MQAMEKWREAKVETEDQK NQYQQTWLSDSASGYRYTKLP FYFRHNLIPLAHLFLDLSYS DLLTAFFMQFWLSAQMSDDQ RGLPGYLLWAEISLLEISELTS GKQDSSWPEVKAGLKKEANYL SSDSARLHPGEINSLVAHTKPV WWSLHMDTHEIWCRRDNNWGD LPWEINPLSSCSLLHEKDPPTTS GPQTATSPRNLPISNPPSKHQE KPPEAISTLPNAAATAAAAVGS LLWSL
25276	55644	A	25414	1644	2010	LGSGLPWEPNPPSSCSLLREKD PPTTSGPQTATSPRNISPINPHTR TSKRLNRSQGAFLQNLPPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPELELWPKAL
25277	55645	A	25415	1	1035	MGKEYSLDVKKSIVFKDNRS QGNRLQKLGLDTRREDAMGF GSHRAKLTVAALGACHCPEN EGQTVLPSSSTSGRSDKRERSA GYTPFFVKEGVPSPLFKLHV RCCSIQSIHISRRSQNCAEDVIR KTKTDQAVSSMSSAPVTVQQL NIIPALLVALTCGWAFLMVSQ EQYDEASKQAASFNNAVIPVY MSHMSKTLYKSEVFPINTYAQK ICFIAHTKPVWWSLHMDAHEI WCRGRSTDLPWEINPLSSCSL LREKDPMTSGPQTATSPRNISP LNQELATRAGNLATRPRNACSL GFLLSRISSVWDPT*KFGLVQLT LGKPLPEPLELWPKAL
25278	55646	A	25416	174	393	LRSGLPWEPNPLSSCSLLHEKD PPTTSGPQTATSPRNISPINPGET KETRFIRGPKTPAPVMDLGRQP SLGV

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25279	55647	A	25417	2	4574	WDVLGAVIGTECGTIESGLSMV FLKDGGERKLCPTSMDDTTGYGN LRFYFVMAKWYIPENVVKGR KEIILVLDFTWCMVHRGICDPG NSHENDIILYAKIEGRKEHITLD TLSYSS/L/SSLYWPVMSQILFW QRTVH*TWLQL*DGIPDIPNVY F*KLWQFQALLP*LLLYPWC* SQLWLWCLGQW*GPGFQQRW AASANYIFP*QLTIQNNLRRTTR *CKAVVNSVQMVA TVSFFPER RCMGY**DYHDICA
25280	55648	A	25418	1	363	
25281	55649	A	25419	1	301	
25282	55650	A	25420	2	309	
25283	55651	A	25421	3	512	YIGPSCCLKFCSGRGQCTRHGCN CEMASQTFFPMFISEFSGSRLSS YHNFYSIRGAEVSFSGCVLASG KALVFNKDGRRQLITSFLDSSQ SRIISVELPGDAKQFGIQFRWW QPYHSSQREDVWAIDEIIMTSV LFNSISLDFTNLVEVTQSLGFYL GNVQPYCGHDWTL
25284	55652	A	25422	2	878	
25285	55653	A	25423	1	750	
25286	55654	A	25424	1	1404	

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25287	55655	A	25425	1	2506	GCSRLLVTVDLNLTAEPFIQFY FMYGCLITPNNRNQGVLLLEYSV NGGITWNLLMEIFYDQYSKPGF VNILLPPDAKEIATFRFVWQPR HDGLDQNDWADNVLSIGSAD QRTVMLDTFSSAPVPQHERSPA DAGPVGRIAFDMFMEDKTSVN EHWLFHDDCTVERFCDSPDGV MLCGSHDGREVYAVTHDLTPT EGWIMQFKISVGCKVSEKIAQN QIHVQYSTDFGVSWNYLVPQC LPADPKCSGVSQPSVFPTKG WKRITYPLPESLVGNPVRFRFY QKYSMDQWAIIDNFYLGPGCLD NCRGHGDCLEQCICDPGYSGP NCYLTHTLKTLKERFDSEEIKP DLWMSLEGGSTCTECGILAEEDT ALYFGGSTVRQAVTQDLRLG AKHDYILLPEDALTNTTLRW WQPFVISNGIVVSGVERAQA LDNILIGGAENPSQLVDTFDDE GTSHEENWSFYPNVARTAGFC GNPSFHLWYPNKKKDKTHNAL SSRELIIQPGYMMQFKPFGCRS DSWQLVQTQCLPSSSNSIGCSPF QFHEATYNSVNSSSWKRITQL PDHVSSSATQFRWIQKGEETEK QSWAIDHVIYGEACPKLCSGH GYCTTGAICIDESFQGDDCSV FSHDLPSYIKDNFESARVTEAN WETIQGGVIGSGCQQLARYAH GDSL YFGCQIKRAATKPL/DL
25288	55656	A	25426	146	10561	GGGGGGGGGGMERSGWARQT FLALLLLGATLRARAAAGYYP RFSPPFFLCTHHGELEGDEQG EVLISLHAGNPTYYPGQEQYH VTISTSTFFDGLLVTLGLYTSVS QASQSIGSSAFGFGIMSDHQF GNQFMCSVVASHVSHLPTTNLS FIWIAPPAGTGCVNFMATATHR GQVIFKDALAQQLCEQGAPTD VTVHPHLAEIHSDSILRDDDFS YHQLQLNPNIWVECNNCETGE QCGAIMHGNAVTFCEP
25289	55657	A	25427	1	296	

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25290	55658	A	25428	1	557	MARSLGLV.LVALFPPLPVGFNAE EAHNIVKEFSPGKSHPRESLSQQ RETLVQAGAFHWFGWRGKEK LKPKNFTFGRLPNEMLEQWLSP TNQCV DGV/LKGGEDVYNHNNI NQWTASIVEQSLTHLVKL GK A YKYIVTCAVVQKSAYGHTASS CFWDTTSDGTCTVRL/WENRT MNCIVNVFCHCLFVL
25291	55659	A	25429	178	2270	VRRLLFCVQTGGSPVGRGSLHHL WLVFHVL.SLLCSPCLLAPGM WGFHDRDLVLRKALYTM MRT GAEREALKRRWRWQQTQQNK ESGLVYTEEEWEREWTELLKL ASSEPRTHFSKNGGTGGHLP EGKPLHGCSLLRSGKGGHV K AEP SRLQQSQAKPPLTSQIRALH FPIPSQINEKPGAGHWSAKLHFP YWQLGEAGEEGSSPPDIMRCL LTCLSV PSTAVIPLTDSEHKLLP LHFAVDPGKDWEWGKDDNDN ARLAHLILSLEAKLNLHLSYMN VTWIRIPSETRAPLAQEPSTAS AGEDVQSLADSLDSDRDSVCS NSNSNNGKNGKDKEKEKQRKE KDKTRADSVANKLGSF SKTLGI KLKKNMGG LGGLVHGKMGRA NSANGKNGDSAERGKEKKAKS RKGSKEESGASASTSPSEKTPS PTDKAAGASPAEKG GPRGDA WKYSTDVKLSLNLRAAMQGE RKFI FAGLLTSHRHQFHEEMIG YYL TSAQERFSAEQEQRRDA ATAAAAAA/PPPPPRP/ERPPRRP ETEGVPVPERASPGPPTQLVLK LKERPSGPAAGRAARAAAGG TA/CPGGRRACERQRTSAWPQ PPGASAPERHPRAGVGRAGRG VRAGRGGAAAVRHVPAAEPLA VVAELQPGARRRPAHRQHGRV AGARGARGPTGRGGDRGGGRA

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25292	55660	A	25430	404	1116	SLGPLMLSGQKLQTSYTM EYY AAIKR/DKIVSLVGTWLELEAII KKLMLQEQKTKYHMFLLDSL GMQQAERVLIADGTMLLSAQY QFENNLLVPILRVSRKSLQRKE EPGRKAKKSQTSSEGIIKKRRFW FEWKEPVALSSQGWYEAAGSE RPEKGHLGLLRAESFQDLRTAL ISKPYFSVPGKVGPAIKCPETLP ELKTYPYQYGVTLGEPVRNEQQ QASSFSLSNTHLSKKRNES
25293	55661	A	25432	1571	1782	WLLCRLPRVPDQL*WCGCQPE KCAGAEFQDGSAMPLPSRTCPI SPRMCTGWSTTCATTD SATTA CPLAL
25294	55662	B	25433	69	1160	
25295	55663	A	25434	14	437	LQTSHPYPTTSKC/PPP/CEKPSP TSL/C*RRSAPHLPPE
25296	55664	A	25435	782	997	MMLCQLQRPV/CGSHSCSRG/C PPAQ/CPSPVPVPSQSAFPVPQS PSSTCPNPSHIPMIPMVPSWSG HWDSK
25297	55665	A	25436	1117	1815	GDAHTEQCLQNLPRGSRPPLP LESHPSSSKHSPKACPTGRS/CG PWK/CPGPEVR*PPPSCTR*DP HFRGLLEGLLEPRHVTCLALCG PQRVLYWPVYHERLGEGWDW CPSSWPGA

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25298	55666	A	25437	1261	2757	ALGKDEKSGQPPQTGGGLGPRLL FRLPSSQGQERRFAAAKAPSSL VPHNGSPKSCWRGLREEGLSL ATLWTPCGVSGVPAAPPSAW CDLGKLLVCRGQNRGRSTQ TDVRRHARSQRRRKCVAAAP VAPRSRRWRCPAALAAPAVAV PVVFALIFLLGTVGNGLVLAVL LQPGPSAWQEPGSTTDLFILNL AVADLCFILCCVPFQATITLD AWLFGALVCKAVHLLIYLTMY ASSFTLAAVSDRCAPVGHPL GRAVGAGVGGGVNLNGLVWL LAALFSAPYLSYGVTRYGALE LCVPAWEDARRRALDVATFAA GYLLPVAVVSLAYGRTLRLFLW AAVGPPAGAAAAEARRRATGRA GRAMLAVAALYALCWGPHHA LILCFWYGRFAFSPATYACRLA SHCLAYANSCLNPLVYALASR HFRARFRRLWPCGRRRRHAR RALRRVRPSSGPPGCPGDARP SGRLLAGGGQGPPEPREGPVHG GEAARGPE
25299	55667	A	25438	1	1624	MKDKSKTLGLEASIFRNNWKC KSIFELKGHQEGYFSQMIISYE KIPSYRKSLSLTPHQRIHNTKS YVCKECKGKACSHGSKLVQHER THTAEKHFECKECKGNLYSAY QLNVHQRFHTEGKPYECKECG KTFSWGSSLVKHERIHTGEKPY ECKECKGAFSRGYHLTQHQQIH TGVKSYKCKECKGAFFWGSSL AKHEIHTGEKPYKCKECKGAF SRGYQLTQHQQIHTGKKPYEC KICGKAFWGYQLTRHQIFHTG EKPYECKECKGAFNCGSSLIQH ERIHTGEKPYECKECKGAFSRG YHLSQHQKIHTGEKPFECKECKG KAFSWGSSLVKHERVHTGEKS HECKECKGTFCSGYQLTRHQV FHTGEKPYECKECKGAFNCGSS LVQHERIHTGEKPYECKECKG GFSGGYHLTQHQQIHTGEKPF KCKECKGAFSWGSSLVKHERV HTNEKSYECKDCGKAFSGSYQ LSVHQRFHTEKLYQRKEFGK FTFHGSKLVHERTHSNDKPYK YNECGEAFWTTYSNEKIDTDE

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25300	55668	A	25439	32	447	VLGGSMMFREGQGRGNRQKGP KKRRNRLALSSALLASTA/PAGG QPRHWRFP*CCRLRQQL*PLQGN WAPVSPILQGHRSQLRAGYSISS FLQMFAP*VQGAARAQAPAPGA AVPRGSGRQGGPRAVDLHGFR VGWNRRLRAASM
25301	55669	A	25440	1	858	
25302	55670	A	25441	147	1088	SRTTYKGGKSSFQTYSDYLRWES FLQQQLQALPEGSVLRRGFQTC EHWKQIFMEIVGVQSALCGLVL SLLCVAAVAVFTTHILLPLVL LSILGIVCLVVTIMYWSGWEMG AVEAISLSILVGSSVDYCVHLVE GYLLAGENLPPHQAEADARTQR QWRTLEAVRHVGVAIVSSALT TVIATVPLFFCIAFPAKFGKIVA LNTGVSILYTLTVSTALLGIMAP SSFTRTRTS/CPQGGPCRAAGRG PGAGCLPRAPAERL*DSPARRG LPIARDGLWTLAPLVPWVGDR SCFPARLQLAVSPGLGPGRPAG
25303	55671	A	25442	1	1596	MGVSVRVDCGARASEFLGRGP RGAVRGADPGSLTETCAQSR TWARARSKGGFRLTLNFGYGR YPSEGTSRGQRSEALPFLDIQHP TPLGRPRMLQSRGEMVRSWGP VVEGKLGFCPLTVFPGGLRGP HPGLAGERENFARGAKQEACL LQPGDAGLTHPCPATGYFPEA SCTSRIRMFINSQERQLADMSL FIADSWLCYSGIICWKSLEHQR GASLSCVYMEGKGGNIWMKAS NVLPLCQMLFTSGHKSDDLFGG LAVEKQMRQDHHILLHDRSGF QLAVTSPLLTRLGKGHIQVPV YVLDAPSRWLGLRLFRDSSCG LVLSLLCVAAVAVFTTHILLLL PVLLSILGIVCLVVTIMYWSGW EMGAVEAISLSILVGSSVDYCV HLVEGYLLAGENLPPHQAEAD RTQRQWRTLEAVRHVGVAIVS SALTTVIATVPLFFCIAFPAKFG KIVALNTGVSILYTLTVSTALLG IMAPSSFTRTRTS/CPQGGPCRA AGRGPAGCLPRAPAERL*DSP

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25304	55672	A	25443	1	2355	MDHPGFREFCWKPHEVLKDLP LGSYSYCSPSSLMTYFFPTEG GKIYYDGMGQDLADIRGSLEL AMTHPEFYWYVDEGLSADNLK SSLRSEILFGAPLPNYYSVDDR WEEQRAKFQSFVVTYVAMLAK QSTSKVQVLYGGTDLDFYEV RTFNNDMLLAFISSSCIAALVYI LTSCSVFLSFFGIASIGLSCLVAL FLYHVVFQIYLGILNGVAAFV IVGIGVDDVVFINTYRQATHL EDPQLRMIHTVQTAGKATFTTS LTTAAAYAANVFSQIPAVHDFG LFMSLIVSCCWLAVLVTMPAA LGLWSLYLAPLESSCQTSCHQN CSRKTSLHFPDVFVAAPEQVGG SPAQGPPIPYLDDDIPLLEVEEEP VSLLELGDVSLVSVSPEGLQPAS NTGSRGHLIVQLQELLHHWVL WSAVKSRWVIVGLFVSILILSLV FASRLRSASRAPLLFRPDTNIQ VLLDLKYNLSAEGISCITCSGLF QEKPHSLQNNIRTSLEKRRGS GVPWASRPEATLQDFPGTVYIS KVKSQGHPAVYRLSLNASLPAP WQAVSPGDGEVPSFQVYRAPF GNFTKKLTACMSTVGLLQAAS PSRKWMLTTLACDAKRGWKF DFSFYVATKEQHTKRLYFAQS HKPPFHGRVCMAPPGLSSSP DGPTKGGFFVPSEKVPKARLSA TFGFNPVCNTGCGKPAVRPLVD

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25305	55673	A	25444	1	1737	MLYAAECLRNVMKQLQVIPSAL NEALQAQSTWSDGLASHALS STWCLHGESA AWSQPAVVECG QPRDQLQTHSEAWLCAVATF SQLEQFAVTGAQISDRQGHAV CTAPPRGRPSILM INLVCASSA DECGGGKTETQTAGGRLQGAE TRSRGQLRLITRTQAAEPRWF LQLLKRSANRSRALTRPFGSLSS DGARRI.RLSFVS AVSSADTKPT VPVSSDSSGRDGCGETRAEAGP GGPHVAQPQRVAPAAAAARDF RKPRGLNRQNVSP/PGPGEQGP G/PRPQKPA GRAP/PEPQGEPL GLFPR/GRPPRSFPGSPADPAAS VSHTQGPSPTGLPGTCQNRLP NPAAVDEQCTTRGSLNCRISRS PRVSERRGPEGTPGRRPAAPPQ CAGTRGLSPRADLGAARTPRA PYRPHGQGRPSRHNCDSVSSQG WPPHSCWKTTSNGMPWKAS FCSRTAQPANQNTGNHERGLRS VAMFGDRASREATPALSLCESQ GCFEDEKEVFSPEPHVETSDEPL PICSGPGDGWGDPIARPGRGNN LSPGTS AWEVPRWIRVTGEDW LSTGPAECVFINDLTT

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25306	55674	A	25445	2	1642	LLSSISAWFGPPASTPAFTMSIR VTQKSYKVS/TSCPRAFSTRSYT SRPGSRISSSFSFRVGSNFRGDL GGGYGGASGMGGITAVTVNQ SLLSPLVPEVDPNIAQAVRTQEKE QIKTLNNKFASFIDEVGFLEQQ NKMLGTKWSLLDQOKTAIRSN MDNMFESYINNLRRLQETLGQ EKLKLEAELGNMQPLVEDFKN KYEDEINKRTEMENEFVLIKKD ADEASMNKVELGSRLEGLTDEI NFLMQLYEEEEIRELQSQISDTSV VLSMDKSRSLDMDSIAEFKAQ YEDIANRSRAEASMFQIMYEE LQSLAGKHGDDLRRTKTEISEM NRNISR/LQAEIEGLKGQR/VASL GGRPLQDAE/QRGKSWPIK/DA NAK/VLSEAGSPPLQAGPKQDMG R/Q/LREYQKLMNVKAGPWITIE/ IATYQESCLEGEEEPGWSLGCQ NMSNHT/KTTQRGYAGRPEPPP MGGFTSPGFSYKPGAPGFGSG AGS/SSFNRHQLSPGAVVVKKIE TRDGKLVSES/INVLPKVKQLR QPLPSLPLLRCPRLGKEAPYP
25307	55675	A	25446	1	1280	MAYLCNAICMTHMTLDPVDQ ALPGATTATSVPGPQCDASCM MLFAVVFPFNGIALAATQGAQS MLPPRVQGSLSKSPSTRRGRDA PGLQVSQAPPPRRGFVAGRRYS PPALAPGRCAAPHGGGRKELPT RRPGHGMAPKFPDSVEELRAA/ GSEFRNGQYAEASALYGRAL RVLQAQSSDPEEESVLYSNRA ACHLKDGNCRDCITDCTSLAL GPFSIKPLRRASAYEALEKYP MAYVDYKTVLQIDDNVTSAVE GINRGPGLKEDTTQKRWNLSLPS ENHKEMAKSKSKETTATKNRV PSAGDVEKARVLKEEGNELVK KGNHKAIEKYSESLLCSNLES ATYSNRALCYLVKQYTEAVK DCTEALKLDGKNVKAFYRRAQ AHKALKDYKSSFADISNLIQIEP RNGPAQKLREQEVKQNLH

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25308	55676	A	25447	1	1297	MHLLSAYFVPGSMLVGSGYM MVNITDVSPPSWSFLCSMLITTT QGAQSMPLPRVQGSLSKSPSTR RGRDAPGLQVSQAPPPRRGFAV GRRYSPPALAPGRCAAPHGGG RKELPTRRPGHGMAPKFPDSVE ELRAAGNESFRNGQYAEASAL YGICALRVLQAQGSDDPEESVL YSNRAACHLKDGNCRDCIKDC TSALALVPFSIKPLLRASAYEA LEKYPMAYVDYKTVLQIDDNV TSAVEGINRMTRALMDSLGPGE W/RALKLPSPFLVPVSAQKRWN FLPSENHKEMAKSKSKETTATK NRVPSAGDVEKARVLKEEGNE LVKKGNHKAIEKYSESLLCSN LESATYSNRALCYLVLLKQYTEA VKDCTEALKLDGKNVKAFYRR AQAHKALKDYKSSFADISNLL QIEPRNGPAQEVAGREVKQNL
25309	55677	A	25448	3	491	GITFTHSPAATGGGAQVRRRRD PPPGVQLRNMAQETNHSQVPM LCSTGCGFYGNPRTNGMCSVC YKEHLQRQNSSNGRISPPATSV SSLSSELVPVQCTDGSVPEAQSAL DSTSSMQSPVSNQSLSESVA ASSQLGQYICGTKAVPETEDVQ ASVSDTAHV
25310	55678	A	25449	1	860	HLLLLAIDYNLPIAGVLMESQY LGASPKRLVIPNLYAHRKSLAT LEPYAPRRPMPAIARYAIPYMS HHNGYIGDVYYRLTVEEKSSF IARRSILTTEFTIRRTKKVPVPSI NMSSASPLEDESRRPSAGVQLRK GRYRLLRDRYRPGCNSVGESPR KSSFDDIMATESRESIFAEPR TGEHSVRGPVSNQSLSESVAS SQLDSTSVDKAVPETEDVQDSL NASPTKQQCG/DVQTVDLYSNN KELFAQKCYRHRYSISRLKKCL CHELVPRDTIKSPESLSVGS
25311	55679	A	25450	880	1196	SPTRRGTPGTCLKPTACAGAA *PGCSARRTCASAPLSTCPPSS CAAPPPAPAAVPSTPRPTSPSPW AAPASPSRRRTQTASTPASTNR APSSCWAPTTRPLAP
25312	55680	A	25451	254	579	IEKISLEPKNRSPQIPNLVGP/R LFLVPGDFQSQVPNLFPPKPSG PHPAAGKGQPFSLPAWRSTGP ERATPGGRPAACSALEAPSLR GPSGYSAQEPPRRPISARI

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25313	55681	A	25452	6	1442	RSELIRHSWPRHAQLRGARART AVSIRECISVHVGGAGVQIGNA CWELFCLHGIQADGTFDAQAS KINDDDSFITTFSETGNGKHVP RAAMIDLEPTVVDVVRAGTYR QLFHPEQLITGKEDAANNYAPG PPTPGGKESIDLVLDRIRKLT ACSGLQGLFIHSGGGTSGGFT SLLMERLSLDYGKKSKLEFAIY PAPQVSTA VVEPYNSILTTHTTL EHSDCAFMVDNEAIYDICRRNL DIERPTYTNLRLISQIVSSITAS LRFDGALNVDLTETQTNLVYPY RIHFLPLVYAPIIAEAKAYHEQL SVAEITSSCFEPNSQMVKCDPR HGKYMA\CCMLYRGDVPVKD VNVAIAAIKTKRTIQFVDWCPT GFKVGINYPPTVVPGGDLAP VQRAVCMLSNTTAAIEAWARL DHKFDLMIYAKRAPVHWYVGR GDWKKGEFSEAREDLAALEKD YEEVGVDSEAEAEEGEEY
25314	55682	A	25453	3	618	SSAGREPDPDLPRRLCFTHRLP AARRWVQLCVHASPEPGGQGV CPGRSERMVIRVFIASSSGFVAI KKKQDQVVRFLANKIEFEVD ITMSEEQRQWMYKNVPPDKKP TQGNLPPQIFNGDRYCGLLVS FSVICIKPNWNHLLIPWSGI NPYCEQDSSFSENVGDEILKNS GVPRDFTSILIQKEREKSEKVG VDQGHR
25315	55683	A	25454	3	424	SWTMAATIQAMERKIESQAHH LLSLEGQTGMA*S*GTPPCPG AAAGSRSSCCAAGSPRSPAASA AARTPAAGSPARPTCPPAGSRT PRLSSRNQPASSRPSRFDLLGKA GEQPAIQSSSPWESWLPSSTK
25316	55684	A	25456	268	445	
25317	55685	A	25457	3	205	
25318	55686	A	25458	27	272	AKCSGQGPGRVRAQGERADHE CPGAGAGGGGCNSAASAREES SRLISG\SLQM\QNVSLASRRKEE EVRAAAAGGAAAGRPRV
25319	55687	A	25459	1	253	
25320	55688	A	25460	2145	2399	

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25321	55689	A	25461	174	1309	HLLCCRAQRRPQTTPPAARGLEA CSEGALKMPEAPPULLAAVLL GLVLLVLLLLLRHWGWLCL IGWNEFILQPIHNLLMGDTKEQ RNLNHVLAACGSPGNAQSVLG GHLTPNCEQKEW/APLNVGDK KGQDSWDALISREQPALPCLLG NLGAYFGLLQLLRMARLLVNO GARLIHHSRFPNDCPPSPKRM VDFAGVKDKALFQVTLVCGAS PETFHPPSLKKKYDVGHNWTW VFLDHWKDRYLAPDTLLEEC G/LLEGGQLLLAEQRLSSPGAP VDFLAHVSRPACFG/CTHYQI VPWKYREVVVDGLGRRPIYKG PGSEAGALTAPRPPSRALSPK PGTEGARPWLLTLVRLRACVL NAKSHARAESLRA
25322	55690	A	25462	2470	3460	SGPCPRCCAECRPYKTRPSRV PGTHGPGPADHGQPPCCMAGA HPPRPQAWMLLQTHSQDCEGK VCGGIFCPCYHCKHTHHHH HHPHHHHYHHHHHHHQHHH HHHHHHYHHYHSHYHHYHHH HLHHH/HHHHHHPYHHYHHH RGQDHHPPHHHH/HHHYHHH HYHHHYHPHHHHHHQPQH HHHQHYHHHYHHHPHHPHH PHHHHHYHYHHHHHHHY/HFY PHHYHHHHHHHHHPHHHHH/ HHHYHHHPHHHYHHHHHPH HHHRPHHHHRHQHPHYHHH HPHPCHHHRLHHHRHHHYHH TSSVQGPSQAGASLPGQACR
25323	55691	A	25463	I	407	DAERQEALGIVRRIGTDEAAT EPAGATVPAAAAAARIGTVGP QPPAMPRRKRKAGSSSDGTEDS DFSTDLEHTDSSESDGTSRRSA RVTRSSARLSQSSSRISRSCSKS GSLALRLSLTLPEE*PVVSSSL

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25324	55692	A	25464	3	2539	RILYIPDGHRA PGASQSGNWEH PLLLL.EPGNLASSPSMSLAYPH CGLTIHQEHRRAHEELAYTPND RASSTGHPAFIEDGNPSVLAFA ASPRPND SYILKREPPESCEKER VFEEATTRGKYGEGAKQETFTF ALTLVFIQCVINAVFAKILIQFF DTARVDRTRSWLYAACSSISYL AMVSSNSALQFVNYPTQVLGK SCKPIPVMLIGVTLKKKYPLA KYLCLVLLIVAGVALFMYKPKK VVGIEHTVGYGELLLLLSLTL DGLTGVSQDHMRAHYQTGSN HMMLNINLWSTLLGMAVSCP DQGPVLVPRCPFVQALEKPSWK NLHQQDLFATCYWHNEGESC SCHGKTLSSKTQGGILFTGELW EFLSFAERYPAIYNILFLGLTSA LGQSFIEMTVVYFGPLTCSIHTT RKFFTLASVILFANPISPMQWV GTVLVFLGSTQIILDNLKILNTS AKTLLYKTPLSWQEELEGERASS CAHKRSASWGSTDHRKEISKLK QQLQRTKLSRSGKEKERGSPLL GDH/VSAGSTEGVPS/RASPOGP LSCDSAPACT/VSLEGLNQELE VVFVKEQGEELRLRIDPDGHR APAPQSGSCDHPLLLLLEP ASSPSMSLASPQCGLASHEEH RGAAEELASTPNDKASSPGHPA FLEDGSPSVLAFAASPRPNHSY IFKREPPEGCEKVRVFEEATHQ
25325	55693	A	25465	845	1316	LSLGDSAQCLLPASWCQVAG HPAFLLEDGSPSPVLAFAASPRPN HSYIFKREPPEGCEKVRVFEEAT S/RRVLTGPFLTSCPDK/NKVHF QPVTGSAFCPVNLMKPLFPGMG FIFRNCPSNPGISSPGQPQATTS EGSGSLQGLPTAIRAMAAHPYH Q

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25326	55694	A	25466	1077	1506	CDACGRRRCRTCTFCLGLQPAG LDGHHHRHPDCWFPWSPRHR* GMIIDVFSTRYSGSEGSTQTLTKG ELKVLMEKELPGFLQILTNEDE PLVTIPLSHSCSLAYLLITSGN RVNALLKWLKLGERWQMT EGIKGQRSGHGPEQAENPLGDS VPQDTTKDVPLTQHRHLHQGLE AGVPKTSVPAAPGLPVPAQLQA QIPGPCERALLHCHNGPQLQH SLQGEEQRETHLRGQDWPC QMRITLKREVALPGGRAGGAA REGLGASICETGEHQMNTFQVP RWPPCFPGQAGPVLGTGRH LDLLSGRPGTVRKSSVARIMK EEVTVTKQSAADLRHTGQGPT CCVLSGGRCGSQACSRPFSL LGDESEPHGRGPF AAAL HHR NPLNDVMLVGDDAGPAGHFAS VYNPLAWTVTTITVLT VG FP RVTD EAGHPVPSQVSGIQ RCLQ GMKAPPVTVTVSGEKGSC SCVLCLEHPYFPLVPWLPVFR DSVIPSS TPQEA VLADVGFRN NVPQRAQLKPKQKILTPF
25327	55695	B	25467	31	783	
25328	55696	A	25468	846	1392	PDPA AHRFHGPTLHPG SLRTSS GAGT WYQNPQHNDHD YYHH HHHHDDHHYHHHHHHHHHH HHYHHHHHHHHHHHHHHHH HHHQHHHHHHHHHHHHHHHH HHHHHHHHHHHHHDQH HHHHHHHHHHHHHHH/HF/H HHHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHHH YP
25329	55697	A	25469	181	412	LRS DQ QTRKFVSRSSGACSPPT TEL SWP PSLLPSL*F HSP SSQP* MNH SAST TSPLPSFITERESILAT EWD TARN

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25330	55698	A	25470	1	848	MPSLNTIVSPLGSPHTSLIPPM L LSANLPFDTTIMIKLQTACSAPI HNLQRPCGENLRTSTFVRLDR NLVKSPQGGGGQPSRQWEAR GAEPQGRDPSEVQ/RPAGRGF GRISRAPRKPSRAPPTPQGLGPP LGAGGGQSLASCRPARKNARPP TRAAAHSAHPHSHWHSHARPQ PQSPSAAGSQGDPWPPARVPPP PLLRLPQRRTAGRTPVDAPARG IFTLSLSSSHKSSGKHGRGKT PEMWPLFRGSLSKLSRRRKVSP SAALHWRLRRTQKRLCC
25331	55699	A	25471	92	1083	TMRTHGHRKGNITPWGLSGVG GL/ETGRALGEIPNVDEGLMGVI AAVAIVLVSLLFVMLRYMYRH KGTYHTNEAKGTEFAESADAA LQQRERALDSSRDHLETLGAC PGRNGGGLALQEATPRDPGRR WPPQRPFPAPRRWEKIWAHGFL GSAGQHQLTGRKVLVEGLGCI CMAHTDLQNTSVAKMAINRPN EYAVQSVLENDVSCVKVAVQAP QRLHWPSVDADTGGRGAVHIA FPKHVEPETPFAHTIPARNSWT KWSSEHILETLSPQKPALPWAP RQQGRPLGLTAPISKRLGPGDG PEGEAGERLAQAHFINTRPPST GPPGTPAAD
25332	55700	A	25472	73	424	RPGMWSTRSPNSTAWPLSLEPD PGMASACTTMTHTTIAEPDPG MSGWPDGRMETSSPTIMDIVVI *CAIAAEAIVLVSLLFVMLRYM YRHMGTYHTNEAKGTGVADS ADACPADPA
25333	55701	A	25473	139	546	RPGMWSTRSPNSTAWPLSLEPD PGMASATTMTMHNHYHCRSLIPG MSGWPDGRMETSTPTIMDIVVI AGVIAAVAIVLVSLLFVMLVAL TCNRA/HRGTYHTNEAKG/TEF AESADAALQGDPAL/QDAGDS SRKIEYFI
25334	55702	C	25474	142	408	

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25335	55703	A	25475	44	727	ARAGSRSRGLPFCGTAGPPPKA TLWGGLLRI.GSLI.SLSCLALS L.L.AQL.SDAANNFEDVRCKCIC PPYKENS GHYNNKNSQKDCDC L.HVVDMPMPVPGA\NVEAYCLR CECKYEESS\STIKVTIHYLSIL GLLL\Y.MVYLTLVEPIKRRLF GHAQLIQSDDDIGDHQPFQKCT RCASPL.PQFEPTCWNKVEYQA QAL.ESFQVQEQRKSV\FDRACC PQLNLGN
25336	55704	A	25476	11	1323	VVLLVSVNTEAESEKAAEQR /PLEGTDQTL.DVEEQEESKAA ACGSKKRVPVGIYVLGHIPPHF QPLHVRNLLSAYG/RSPSHYDL WNLKYL.HHFTWSHHSEHLAFE RQVC\HRQHLRVEVTQAKCETI FYLQSVIEWGQCF.LAVDGD.LAH PDGSWTF.AQRPTQELRARKA AQPVGKVLNYYPTQLSLECEVP SQPMGTGHSRGLCQDVKVIN VPVSFVWCALVAGLLVVVPPPP PQAPAEVSDISLKRGLQREIEQ CRRDIQNFPFPCASEELASQL.FP LMEVPQGRGTTGFMNAPL.TTS EVRGL.KKELKPL.I.DDPERVAEQ IDQFLGSKLYTWTELSILGILF SKEERNMICRAAMGAWERDYP AGQNIPAA.DVTF.PARDPQWNN NNAAHQKNMRDLQELIIGIKE SAPRPQNLTKAFDEQEQEKDEGP
25337	55705	A	25477	1	490	GTSGRPLVSVNMEAESEKA\ ATEQEPLEGTEQTL.YAEEEQEE SEEAACGSKKRVPVGIYVL.GHI PPRFRPLHVRNLLSAYGEVGRV FFQAEDRFVRRKKAAAAAGG KKRSYTKDYTEGWVEV\RDTR\ IAKRVA\AILLK*PMGARRRSP FRYDI.WNLKYLHR
25338	55706	A	25478	2	574	

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25339	55707	A	25479	160	1548	KTSSQTLSLALTMFQRLNKMVF GEVSSSSNQEPEFNEKEDDEWI LVDFIDTCTGFSAEEEEEEEDIS EESPTHEPSVFSCLPASLECLAD TSDSCFLQFESCMPMEESWFTTP PCFTAGGLTTIKVETSPMENLLI EHPSMSVYAVHNSCPGLSEATR GTDELHSPSSPSILPNKMLSVHV GTAIHNQAALCQSVESYWQCGI QLLTQFQSQSKLGQLLAATCKE LPGPKESRRRTAKDLWEVVVQIC SVSSQHKRGNDGRVSLIKQRES TLGIMYRYVLEPLVLTILSLFV KLHNVDREIVNDITAHEHSIWPS SIPKKQMSRSTFMSQEETVCRA AHTPSLPEEKWVEQLIYALVVA AARIMAMWGPNAAWLVFLAA AGPPPLTPPHSP/PPPPPALGR WMGPPLRDSASGLPRPPGRISE DSGAWACGPALCPRPAIPSPAP ALRVPEALRLWGTCSEV
25340	55708	A	25480	1	380	FTSPKTARNWGLMQVRNQR LVLGKAGGKKGSPLEQRGGNG HHGGTRLICALVLSMRPLAT FAEPQTETCTVAPRERQNCGFP/ GVSRPPQCANCKGCCFDDTVRG VPWCFCYNTIDVPPEECECF
25341	55709	A	25481	3	2367	
25342	55710	A	25482	2	1230	WRRSRRRRPPAPQAGGGDFRA GISPPTGKKSGLMEPQGNHYR CRCLQVAGSQAWARCVSMPEL VVQKVVGHP/LVLSVVDHFN IGKVGIQKCVIGLFWGWSQKK VLDVLNSFAVPFDEDDKDNSM WFLDHDYLENMYGMFKKVNA RERIVGWYHTGLKIHKNGITIN ELMKRYYPNSVLIIDVNPDKDL GLPTEAYISVEEIQDDGTPTLKT FEHVTSEIGAESYLEKVA TGKL RINHQIHYELQDVFNLLPDVSLQ EPIKAFYLRNDQM VVVYLASL IHSVGLTDPPCIVALHNINNKI ANQDGDKKEGQEKES/KKDR KADKGDKDKESDVKEQK NHCLKERYFRQDSL PDDPRVL GLELTPPVARQYSPQDLSEIPRH ADFRCDPAHFQLWWSQGETPS

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25343	55711	A	25483	3	1042	DRYCCRCRLRVAGSQAWRAGC VAMPELA VQKV VVHPLVLLSV VDHFN RIGKVG NQKR VVG VLL GSWQK KVL DVSNSFAVPFDED DKDDSVWFLDHDYLENMYGM FKKV NARERIVGWYHTGPKLH KNDIAINELMKRYCPNSVLVIID VKPKDLGLPTEAYISVEEVHDD GTPTSKTFEHTSEIGAEAEV GVEHLLPDIKDTTVGTL SQRITN HVGHLKGLNSKLLDIRSYLEKV VTGKLPINH QIYQLQDVFNLL PDVSLQEFVKG FYLKTNDQMV VVYLASLIRSVVALHNLINNKI ANRDAEKKEGQEKEESKKDRK EDKEKDKDKEKSDVKKEEKKE
25344	55712	A	25484	257	1566	GLEHL CNPRWLLFLRAMDST VPSALELPQRLALNPRESRSP EEEPHLLS/SLAAVQTLANVIRP CYGPHGRQKFLVTMKGTVCT GCATAILRALELEHPAAWLLRE AAQTQAE NSGDGTAFVLLTE ALLEQAEQLLKFGLP RPQLR/EA YATATA/EEKQVQGL/AAAGIN VAVVLGEVDEETLTADKYGI VVIQARSRMEIHYLSEVLDTPLL PRLPPQRP GKQQRVYRQELGD GLAVVFEWECTGTPALT VVLR GATTQGLRS AEQAVYHSIDAYF QPCQDPR LIPGAGATEMALAK MLSDKGSRL EGPNGPAFLAFAR ALKYLPKTLAENAGLAVSDVV AEMSGVHQGGNLLMGVGAEGI INVAQEGVWD TLIVKAQGFRA VAEVVLQLVTVDEIVVAKKSPT HQQIWNPD SKKTKKRPPPEVK

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25345	55713	A	25485	145	1918	PLEYFQSRVSGVPQLLFLEHL C NPRWPLSLRAMDSTVPSALEL PQRLALNPRESRSPEEEEPHLL SSLAADVQLASVIRPCYGPGR QKFLVTMKGETVCTGCATAILR ALELEHPAAWLLREAGQTQAE NSGDGTAFVLLTEALLEQAEQ LLKAGLPRPQLREAYATATAEV LATLPSLAIQSLGPLEDPSWALH SVMNTHTLSPMDHLTKLVAHA CWAIKELDGSFKPERVGVCA LP GGTLEDSCLLPGLAISGKLCGQ MATVLSGARVALFACPPGPAH PNAPATARLSSPADLAQFSKGS DQLEKQVGQLAAAGINVAVV LGEVDEETLTLADKYGIVVIQA RSWMEHHYLSVLDTPLPRLLP PQRPQKQCRVYRQELGDGLAV VFEWECTGTPTALTVVLRGATT QGLRSAEQAVYHGIDAYFQLC QDPLIPGAGATEMALAKMLS DKGSRLEGPSGPAFLAFAWAL KYLPKTLAENAGLAVSDVMAE MSGVHQGGNLLMGVGTGHIIN VAQEGVWDTLIVKAQGFRAVA EVVLQLVTVDIVVAKKSPTHQ EIWNPDSSKAK\KHPPPVETKKI
25346	55714	B	25486	1	642	
25347	55715	A	25487	3	395	FLPVNLTHDWQSSALATLERP LSQVRLKRFVGTLIAFMVSAIVI LATASMAVASITESVQTAAAFID NMARNVSNKLLLQQGIDQKIL ALLQSLAALLEYVGEQDALA FQQQ*NCNWGHKHCIIISLPWN
25348	55716	A	25488	3	358	HEPMCGETHQALQGAMEKILW SRFMELMQE/KKVDLKERVEEL EHCCI*LSGERQTPSGSGKPGHG KESCTLVRGAPASESCPPAGEYI ALYQSQRAVRKEECISRLAQD KGEVKVKLLE
25349	55717	A	25489	1	250	VQCGGIPPGQNNKEEMEVLP PEP PPPIRNRKDKSYATAMGPFLRQ EALSGELLAACLVIQD*QGNWV YKPSIFNIYKKLRKSIRG
25350	55718	A	25490	1	702	
25351	55719	A	25491	1	252	
25352	55720	A	25492	1	122	LAPLVITYFSSLSLGFNFKGKL APSSWRC*GLNEIIRGKH
25353	55721	A	25493	3	505	

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25354	55722	A	25494	1	3345	MRVGF RDIVGSLSEYSFGCPVN YEVFHSVWITILCCLMANDRKP QFLYFFQFSSFHGGRNLMSSFH PGNGHNSRRRSVFFYANEKWEF LDPTPKDLEESIVQEEKKEPTPE GNKVSQRLKNLPHSTLKAQKL LQTSSTNRGTVITATRLAFDLRT QSTKCSHPASGSSGHSTDFQLE GEWGLWDLGTKGFKLPYLSI DIDNVKSPHFPHEKLTLTVSLGS NRRMGLEKKECHQKQGALREQ LQVHIQNV EILVSE
25355	55723	A	25495	296	1350	TLWLQGEQPSQTEIHEKV/LNE AMGAMMYHTILTRDLEKFK APRVIVQIGSGYDNVDKAAASE LGIACVNIPSAAVEETPDSTICHI LNLYQRNTWLYQALRGQAVA VRAKAFGSVIFYDPYLDQDIE RSLGVQRDLLYQSDCVSLHCN LNEHNNHLLINDFTIKQMRQGA LVNAPHGGLVDKKALAAQALKE GRIRGAALVYRESEPFSAQGP LKDAPNLICTPHTAWYSKQASL EMREAAATEIRRAITGHIPESLR NCVNKEFSVTSAPWSVIDQAI HPELNGATYRYPGIVGVAPGG LPAAVEGHIPGGIPVTHNLPTVA HPSQAPSPNQPTKHGDNREHSN
25356	55724	A	25496	694	1185	PKPFKEGTIRGAALDMHESEPF SFAQGGLKNAPNLICTPHTAWY SEQASLEMREAAATEIRRAITG CIPESLRNCVNKEFFVTSAPWS VIDQQAHPPELNGATYRYPGIV VGVPAGGLSAAMEGIIPGGIPV THNLPTVAHPSQAPSPNQPTK* MK*KQMG EVA*GAARIGETL GLNGFGCTQA/VAVRAKAFG FSVIFYDPYLDQDVVERSLGVQR VYTLQDLLYQSDCVPLHCNVN EHNHLLINDFTIKQMRQGAFLP PKPFKEGTIRGAALDMHESEPF SFAQGGLKNAPNLICTPHTAWY SEQASLEMREAAATEIRRAITG CIPESLRNCVNKEFFVTSAPWS VIDQQAHPPELNGATYRYPGIV VGVPAGGLSAAMEGIIPGGIPV THNLPTVAHPSQAPSPNQPTKH

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25357	55725	A	25497	290	1251	PFMLYVSISTLYIAFCHILNLYR RNTWLYQAL.WEGTRVQSV EQ MGEVA*GAARIRGETLGLNGF GCTGQA/VAVRAKAFGFSVIFY DPYLQDVVERS LGVQRVYTLQ DLLYQSDCVPLHCNVNEHNNH LINDFTIKQMRQGAFLVNAARG GLVDEKALAAALKEGTIRGAA LDMHESEPFSAQGLKNAPNL ICTPHTAWYSEQASLEMREA ATEIRRAITGCIPESLRNCVNKE FFVTSAPWSVIDQAIHPELNG ATYRYPPGVVG VAPGGLSAAM EGIIIPGIPVTHNLPTVAIIPSQA PSPNQPTKHVDNREHPNEQ
25358	55726	A	25498	1	1538	MLLQKTQFEYAFKRRKLEES KKRGAGPASSDPWRGSSQTA PHASEVSGAPLGRSCETTRDTG VGSPRQWL GAGAGTWQHRA RAASTPSSRGLRALQTWGGGE VMNGPLHPPPRVALLD/SRNC TVEMPIPKDLATMAFCDDHSTQ EIHEKILHEALGAMRYHTITLA RADLEKFKALG VIVRIGSGYDN VNIKAACELEIAVCNIPSAVEE TANSTICHILSYRRNTWLCQA WARKHVCYSMGQIREVALGG AHIGGETQGLIGFGSTGQAVPV RAEAFGFSVIFYDPYLDGIERS LGVQRMSQGAFLVNAARGALV DEKALAAALNNGKIR/GAALDV PQSELFSFAQG/SLEMREAATE IRRTITGCIPESLRNCVNKEFFVT SAPWSVIDQAIHPELNGATYR YLPGFVCVAPGGLPAATEGIIPG GIPVTHNLPTVAIIPSQAPSPNQ TKHGDNPEHPNEQSRERCKVII QIHLRPDSEKLMNSEKTNLTV FLADSGHMHY
25359	55727	A	25500	1	2595	
25360	55728	A	25501	561	1023	SGHDAYREQIQEYRVISLLNP NDHVNKQSTNDAYPTGFRIA VYSSLIKLVDAINQLREGFERK AVEFQDILKMGRQTQLQDAVPM TLGQEFRAFSILLKEEVKNIQRT AELLLEVNLGATAIGTGLNTPK EYSLAVKKLALKSLAFVGNLF
25361	55729	A	25502	2	227	
25362	55730	A	25503	262	428	

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25363	55731	A	25504	389	2310	ATSGPPGRSLGSACTIWLVLVWT GSIPIYSFHGKVEKYMCFHNMS DDTWSAKVFFPLEVFGFLPMG IMGFCCSRSHILLGRRDHTQD WVQQKACIYSIAASLAVFVVSF LPVHLGFFLQFLVRNSFIVECRA KQISIFFLQLSMCFSNVNCCLD VFCYYFVIKEFRMNIRAHPRSR ATEEVSKNLVAMKEILYGTNE KEPQTEAVAQLAQELYNSSGLLS TLVADLQLIDFEASLGLHGLEQ AVDLALPIAQAQGEVLNNGKC MDQFPVDVYQGGAGTYVNMS TNEVLANIGLGLMGHQKGEYQ YLNPNHDHVNKCQSTNDAYPTG FRIAVYSSLIKLVDAINQLREGF ERKA VEFQDILMKGRQTQLQDA VPMTLG/QE/FRASILLKEEVKN IQRTAELLLEVNLGATAIGTGL NTPKEYSPLAVKKLAEVTGFPC VPAEDLIEATSDCGAYVMVQG ALKR/LAVKMSQ/CNDLRLSS GPPGSSIMPAKVNPNVPEVVN QVCFKVIGNDTTVTMAAEAGQ LQLNVMEPIGQAMFESVHILT NACYNLLEKCINGITANKEVCE GYVYNSIGIVTYLNPFIGHHNG DIVGKICAETGKSVREVVLERG LLTEAELDDIFSQNLMPHAYK
25364	55732	A	25505	133	375	
25365	55733	A	25506	3	505	ARGREGVSRREPLLSARRLGA EWDSSAGAETASGLQVPRLGGS WPQTSVFSAAVKARGCRIATLP MDLIGFGYAAALVTFGSIFGYKR RGGVPSLIAGLFGVCLAGYGAY RV/SNDKRECKKCHWFTAFLPG LPSMGVRFKRKKIMPAGLVA GL/SLM/MILRLVLLLL
25366	55734	A	25507	244	696	

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25367	55735	A	25508	1	1442	MGQLHQAAQASADIATSRLLQQTSLTDVTRHQQFFSTYNTDDFIQFTATYREQTRTRRQRYAVNHVTFFFGKCTFRDRHRHRVIGIVLNIGLTFPAHQTDGIGSTRSQRQSRLVANKVATRNLVKHFDDDDREANRGIEAQTEHHHRGVLVNESRQRFGCQQHNRHRNHYYRRHHHRQMVMNHPYCSNYRIQREDGVKDDNLCDHPETGIQLYASLLQVFFFAANIYGWYASRQTSQNEAELKIRWLPLPKALSWLAVCVVSIGLMTVFINPVFAFLTRVAVMIMQALGLQGVMPELQADAFVWDSMMVLSIVAMILMTRKYVENWLLWVHNVISVVFIALQGVYAMSLEYIILFTIALNGSRMWINSALIHQVVLDLIQQGIVIVWRDHLHMQRHLRLAYHPCMYLVHIADFRDFPAHTRLQVQRFPAPVHLQVIHSRYLSTVATRYAESEATPVSGALGLLCPTLPV
25368	55736	A	25509	133	375	AFAQRETAGRRVQGRWCGDCFRTPTGALGGSWPQTSVFSAALKARGCGRIATLPMDLIGFYAALVTFGSIFGYKRRGGVPSLIAGLFGVGLAGYGAYRVNSNDKRECKCHWFTAFPLGPLSPMGVRFKRSKKIMPAGLVAGLSLMMLRLVLLLL
25369	55737	A	25510	2	471	
25370	55738	A	25511	3	432	NSRVDDFVAAQDAKGGKVAPAPAVVKKQEAKKVVNPLFEKRPKNFGIGQQRLLARAEEKKAAGKGDVPTKRPPVLRAGVNTVTVTLVENKKAQLVVIADVDPIELVFLPALCRKMGVPYCIKGKARLGRVLVHRKTCTTVAF
25371	55739	A	25512	59	882	SRLKNASIFVASPGKKAAGKKVAP/APAVVKKQEVKKVVNPLFEKRPKNFIDIGDIQPKRDLTSFVKWPPLYQRQRAILCKWLKVPPEINQFTQALDHQTAALLQLAHKYRSETKQEKQRLLALAKKKAAGKGIPTRKPPVLRAGVNTITLLENKKAQPVVIAHDVDPIELVFLPALCHKMRVPYCIKGEARLGRVLVHRKTCTTVAFIQVNS
						EDKGALAKLVGAIRTDYNDRYNEIRRHWWGGNVLGPKSVACIGKLEKAKAQELATKLG

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25372	55740	A	25513	1	833	GTRPKMPKGGKAKGKKVAPAP AVVKKQEAKKVVNPLFEKRPK NFGIGQDIQPKRDLTRFVKWPR YIRLQQRRAILYKRLKVPPAINQ FTQALDRQTATQLLKLAKHYR PETKHEKKQRLARAEEKAAAG KGDVPTKRPPVLRAGVNTFT PLVENKKAQLVVIAHVDVDP RGWLSFLPALCRKMGVPYCIK GKVARLGRLVHRKTCTTVAF QVNSEQRRLWAKLVEAIRTN YNDIRYDEIRRHGGNDLRPK SVARNAKLEKAKAKELATKLG
25373	55741	A	25514	1	1176	MEKELVDHTGLFLSAHASEAL ALKLMIYSEVAHKLRVRSQH PDMGVSLPLTPANSCPKTIEM RRSRELEREKDQSIETDHLPA FGSTFLKTPLSCKTLMKYICYA FIINLSFVKGSVATLMMSEES NMQMQFSVSITSGFGPFKSHIA AIPNAERKESQGEKMAPAPA VIKKQEAKEVVNPLFEKRLNFGI GQDIQPKRDLTRFVKWPHYIRL QRQRAILSAHKYRYPETKQEK QRLLAQAKKKATSK/EDIPTKR PPVLRAGVNMVTTLVENKKAQ LVMTAHDVDPIELAVFCLPAPC CKKGVPYCIKGGKARLGHVHR KTCTTVVFTKVNSDEKALAK LVEAIRTNDRYDEIHCWWGG NVGLGKSVAHIKLEKAKVKEL
25374	55742	A	25515	2	524	
25375	55743	A	25516	144	412	AGSCPFAAGPGLSGRCFVLIR FILIQNRAGKTRLAKWYMQFD DDEKQKLIEEVHAVVTVRDAK HTNFVGVSgtfkiilPPLWLASN
25376	55744	A	25517	38	476	
25377	55745	A	25518	235	892	RSRVGTNRLFGETYPRASPGPQ STALLTAYKKMTDLVAVWDV ALSDGVHKIEFEHGTTSKG/REV VYVDGKEIRKEWMFKLVGKE TFYVGAATKS/ATINIDAIISG AYEYTLIEINGKSLKKYMEDRF KNPPILWVLHMDG/ENFRIVLE KDAMDVWCNGKKLETARDFC KMSDTISDDTKVDEQERALSRT PEDKWNFRPAVPMRGERGSPS HCGQAH

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25378	55746	A	25519	1	1233	MQLKFPGRQKIHISKKWGFTKF NADEFEDMVAEKRLIPDGGCV KYIPNRGPLDKCHHGKCVATG TSYMCKCAEGYGGDLCDNKN DSANACSAFKCHHGQCHISDQ GEPYCLCQPGFSGEHCQQGLLG GVREMLRCKVRSNIVTMKAKL SFRICMTLTILANMWPRPILGG VDQIPKPKSKVLVLGAASGTT VSHVSDIIGPDGLVYAVEFSHR AGRDLVNVAKKRTNIIPVLEDA RHP/HQPDQARSVALNAHTFLR NGGHFLISIKANCIDTASAEAV FASEVRKLQQENLKPOEQLTLE PYERDHAVVDYSSSSATEQRRT ENDSDKLTEVGFRLVINFSKL KEDVRTHHKEVKNLKRLDEW LTRINSVEKTLNDLMEAHNGT KKYVTQAQASVAYLIKWKKG
25379	55747	A	25520	78	978	AAGHSAKKSCLSLPAWSFPLG STRAQWHVRRQLQARISGGGRH RCGRRQGKTRRRMGPMVVS VEPHREHGVFIYRGAEDALVTL NMVPGQSVYGERRVTVTEGGV KQEYRTWNPFRSKLAAAILGG VDQIHKPKSKVLVLGAASGTT VSHVSDIIGPDGLVYAVEFSHR AGRDLVNVAKKRTNIIPVLEDA RHPLKYRMLIGMVDVIFADVA QPDQSRIVALNAHTFLRNGGHF LISIKANCIDTASAEAVFASEG EKLQQENLKPOEQLTLEPYERD HACVVGVRPLPKSSSK
25380	55748	A	25521	230	314	QMPGNPNPFSFA*CDAGASYQA YVNSAIY
25381	55749	A	25522	1360	1848	RFRALV/TEGFSRLRFPVATVL VASSTVTKRIFLLAADIVRLA LRRSITHPFVRKQELTVYTLNN ELENLLTNVNVQAQQGGKVML DSVVPDPNMLNQFQSTMPQVK EQMKAAGKDPVLLVPPQLRPL LARYARLFAPGLHVLSYNEVPD ELELKIMGALM

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25382	55750	A	25523	91	1184	AAACSPPPPARLTYGSETLRGG DCSKMAAGCGVKKQKLSSSP PSGGGGGGGASSSSHCSGESQC RAGELGLGGAGTRLNGLGGLT GGGSGSGCTLSPPGCGGGGG GIALSPPPSCGVGTL\STPAAA TSSSPSSSS/APASSSPGSRK\M VVSTE\MC\CFCDVLYCHLYGI VQPPRPFRFTNEPYPLFTWKIG RDKRLRGCGIGFSAMNLHSLGR EYTLTSALKDSRFPPMTRDEL RLFCVSLLTNFEDVCDYLDWE VGVHGIRIEIHQCKKASKR\TA TYLPEVAKEQGW DHIQTIDSL RKGGYKAPITNEFRKTIKLT RSEKMTLSYAEYL AHRQH H QNGIGDPLPAYNHYS
25383	55751	A	25524	3	154	
25384	55752	A	25525	575	1707	TALLLTQSLFGGLFTQTHMKFG AVTRI*NRKTGNSKKQSTSPPPK ERSSSPATEKSWMENDFDELRE EGFRRSNYSELREDIQTGKGEV ENFERNLEECITRIINTEKCLKE LMELKTKARELCEECSRLRSRC DQLEDCLLKKLHSHQANPEFDL ITEHLTLCIRISIQIKAYLSLSKA QSSLSHRPPTYLAYLFNGFRLF KNLKAYLHPGEINSFIAHTKPV WWSLHTDAHEIWC RDSDLKLV PTLPLIPLEAALRNITHSLSIPPP KNFRPNTSTLFCVIFLINIRRQE YQASEPKPSHRIPCDLQRIKYL IQLTRDVKDLFKENYKPLRNEI KEDTNKWKINIPCSWVGRINIVK MAILPKPLLVI PRQTGSGMDPQ QTSGLDQKCLTVLRKTNKQKAI ASTSRKRMTMQKLHLKEKLINS KDQRTNDKNHMIISDAEKA FN KTEHRFMLKTLNKEINSRWIK DLNVKPKTIKTEENLGNTIQDI VMDKDFMTKTPKAMATKAKI DKWDLIKLSFCTAKETIIRVY RQPTERESIFVIYPSDKGLIRIY KELAIPEGKGNSSNVSKDSKMSK HQKMQGENKHD

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25385	55753	A	25526	110	569	TALLLTQSLFGGLFTRTRMKFG AMTRIGADLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGCLPWSFTLSGKSR FSGEGANHGHGRASGNHSHSGS
25386	55754	A	25527	2	464	LFGGLFTRRRMKFGAVTRIR/DF PWEINPLSSCSLL/CEKDPRTTS GPQTDQPSKHLTNLKSASTPPP YNPFITSPPHTRSGLQFRSTSSPP APAQQFTLKKVAEAKGIVKVN APFSLSDLSQLSVRLGSFIKYEKS SPVHGSFGSNPETLYSPRP
25387	55755	A	25528	162	206	
25388	55756	A	25529	74	446	TAMLLTQSLFGGLFTWTRMKF GAVTRIGADLPWEINPLSSCSLL SRFKKIKACYHSPATSWPFKTY KLSLQLPHFTCPKTRQALQVSS GAVPYQPNCFAYPCCGAQPVPS FVLNTFLHNSLCRA
25389	55757	A	25530	66	311	FGAVTRIGADLPWEINPLSSCSLL REKEPPTTSGPQTNQAKKHLTN FKSGACYTCRKS GHWAKECPQ PGIPPKRPICVGP
25390	55758	A	25531	728	825	MKFGAVTRIGADLPWEINPRSSC SLLHEKDP
25391	55759	A	25532	291	311	TALLLTQSLFGGLFTQTHMKFG AVTRI*NKKNNTK
25392	55760	A	25533	1	1056	
25393	55761	A	25534	245	487	TALLLTQSLFGGLFTQTRMKFG AVTRIGADLPWEINPLSSCSLLQ EKDPPTT/SGPQTDQPKKHLTNF KSTSEVFFSSCIP

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25394	55762	A	25535	818	2391	TALLLTQSLFGGLFTQTRMKFG AVTRIGDIPWEINPPSSCSLFLP/ RLPLLHFFGAGPSTPQPLL/HSPS AASPAFLGQGQDLINLVKVVYN NRKKLQFLASTVTQTPTATSPAH KNFQTPEPQPGVPPEPPSPGAC YKCQKSGHQAKECPQLRIPHLS YAWTFNDNPLYVQEDNRRFVS QETGNLYIAKVEPSDVGNVTCF ITNKEAQRSVQGPPPLVQRTD GVMGEYEPKIEVRFPEITQAAK DSSVKLECFALGKIDDSIREKG AIRIKPSSILMRCNCLVQSPILVG EGWTGARCQGSSTANPKLSL KSRTSNKKMKAFMSALQATFE EETLQRVNSFFMHNVLNCLLP NSGTCLFETAPPEWEQKIQNT LSIYDNLLWECKASGKPNPWY TWLKNGERLNPEERIQIENGTLI ITMLNVSDSGVYQCAENKYQI IYANAELRVLGSQLVHFRENGT CLSDEVIRDSDFMSGMTVVHAF TSGSQGTTTENQDELQIKFISAR HSQATEGINSTSAKFD
25395	55763	A	25536	425	749	IASLLTQSLFGGLFTWTHMKFG AVTRT/RGDLPWEINPLSSCSLL HEKDPTTSGPQTDQPKKHLTN FKSAQLKASGK/DLQKPYQHFO TLQQLLPLQWAPCYGPSSVSI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
25396	55764	A	25537	2	2204	IDMIFTGPGPSTPKHKKSQKGS FTFPPSQSPRNEPYVARPSTSEI EDQSMGKFKVVERVQVQDMG KKLDFLVDHMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSCLKTHICNYSETGPPPEPYSF HQVTIDKVSYPYGFFAHDPVNL RGGPSSGKVQATPPSSATTYVE RPTVLPIITLLDSRVSCHSQADL QGPYSDRISPRQRSSITRDSITP LSLMSVNHHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDITDTPFTPSGSMPLSST GDGSDSTVPLFLSSEILQKQVG QSITSMGLGFLSRGSPMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKFFSLSVTSYS SFAHFKSVAVYNIINLKTVD AKFPTRYCYCLNNRTNDLSDF ALLVDIIGNSTSYLTFIKSTSL SVNQSNESDCIFICVMTGKSGR NLSDFWEIEKYPIINYTFTSGL SGVLALLTQSLFGGLFTRTRM KFGAVTRIGDLPWEINPLSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARFTLGGQGVPLNPF SFTLSGKSCFPRRQEPNNRLFPH PNLLSLCPNPLFCNPFSTFLE GKNHHHPHFSVSQVFLGLP LWEHSPMAHRLRVQPRQPPDI HKQVISLQSGHSLVKSSQWSQ DPIKFLPHHHKNTASVCINPSV
25397	55765	A	25538	110	542	TALLTQSLFGGLFTRTRMKFG AMTRIGDLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGCLPWSFTLSGKSR FSGEGASCSLPG
25398	55766	A	25539	1	781	MPLQPLATPFTSPGSPVAQVT TNTGEPGFAQQEYAEPTQTAR PPHPALRALQASVHQTPRLG DCLGSSESATLHGSGEPNKLA PPGRPTERGGLFKCSVPLRTVR GCRAGLRGTETVPSLQRPAG DVGWINNKSTTALDRTPDTQ RTRRPRPPKQQRGRALKERPR DSDSAREGPLKAVAGLFGGLFT RTCMKFGAVTRIGDLPWEINPL SSCSLLHEKDPPTTSGPQTDQPK KHLTNFKSLLSLATED

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25399	55767	A	25540	1571	1781	TALLTQSLFGGLFTRTRMKFG AVTRIGADLPWEINPSSSSLLRE KDPPTTSGPQTDQPKHLTNFSA
25400	55768	A	25541	2150	3195	TVLLLTQSLFGGLFIWTRMKFG AVTRIGADLPWEINPLSSCSLLH EKDPPTTSGPQTDQPKHLTNF KSEDED
25401	55769	A	25542	4688	5149	TAMLLTQSLFGGLFTRTRMKFG AVTR/IRGTDLPWEINPLSSCSL LREKDPPTTSGPQTDQPKKHVL TNFKSGACYCCKWSGHWAKER PQGPPIPKPRPICVGPLKIRTCS THLGQATPRAPGTLAQGSLTDS FPDLLGLAAEDSHCLIAEAP
25402	55770	A	25543	1	433	MAAFPAALNRPTRARARRRRIS AHSASASAAAVVAGTARGM VPGSEGPCRA/GDEVADWEIVI EGTANLGPYFEGLRKHLYLLPAI EYFNGGPPAETDFGGDYGGTQ YSLVVFNFTVDCAPESYVQCHA PTSSAYEFVTWLDGIK
25403	55771	A	25544	1	235	
25404	55772	A	25545	1	301	
25405	55773	A	25546	2	438	
25406	55774	A	25547	1058	1494	KSVRLVFN/YLRTQKAVVRVSP EVPLQNILPVICAKCEVSPHEHV LLRDNIAGEELESKSLNELGIK ELYAWDNRRVPSAVPMQGPWP AEHFLQVNEQPPAGSPSPCPSSS SSSSGLRGGMQTANGPACALTP TCAQTDCCPTSH
25407	55775	A	25548	1	3965	RRFQPLPSAALRRCPPARVGG RWVSAEKVNEGGSGGGGSQRL TRRARSTARVPAGTMDAPRAS AAKPPTGRKMKARAPPPGKA ATLHVHSDQKPPHDGALGSQO NLVRMKEALRASTMDVTVVLP SGLEKRSVLNGSHAMMDLLVE LCLQNHLNPSHHALAIRSSETQ QPLSFKNPTLIGTLNVHTVFLKE KVPEEKVKPGPPKVPEKSVRLV VNYLRTQKAVVRVSPVPLQNI LPVICAKCEVSPHEHVL
25408	55776	A	25549	1	388	

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25409	55777	A	25550	1	1748	MVLARVARRPAGSAEAQASLA GKAALPERARKMSSPGIDGDPK PPCLPRNGLVKLPQPNGLGAA SITKGTATKRNRPQPPPPPTLP PPSLAAPLSRAALAGGPCTPAG GPASALAPGHPAERPPLATDEK ILNGLFWYFSACEK\CVLAQVC KAWRRVLYQPKFWAGLTPVLH AKELYNVLPGGEKEFVNLLQGF TARGFEGFCLVGVSDLDICEFI DNYALSKKGVKAMSLKRSTIT DAGLEVMLEIQMQGVVRELS GCNDFTEAGLWSSLSARITSL VSDCINVADDAIAAISQLLPNLA ELSLQAYHVTDTALAYFTARQ GHSTHTLRLLSCEWITNHGVVN VVHSLPNLTALSLSGCSKVTDD GVELVAENLRKLRSLDLSWCP RITDMALEYVACDLHREELVL DRCVRITDTGLSLSTMSSLRSL YLRWCCQVQDFGLKHLALGS LRLLSLAGETPVSALTAVTTH PHLVHPPNLPGPCANSHPARTH SPGSEAEFEGGAARPPPEPWA ARTEPPSDPAAGCPLLTTTGLS GLVQLQELEELELTNCPGATPE LFKYFSQHLPRCLVIE
25410	55778	A	25551	1	377	MRRLTRRLVLPVFGVW/DGA AVLLGNQEEVGGAD/WDLKCR PL/EVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTSGDNHTL/SRPSLR* CIRSQHGNRKRIIPRRJFI
25411	55779	A	25552	222	287	
25412	55780	A	25553	2	918	GHCEVNRDNLQPLLHRVKEDY TRVVCPIVIDINLDTFTYIESASE LRGGFDWSLHFQWEQLSPQK ARRLDPTPIRTPIIAGGLFVIDK AWFDYLGKGYDMDMDIWGGEN FEISFRVWMCGLSLEIVPCSRV GHVFRKKHPYVFPDGNANTYI KNTKRTAEVWMDEYKQYYA ARPFALERPFNGVESRLDLRKN LRCQSFKWYLENIPELSIPKES SIQKGNIRQRQKCLGISKGRTTK KPQT*S*ALCQGGRRRCQSPRV WGLSHYTQADSFQGELVALFSS FTFVSLGAPVVCSCFARMGD

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25413	55781	A	25554	84	2804	PRGSWRCRRDLKCRPLSHSDA DWDDI.WDQFDERRYLNAKKW RVGGDDPYKPVCFSTSGRVSGSP AIRAIPDTRHLRKKATSNLSRQ QLASPLPRSSYCGVTPGPIAIGP LWTSGSLRTPNHIDTVFAPGLP QPWFIHLNLYLRAMPSSLSSAPKCT LLVYCTDLPPTSIIITFHNEARST LLRTIRPPAVSTSQMAMTAAA LTPAPLRTYSVHLSRAHQLVP MPQRKKYDETWWREHTKHSKI SLFPSCRLHFSCLSRRRMAVGS GKFGVMGDLGEPFLRVRWLRI WTLGPDFHGSALNSVLNR/TPT HLIREIILVDDFSNDPDDCKQLI KLPKVKCLRNNERQGLVRSRIR GADIAQGTTLTFLDSHCEVNRD WLQPLLHRVKEDYTRVVCPI DIINLDTFTYIESASELRGGFDW SLHFQWEQLSPEQKARRLDPTE PIRTPHAGGLFVIDKAWFDYLG KYDMDMDIWGGENFEMMTVQ VLQPRREALICTWKVHHLTRE STALLIALVQAPFTGPQAKKLQ QSPCPAMLAP EYAPEASVLVCT VSLLTYTTLQSEISFRVVMCGG SLEIVPCSRVGHVFRKKHPYVF PDGNANTYIKNTKR TAEVWMD EYKQYYAARPFALERPFGNV ESRDLRLKNLRCQSFKWYLENI YPELRYPSYLLLEWLAE SRGPQ LAWSGEETDNDQLDEGFYVYQ

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25414	55782	A	25555	1	2439	MPLKKKGDEPQMEKYIQERSM LAPPCSDHRDTHSRCIPHQR FQCPLGPWFQGEQRNQARGEG GALHPLPVTAGTVALPGAAQPT PARGNVTESLQGATVKLVCKK TSFIFYCQHPAQCLALACDHEC IDLCTHIVASTSLCLRGYQGMKR TIERALTATLAQGTAVPPFPSDV PSQKDAAVRGKGDGSEWERTL TMKRSNLNSEKILPAILLTEFP RHQSPCSFDKPHHPNTLGCWLP TVLETRGGTNGQSSGKREATLC PCPLLGLPISEEDCVPPALLPPR GALPPGLQLSWAPVPQFPPLGPS SLGIPA/LPLVLNLGCLPSLVCPP TSAHTSEVAPSLKSPAESPAPAR LPRSHQPALREMRHSDYSVSV HAICWDHDFYTLVTHYMNNTS PISSKRSSDKLNPHVLVVQDSM TILSLHNHLALAGQDMMVWEP RKTLQRRQQPDSSSHSPPALV ECHPLEPEPLVAGIMYSFSGLQ GVGLRDRAVDETNRNEKRTL EMSRVEALSSFENSEFGCPPSIN TREITGNSLEGNVKKGVSVFNC TAPGKRTEKKYSKIHVMVKHS GNCKRTDGIWEEYGWSWRLH MKKVFPFGLVLVKGGEAAPGT KEIKSVSGIFQRGKKKPRGRKE KNRKKRGFAFSKETNFVYLLIL VCLIGKVVVWLTSACAEKPKP HGEATCRHSGSPAFLNFQPTRV
25415	55783	A	25556	2	1178	AKCVEVCGKREPPMSPLNQSA EGLPQEAASNRSLNATETSEAWD PRTLQALKISLAVVLSVITLATV LSNAFVLTILLTRKLHTPANYL IGSLATTDLLVSILVMPISIAITI THTWNFGQILCDIWLSSDITCCT ASILHLCVIALDRYWAITDALE YSKRRRTAGHAATMAIVWAISI CISIPPLFWRQAKAQEEMSDCL VNTSQISYTIYSTCGAFYIPSVLL IILYGRIRYAAARNRILNPPSLYG KRFTTAHLITGSAGSSCLSLNSS LHEGHSHSAGSPLFFNHVKIKL VTVALKRKEDSAERERKATKIL GIILGAFIICWLPFFVVSLLVLPIC RDSWWIHPALDFFTVWGYYLN SLINPIYTVFNFEFRQAFQKIVP FRKAS
25416	55784	A	25557	3	146	

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25417	55785	A	25558	45	592	PSPPPPARAPSAARTRRAPIPAAG QGRARPPRTVSRCSAAMATKI DKEACRAAYNLVRDDGSAAVIV VTIKYDGGSTIVPGEQGAEEYQHF QQCTDDVRLFAFVRFTTGDM SKRSKFALITWIGENVSELQRA KTGTDETLVKEVVQNFANEVVI SDRKEEEFEIKSELKKAVGAN YDAQTE
25418	55786	A	25559	249	1808	INGGTLTVTLVSVTNQGAETLPF GTGWHYPYFPLSPQTRJQAQASG YWLEREQWLAGEFCEQLPQEL DFNQPAPLPRQWVNNGFAGWN GQARIEQPQEGYAIIMETTPAP CYFIFVSDPAFDKGYAFDFCCL PMSHAPDDHHRPEGGDLIALAP GESTTSEMSLRAYNDTNRRSDK AFTPHPTCFPSNQNNASAPPTIT PDTATIAPVSHKAFAGNALRSII SDGKLTAGSVINNASAGAVPIP ASIIIVCTIGISAAVGMTNKHPT AIDTTHIMLLSTAPSAWGNQNT RAAPNTSLAAYRFLIDSRDTE TDSRLDGLSDAFSVFRCHSIMN CVSVCPKGLNPTRAIGHIKSML LQLPPNVEKFAGAYLIQFALFQ PLTHNRLMFFGAFADFLHADQ TFPGQITAAVKGQFVRRRLRF AIISPSRTL/YHTP*PRR*PR*SN FVTGRDAGRGLYNRQ*KTS/PS SICSA*GANPVVHHAMTVKFA* WQPMKISSTSPSMRPLSHMK TINGLTTFFVAW
25419	55787	B	25560	1	567	
25420	55788	A	25561	1	741	MLILISPAKILDYQSLTITTRYT LPELLDNSQQLIHEARKLTPOI STLMRISDKLAGINAARFHDWQ PDFTPANARQAILAFKGDVYTG LQAETFSEDDFDAQHRLMLS /GLPYRLEMGRLENA/RGKDLY QFWGDIITNKLNEALAAQGDN VVINLASDEYFKSVKPKKLNAE IIPKPVFLDEKNGKFKIISFYAKK ARGLMSRFIENRLTKPEQLTGF NSEGYFFEDDESSNGELVFKRY EQR
25421	55789	A	25562	3	320	IGLVLPISVRKRHAASARCLVN RRPMPRLHGLPGIPMRPPLPRV RHAGTVFRRHRKRGSPMAY*Y GHSDVVKHREALVADLCHKAA FQLCRGQRHCRPALWRHR

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25422	55790	A	25563	1600	1908	
25423	55791	A	25564	142	326	TRRAPSAISSRCCNSHQTSKSS LVRTSSSLRSSHLRTIA*CSSV HLPISCMQIRPSQAR
25424	55792	A	25565	1	1599	
25425	55793	A	25566	393	611	HSRAVCRFYPAKTSPPFVRRCR YRQFVPR*HQNE*AGRE*QPCSI ATVLPYRALPSLAHPRLSADQL PAAHL
25426	55794	A	25567	971	1628	
25427	55795	A	25568	3	1895	
25428	55796	C	25569	1	2505	
25429	55797	A	25570	1	3345	
25430	55798	A	25571	457	790	PSFRRRYRQVVVISVRKRHAAS ARCLVNRRPMPRLHGLPGIPMR PPSLPRVRHAGTVFRRHRKRG PMAY*YGHSDVVKHREALVAD LCHKAAFQLCRGQRHCRPALW RHR
25431	55799	A	25572	1662	1767	
25432	55800	A	25573	3	603	RLRSLFFLPDKMKLKDCVMIKK IFALPVIEQISPLSRRLDELDEL IVVDHPQPPSGDYTLHPLPIIR ANRPNRFRINAGCTRTFTLSTPI NVFRHKILRTQEFPSLTHHAYSP LLVVKAKFTDGLSPEFQALV SSAQEAGNYQRKLVAED/LAK NHRRHERSGRS/LSPISTAKPL ATHWGIRFATCLLKMCRRELIC
25433	55801	A	25574	2271	2519	HRQLVIVFQQPLVSGFHEAELS LDDAKWVLHPARMLAFMYSM LMAVFLRGCCFKVLTLPGRSA ISQSTSTSASSSRGAPW
25434	55802	A	25575	931	1213	
25435	55803	A	25576	1	2767	MAILSGLRCSIVANYIYAENNL FWLRLNNPKAIWCLRICITFATV IGGTLTLLPLMWQLADIIMACM AITNLTAILLSPVVHTIASDYL RQRKLGVPRVFDPLRPDGRQ LSPDAPLTTRYTLPELLDNSQ QLIHEARKLTPPQISTLMRISDK LAGINAAARFHDWQPDFTPANA RQAILAFKGDVYTLQAEFTFSE DDFDFAQQHRLRLSLGYGVLR PLDLMQPHYREMGIRLENARG KDLYQFVWGDI
25436	55804	A	25577	395	467	
25437	55805	A	25578	1	675	
25438	55806	A	25579	1	4014	

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25439	55807	A	25580	1802	2385	RKISAPALIKSRTG*EMASLPTS/ HDKQIEQALADVDVPIVGVGGS YHLAESYPPVHYIATDNYALVE SAFLHLKEKGVNRFAYGLPES SGKRWATEREYAFRQLVAEEK YRGVVYQGLETAPEWQHAQ NRLADWLQTLPPQTGIIAVTDA RARHILQVCEHLHIPVEKLCVI GVMNRRTVRSPFRESLKISP
25440	55808	A	25581	1	1568	MVKQLKLVSFLLRPGDSKQGY DKHSSLVGLMIPVCSIRFRKP SEQSFKEEGTDAAHGFWLW PCTMLNVTPIKGMMTVIYEFV DSETTLQNYDIYFTNEELTDEQ KSLIEWYRDVFRPEDLRLVESV QKGLKSRGYRGQGRIMADSSG SGISEHAWCMSRGAQGRQFCK GAKMSQVLITGATGLVGGHLL RMLINEPKVNAIAAPTRRPLGD MPGVFNPHDPQLSDALAQVTD PIDIVFCCLGTTREAGSKEAFI HADYTLVVDTALTGRRLGAQH MLVVSAMGANASPPFFYNRVK GEMEEALIAQNWPKLTIARPSM LLGDRSKQRMNETLFAPLFRL LPGIILLEELNWKTWAEWNS MLGPRAVKVFFSLAFLPGTLEP AQILFPTQRQGGKAAALLGLW KLEIYSDNRRSPEVSTAWNSPP TGKLDNKQYMIMIPRKRENTT TRGASNARLDPPSRKGYKGHY ETIGHALEHDKQSQGSYNVEHT IKRQTPVRVRCSTIIAGIYQELG
25441	55809	B	25582	1	1560	
25442	55810	A	25583	1	2115	
25443	55811	A	25584	3036	3957	RIYDAVSEPAEPVDCPRNPVCR FY*QYRDHRGKTVYDVASGDA LFISELG/PLPENVTWLSPEGEFQ KWN/GTAWVKDTEAEKLFRIRE AEETKNLMMQVASEHIAPLQD AADLEIATEEEISLLEAWKKYR VLNSRAMALILTPDLIRSNTACF CSSFVLAGQTAKAAADDGLFPP IFARVNAKAGSPVAGLIIVGILMT IFQLSSISPNAKTEFGLVSSVSI FTLVPYLYTCAALLLLGHGHFG KARPAYLAVTTIAFLYCIWAVV GSGAKEVMWSFVTLMMVITAMY ALNYNRLHKNPYPLDAPISKD
25444	55812	A	25585	1	2490	

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25445	55813	A	25586	368	761	LYCEACIMAFRMSEQPRTIKIY NLLAGTNEFIGEGDAYIPPHGTGL PANSTDIAPPDIPAGFVAVFNSD ESSWHLVEDHRGKTVYDVASG DALFISELGPLPENVTWLSPEGE FQKCSGTRVRKNKA*TLF
25446	55814	A	25587	1	809	MPVSSYERGHAEKRVVQECCE INLTSSANTILSDCERNVGYCVL CHTTRALVTGNHHRNAVYAET PSNSRINYVSSHNAFRMSEQPR TIKVYNLLAGTNEFIGEGDAYIP PHGTGLPANSTDIAPPDIPAGFVA VFNSDESSWHLVEDHRGKTVY DVASGNALFISELGLSPENVTW LSPEGEFQKWNGTAVWKDTEA EKLFRIREAETKNNLMQVASE HIAPLQDAADLEIATEEEISLLE AWKKYRVLNRRVDTSTAQDIE WPALP
25447	55815	A	25588	1	2301	
25448	55816	A	25589	718	1131	
25449	55817	A	25590	279	513	CRRIDTWQPIYQTCGRMLAVEL LTVVTHPLNPSQRLPDRYFTEI TV/SHRMEVVKEQIDLLAQKAF SLAYLSPCESGL
25450	55818	A	25591	1	407	PQDNAKKLRPHQLSSDEGHTG MGGTAKDVGFVSMRTYSWISS ALPKRLGGGVMPIGATIAITEEV FSVLLGNPFLHTTTFGGNPLAC AAALATINVLLGRITYRLRLSK KAICCWTVSVNWRGNIPIWYR KRVVKGK
25451	55819	A	25592	1	2079	
25452	55820	B	25593	1	700	
25453	55821	A	25594	1427	1845	ACISGFSTETSASGRSVITDAS LFRVLPRVCGMAVAATKRSGR TTSEALCCANQLRRRPCVSPTR STPSWLSCAV*ICTSGTT*MKR VPNARHCWICSSLIPHSLHPQP ITAKFAPIALSSSVTSPFSSVTFG *IN
25454	55822	A	25595	2	295	
25455	55823	A	25596	1	900	
25456	55824	A	25597	1	1422	

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25457	55825	A	25598	2	535	YGNREQRAVSSHTNTWVNRAL ARGWSSLGYRWVWSAWTPSR RFISQLMSRPVDASAAKVKRSL SVPCGSIPIFGNCFVRLRLSASC GCILPVRFSSSSGSEIPSTISSGSI TLPLDLDFWPFSSSRIRPVMTV WNGTCGLPFSSLMKCMVIMIM RAIQKKMMSKPDITITLVGWN
25458	55826	A	25599	442	1368	RRTMAAFACGVVRDASEVIRPS STLVPLVGEKHAKGLFGTIVDN FYLVALIFAMGTSLGLATPLVT ECMQWLFIPHTLLGFI/LYNAI CVACGLQKGVRIASDVRSYLSF LMLGWVFVIVSGASFIMNYFTD SVGMMLMYLPRMLFYTDPIAK GGFPQGWTVFYWAWWVIYAI QMSIFLARISRGRTVRELCWIL WTVLGSNTLLIDKNIINIPNLIE QYGVARAIETWAALALNNGN MWGFFILWFIGPGLVNAWQNI RAQFVHHILRRNGIADGFRHLA ALTIHGKAVGQYLTIRRTFLHR
25459	55827	A	25600	2468	3907	
25460	55828	A	25601	3	3738	YKNTYTDNSEYYANVGFNVPK VKRDGKMSVMSPDPTAIYPPFP KPTPLSIDEKAYYREKIKRLLTE RNAVMVAHYHYDPEIQQLAEE TGGCISDSLAMARFGAKDPASN LLVAGGGTCRSVINAVFSYVT NVWGWAFEWYMVVMLFGWF WLVPFPYAKKRLGNPEPFSTA SWIFMMFASCTSAAVLFWGSIE IYYIISTPPFGLPNSTGAKELG LAYSLFWGGLPWATYSFSLSV AFAYFFVVRKMEVIRPS
25461	55829	A	25602	1331	1456	
25462	55830	A	25603	549	588	
25463	55831	A	25604	19	1629	

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25464	55832	A	25605	1	1995	MVGVRFALGLMWLTLIVAETIS ANSIGIGYLAMNAREFLQTDVV VVAIILYALLGKLADVSAQLLE RLWLRWNPAYHLKEATLSAEQ AARIREMTVITSSLMMSLTVD SDLSVHLVGRKINKREWAGNA SAWHDTPAVARDLSHGLSFAE QVVSEAHSAIVLDSRGNIRQFN RLCEDYTGKLEHDTVIGQSVFKL FMSRREAASRRNNRVFFRSNG AYEVENVPDPGVEQADDIILRIT ATAICGSDLHLRYGKIPQVKHG DIFGHEFMGEVETGKDVKNL QKQDRVVIPFVIACGDCFFCRL QQYAAACENTNAGKGAALNKK QIPAPAAALFGYSHLYGGVPGGQ AEYVRVLKGMWGRNDAAQPG FRSSRPLRYGAGIMTLNLSGLS HHYAHGGFNGKHQHAVALNN VSLTLKSGETVALLGRSGCGKS TLARLLVGLSPAQGNISWRGE PLAKLNRAQRKAFRRDIQMVF QDSISTVNPQPNRLHIV/RFP RLNQYQPSFSTDLYHGTLKPAS LTMSGVVLGRM/PRKTSQQV QWACIARTDKASMPVTYSESL FVEPLERVLRYAVILTQIHRGLR DTEIETINPDIAVHFALCFHGLG SIPTKGAEKSPFLTHKVRVKPD IPSPVSIMAPCRAHPTCEALFNN STALHSPWFCDSL
25465	55833	A	25606	179	371	CVLQYTHWPACSTVAHSRRW* NRRRLRLAVTKGSLFSHRCAG ARLAFSKKLRCDALPASRS
25466	55834	A	25607	544	983	SVQNPRVNWIIAALQRTGRGR RRHEQHGEDHFVNGAAGVHV AANGLVNPQRHVFGAHQAKG DGENHRQRGAPDGLQRDGHF GEVILPLAEIGREEVVGERRHV AAVFDQ/S*AGPFP RPATRRPTR RVQRPSSEARTSCAWVGRW
25467	55835	B	25608	1	1746	
25468	55836	A	25609	1	858	
25469	55837	A	25610	98	288	LCRNNGEPLARSGAAMGALLD REHSRHP/PDLEG/SGSQQVCD GGSVTAANTSGGQVKAQLEL

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25470	55838	A	25611	1934	2812	RPQTYSDAQPGFSSRPLRYGA GIMITLNLISGLSHHYAHGGFNG KHQHQAGLNNVSLTLKSGETV ALLGRSGCGKSTLSRVLVGLES PAQGNISWRGEPLAKLNRAQR KAFRRDIQMVFDSDISAVNPRK TVREILREPMRHLLSLKSEQL ARASEMLKAVDLDDSVLDKRP PQLSGGQLQRVCLARALAVEP KLLILDEAVSNLDELQAGVIR LLKKLQQQFGTVASLFITHDLRL VERFCQRVMVMDNGQIVETQV VGEKLTSSDAGRVLQNAVLP AFFVRRRTTEKV
25471	55839	A	25612	1	515	MLAVECRSLPFPLVQPVRYTD VTVKDDYNPETEQYTLTISQRT PATPDQAEKQPLHIPFAIELYDN EGKVIPLQKGHPVNSVLNVTQ AEQTFVFDNVYFQVPVALLCEF SAPVKLEYKWSQQQLTFLMRH ARNDFSRWDAAQSLLA/ILHQA ERRASSARSAVVSAGACG
25472	55840	A	25613	1	1053	
25473	55841	A	25614	1	1521	
25474	55842	A	25615	430	1120	QTASTFLKRGKCSARQSKLCGN RRRKRQRISSYCLLRGTACSP AHQPDAFHQKRGNAGRHYAEC VLQYSSCSTRYSIPGR/TQLNLF EVADGKRLVDLPGYGYAEVPE EMKRKWQRALGEYLEKRQSLQ GLVVLMDIRHPLKDLDQQMIE WAVDSNIAVLVLLTKADKLAS GARKAQLNMVREAVLAFNGD VQVETFSSLLKQGVDKLRQKL DTWFSEMQPVEETQDGE
25475	55843	A	25616	407	1176	AYSTSLRVKICRKTSTLLRSRV TQIRSNKSTKRAAHCSLTASC PPRCISIHATTVTSTTPCLWRIA TMLRALARILLRICFSGRTLKIA CLLLLVAGATILIAIDR/AALYHA GKVKWLLVSGDNGRKNYDEA SGMQQALIAKGVPAKVIFCDY AGFSTLDSVVRAKKVFGENHIT IISQEFHNQRAIWAKQYGIDAI GFNAPDLNMKHGFYTQLREKL VIAKGHGSLTDLPAKAGITM WAIEIDDVARHSRSHL
25476	55844	A	25617	3	168	NPFYSAMR/KSAGIRHILARHVE GASHMAEGYTRATAGNIGVCL GTSGRCCFRLCW
25477	55845	B	25618	169	1227	

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25478	55846	A	25619	489	740	AIARSCADYHPANFRHHRAAA RAGDDYLSRRAERQPGAKAGG SRLRAGKRPCSAFRYW*CAAG E*SVGEKIMAGDVISPKRRL
25479	55847	A	25620	146	475	
25480	55848	B	25621	38	191	
25481	55849	A	25622	662	4568	
25482	55850	A	25623	20	2661	AGHIHRPRYQHGVGTESTSIMS VASRSAERVFLTKFESWKNFPI NRGRNKMAMRAVDAAMYV LKKEGVTAFGVPGAAVNPFI SPMRKHGVRHILARHVEGAS HMAEGYTRATAGNIGVCLGTS GPAGTDMITALYSASADSIPLC ITGQAPRARLHKEDFQAVDIEAI AKPVSKMAVTVREAALVPRVL QQAFHLMRSRPGPVLVDLPF DVQVAEIEFDPDMYEPLPVYKP AASRMQIEKAVEMLIQAERPVI VAGGGVINADAAALLQQFAEL TSVPVIPTLMGWGCPDDHELM AGMVGLQTGHRYEKYTEGRKI VHIDIEPTQIGRVLCPLDIVSD AKAALTLLVEVAQEMQKAGRL PCRKEWVADCCQQRKRTLRLKT HFDNVVPKQORVYEEMNKAFG RDVCYVTTIGLSQIAAAQMLHV FKDRHWINCGAQGLGWITPA ALGVCAADPKRNVVAISGDFD FQFLIEELAVGAQFNIPYIHVLV NRPAANGAQGSCHPDAPAVFR SSIFIRKSEELVVTMNELSASR ALPEETMPGRFELKPTLEKVLH APDNFLFMDPLPPMHRGIIIAA IVLAVGFLPSDDTPNAPVVT EAQLDIQSQSQPTEEQRLAQL VTPQNDPDQNLVYRKASQKSSR KLPKRDLPHILTPFRAPMASVC AKRKGQVLHQYSLKKYRYK
25483	55851	A	25624	1	570	
25484	55852	A	25625	312	873	APRSRVQAKIAASNTGELNALQ QLGFSVLVEGEVDLALPVNNA\ SDSGAVVA/QETDIPA*RLASA AFAQSRFRAPWYAPDASSRFYA QWIENAVRGTFDHCILRAAS GDIRGYVSLRELNATDARIGLL AGRGAELMQTALNWAYAR GKTTLRVATQMGNTAALKRYI QSGANVESTAYWLYR

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25485	55853	A	25626	2	922	FSPPLHDAGEAVFWRVNKSA NYGVLDKLARGYADLSKAESQ WDEMMRTAGSKLGLTIHASINS LFENITAAPADPILGLADLFRAD ERPGKINLGIGENPSCCRTSSSP VFDAAIWPAVNNASD SGAVV AQETDIPALRQLASAAFAQSRF RAPWYAPDASSRFYAQWIENA VRGTFDGHQCLILRAASGDIRGY VSLRELNATDARIGLLAGRGAG AELMQTALNWAYARGDHMI/R I*RTAGGGNRTRLYAVGNG* RVWRWRFYPSLPAVAGATFWQ RQSVTD AVLHRFAGDGGAAAR YPAWR
25486	55854	A	25627	911	1441	AIPISCFLLAIKALILSAIWLNA TPSRKLEPSSKWIRSLRCPSPN RCAAASSFNISQWFLSEYGPP NQVASGKTSPPVIVFKQPRYRA VTKPNCRLMMRNGCSTLARML PVMYAMLMPVFLRGCCFKVL TLPGRSAISQSTSTSASSRCGA PW*PASAETNCSSPCSRPLPS
25487	55855	A	25628	1	1247	MERVLDNLLNNAIRYCHSTVE TSLLLSGNRATLIVEDDGPPIAP ENREHIFEPFVRLDPSRDRSTGG CGLGLAIVHSIALAMGVNAQA DFMKLTGADEQIAAYCFKMPP VFHLIEEVS RNFGYALCLINIDH KAALNITQRTAANILLDGQMQ HADVQAFQTQRTARQGSTFVQY ARLARKLATANICWSYFVPR ASIEPLTWENAFFGVNSAIVRIT SEAPLLTPDALAPWSRVQAKIA ASNTGELDALQQLGFSLVEGEV DLALPVNNASDSGAVVAQETD IPALRQLASAAFAQSRFRAPWY APDASSRFYAQWIENAVRGTFD HQCLILRAASGDIRGYVSLREL NATDARIGLLAGRGAGAEMLQ TALNWAYARGKTTLRVATQM GYTAALKRYIQSGANVESTAY WLYR
25488	55856	A	25629	1	1925	
25489	55857	A	25630	402	664	TARRLLFFRD/RTARVAVPNAA VVLPFPLPVKTMIPRSLGRRRS GGICRPLGYLVAMDAIDGLQN ADNSNGESRIATSSFRSRSARR

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25490	55858	A	25631	920	1237	IARPGCHLSHCHSEPSGRLSK*P FSCNSLKTGDF*PI*GLIQTQIFS PFAFRRIIPSGSGKVS GSHSKS HHWKAFIQKQSKWKTC SGRLR SAIPSIKLFTVASS
25491	55859	A	25632	1	1341	MVHRFGIRVRFV ALGFIYQDVIL PVRAHRHEWGHYVHL CASIQR QIDVSFARDATSHSSCPVTGVR FWGYPPAANKVVIAGFELEGET MTRPGLICAEGLLVMIVSLRS ELYDSYHEFTQRVTEIVEKAA NHLPAVVEMMTLHRCATNRHN FVRRVGPAGISTFFASSPDGVN AGFSTFRVVFTCQSRPLQRHS HADVQTATLLNTVNLEQKQA NAILSGLSMDIPNSSPESAPEIQL LQSRMILGKTIAELNLRDIVEQK YFPVIGRGWARLTKEKPGELAI SWMHIP*TL SKNRPTPFS/DGLS DMIPNSSPESAPEIQLLQSRMIL GKTIAELNLRDIVEQKYFPIVGR GWARLTKEKPGELAISWMHIP QLNGQDQQLTLTVGENGHYTL EGEFTVNGMVGQRLEKDGVA LTIADIKAKPGTQFVL SQRTLE AINALQETFTV SERSKESGML LTMTGDDPQLITRILNSIANNYL QQNIARQA A QDSQSLEFLQRQL PEVRSELDQRKKNSTFIASSAIR
25492	55860	A	25633	170	935	LTQEDTRINLIPMAVESLHLPTQ MLINGGETYA WRNWKRGQY KSATLNTGQPHVRARELVDS TLASDAARLTCRHGLALPALFT LIAVVTSLSPQFIRQLWSRLT KTR*AGDQLDAYSTTEWSGSA TDTGWGKRPLYTGR*RVHRQ WYGRPASGKRWRCADYRGH* GQTRNTVCPEPAYRTGSD
25493	55861	B	25634	42	755	

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25494	55862	A	25635	793	2127	RYCKGTVMDQIRLTHLRQLEA ESIHIIREVAAEYSNPVMLYSIG KDSSVMLHLARKAAYYPGLTPFP LLHVDTGWKFREMYEFRDRTA KAYGCELLVHKNPEGVAMGIN PFVHGSAKHTDIMKTEGLKQA LNK/YTTSRAKERIYSFRDRFHR WDPKNQRPELWHNYNGQIMIK GESIRVFPLSNWTEQDIWQYIW LENIDIVPLYLAAERPVLERDGD MLMMIDNRIQLQPGEVIKKR MVRFRTLGCWPLTGAVESNAQ TLPEIIEEMLVSTTSERQGRVID RDQAGSMELKKRQLIELINVH NLLKNGGFGQVKVNRIALLAIN VEFFFRVLVQLAAHFSSGTLAQD KLCSWFGLNVRDSQRNAIFFQT LADHTIDGELFTFCIVAVFPNL PIYSYATIYVSSSSIPISSEESPSIR FACSQTSRQPPVSDSRFCVSVQV
25495	55863	A	25636	360	566	GAETMGDILLVVGILLMCSLS TLVLVWLDPRLS*RT*A*CGA LTSHQAINNGRNEKRKPIRESDP LKA
25496	55864	A	25637	1	312	LLRKSVSIIKGTIKTIIGFMLLQ AGSGILTSTFKPVVAKMSEVYG INGAISDTYVMQDG*APELGLS PGRFLRHDTFVLQLGIVMVRL AGDGS LNIN AQANN
25497	55865	A	25638	517	796	PTARFGVWKGVDPAD/CNRQ DRFAIDVRVQGS*WGCVLPLF RVLLFVSCALLVSVCVLRLL FCSSSLSLFLSGLGGGRSPKAG DVFRDRR
25498	55866	A	25639	47	411	AIKVRLESIKLMC/YSLIKTLH G*KYRNFMVIGSMVFGKKAITH VAGVKRRTAVVVGKVFQDIQR SQFRIVVTGDLAQLLYRVIKVIT CGHFVRQHGIVLCAGVLHVGD RYQAHVKTLGGLI
25499	55867	A	25640	1	1488	
25500	55868	A	25641	2	298	CCICL/YSYAPIDVW/WG/WNTA GQVQAA*TLKAASSIVTIPLRN TIFNYSLSGLRRRLIIRSRHS THASNITLJAASTASRIGWFASA YHTRSNHGR
25501	55869	C	25642	1	2064	
25502	55870	B	25643	1	1116	

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25503	55871	A	25644	312	620	SACRCCLVVVPLFVCL/GSSLSL APTFFLLAS/SSSRASRVVAFGL GSLRAGSALCLPCAAVVVALRS AGTCLEWW/WHSVLPPETK RLP/STSLIPYASVSI
25504	55872	A	25645	2	2237	
25505	55873	A	25646	692	6383	RMSRSSDYDQYRSRNLIRRH EKMDASLHVGTKEFDISKVSEV DSVDDLIDNAARYLLKDWKG VGELVNGVEVALEYTAERGIAL LKQNPELYWQILAEASIAQVG GEVWIAPKFERNGRLRLANSEI GAASQLQTYHRVDPGRPKLD LSGGMSQRYMIAMAIACRPKL LIADEPTTALDVTIQAIIELLE LQKQENMALVLITHDLALVAE AAHKIIVMYAGQVVETGDAHA IFHAPRHPYQALLRA
25506	55874	A	25647	856	1467	
25507	55875	A	25648	1823	2014	SQEIALMQFRPRLTGASGSP*RP PHRTLRLSDQNAATIPQKRASA LIPLMRILPVRVYGHLLC
25508	55876	A	25649	1	218	
25509	55877	A	25650	2740	3293	IFAVNLILQCHVGTHHQRFL FAGNGDAGNQIRERFPNAGG/E LQSPDVALLRPAFWRRPQSSA AAAHGE*SRGVSYPEAPYTRRQF ALPAPPIKCAPLERQRPSPSR HLRLPACPGYKNRASSAKPSYS FLAQRQHLQRLSPLPQNQNLPQ RRRDQRQRAGAMSARVPDLISS SRSMRRTS
25510	55878	B	25651	1	1875	
25511	55879	B	25652	1	2981	

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25512	55880	A	25653	1	1649	MTFRNCVAVDLGASSGRVMLA RYERECRSLTLREIHRFNGLH SQNGYVTWVDVDSLEAIRLGL NKVCEEIGIRIDSIGIDTWGVDV LLDQQGQRVGLPVAYRDSRTN GLMAQAQQQLGKRDIYQRSGL QFLPFNTLYQLRALTEQQPELIP HIAHALLMPDYFSYRLTGKMN WEYTNATTTQLVNINSDDWDE SLLAWSGGQQLVWVAEASGE WGVLACTIONFAWNRNYFVLLFV GVFLSSFGSTANPQMFALAREH ADKGTGREA VMFSSFLRAQVSL AWVIGPPLAYALAMGFSFTVM YLSAAVAFIVCGVMVWFLPS MRKELPLATGTIEAPRRNRDRT LLL FVICTLMWGSNSLYIINMPL FIINELHLPKLAGVMMGTAAG LEIPTMLIAGYFRQTSGPAYGR SVGRIRSRIRQSCYYQRIFSL LACELANALERPENFCGMHFFN PVHRMPLVEIRGEKSSDETIK VVAWASKMGKTPIVVNDPCGF FVNRVLFPYFAGFSQLLR/ERRG FPQDRQSDGKTVWLADGPGIS AGRCGH
25513	55881	A	25654	1590	2855	RNLLGEAADVPVSGPHSAIYRPD WPKSGDCACQGPICKSARNP VVPVHVHGPSEDLEVLNVFGE LPOPLIDTQLAAFCGRPMSWG FASMVVEYSVGTLDKSESRTD WLARPLPERQWEYASPNVWY LLPITAKLMVETEASGWLPAAL DECRMLQMRRQEVVAPEDAW RDITNAWQLRTRQLACLQLLA DWRLRKARERDLAVNFVREE HLWSVARYMPGSLGELDSLGL SGSEIRFHGKTLALVEKAQTL PEDALPQPMNLMDMPGYRKA FKAIKSLITDVSETHKISAELLAS RRQINQLLNWHWKLKQNNLP ELISGWRGISA VKSSEAGLGAL SATSGFGKLQIQHQAFTLRTRT TDQHTLLAGTLFIKILIPMVSF TFQYCCFAVPQATYCHRIAPIL GNGAMKPGRKIS

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25514	55882	A	25655	1	3315	MDELRLVLMTHIHLPPIRRAD GSFGNDLTTGAGFNDKRTVPR YARVHVYRCRKVICIFTKRIFPC LDVPAHRLVVMKGTLYGMP VVAAAFEFAMGGSMGVS VVGA RFVRAVEQALEDNCPLICFSAS GGARMQEAALMSLMQMAKTS ALAKMQERGLPYISVLTDPMT GGVSASFAMGLDNLIAEPKALI GFAGPRVIEQTVREKLPPGFQR SEFLIEKGAIMIVRRPEMRLKL ASILAKLMNLPAPNPEA
25515	55883	A	25656	246	422	RHADTDLRR*ISDRFSPAPPADP ANGGR*TPRHAARKRRDPGTPV QPARKPSKPTRLLR
25516	55884	A	25657	884	1276	LVTRQLSPGNRCNVFAFSSAVE TSLTCQGWLSVCAVCQAISSS HNASIQVRSPAASCGSPFCSKRP SALWWTVSVPFLSPRRRTSGAN AESVSAT*SKRRSSARRSASARS TSLGAALRSRTASNEWRS
25517	55885	A	25658	649	1427	LPLLGSMSPRMTAQLACDAL QMALWRRKRPRNVIVHTDRGG QSVQQFRALKRHITASRETERF YLDVQKQFPKVTAAQKVIVSEA GASVYSASELAAQEFDPDLVSL RGAVSIARRLDPLAELVKIDP KSIGVGQYQHDVSTQLARKL DAVVEDCVNAVGVDLNTASVP LLTRVAGLTRMMAQNIVAWR DENGQFQNRQQLKVSRLGPKE AFEQCAGFLRNHGDNPLDAST VHPEAYPVVERILAAATQQALKD LMGNSSSELRNLKASFLDNEEN WPLLLDALIPVANTCEMILMPA CFGLADDKLWRWLNEKLPCSL MLLPTLPPSVLGIRLQNLQRO FVRQGGVWIECDGGGDTTTITI TQR**PAGRVYRSPGSLSGGGT HSGSNTAGTERSDG
25518	55886	A	25659	1	1878	
25519	55887	A	25660	1	4329	

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25520	55888	A	25661	2514	4173	PTSCLPDDYVGHCRGVSAAHF AGSVSCVRLLSACARPLWRHL GLALLRVWCRTFLLLSALASVF CPCSVVWGRLLFSASLSVVVW GGVFLSPLGSLSPRG TARLGAA CRSRED/RRR*WRGIFNRDIFAS AVPASVNPDKPCAPAAICIRFTS TSAV*VGCSDRNA/DAEASGEG WRRFGDATLSTGQFGGEAREE VILGLIGSQA/KTGGNTPKASAV RKITLVAWPALETGLTMLS** IG*ETRVFSVFEPSSKSIVPSSRT VTFSSNASRRIAL*ISGSASFDSL IVFA*QPPSKLNTPSSQPCSSSP IRRRFGSVERVVLVPVPERPKNT ATSPFSPTLAEQCIEAIPSAVFA APVRVAASMIISGFICALASIRPS ASTRRPSASVFITSTFLPLR*VMI SPSLNALPLIRLSAQQRNSFTRL FSPRVMANASAPVTVAAPPMS DFIESINAVCLMQARVHWRFFI ASWVVIQPPAIPENVLNRVRLC AAPGTLCLTTVFSSSGDR*NAL CNRCNRPAFCFRSSAIRFATVLA ARRHDWVWPISLIPRPSS

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25521	55889	A	25662	2221	4400	RGCVVSGKSSCSKTNLPSDDKR TGASCPRLDLFLRYLRAHALVT AEQLAHEFSLGIAIVEEQLQQLR EQGLVMNLQQDIWVSDEVFRR LRLRSLQAAREATRPVAATTYA RLLLERQGVLPATDGPALFAS TSPGVYEGVDGVMRVIEQLAA SAINASLWESQEFVYGKPVYAV GENYSQGQYYLASFANKIWLSP QGVVDLHGFAITNGLYYKSLLD KLKVSTHVERVGTYSKSAVEPFI RDDMSPAAREADSRWIGELWQ NYLNTVAANRQIPAEQVFPGA QGLLEGLTKTGGDTAKYALEN KLVDALASSAEIEKALTKEFGW SKTDKNYRAISYYDYALKTPA DTGDSIGVVFANGAIMDGEETQ GNVGGDTTAAQIRDARLDPKV KAIVLRVNSPGSVTASEVIRA ELAAARAAGKPVVSMGGMA ASGGYWISTPANYIVANPSTLT GSGIFGVITTVENSLSIGVHTD GVSTSPADVSITRALPPEAQL MMQLSIENGYKRFTLVADARH STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASVQVRS PCLTYILLFRYHSYQYHAKEN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA
25522	55890	A	25663	1	1665	
25523	55891	A	25664	475	1182	
25524	55892	A	25665	242	3059	
25525	55893	A	25666	1761	1970	
25526	55894	A	25667	455	1137	GTKPRDIDHILGTFITPGMPKGG KLDVYAAPLPLKLLGRPTEGE YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLK /IADQLIVGGGIAITFI/AAQGH VGKSLYEADLV/DEAKRLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDDKISYISTGGGAFLEL WKVKYLPVAVAMLEERG
25527	55895	A	25668	1108	1932	
25528	55896	A	25669	1496	1631	
25529	55897	A	25670	462	1152	
25530	55898	A	25671	545	598	

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25531	55899	A	25672	1	1761	MRGHNWIDMDQARQSTPHT DRKICHKNDRPRTTPLRKIDAH PHTLILPAESTLSTTKYKLRLAL LVENTNKDKSAVS SVVFRGSVL HQAANFPNMLCFQLKNGVN ACNDFIMLFVDDNAAGSIERAA SPCINEKQHAFSESVPAIAAVRG LGSMIAVEFNDPQTGEPSAAIA QKIQQRALAQGLLLTCGAYG NACKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDCLKT PVIQPRASGEYNEEFSLLPVVN YLKDKLSNPVRLVKDYLDGVD VAEGLVVLNVFNKGEKKD DETLSKYYAALCDVFVMDAFG TAHLRAGFLLTGIGKLRCSLRC AGPLAAELDALGKALKEPARP MVAIVGGSKVSTKLTVLDSLK IADQLIVGGIANTFIAAQGHD VGKSLYEADLVDEAKRLLTTC NIPVPSDVRVATEFSETAPANL KSVNDVKADEQILDIVRDLAA NVVINAVFSYVTNVWGWAFF WYMMVMLFGWFWLVFGPYAK KRLGNPEPFSTASWIFMMFAL LYVCCRTVRLGREIHRRAQIVH IDIEPTQIGRVLRCISVLSMLKR
25532	55900	A	25673	1	984	
25533	55901	A	25674	1	1181	MMAVSAPYVGDNIDGGIYTQ SETHTISSDCVLDTAAMWTPLS AVIGCTTNPAQYPANAEEVYN KDGKLDLYGKVDGLHYFSDN KDVDGDQTYMRLGFKGETQVT DQLTGYGQWEYQIQGNSAENE NNSWTRVAFAGLKFDQVGSFD YGRNRYGVVYDVTSWTDVLPF GGDTYGSDFMQQRGNGFATY RNTDFFGLVDGLNFAVQYQGK NGNPSGESFTSGVTNNGRDALR QNGDGVGGSITYDYEFGIGY TQTYNATRVGSLGWANKAQNF EAVAQYQFDFGLRPSLAYLQSK GKNLGRGYDDEDILQICCMSDP TQNRQASAKLAPCQVALLSSA SPHHAFTPSTSIQPAHIIHSSPP PWASSHSISTHQHTQCSSSNT LAVH
25534	55902	A	25675	1	147	

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25535	55903	A	25676	683	947	QVRDSLQQGRERRIALSIGWL VWREGCQDQCELEAGGASALTR RGSCRELDPAFPATMLLFCPGC GNGLIVEDGQRCCHASTDAVPP
25536	55904	A	25677	12	393	RGSCRELEPAEFETMLLFCPGC GNGLIVEEGQRCH/RAVACNT CPYVHNITPQGNITWKYPKLKE CGSDVLGGAAAWIENVSTAE SC/PKCEHPRAYFMQLQTRSD EPMTTFYKCCNAQCQGHWRD
25537	55905	A	25678	234	567	YVDETDDCFENNRCQGPVNGA YSPAGLSRVAADASLTTPHAK* TLRSLTLHQHDKTRTELLNDVA GALALDDKLGRSTNQLSGGEW TPSLARPFLLLGPRKMRLPLH LPP
25538	55906	A	25679	1	794	HCDGKHFTGVGKIMSIGMQLQ DVAESTRLGPLSGEVRAGEILH LVGPNGAGKESLTGREWPEMP TVKGTIQFPGHPLEASAKK/L ALLRAYL/SQQQTPFPFPVWH YTLHQPKTRPELLNDVAGA LALDDKLGRSTNQLSGGEWQR VRLAAVVLQITPQANPAGQLLL LDEPMNSLDVAQQSALDKILSA LCQQGLAIVMSSHDNLNHLRH AHRAWLLKGGKMLASGRREE VLTPPNLAQAYGMNFRLLDIEG HRMLISTI
25539	55907	A	25680	12	414	RAAPSRNLPPRMPIPIAIAAR PIITAAAMYRSIRFSMTVSSLF QLKRSSVGKLMFFRRHRQIDDR QNHDEGLQRNDQDVENGPRH IQDPL*PPRQETSNQNEQLSGV HVTESQQTGGSWFGQHA YPF
25540	55908	A	25681	568	724	RFSGLTVLDGIYPHQYDGYSR WSAKRYL*WRNL*SGTHRSC* VNNFTRSNKK

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25541	55909	A	25682	1	974	MNGKLGSSDVKNETPYNIPLLI NENVISSGISLWHTYADEHY RVIWPRDKKKPLIANSWVAVY TVTGCNSDRLNNIRTLRA/MA REFSIDVLEMLQQFRVVTDPDR PEHKQLPQHELAERQEKISTWL ELMKADGINPEELLGN/SSAAA PRAGKKRQPGSAKYLF\DVN GETKTWTGQGRTPKPIAQALAE DCHGKPEYGSVHGCRCDDGS AGNLCFDLNRHCGLGVRLRPR KINGDYRSRCHAGETGVCAG AETTQMAESGVSGAGLA VRGE RDGKRSPLQIAIMMNGSSGQAI SSNVIIQLFLVEIKSLRMLYM
25542	55910	A	25683	1	1359	
25543	55911	A	25684	1	918	
25544	55912	A	25685	72	690	PAPVAGAHCPGLHRSHSEHQEP QLRHVARWPSS*SWLCHGTFR KLLPGKKRRGGNKKF*GRRAR GVGCVVSRYWCGPACACSLRR WLAHTVHVVFTEAQSIKSHSS DMWPDGLALSPGCAMGPSGSC SRGKNVGGATKNFRGVHNIYC HKPIPTTQHESKYARQTTTEEC TQTSSHDFRITTSVAVMQRLQI ARNLVTHPKLVFMDPTGGLD VSVQARLLDLLRGLVVELNLA VVIVTHDLGVARLLADRLVLM KQGQVVESGLTDRVLDDPHHP YTQLLYSSVLQN
25545	55913	A	25686	1334	1545	RSQSRLESCSVTGSM*RVSPA RSFRITKRVLAAARLAT*LPAS GRRITGVGVSVDEFPSELLSSSF TD
25546	55914	A	25687	1784	2125	WLQHIHPQLLRCPVLRAQNVW IRLTLYDRH/RFVTRGTGLGWIEG DF/DKVPDDLRFAGGDRSI/RG YKYKSIAPKYANGLDIGKSPAA GAISFCLTFVMSARRGGHRGQS ASGCRA
25547	55915	A	25688	931	1213	NLHPAPAKRRAPARPQSRLAHR QGRMRGAPRFRQRQIKLCY ARCTPTICTKVKSRNTVTSG* TWSPRQRAKWWKSAKPPSAGL TSSARHP
25548	55916	A	25689	999	1243	VDPVPWLPMALDITSTAPARQF RKRIIASLMPT/WGTSLRRYSVP PRRSGWKRWRFPPTGSTTCRPP FPAVCSSVCLPATW

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25549	55917	A	25690	1225	2341	ARTFRLSNFGGSTRARGVYWD PNSDLCPITLDFSYKMPLLNPL EQYYLVQGGFKRTDLNDTESD STTLVASRYWDLSSGWQRAIN LRWSDLHFTQGEITNTMLFYP GVMISRTSRGGLMPTWGD SQ RYSIDYNTAWGSDVDFSVFQA QNVWIRTLYDRHRFVTRGT LG WIETGDFDKVPPDLRFFAGGDR SIRGYQYKSGPKLPNGDLKG ASKLITGSLEYQYNVTGKCTK WQFGEWLAPGEVRLAPGATLA TPELVASCSTEGNLGAANFHA ELRARLPWHGGAMKPRPVHLN TWEGFYFDLPDKVKALATAA AALGVERFVLDGWFNARHH DRAGLGDWWPDA TKFPQGLG ELVAHVNP FYA
25550	55918	A	25691	45	233	SSYPWWAAWWASTTARPSTR WRSSPR*SA TTWASSPSP TS* HDRPGIGATHSSRFPLK
25551	55919	B	25692	1	558	
25552	55920	A	25693	324	657	
25553	55921	A	25694	831	1244	WQPGGR*WSRQRSADGTGPDD LAAAYFPGRDFYRN*PSERC*H RRG
25554	55922	A	25695	1	1215	
25555	55923	A	25696	1	840	
25556	55924	A	25697	1	1365	MPQNRGGFLDKKNPGAPLEGA VYVNCFTFRPGIGYEGRTAVFC GAAKVPPGLNRYRGIAFPGGNF ASKRSRGRNLGARGCLRFCPK\ WQ\NYSETASVQQQN*SVLARA IERGINAPLA\SSCGRFFDAVPA ALGCAPATLSYKGEAACALEA LAASCHGVTHPVTMPRVNDQL DLATFWQQWLNWQAPVNQRA WAFHDALAQGAALMREQAT MRGITTLHPEGLERMSAGHES WLERRNGELGEGKGS KAYPTG DHKGADLYDDSNFLIQNIFVED TRGLLRQGGREDLIERYKDP LNE NPKRCVEQLANWHKELEYKK ASRIDIKPSREYASTIMNAIWTG EPSVIYGNVRNDGLIDNLPQGC CVEVACLVDANGIQPTKV GTLP SHLAAMMQTNINVQTLLTEAIL TENRDRVYHAAMMDPHTAAV LGIDEIYALVDDLIAAHGDWLP

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25557	55925	A	25698	1	950	MPDEENRFNALKAVFSQLMTD ATLTPLFNYHYRISAPPGVNGL SMKRAYVVFSGGQDSTTCLVQ ALQQYDEVHCVTFDYQQRHRA EIDVARELALKLGARAHKVL VTLLNELAVSSLTRDSIPVPDYE PEADGIPNTFFVGRNILFLTLAA IYAYQVKAEAVITGVCETDFSG YPDCRDEFVKALNHAHKEKLD EDCKRRMYTNPLRVLDSKNPE VQALLNDAPALGDYLDDEESRE HFAGLCKLLESAGIAYTVNQRL AVNPEFKADPVVDIYLVASGA DTQSAAMALAERLRDELPGVK LMTNHGGGNFKKQFARADKW GARVAVVLGESEVANGTAVVK DLRSGEQTAVAQDSVAAHLRT KEKDSVEIYENENDQVEAVKRF FAENGKALAVGVILGVGALIG WRYWNSHQVDSARSASLAYQ NAVTAVSEGKPDSSIPAAEKFAA ENKNTYGALASLELAQQFVDK NELEKAAALQQGLADTSDEN LKAVINLRLARVQVQLKQADA ALKTL*IPD*RPDAGLRCKRSR SPAVCTDRQNAHEIPRPSHLM PERR*EAPALPDFLNPARAAG
25558	55926	A	25699	1	3314	MKISRGLGEAPDYRFSLANERTF LAWIRTALGFLAAGVGLDQLA PDFATPVIRELLALLCLFSGGL AMYGYLRWL RNEKAMRLKED LPYTNSLLIILMVVAVIVMG LRAMLAMAPIWESDFHTLSY GFRPERSVHHAIRTVKLQLTDC GETRGRWVIEGDLSSYFDTVHH RLLMKAVRRRISDARFMTLLW KTIKAGHIDVEDKRAASEGVPO NKIISPLI.SNIMLNEFDQYLHER YLSGKARKDRWYWN
25559	55927	A	25700	997	1716	PYLTAASSAFQQLHLSGENHRD DGCAGYSRRTLAAQLQCHCEC DHNLPDTPRLPRSGVVLPA PRPLHTLISALHRRVLTTRHARH ESSTLNPQRLPPAHRFFACQSRY VPGPAEYSYAVRSTDESG*A*W LRVPPNLIALTQVRSPLDLALPA QNCPPCRSMLEPAPYILLGMLA TWPACPGHEVG*SHSAHPDEP ETLQTVSR*YRRFGRPVH*SVH VVGRYPHQACQCYLSSTAE
25560	55928	A	25701	1	769	

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25561	55929	A	25702	1	3707	MVRSAVVAGIAQAALPQSVVA WEYLVEDYDRINDIEAVLPEF ADYNQRIHHPGGFHLINAAER RWMTSGKANFITSKGLLEDPS SAFNSKLVMATVRSHDQYNTTI YGMDDRYRGVFGQRDGYRDN CEEIAQLAEDCGNLFAVTVFRC PAGANLQGNRVHCIDDLGKD RFNDIRNVQAAELAEAMAISAA QRRMRAAKKVVRKKLTSGPAL PGKLADCTAQLNRTEFLWK GEQNALLRGFPVAVRLHSL
25562	55930	A	25703	1	369	LPSHGAGLGTCSLPCLSLPPTP WAPVQPEPRRAPPPWVRPVP LTTQGLRN/DEHRVQDWQAAP PAAPLKVKCYTNQHPVFSTRFV NAPIDTLYLAALVRTWRTFMSS SRIVNTPIGTLYLAQ
25563	55931	A	25704	1	444	MRLHSSALGRSMGLGAVEQGA ALVGEAPAAQEPTEAGEGSGM AGCSPKACAPAGRQLRPGPA/AA PSAGPPSPRPPTGAPGQAAPRAA PVPARASPTPPCKLRERAAAF A/EPRKGLPQCSGGLKGSSAA KVGAQAEAPRASESCEDC
25564	55932	A	25705	1767	2130	YTGQRLRRVYVWPQQCQPTCA ALDFSPSLSCLPA/AAGLRTYSQ PCLSLPPTPWAPVQPEPPQ*APP PAPRRP/AHRPPKG*GVQAHA G/RQAAPPAAPVRDPLG/KPAGL LSLVGTWRTFMS
25565	55933	A	25706	654	832	RRCARFLAGP/LPSHGAGLGTC SPPCLSLPPTPWAPVRPEPPRA PPAPRRPVLGVFS
25566	55934	B	25707	1	537	
25567	55935	A	25708	1	455	HCGSVIGFLVSLTLRTKLRTL AVSVTALTVCLEFIPSDVRMR SVSSFVWVRSLAGSRVKLQTF AVTVTALKAASLELVPPGGVL VSLASGVKLQTAAGK/RCLPV LRHAPALLSPVVVDGTGHRGA GGGAHRGSGRPGAHGGGGRL
25568	55936	A	25709	1	314	SACREVVRRERHEREPGLRGAL AGQLEFRVGVGLVRPALGGAG QPGAALDFSPGLSCLPA/AAGL GTCSPCLSLPPPWAPVQPEPP RRAPPPVHGAQSHRPPKG

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25569	55937	A	25710	144	519	HPGQRLRRVYVWPQQCPIGA ELDFSPSLSCLPA/AAGLGTCSP PCLSLPPPWPAPVQPEPPQRAPP PAPW/WLSPIDHPRAEECECTA QDWQAALPAAPVWDPLEMSG LFDRAEKRYIRSFARKDSM
25570	55938	A	25711	271	743	ARTWNVKVCVRIKANSHSIFT GLSCLPAGQGSGPAARIA*ASD PLRGLLCGPSLLDE/PPPPAPWR PVPSTTQGLRSAGEQRTGRQL HLSAAPVRDPRGEAIWAPESGR SAASILKPARPPAHREERTTPDA PP*EL*HSPRRSAASLREDPWLH S
25571	55939	A	25712	1043	1348	GPARNRAQRRRAGTAGGPITPS AAAGPGAKPLIARRRQGWPA PSAGPAKPTPTRISSWPAS/QPA AAVPARASPSTTLFKLREWAPA LASPERGSHSATVG
25572	55940	A	25713	22	226	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIACTGHI VTRFRPRAR*GSSHRNKA VDTQ RH
25573	55941	A	25714	166	714	
25574	55942	A	25715	1	462	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25575	55943	A	25716	1	924	MFAHSYSSLAALLTATLTAAG IISFPVALCLVIGANLGSGLLAM LNNSAANAAARRVALGSLLFK LVGSLIILPFVHLLAETMGKLSL PKAELVIYFHVFNLRCLVML PFVDPMARFCKTIIRDEPELDTQ LRPKHLDVSALDPTLALANAA RETCALATPWTDDGRKYAYSA ASGGRRSATKVMVVVTDGESH DGSMKLAVIDQCNHNDNLRFGI AVLGYLNRNALDTKNLIKEIKA IASIPTERYFFNVSEAALEKA GTLGEQIFSIEDMDLGDEVYTV GRPHPMIDPTLRNQLIADLGAK PQVRVLLDDVIGVGATADPAA SLVSAWQKACAARLDNQPLYA IATVTGTERDPQCRSQIATLED AGIAVVSSLPEATLLAAALHPL SPAAQQHTPSLLENVAVINIGLR SFALELQASKPVVHYQWSPV AGQGWLANPELLEADAEY AAVIDIDLADIKELCAPNDPD DARPLSAVQGEKIDFVIGSCM TNIGHFRAAGKLLDAHKGQLPT RLVWVAPPTRMDAAQLTEEGYY SVFGKSGARVSSIPCAVPCVWA RVADGATVVSTSTRNFPNRLGT GANVFLASAEALAAVALIGKLP TPEEYQTYVAQVDKTAVDIYR YLNFNQLSQYTEKADGLLKPRF RPWQRKILDLTATYHEQHRDEP GPGRELRRLMPMEDEALVL
25576	55944	A	25717	1	417	MGLVNNWLSEESLWQSRHIL RALRYYSNWRQYFAGYTFGRQ YWQSPEDDHLPLLEFLARYER PMKNCWKILDIETTDVDIIRRA YLALLPSFHPETDPQDFKQLRQ AYEEALRIAQSPAKSVWQPEEY EVAEHEILLAFRALLASDSEFL PSAWQRFIQQNLNYCSMEIDEL RWSLCTIAMNTAHLSEFCVVLL AERLRWLQEENTGEIDEEELGS FLYAIAKGNVFNQITLHLPVA RRPDICTQHNDQSRCEGYQILS DKRGHQHGGITALYQCNGNAD PRAKGERLFFDAPA*CSSARV CVLSLAGASKKSRSPFARGSAL PHWYRAVMPPPCW

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25577	55945	A	25718	1680	2058	YRAYAPAFLLPSPSCPPLWRHC GSGRGENRRRDSAAHGPIAPRR QPDMPAHRQS*SFV/PASCSAC MDEPHKRLTVTAGTECGTSASS AALRAILKPCSSVCSFFLLLLL PPPPSSSSSSFFFLF
25578	55946	A	25719	1115	3549	NPDRLQLNLIETSK*QOMGD TRKKRS/NLTVAPIHSLKRYEQ HTEL SRHINVNLGDRNRQQL ILDQKGSSQRNIYLSHVAQKIPG RATYALSHSVDMITIQGLTLR CAPPHRRRYAGRFRCRSAGNFL NVQGFDAVLVAVKIIDLCLLT IAPSLIVCTRLRSPWCGALRRCS TDGRSDLASSGVMSIDTESAL TRWCLSLPHGALGKIIAEGLLS VIASKASAIVTTVA VVPVTRRSS LVNWHSGGSLWRCNRTDERD QQASQGTTRMGRTQRNYSPT QAIHKGTSPMTATTSNTEQPPH EKPNLTQHPNPDRTIHPKAT HNELTQDTPQRDAKQNGEKTQ RKKNCSELNDAEDQAERFQD RLMLKLQVTTKPCSMTRLRDC AGIWSAANRWSGIGIDRMIMLF TNSHTIATLFSSRRCAHRNKFH LMNEAVRRLRLSSFRKSVLRD ASFHDNQRVHSLQLLKERKKSL IHGRICAAKASLFQTRRYRWQK APLFSAQFGRNRNAVTHNRVW TTTTAIERTRARGLRPNSGRGF HSSPAWQLRHRKCRRCARRYH TVYWKRRRSVARASTVVSGR TSRRGENRRRDSAAIHMLHAA KQTCRLRIAVMIIRAASCSACMD EPSPDLTVTAGTDAGLAPAGYA LNERRDLHLATKSTALRTAHR GPNRTGWLNRRIVRVMTALF
25579	55947	A	25720	606	1562	
25580	55948	A	25721	688	762	
25581	55949	A	25722	492	737	SLPSGATLPPALLLASAPDTA* WRCRER*YHLPAYAAALSPAVA HRASLYSTLPSSVPWRRQCAGF RARRSPEQAWAYPAR

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25582	55950	A	25723	335	903	WVHDLPAKGGSSARNIMLKSA PLRGHTRTRKKMNIIEANVAT PDARVAITTIARFNNFINDSLLEG AIDALKRIGQVKDENITVVWVP GAYELPLAAGALAKTGKYDAG IALGTGIRGGTAHFYVAGGAS NGLAHVGDSEIPVAFGLTT ESI/EQAIERAGTKVGNKGAEA ALTALEMINVLKAIA
25583	55951	A	25724	3644	4545	SEAWPWRTAGTCLLCNTT/AH VDKAIESRTVVADVLAKFENAL TGKLLTVSFQAHEAVIHGHPA PEENLQVLAALRLQYLQGDYT LHAAIPPLEEVYSLQRLKARISQ STKTFTPCERLEKRRTSFLEGT RRSFRTGSVVRQKVVEEQMLD MWIKEEVSSARASIIDKWRKFQ GMNQEQAMAKYMALIKEWPG YGSTLFDVECKEGGFQELWL GVSADAVSVYKRGGRPLEVF QYEHILSFGAPLANTYKIVVDE RELLFETSEVVDVAKLMKAYIS MIVKKRYSTTRSASSQSSSR
25584	55952	A	25725	1	735	
25585	55953	A	25726	147	504	STCPASAPPRPSAGPRILSGSSAS GSPLGSSASSPAVHKG*RFWL TG*CGP*VSAGNK/LFERWDGS VQSIHPLQILESQGSKNLEVFVRG WMVAMDNRFVGLKGDSQQLS GQRIFKLG
25586	55954	A	25727	1	639	
25587	55955	A	25728	1	1247	

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25588	55956	A	25729	1	2376	MAEEVEKKQRIKFKFTYRGVD LGQLDMSFEQLRQLYGARQL RRLNHGLWRNAEAQAFAAE APMLGQEGGADHREAGSGEDA PAGYDHPSQDGGQQGRLQRQ DLQPGGDQAGDDRPRPGRVLH HLQAQRGKKPM/ISTVTFGQ*P DPPLRAGQRL*RC/RLIYGRGK CWALSGNP/RSKGTTLLKSISAR LTPQQGEIHYENRSLYAMSEAD RRRLRLTEWGVVHQHPLDGLR RQVSAGGNIGERLMATGARHY GDIRATAQKWLEVEIPANRID DLPTTFLRATHTVKMFSIPGYSS PGQLDPETNINIGTSYLQYVY QQFGNNRIFSSAAYNAGPGRVA TAIVLTLYIIMVGGFATSGELT YEVWIGFFASAFKVFLLALF SILIHAWIGMWQVLT DYVKPLA LRLMLQLVIVVALVYVYIGFV VVWGMRAALQISQSGQTCALL SKVFPTRSHTVSAOGGITVALG NTHEDNWEWHMYD TVKGS DY IDAGRKRQEEDWNSGVGDPS DAGDRKHQLKAAQLRPEAIKQ RRIANRLKRRTOFPRHLKGFVN TLKPIHGGCSVGTKCPQMASLP EGLHHPVKLVFLGKPGCLLTDR PLKGPNTAKPVAVDLNASATAI TSYSLYGGSMILLFASTLYHAI PHQRAKMWLKKFDHCAIYLLI AGTYTPFLLVGLDSPLRGLMI
25589	55957	A	25730	219	652	SASWREAIKLSRCLRPSATAR GAGRGGCGLADRRASRQGNL EAEQAQEQNGHQHRIHESQHPC QGGAPVSHQAAVRLRESQIQ GAAEKR*PTGDV/IHPGPVSGG /LK*YPSIPTCLLTTRTASLLKPP GVRTSVCWQQLPR
25590	55958	A	25731	1902	2100	RKFFSSSSGRS*PVRC SKL*SSID A*PLERIKRSRYQVGSVGLCL RKSFHSTSAISAMPIGAPG
25591	55959	A	25732	3223	3669	

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25592	55960	A	25733	1	4325	MPEPPTHSMGSCAAGASLTSTA PCSTAPSPIDHLRAKECERTAQ DWQAAPPAALVRDPLAALVRT WRTFMSSSRIVNTPIGTLC LAQ GFQWFSVLSQVHASTDQEIQE MHDEQANPQNAVGTLDVGLID SVCASDSPDRPNFVIITANRVL HCNADTPEEMHHWITLLQRSK GDTRVEGQEFIVRGWLHKEVK NSPKMSSLKLLKRWFLTHIPG LLQEFREDALNWGPDEKIFKET ELVNDMDKINGRIERA E
25593	55961	A	25734	501	2871	TGCCCLRKTDCCRRESARGVH AVYRRCARSMLLYRESVRPKA VTARVAVEAGIADYWKYVVG LNGAIVGMTTFGESAPAE LLFE EFGFTVDNPLASRAVRLRLPFN NDQVEAAVGVWKL AVERHNGP TALILSRQNLAQVERTPDQVKE IARGGYVLKDSGGKPDII IATG SEMEITLQAAEKLAGEGRNVR VVSLPSTDFDAQDEYRESVLP SNVAARVAVEAGIADYWKY VGLKGAIVGMTGYGESAPADK LFPFFGFTAENIVAKAHKVLGV KAGSHIPRKKYDVP GKKSFSVP KYSTIGSPSPERPVSIITIPNSFVI ITANRVLHCNADTPEEMHHWIT LLQRSKGDTRVEGQEFIVVEKL IRGLAMEDSRNMFALFEYN GH VDKAIESRTVVADVLAKFEKEP VGKHLPTYDGGQIAMGLESTAS VTRKHSSPSSLQNALSCETATSL IERRVRMALGTGDRRGLNTWL ARLPMEAKEKDEWRYWQADL LLERGREAEAEKILHQLMQQR GFYPMVAAQRIGEEYELKIDKA PQNVDSALTQGP EMARVRELM YWNLDNTARSEWANLLKNKS KPDRAHLPGYASTTQWWILSV QATTAGNLGDHLKERFPLANN DLSKRYTSGGKIPQSYAMAIAR QKSAWNPKVKSPVGASGLMQI MPGTATHTVKMF SIPGYSSPGQ
25594	55962	A	25735	1	1195	

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25595	55963	A	25736	1931	2676	PCGNTHQTYLGVWVGGVANSEA *GEKWTGTPDLVG/AERTETIQ LLGVCPEQGEGKIYIDGKQVDI RNCQQAIAQGIA MVPEDRKRD GIVPVMAVGKNITLAALNKFTG GISQLDDAAEQKCIIESIQQLKV KTSSPDLAIGRLSGGNQQAAIL ARCLLNPRILILDEPTRGIDIGA KYEIYKLINLQVQGQIAVIVISS ELPEVLGLSDRVL VMHEGKLG ANLINHNLTQE QVMEALRSE HHVEKQSV
25596	55964	A	25737	1491	1667	TNGQWRAFYC*MRSGRNRIR GEDISGGAGVSPRESPE*REVPE MGPGGAANRGTKRV
25597	55965	A	25738	419	823	VTLVAITRPIHVNRLRQYLVAIS LNETFGPSCKPSRSPSSLSTCC WNAGVMHKK*VQGGRLCSYR N*SICLVVISPVVMGKRCIS*RC TAVLAALT VTVPSGVVAAHSV MLPRLPMKRSSIVPLPSNWRTS
25598	55966	A	25739	591	968	VKQCKQADEH*EQSLPLERRR TTPLSVPL/GKALTTSVFCASG GTSVNSLSHTS*ECMASAVAVK FTFPNLA VNFCTAAMAGPKVA LTSTLARIQAGSLARTGGRAYR WSRSTMLAKSFWCLMAL
25599	55967	A	25740	764	1005	QARPRAPRAPYPIIRSSITLIY /DGQRLGHLDDGTD SWNHVPT LNGQCTLVLIHEYVDTRGPEIK TILVISWWNILVFH
25600	55968	A	25741	463	786	
25601	55969	A	25742	3	646	
25602	55970	A	25743	1	3008	MTMLQIVGAILILLIAGFAILRL FRALISTASALAGLILLCLFGPA LLAGYITERITRLFHIRWLAGVF LTIAGMIISFMWGLDGKHIALE AHTFDSVKFILTALAGGLLA V PLQIKNIQQNGITPEDISKEINGY YCCFYTAFFLMACSDQRRLRG AMDKRYKFILVGFGEVVFVNLE SLDSGKKIHLRRSHEEVMGVS MRTGTIDKGILPFIHTRGNEIL FIPALFILFSLGGAVFGMGEEAV AFAIIA

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25603	55971	A	25744	2	3494	TITNLRPAAPGICEMAQGLSAG GEYTGASIFVAEYSPDRRRGFM GSWLDLRSIAEIELGAGGVGLIS TIVGEANFLDWGWRIPFFIALPL GIIGLYLRHALEDTPAFQQHVD KLEQGDREGLQDGPVSLKEIA TKYWRSLTCTGLVIATNVTYY MLLTYPMSYLSHNLHYSEDHG ALIIHAIMIGMLFVQPMGLLSD RFGRRPVLLGSVALFVLAIPAF ILINSNVIGLNLPPAMFPPTHIRYS ALLLEMKN
25604	55972	A	25745	1	277	
25605	55973	A	25746	902	1006	
25606	55974	A	25747	2	1265	
25607	55975	A	25748	409	525	
25608	55976	A	25749	91	431	NHKPGNIDVARRIQRGFAGDQI GHLRPVERQCSPKRRFIAADG REIRGKQRAGHIFQLLSRCLLQI LNHCQRRAAHFRQLSNQRHQ QLLPV/HYHAAEREYPAGACLV RWLL
25609	55977	A	25750	3	71	
25610	55978	A	25751	1	1212	
25611	55979	A	25752	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVDIVWNATAAFIAVIII SLLLDESGFFEWAAHLVLRWG YGPGRLPFNRIQLIRIRIRQR LLFGLVTFILLNRSQNP AQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGGCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQGLKRVYHSPG APDIREFTRDAIP
25612	55980	A	25753	5	402	EIFSVMVIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFRLFHRI
25613	55981	A	25754	48	219	PETCGHLWAYVWPSCAAVIGL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25614	55982	A	25755	1	912	

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25615	55983	A	25756	1	1857	MRVCARACVTRTRMCMVYAH TCVCVRTYAYVVRVRVHVRA RVRVCAYARTRVRNLSLIPFIQ LTLATPIHHIQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPRLIRMLEQTALEHN IPVQREVPAGVITETGYIQLFLP GWEIGFSLALLAFLCSTSPGF GDPDLGVIAVYQDTPVRNAAT AISELNALAVKGVILTGDNPRA AAAAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMSGTVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTLLDDRVRVAGSAGRYGGDGA GDSECVKIVAEIRQTDNR DRSPRPSGERVVRVGKGGIEAN QPLSTAFNTQITIRQSIRLFSNQF VFHKGISRVVAGSSAHSNVS CILRTPNCRGFPISCTGEGKAA YGWQRDGGHAEYLLAEKDLI LLPDALS YEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDVYV*IGVARVSWMNGRID SELRTVRVAYAHTRTRARTCTR TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
25616	55984	A	25757	3	1180	SKLGTTRRSVVWA*SPSTPTLW CSTFSAAGHSSMKRMNEFDL LPAQQRMKGENVYRGTDADAV TQNLDIIRRYKAEYVVLADHII YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIEFVEKPANPPSPMPNDPSKS LASMGIVFDADLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHPPPLSCVQSDPAEPYLAR CGYAGNFMESSEPRGLIRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRVPDPVELVLV AAEFITPGDTPRLHGSGFIDIR QIIHHQTRSHLEGVKTGIRFLNH FSGNPQGGIAHVNGVARFQVK QCHQAWGQYAAARLRFQARGI SLQIAIHRVDIIHRFDRVQL
25617	55985	A	25758	16	543	
25618	55986	A	25759	1	3387	

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25619	55987	A	25760	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTPFGVC TSASMNVPVLTLRIRTRVTGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/VVAGTFD*SVWF GHDTDVVTLRYFHEALCYSVT LRTPHRRVLRFKSOHPGELACFI SPVA
25620	55988	A	25761	905	4762	PPHNWMPNSATPGIAFVWCAY GAI/LPGDAPVPVDDYRKVVVR KDTKGLIARWKYFWMVSIALG VAFALYLAKGKTPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTDLGLDGLAIMPVVFV AGGFALVAVATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAVLLRQEFLLVIM GGVFVVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25621	55989	A	25762	1	1448	MCHVLLAGRQRTAGPEHALT PPECGSAIGAIPAVYKWAHATG VMIPDRPRSPHAGAEERHWHH PQPELISQRLGSFSSGPTKYIHEF QYLTLSYNLTWSDLNVLTFILP LDEWERVFSLAQSHTDNCRLH KPDLEQEGIREVPQEDPQWNYQ ENSPGIARRDYMISCLVEGLKK AAYKAINYDKLKETTQGTDKN PAQSMACLAATMRHFAALDPE ALAPHRDVNHGKLTCKTIRSSI DISREIRAPRECRSTEMASWHPP ADLTECPVESGYSVLSGRDTCQ YSHTVRRACLTIDSRPAVRQL LKIREVQLLSLLRGCVSRSSGS INAQYRCCLERVVTLPPFDSGPS LMNHAPHLYFAWQQLVEKSQ MLRLATEEQWDELIASEMAVY NAVQEIHLTEEDVPSTTMQEQ LRPMLRLILDNESKVKQVLQIR Q/DGLAKLVEQLRHLSKKHHLD TDSTSSSLPGVTRTPYSPIRGEE

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25622	55990	A	25763	1029	1665	RPEISSVASKTRLGRSFHGAAR RTREYHSSTCNASIAAAATVA AQGHDPDTTSTPPASVDTTATNT QTPAVTAPAPAVDPQQNAVVS PSQANVDTAATPAPTAAATPDG AAPLPTDQAGVTTPVADPNAL VMNFTADCWLEVTDATGKKLF SGMQRKDGNNLNLGTQAPYKLLK IGAPAAVQIQYQGGKPVDLRSFIR TNQVARLTLNAEQSPAQ
25623	55991	A	25764	658	1307	SNRLYTDVESINEIEGIYMKLRF ISSALAAALFAATGSYAAVVDG GTHIFEGELVNAACSVNTDSAD QVVTLGQYRTDIFNAVNTSAL IPFTIQLNDCDPVVAANAFAV SGQADAINDNLLAIASSTNTT ATGVGIEILDNTSAIKPDGNSF STNQNLIPGTNVLHGLAFRR CVSTANLRVPRPICDFPGSSYQA NTIGSGRCADCQPDPA
25624	55992	A	25765	167	232	
25625	55993	A	25766	441	686	
25626	55994	A	25767	206	331	
25627	55995	A	25768	674	900	VVPICTMLEALERQNLATSLC G*LKKACGRSWQTSPIKRSLNG AKFSRTSIIMGFITAEKWSGWEI WSARNVTS
25628	55996	A	25769	41	222	
25629	55997	A	25770	17	525	ESLECSGSPWNASGTQSGFYCH RIAPILPEKRLARMVEKTWGLG LRRRTGFRRLNGLGGGTGLTVE CTSENSKPSKSSFRKQRRGQRR EGH*SLRR*IRRERTERMQASR VTWNSFPQVPAACKPSSLSESG *P*ATNYTREQDSMNWCVHHY WQPPTSVSRLVHLNSG
25630	55998	A	25771	698	1051	PYLRLITLISRSSTVMRLFAI SKRPIT*PKRPKPTTMTWGLSSL THGFSSSSGPNLWRDLSHLSTSF ISNGVVIMESVTVTSNNAIWSPS SSVAAVNTSRTEPAAIKRNTRGR SK
25631	55999	A	25772	1	2204	

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25632	56000	A	25773	3	891	RYRNQDDHELQIHTGTRFYVEL CGFRVNPWWLATDVTHAAMAL LTLVTTGLHIVGEWGKHATPPV PYSICSNPPRRAAYITVWRNRP TLGDHLFSIAYPRGLRYDMGG GGEGTAWANVRQALARTTGR AQHWTKDNAKSSREARHPRQN KTKTHLGKPVLRWV/DPSFDQS KYDSIVWNP/ITYVPVKPSQV GQKV/LDKILNYNTEMKEAIA H/DTSKEGLQFYEVVPVALVVA GTQMATGLRTMDTRLFYFEGELI DAAPNKPVIKVVRQGEEDWP SKGDAGDGEKVPSSLSSEG
25633	56001	A	25774	1	285	
25634	56002	A	25775	1	302	SFSSFTQRTASVHISTSTQSRLLA TSPILAIARARTSRRCEPKQLG YPDSAAHVQQDRATKYVINR NSKKP*ICSACRSTVSTRQHRR WRGSLQPLSQ
25635	56003	A	25776	307	473	
25636	56004	B	25777	67	809	
25637	56005	A	25778	44	301	
25638	56006	A	25779	1	1519	MINRLQHTVYTHKWNSYRTEP DRRHTALRNSFCLVRLNDSSHS RSLDSKQGHTEITFAATEHPPSP VSLRIHDVAFDDGRQTSRAPCF NLEQPGKLDCTKRLISDCWVM HPGESWHGFKDIPDNWSMLDPI KISILAPGMGEDGELEETGVPA ALVTAWLGRHGIVPTRTTDFQI MPLFSMGVTRGKWGTLVNTLC SFKRHYDANTPLAQVMPPELVE QYPDTYANMGIHDLGDTMFA WLKENYSGARLNEAYS/GLPSII ERHVVDAAQYRGGGMLCSCES NFCVSLRLIQAS
25639	56007	A	25780	461	789	HHVLSELQQLYTAIRSVDDHID HSLAIARAPQRRRCPEKPLGY PDSLQHVQQDRATKYVINGTS KKP*ICSACRSTVTHGHTDAGE EVWNPFAVLVPSGKDARVWG
25640	56008	B	25781	1	990	
25641	56009	A	25782	1	3066	
25642	56010	A	25783	583	904	WGIRTTDFQIMPLFSMGVTRGK WGTLVNTLCSFKRHYDANTPL AQVMPPELVEQYPR*FTGVVK KSNN*FRQFGGVDTAGNNLSEI FSASASAEIFPANSFCNRLA

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25643	56011	A	25784	331	660	TGIQLPGAP*SQPWSTRRAVV RPLYRVN*AVP*NR*VIRSKRA MPKRTDIKSILILGAGPIVIGQRL GWRDSGCVRLCGVLGSQENVC ELDEKGEERWSISGTSSSEFTR
25644	56012	A	25785	1	798	MSDAEDGARTTLGSGNAVERL ADALSQONVTVIKSTSLDDGFA ILSSNEAIDCLMFSYQMEHPDE HQNVRLQIGKLHERQLNVPVFL LGDREKALAAMDRLLELVD EFAWTLEDADFIAG\RAVAAM TRYRQQLLPPLFSALMKYSDI/Q SEYSWAAPGHQGGVGF\TKTPA GRFYHDYRLLRVAVWLHKTE CRLINFETPIFGNSFRYDIEVSN ESPDEEVKLRRHHLARCMKNF KTDIYFVSTFEPSTKSVDLLTVE TFAGT
25645	56013	A	25786	211	414	RVCECIQLRRIEIFRMISSQPNL PEDLHPQIIAKPSQKRLIEQ*SSK LTVTKARRQGSRYKSSRFFS
25646	56014	A	25787	1694	4974	LSLLSAK/PVYMPVPSRNRYYGIG PI/YPQEMQPETLQKKISE/SPLT KDKAGQKPSYCVV/TNCTYDG VCYNAKEAQD/LLEKTSDDLHF DEAWYG/YARFNIYADHYAM RG/EPGDHNGPTASYIHVREGV GRLNFFRFNQAYMMH/ATTSP YAICASNDVAV/SMMDGNSGLS LTQEDCWVMHPGESW/HGFKD IPDNWSMLDPK/VSILAPGMGE DGELEE/TGVPAALYSNLCSSG TTGLSTEALLE

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25647	56015	A	25788	1	1709	MSKPKYPFEKRLEVVNHVFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSDAP ELRIKVVKAIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIASVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK LSASLTSMRTLKSVFSEIYHENR GRYGYRRVTLSLHREGKQINH KAVQRLMGTLSLKAIAIKVKRY RSYRGEVGQTAPNVLQRDFKA TRPNEKWVTDVTEFAVNGRKL YLSPVIDLFNNEVISYLSERP MNMVENMLDQAFKKLNPHEH PVLHSDQGWQYRMRRYQNILK EHGIKQSMRKGNCLDNAVVE CFFGTLKSECFYLDSEFNISELK DAVTEYIEYYNSRRISLKLKGL TPIEYRNQTYMPVNCPLFDL RIPDIGGVVRARAIAKLLNDTD MAIIDKRRPRANVSQVMHIIGD VAGRDCVLVDDMIDTGGTLCK AAEALKERGAKRVFAYATHPIF SGNAANNLRNSVIDEVV/DLRY HSAER*NQITAERAYSDPVRKI
25648	56016	A	25789	2902	3271	SSAARHCAGCGDVRSVCRSGR ADAPRMHPGESWHGFKDIPDN WSMLDPIKISILAPGMGEDGE/P TRTTDFQIMFLFSMGVTRGKW GTLVNTLCSFKRHYDANTPLA QVMPPELVEQYPAFVINQ
25649	56017	A	25790	185	663	SPVPSSRPSTRHRLPDGSSSSQFS SAIAARKVVNSCILCSKICQN*F NRRASPLKRLP*SGASGMITP NQPAPAQ/PAK*LYTRLDEVKP* *KITHGNGVSFCPTG*A*RTGIS ASSRDLVQSKKRSFPALNWPA VYCCSALGSAPKCKPIPLRAT V

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25650	56018	A	25791	684	4208	NGLFWLFPWLFADETRRLERFRDRYQIIHSSQVCHSDQA VYVLTQERVNERDDIVDIDLFV IDEFYKLAFRQLKSGDIDHQDE RVIELNIALSKLLKVSQFYLTG PFVNSIRGLEKLGYPHTFVSTDF NTVALDVKTSASKRMTTKPSS KRWGKSRTCVDADHIKNGIGL HFGALPRALQYTTADQFNAGK LRFLCTSTHIEGVNTIAKNVVIY DNRAGSTRTISADIINSVICGLN TLKSFDRWALL
25651	56019	A	25792	1	896	
25652	56020	A	25793	231	721	IITAEGGRSREQLAIL/PLNLAD MRQLQQHSQTRLADTAADGL RHFTAQQRLMPLQLQAIFVTGQ RQLMLQRVGY/R/LHGSPWRKA QTHLPVPGSTPEYRRSDPHGPA LTGCSHHNPVRARRGMTIAQL AANPDKEYRARSFAIARSPLA SRSGYETVTPGC
25653	56021	A	25794	1	933	MLEAAVCLCVFVCSLAEGRA CCRVAVSIPVSVRARIHLES LGRFREPKSIPRKDAQMDTFR MVREPATFLDQVGLQSDDI RLLPPELATLGITELEYEFYRRL VEKQLTYRLHGESWREKVIER PVVHKDYDEQPRGPFIVCVDT GSMGGFNEQCAKAFCLALMLI AIANKWRCYIMLSSITEIVRYE LSGPQIEQAIRFLSQFRGGTD LASCFAIMERLQSRWFADADA VVISDFIAQRLPDDVTSKVKEL QRVHQHRFHAVAMSAHGKPGI MRIFDHIWRFDTGMRSLRLR
25654	56022	C	25795	83	1108	
25655	56023	A	25796	1	747	

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25656	56024	A	25797	25	1741	IMERLKRMSVFQKVVEFGSFTA AARQLQMSVSSISQTVSKLEDE LQVKLLNRSTRSIGLTEAGRIYY QGCRRMLHEVDVHEHLYAL NNTPIGTLRIGCSSTMAQNVLA GLTAKMLKEYPGLSVNLVTGIP APDLIADGLDVIRVGALQDSS LFSRRLGAMPVVCAAKSYLT QYGIPEKPADLSSHWSWLEYSVR TDNEFELIAPEGISTRILIPQGRF VTNDPMTLVRWLTAGAGIAYV PLMWVINEINRGELEILLPRYQS DPRPVYALYTEKDKLPLKVQV VINSLTDYFVETPTPLSSLTSLPT IEICCMVSIPGTNQRLRPFTGFA THRLQSDLLQVMTISRGRFSR SARFNGPTPSGRRLIRVIISTESG SRSSNPRTTGCFEHCDHYRAII DSADGLPMVVYNIPALSGVKLT LDQINTLVTLPGVGALKQTS GDLYQMEQIRREHPDLVLYNGYD EIFASGLLAGADGGIGSTYNIM GWRVYQGIKALKEGDIQTAQK LQTECNKVIDLLIKTGVRGI.K TVLHYMDVVSVP LCRKPFPGPV DEKYLPELKALAAQQLMQERG
25657	56025	A	25798	1	1005	

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25658	56026	A	25799	1	2392	MEMVAASKMRKSQDRMAASR PYAETMRKVIGHLAHGNLEYK HPYLEDRDVKRVGYLVVSTDR GLCGGLNINLFKKLLAEMKTW TDKGVQCDLAMIGSKGVFFNS VGGNVVAQVTGMGDNPSLSEL IGPVKVMILQAYDEGRDLKLYI VSNKFINTMSQVPTISQLPLPA SDDDDLKHKSWDYLYEPDPKA LLEQCSCMLRSPA WGI TSDTT RARTDLACPIWLLDPYPKLMG NAPKALASVDKRGVPVNTILVS ALVTALCVLINYLAPESAFGLL MALVVSALVINWAMISLAHMK FRRAKQEQGVVTRFPALLYPLG NWCILLFMAAVLVIMLMTPGM AISVYLIPPLQTNTFNSTTIAMA DYQMESLSAEINFAAALKLARA CADEWTARTPEKPRYVAGVLG PTNRTASISPDVNDPAFRNITFD GLVAAYRESTKALVEGGADLIL IETVFDTLNAAAVFAVKTEFE ALGVELPIMISGITDASGRITLS GQTTEAFYNLSRHAELTFGLN CALGPDEL RQYVQELSRIAECY VTAHPNAGLPNAGFEYDLDDAD TMAKQIREWAQAGFLNIVRGC CGTTPQHIAEMSPGRKRLTRAE SSSVFSTLPGKAWLEHALPLIAE QL/QGRRSAVFIPFVAGVTQTWD DYTAKTAAVLAPLGVSVGTGHS VVDPVAAIENAEIVVGGGNTF
25659	56027	A	25800	412	1115	LAGEVMDLLLLSNSTLPGKAW LEHALPLIAEQLQGRRSAVFIPF AGVTQTWDDYTAKTAVVLAPL GISVTGIHSVVDPVAAIENAEIVI VGGGNTFQLLKQCRERGLLAPI TDVVKRGALYIGWSAGANLAC PTIRTNDMPIVDPQGFALNLF PLQINPHFTNALPEGHKGDPR FRURELLVVAPELTIIGLPEGNW ITVSKGHATLGGPNNTTVFKAG EEAVPLEAGHRF
25660	56028	A	25801	1	360	MDHAIAGIAVQFRGGNLLRFK AFQQRVKYRMCQAERAINRLF NIAVKRLTGNRLDDKSKQHIDI AVDIPKWSDDLHIIRKHHDP QDSGTHLPAVADDGFRSTVRN RSA*HIRYLTRC*KALNRNKLPP RN*TAIPAMA

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25661	56029	A	25802	1032	1233	LVQFLRICFHILQRF/LPSH*RQK DESLRALPVSFCLWRTDSDFFA DISYQNYR*YNREPYLPRPDSG
25662	56030	A	25803	1	1394	MTRDGLANKALAVARTLADSP EIRQGLQKKPQESGIQAIAEAVR KRNDLLFIVVTDMSLSRYSHPE AQRIGQPFKGDDILKALNGEEN VAINRGFLAQUALRVFTPIYDEN HKQIGVINDSRWSIWSVLFMG LVGLIGTCILVKVKKILFLEP YEISTLFEQRQAMLQSIKEGVV AVDDRGEVTLINDAAQELLNY RKSQDDEKLSTLSHSWSQVVD VSEVLRDGTTPRDEEITIKDRLL LINTVPVRSNGVIIAISTFRDKT EVRKLMQRDLGLVNYADALRE RSRLEHILHNQRPVPMKLHHR MLRHFAASVIVLTSSFLIFELV ASDRAMSAYLRYIVQKADSSFL YDKYQNSIAAHVMRALAAEQ SEVSPEQRRACEAFESANNT GLNLTAAHKISRAYAAHYKPHPL TATQLWKRSITITR*SGSGRQP PPG*LRFRSWDGRREISLLSRSL
25663	56031	A	25804	3	219	
25664	56032	A	25805	14	265	
25665	56033	A	25806	744	1566	FASWLRVFSITNCAAPVTSESC ALDLGSAEAKAWIGVENPHRA DVLTELRRSTVARVCTGRAGPR PRTQALLRFLADHSRSKDTVLK EVPPEWVKAQGLLEVRSEISDK NLYLTRPDMGRRLLCAEAVEAL KAQCVANPDVQVVISDGLSTD AITVNYEILPPLMAGLKQAGL KVGTPFFVRYGRVKIEDQIGEIL GAKVVILLVGERPGLGQSESL CYAVYSRPMATTVEADRTCIY NIHQGGTTPPVEAAAIVVDLAKR MLEQKAFGINMTR
25666	56034	A	25807	596	745	
25667	56035	A	25808	151	660	STTERLGDDFVRANILHCEG KVVVSGIGSGHIGKKIAATLA STGTPAFFVHPAEALHGLDGM ESRDVMLFISYSGGAKELDIIP RLEDKSIALAPNSRTVIT*CWFS AGDGGLPDPYQDFAAHPAG AGALYKCRDLINDNLRVTSQ SHDDGDIRGMAFARQ
25668	56036	A	25809	314	583	
25669	56037	A	25810	1	2982	

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25670	56038	A	25811	120	790	EGLKTKGEKASPPSCLSPCKNE FVISSTDYALSSQSGGVMHRQ SFFLVPLICLSSALWAAPATVN VEVLQDKLDHPWALAFDPNH GMLITLRGGELRHWQAGKGLS APLSGVPDVWAHQGGLLDVV *APDFAQSRRIWLSYSEVGDDG KAGTAVGYGRLLSDDLKSVTDF RAVFRQMPKLSTGNHFGGRLV FDGKGYLFIALGENNQRPATAQD HRVPSWYK
25671	56039	A	25812	707	1141	ASHTATSPRPVRLSSSIASITLAV NATCGMASSRRIR*CTLFSKRA PSAPAGWERAKSSSLNPRACMT AIASASPIIRVLTVEVGAKCIG QGSRSDESTLSPFIKMVPPNSLT TALAIVPPFSLSDTLPEVLISLSLI YNTLF
25672	56040	A	25813	215	2160	EINSITSRLSIIPRSPCSASAGWT KKAGVPLASVAIIFLPMWPD LPPIETTTLPQCKMILAARTKS SPR/RSNIMTHIRIEKGTGGWGG PLELKATPGKKIVYITAGTRPAI VDKLAQLTGWQAIDGFKEGEP AEAIEIGVAVIDCGGTLRCGIYP KRRIPTINIHSTGKSGPLAQYIVE DIYVSGGKEENITVVGDATAQPQ SFVGPDYDTSEKLMIVRKKPIG VQMLYQVGTVMMLLYTRTIQT KMTPTRTIVTISHSVRNAGDSFFS IASNQMPMPPTAKKIEPLAISLLS AEAPTRLSELKARIGEPWVSEIA IKPMPISTHKNPMQAITPPARRA ILSPCACESRSRQEPCCPPGCHCS CPNHSCRSRLKGVLSEMEQYLL QQKHVGTTPGPFRPPDTNQPCW KTKPSQREYTRRVGFTGHSNQ GAKIIRTHICRRRTSFALERPGD GFQAVVGGTVLMGLPRTKNVG LPVTILGRVHRRSSERFPRTSES AINRKDAGPKDPVRQRLAYKK HPMERRHGHVVARVTFGRAIPT LGPHTRTLSTRFQVAKNPLGPI GPSPLAVLTWTVPKPNNGRRG GKQARAIICQSRREASCNVCL ARSSGVFKGFSPVSSSGEHTGN KYSAYSFSLCLFVFLPLSGRL

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25673	56041	A	25814	11	613	RLSSVFVSKSLASWRSCNCSFS GPLVRLTIRPLSPDVRLLLSPS VVHAYNCPHQETQRHHTHHLT P/RLPNHGQIAISAMVYSSPATN/ SMLRQLLIQHVEQIGSVPLVMD AISLVEAHD/RSAA*SRPLY*R AN*SSRY*VSYARKRVROAKSR /HGKPSKKVLAKRAVPNRVCRC CNRVKRRRCICQPKRRKCMTLPV RATR
25674	56042	B	25815	1	1920	
25675	56043	A	25816	247	1182	EAVMRQTKTGILLANLGTDPAP TPEAVKRYLKQFLSDRRVVDT RLLWWPLLRGVILPLRSPRVAK LYASVWMEGGSPLMVYSRQQ QQALAQRLPEMPVALGMSYGS PSLESAVDELLAEHVHIVVLP LYPQFSCSTVGAVWDELARILA RKRSIPGISFIRDYADNHDYINA LANSVRASFAGHGEPDLLLLSY HGIPQRYADEGDSLRELYAVA NPNPGPGMGVLLAYMFFGRGS AKQSAGGSGLDGLLRTPPITP GGYFSVFVWKSLSGWSRSCNCS FSGPLVGLTIRPRFTAGRSPTSF AQRCTCL
25676	56044	B	25817	1	651	
25677	56045	A	25818	1	1647	
25678	56046	A	25819	1	1506	

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25679	56047	A	25820	645	2161	LDRCALNVTAQPSIECQVANAC LSPKGEFEYLQIDAPTPQALLSE IEKCWHRHRNVWPDHTINLAL AIHQGVDPVTGVSQTMPQAPW TTPVEVKYLLEELGIRVMVDN DCQLHIYCKTAILNWSRKMALS RQKFTFERLRRFTLPEGKKQTF LWDADVTTLACRATSGAKAFV FQSVYAGKTLRMTIGNINDWKI DDARAEARRLQTLIDTGDPRIA KAVKIAEESLQAESRKTCTVF SVAWEDYLQELRTGISAKTKRP YSTRYIADHINLSSRGGESPLG LLLAFTLFGKGMSKRSAPGAMI IHFLGGIHELYFPYVLMKPLTII AMIAAGGMSGTWFMNLDGGL VAGPSPGSIFAYLALTPKGSFLA TIAGVTGTLVSFAITSLILKME KTVETESEDEFAQSANAVKAM KQEGAFSLSRVKRIAFVCDAG MGSSAMGATTFRKRLEKAGL AIEVKHYAIENVPADADIVVTH ASLEGRVKKVTDKPLYGPAVV
25680	56048	A	25821	2	341	
25681	56049	A	25822	218	469	LICAQGRRSRSTRQPKVLTL ACHNGSVSVVLSPLNSLYIEVV VPS*CNAATGPVVTCLYKGGFKQ PILILLVTSTRVSSCI
25682	56050	A	25823	1	3966	
25683	56051	A	25824	2	728	
25684	56052	A	25825	528	1123	DAEEGPDHRYLSSAHGGGSAS QPPSCAVTACRWPRGRGCRA GVWNQPTAQGRSWPVGKTSC *GGGSTCKSQTWGFRGQRLPQ DAPAPPASLCASFHLVEAGASA DSGDTRRMTRIR/FASKTVARAK RIIRVLRFSPLWVATRSLASTAI KIACCASEPGSFLQLWKPRSMA PVHRCWTWHEACPEGQRQMSCV SSTGL
25685	56053	A	25826	1	492	

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25686	56054	A	25827	1740	3858	ADAAGTEKTATVSRYHFYLRYP PRSGRSVIDVRSWWRFSIMDAL SR SIPRAISICARGKPVVTAKF QGTMPSPSNKAIILPIRFFPGVV LMIKKSGGRWQLSLLASVVIS AFFLNTAYAWQQEYIVDTQPG LSTERYTWSDHQPNDYNDILSQ RIQSSQRALGLEVNLAETPVD VTSSMSMGWNFPLYEQVTTGP VAALHYDGTTSMYNEFGDST TTLTDPLWHASVSTLGRVVD RLGDLRPWAQISYNQFGENI WKAQSGLSRMTATNQNGNWL DVTVGADMLLNQNIAYAALT QAENTTNNSDYLYTMGRTRWL TLIGTIITQFALGSVYTWSLFNG ALSAKLDAPVSQVAFSGLLSL GLAISSSVAGKLQERFGVKRVT MASGILLGLGFFLTAHSDNLM MLWLSAGVLVGLADGAGYLL TLSNCVKWFPERKGLISAFAGS YGLGSLGFKFIDTQLLETVGLE KTFVIWGAIALLMIVFGATLMK DAPKQEVKTSNGVVEKDYTLA ESMRKPQYWM LAVMFLTACM SGLYVIGVAKDIAQSLAHLDDV SAANAVTVISIANLSGRLVLGIL SDKIARIVITIGQVISLVGMAA LLFAPLNAVTFFAAIACVAFNF GGTITVFPSL ICGSHASLFGGFY VTFYVIFALLLSLALSTTIQPE QKMLHFTYLTTSALFPAGPKRN
25687	56055	A	25828	2	356	
25688	56056	A	25829	1	1307	MYETLEEVLRSSGDPADQKYV ELKARAEKALDDVKKRKL YCWRRQICALRRISRPYGHQL ECIASFDRNFEMQKEMYGQF ENTFMMYLPRCLCEHCLNPSCV ATCPSGAIYKREEDGIVLIDQDK CRGWRLCISGCPYKKIYFNWKS GKSEKICFCYPRIESGQPTVCSE TCVGRIRYLVLLYELTAQOFF PVWPPDHFVHPF*TLVYLPAPP SR*CDRVQLMASLQSVARASRE YRWYGFSR*TPRKALALQLRP AESSPTAPDCN

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25689	56057	A	25830	583	1369	RHQLNSIASPAGGRWKDIGWF NFPQSNLCLKREKQDESCSLTQ ALPSELKVSADNVSLTGAVSLA SMLTEIFLLQQAQGMPEPGWG RITDSHQWNTLLSLHNAQFYLL QRTPEVARSRATPLLDLKTALT PHPPQKQAYGGTLLPLPVRFMA GPDNLNANLGGALKFNWTLPG QPDNTPPGGELVFERWRRLSDN SQWIQVSLVFQTLQQMRDKTP LSLNTPPGEVKUTLAGCEERNA QGMCSLAGFTQIVNEARIPACS
25690	56058	A	25831	199	543	
25691	56059	A	25832	1	642	EASIFRRLSVYDNLMAVLQIRD DLSAEQREDRANELMEEFHIEH LRDSMGQ*SARPGRCRAGAQ* CV*CR*PRSGQPRQTVRRAE*IS DSQPVRGQFLHG/VRSPPESDCP MLSRRCM*NSSISSFARSSRCS ADKSSRICSTAIRLS
25692	56060	A	25833	3	329	
25693	56061	A	25834	1974	2195	
25694	56062	A	25835	1	615	
25695	56063	A	25836	2	166	
25696	56064	A	25837	2	189	STPGNWRFTTITYPLNCATRWK M*FLIVATMAPSVVWSLPRNIA AAKPTTPTPSRRSGARGK
25697	56065	A	25838	64	354	
25698	56066	A	25839	1123	1845	
25699	56067	A	25840	1120	2097	
25700	56068	A	25841	124	548	CRQMVGTRRGGEQGKEVIDGY GKPATFYQMQDNGKPVYEGHAS QMHYELAKDFVLTGNAYLQ QVDSNIKGDKITYLVKEQKMQ AFSDKGKRVTTLVPSQLAKA YKGVAV*KTSA*PSTPGKLSV CWGQTVVPRPPLSTWL
25701	56069	A	25842	77	514	
25702	56070	A	25843	2487	5738	RRAAGLPGRNDAGLARSHQWA GSADTGSEKQHELQRIQGEVP SQQLNLAGSFDRKEERWKG/TL SNTRFQTPVGPWSLTRDIALDY RNKEQKISIGPHCWLNPNAEIC VPQTIDAGAEGRAVYNLNRFD LAMLKPFMPETTQASGIFTGKA DVAWDTTKEGLPQGSITLSGRN VQVTQTVNDAALPVAFQTLNL TAE LRNNRAELGWITRLTNNG QFDGQVQVTDPPQGRNLGGNV NIRNFNLAMINPIFTRG
25703	56071	A	25844	538	777	

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25704	56072	A	25845	489	2797	TRRRRTMIALIQRVTRASVTV EGEVTGEIGAGLLVLLGVEKDD DEQKANRLCERVLGYRIFSDAE GKMNLNVHQAAGSVLVVSQFT LAADTERGMRPSFKGMSQLP GLSRETRESIAMYHLRVPTTEE ELERYYQFRWEMLRKPLHQPK GSEDAWDAMAHHQMVVDEQ GNLVAVGRLYNADNEASIRFM AVHPDVQDKGLGTLMAMTLES VAPYFSGSETGMMTLNRYRLR HMAKQGNRSKRVEKLLRKPD RLISLVLIIGNNLVNILASALGTI VGMRLYGDAGVAIATGVLTFV VLVFAEVLPTIAALYPEKVAY PSSFLLAPLQILMMPLVWLLNA ITRMLMRMMGIKTDIVDMLLS VLDLEKM/TVDDIMLPRSEIIGI DINDDWKSIL/RQLSHSPHGAIV LYRDSLDDAISMLRVREAWRL MSEKKEFTKETMLRAADEIYFV PEGTPLSTQLVKFORNKKKVGL VVNEYGDIQGLVTVTEDILEEIV GDFTTMSPTLAEVTPQNDGS VIIDGTANVREINKAFNWHLPE DDARTVNGVILEALEEIPVAGT RVRIGEYDIDILDKLSFCFRYSN HRRTNRTTIQRITFLHNAQYVT WRNVIRFHHCDGLMHIRVQWD VSFGDHFNAKLTHNIQHLRQRQ LNAFNHRRHIRVSFISHFQRTIQ AINHRQQVFDEFQREFVGFENI
25705	56073	A	25846	87	199	QPASVQTAGAGCRL* ^L HQRQW RECLVLD ^{SKRR} GDGVL

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25706	56074	A	25847	1167	3306	GKSMDELPWLADNAQLLEK YKKGKTPLSHRRWPGEVSVIT GSLIQTGLDELQKAEKKKNIV WRYENFSEWQSAITQAINLIG EHKPSIPARTMAALACIAQNDS QQLLDEIVQQEGLEYATEVVIA RQFIARCYESDPLVVTLQYQDE DYGYGYRSETYNEFDLRLRKH LSLAEEESCWQRCAKDLIAALPG INKVRRPFIALILPEKPEIANELA VPALREFLAATKMPATCTLKGL GAVEADYPYYLGMGLMHGK AANFAVQECDLLIAVGARFDD RVTGKLTNFAPHASVHIHMDIP AEMNKLRQAHLRDEHSWRYD HPGDALYAPLLKQLSDRKPAD CVVTTDVGGQHMWAAQHIAH TRPENFITSSGLGTMGFLPAA VGAQVARPNDTVVCISGDGSE MMNVQELGTVKRKKQLPLKIVL LDNQRLGMVRQWQQLFFQER YSETTLTNDPFLMLASAFGIH GQHITRKDQVEAALDTMLNSD GPYLLHVSIDELENVWPLVPPG ASNYKKHHKLKQTFGVKIHFDV HDSQAQPVADVNVNVIQPAFL ARQTDLVETHGENRPGQMGNI VDKFKEGGNEKVLCDRGNF GYDNLVVDMLGFSIMKKVSGN SPVIFDVTHALQCRDPFGAASG GRRQAVALARAGMAVGLAG LFIEAHPDEHAKCDGPSALPL
25707	56075	A	25848	1	695	MATRASVTPLMSLFSAGTCLLST SCVLSPVGDTAEEESCWQRCA KLIALPGINKVRRPFIALILPEK PEIANELVGLECPRTFHFSKEW LKVVDNDPTAVRKLHYWSQD IFSREASYMSHENHFGYAACA ALLREQGLAAIPRLAMAYHKE DCGSLVQINHPQVIRTLTLLVA DKNKPSLQRVAKYHKNFPHAT LAALAEALLATEPPA/RPWLNS HRRQKAECTAKSTR
25708	56076	A	25849	823	1091	CVRFARINCSRRSRCFAGFNH VLNKGALGVHINHFG/YSAACAP* CRYPPHAAAGEFYDPDCRHGTT GYRHRQGYPPPGPEPPRASWLD LR
25709	56077	A	25850	714	875	EFSSARISRTSLKYTGNCCLL WSAFRCRLRTATTVPARP*QLR PDRSRAQCQ

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25710	56078	A	25851	2730	2893	WPVGERLAPGDYVPVI*TGQLCT AAGD/EWRR*KVRRHQPLWRG FPNRRYMAWRSA
25711	56079	A	25852	750	929	SFHPAGRRYLYRHSSRSRGNITN GCCRLWSAFCLRLRTATTVPARP*QLRPDRSRAQCPV
25712	56080	A	25853	2	2427	CRQHHRWHSGSTAVYRRVLITS KCWNVFIRTKTWTVSILTTSVV CASARRVCVPAPRAVSSRCLSV TTLIPSASTPW*LAHRISLAAR* AFWFNCRIPAGIDNVKVLRIH PDKDVGDFHPYVGRLCQRAP RLRPCTPRGIVTLRLERYNIDTFG LNAVVGASNIVGRPMSMELLL AGCTTTVTTHRFTKNLRHHVEN ADLLIVAVGKPGFIPGDWKEG AIVIDVGINRLENGVVGDVVF EDAAKRASVITPVPGGVGPMT VATLIETRYRQGMFDDGSSIGG WKGINESDMVLMPDASTAVID PFFADSTLIIRCDILEPGLTQGYD RDPRSIAKRAEDYLRTSTGIADT VLFGEPEFFLDDIRFGSSISGS HVAIDIEGAWNSSTQYEGGN KGHRAVAVKGGYFPVPPVDSAQ DIRSEMCLVMEQMLVVEAHH HEVATAGQNEVATRFNTMTKK ADEIQIYKYVVHNVVHRFGKT ATFMKPMFPGDNGSGSPSPQ PQSQPTPEILLQALLSAGCFYAVY YVYTKRLRKRVRADVPRRPLFT MNRVETNLTWVILMGIALVSV GIFFMHNGFLLFRLNSYSQIFSS EVSGVALKRFFYFFIPAMLVYV FLRQDSKAWLFFLVSTVAFGLL TYMIVGGTRANIIIAFAIFLFGII RGWISLWMLAAAGVLGIWGMF WLALKRYGMNVSGDEAFYFTL
25713	56081	A	25854	502	885	
25714	56082	A	25855	233	738	SNCKRRTKIISDVTSVFHIAIFPAI KITAPNSPRLRVNDSATPLTSAG ESSGSTTLQLKCORVAPSVSAA SSYSGPNLFQHLRHGTHPKRNA GKGHSHRNPPQICGDFDIKLRLQ PFTVKTLYVKEKGQR*GGDRV LPAQRVNPSAHQAACGLGSDS GLGSTPSADRKRR

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25715	56083	A	25856	1	2363	MRRQDTGRRGRKRRDAGRWQ WRYWGKGSFTPMNATWDVAG KGEWHDSTLTLDLSTGFDQLQ YGTMTVEKPRLLDKPIVWVRD AQHPSPFSGALSLDAGQTLFTGG SVLPPSTLKFSDVGRDPTYFLFK GDLHAGEIGPVRVNGRWDGIR LRGNAWWPKQSLTVFQPLVPP DWKMNLRDGELYAQVAFSAA PEQGFRAAGHGVLKGGSAWM PDNQVNGVDFVLPFRFADGAW HLGTRGPVTLRIAKQRKEMRN NNLRQFKLLGPDVGFDSINDRP MAEELSKLLSKQNEENLLPKTI LYCLNPRDNEVLGTMIENGASF AANPLYFDPKNIVELAIEAGCN CVASTYGVLASVSRRYAHRIPP LVKLNHNETLSYPNTYDQTLTY ASVEQAFNMGA VAVGATYIFG SEESRRQIEEISA AFERAHELGM DGGWIGLMIKPLGRWSLIMEID EGFAVGMSPAELSAEQLLSKL WLWEGKAERYGWGRKSMCKE LPRLADNAQLELYKKGKTPLS HRRWPGEPSVITGSLIQTLDG ELLQKAEEKKNIVWRYENFSLE WQSAITQAINLIGEHKPSIPART MAALACIAQNSDQQLLDEIVQ QEGLEYATEVVIARQFIARCYE SDPLVVTQLQYQDEYGYGYRS ETYNEFDLRLRKHLSLAEESCW QRCADKILALPGNKVRRPFIA
25716	56084	A	25857	1	4440	MNRFDGAKQNVVGADAHHLA DTAVKRNQSLFQLRASGHPRLP AGGGKAVFHGRFAAKKIEAVA FYFRHLIALLVVQMHFKLKVG NVDVVFTAQLIDSTVQLIDSTTT VTQFTHIQTLMRSEWLTDN GSCYRANETRFARMLGLEPK NTAVRSPESNGIAESFVKTIKRD YISIMPKPDGLTAAKNLAEAFE HYNEWHPHKAGTLTNEQWQWQ VTAELHDMMETVFFALDDAE QLFAHHQTPVTSVDLLGQG

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25717	56085	A	25858	1	3705	MEEYGGVDVRLYRIPDPMFL RQQKNLHRIVVQPQYLGDLN NTLTWLWDNWKSRVMQR TFSSQSRQNVQALPELQLGNA IIPSRVYVQNNQFSPLKKYPLVK QFRYPLWQAKPFEPQGSRL YLVEAMVGGYRATTGGVSDT VALSKVSSKELLVWTAGKKQV NEPGSEIFGLTALRITAFNQDCA SLTPETFLPRIHVIGVNIATV CRQCEDAPCANVCPNGAISRDK GFVHCEARTLHLFAKT
25718	56086	A	25859	123	923	TDSPYERGHMSNLLGPRDAN GIPVPMPTVDESIAASKALLKKI KRSAYVYRVDCGCGNGCEIIF ATLSPLFDAERFGIKVSPRHA DILLFTGAVTRAMRSPALRAW QSAPDPKICISYGACGNSGGIF HDLYCVWGGTDKIVPVVYIP GCPPTPAATLYGFAMALGLE QKIHARGPGELDEQPAELHGD MVQPLRVKVDREARRLAGYRY GRQVADDSFTQLGQGEQVAR WLEAENDPRLNEIVSHLNHVVE
25719	56087	A	25860	1337	1516	KLKSKSAKRHKFITPILAWRILI HYLQRVAV*WGSRL*LFILITIP SRWRLLPHNTGKG
25720	56088	A	25861	1	545	MARLAALKACETVYSMGVRSR RRSPLEHLWQLKDQLVNEGEL VLETVIDGDENTVLVPGRDRA QMRNVYFIPSAALKNWLKCC GFVDIRIADVSR/ITTEEQRRTE WMVTESLADFLDPHDPGKTVE GYPAKRRARNRRAEDHRQRL RHRTRKKQTHGQRRRRRPEPA QRQPQTGTDT
25721	56089	A	25862	620	1117	
25722	56090	A	25863	1	1188	
25723	56091	A	25864	231	407	
25724	56092	A	25865	1	501	
25725	56093	B	25866	1	2373	
25726	56094	A	25867	1	2211	

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25727	56095	A	25868	2093	3589	GGINGKNFWFFLSPTPCVGRCHSRVQLANSHLVVDDETPSSAAVHLYATDADSIGNCGTDREFCPCNPIRRHAFCCERLQNGYHRS GYAFHLGHYGDRKVITNFYSLIAKNHLSHWLETLPQAQIANWQREQQHGLFKQWSNAVEFLPEIKPYRLDLLHSVTAEESEPLSAGQIKRIETLMRNLMPWRKGPFSLYGVNIDTEWRSDWKWDRVLPPLSDLTGRTILDVCGSGGYHMMWRMIGAGAHLAGIDPTQLFLCQFEAVRKLLGNDQRAHLLPL/GIEQLPALKAFDVFSGMGLYHRRSPLEHLWQLKDQLVNEGELVLETLVIDGDENTVLVPGDRYAQMRNVYFIPSAALAKNWLKCKGFVDIRIADVSVTTTTEEQRRTEWMVTESLADFLDPHDAIFQIWPCTFMHAYHAFFDPVSHHRACQNLTTFVPDTHQIAIRNTKACSIFVSFALRTTHSCAISHSSLEDPPIALFKIADRMEQNLELLATAGNLG
25728	56096	A	25869	231	1785	DDEVHRYSELRTRTVPSYPERSGEAKTAAQRAGTAFRRGRGAGVPPFNLQQRSDRWCS*RSQQNA*RLIGLHGQNSRSPQLPMESASVA*RCGSIIKTTLSSRPFYWCPGCQHYADRFGA

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25729	56097	A	25870	1818	3311	RMAIQFRTLRLRWCWKISLVSS FTVVKAMTRIVAMRQLLRQQ KQRTFVC*SS/TVDGVLSDGLIY MGNNGEELKAFNVRDGYGIRC ALTSIDIEVAHTGRKAKLVEDR\ LPHWGSGLTCIRGSQTN*SPLAIC WKNWRLP/QENVAYVGGDLID WPVMEKVGSLVAVDDAHPLL GTEIDAYIENADYQYNKKRLRE IDRRVRYLT/KCLENLKIVDYSP QQEGKVFFGAWVEIENDDGV HFRIVGYDEIFGRKYDISIDSP MARALLKKEVGDLAVVNT PAG EASWYVNAIEYVKPRLNQTVR L.I.IHEMGGQVWISGEISNFTQP ASGHWYFTLKDDTAQVRCAM FRNSNRRVTFRPQHGGQVLVR ANITLYEPRGDYQIIVESMQPA GEGLLQKQYELKAKLQAEGL FDQQYKKPLPSPAHCVGVTISK TGAALHDILHLVKRRDPSLPVII YPAAVQGDDAPGQIVRAIELAN QRNECDVLRPCVWCRRVRCRR
25730	56098	A	25871	1	3465	
25731	56099	A	25872	1	3126	
25732	56100	A	25873	1	1722	MSSLSQAASSVEKRTNARYWI VVMFLFIVTSFNYGDRATLSIAG SEMAKHIGLDPVGMGYVFSAF SWAYVIGQIPFVDIFSGFGIIV ALFTLRLVLGLAEAPSPFGQSR VGDWFPADRGRTGVSIPTFIL RKGDRLRPIWVVILMAGQLHAL MSTLEDTPFSNKAGMRLRRWI NAAVMRLNPLACLATRSNQVN WLLL.TGNISVYPVGSSEPTRR STPINSTPHFNKLTILINARYSPT LPSSDGTWTRIDDKPTWGHK FARYWDVELREIPMRPGQLFR DPKRMIEGCAENPLGVVPTFG VTYAGNYEFPQLPDALNKFO ADPGIDMDHIDAASGGFLAPF VAPDIVWDFRLPRVKSISASGH KFGGLAPLGCGWVWRDEEALP QELVFNVVDYLGQGIGTFAINFS RPAGQVIAQYVEFLRLGREGYT KSTQPARGSPANNCAQPETP DRAVIHPTDGYESAATHIVLSP TASDSDPAHRDQRRVVKTDWS VVPGSTSEYPRRYKAEWFQCPF AVLPAILAWSAALWRYQPRAR RRKADYGCRLNSLKNELTTP

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25733	56101	A	25874	1	2385	
25734	56102	A	25875	1	1767	
25735	56103	A	25876	1	2079	
25736	56104	A	25877	368	1261	TSPRARPAAQSGRAFL/HLTE KGVNRFAYGLPESSGKRWAT EREYAFRQLVAEEKYRGVVYQ GLETAPENWQHAQNRLADWL QTLPPQTGIIAVTDARARHILQV CEHLHIPVPEKLCVIGIDNEELT RYLSRVALLSSVAQGAQRMGYQ AAKLLHRLDKKEEMPLQRLVP PVRVIERSTDYRSLTDPAVIQA MHYIRNHACKGIKVDQVLDAV GISRSNLEKRFKEEVGETIHAMI HAEKLEKARSLISTTSLINEISQ MCGYPSLQYFYSVFKKAYDTT PKEVFAIVNSEVML
25737	56105	A	25878	1	868	MTSLKNSMKWDEERFGLEYDL DIYMIVAVDFNMGAMENKGL NIFNSKYVLARTDTATDKDYLD IERVIGHEYFHNWTGNRVTCRD WFQLSLKEGLTVFRDQEFSSDL GSRAVNRJNNVRTMRGLQFAE DASPMAPHPIDMVIMNNFYT LTVYEKGAEVIGMTPLPFGQE NFQNVILTCALEDPTRKVVLPK LCRPPLSLCNRRKRVMCRIFTSS ASTLRLSRRCACVWNRSRITVSM RSSRRVTSVWLSAPTPILSPAIF IVRWLLDSNPLIYYKAWSCW CSRK
25738	56106	A	25879	2097	2512	NTPVRPDVGT*TEEHGAESGE *RNSRELRENDKA* LHQYHAQP DGKNLAEAFEHYNEWHPHSAL GYWRTVD/DMRGR*PQEPSLMI RAGRSSSPVQWQRIPLLIPGRKG DRMQKTVIPGSLFAGMPYAQPS IKTELAG

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25739	56107	A	25880	71	2613	QRKPTSSRKGLSARMMSSGLTG TITTVSTGWCTTRGHNMKSRW SKVAIFTTRSGRRVAKRVWRR ERDLTGWMSLSRKPKQVTWYG WDGDRLLTIQNDRSRIQTIYQP GSFTPLIRVETATAVRRRRRWQ WGIPAGTVQMLDRLESEILADR VSEESRRWLASCGLTVEQMKK TSIHASIVRHKLLTAEQALKLLG EMFVYHMPFNRLGMELERYE KEFAQLAFKNQPMVMGNWAQ SILHGGVIASALDVAAGLVCVG STLTRHETISEDELRLSRMGT IDLRVDYLRPGRGERFTATSSLL RAGNKVAVARVELHNEEQLYI ASATATYMSKSMFLAVATILIS KSSLRLRRPSTIVCGIPISSISAN ITPGRSLRSSSTSKTLCTQFAV QFLSKLLYAEGFVHVHRQNRH LERRDSVRPYDASFVVLLNRR SYHTRYPDVTATHRQDLVTAIF TLYGGFCQFVLGTQLEDVTNF DTTFDQPTLAIRAWIASHHVT DICNFRGSDIAPVDAEVVFTID VSTSSEITHRRNVDLFPDQLTVT RSQFTTAYERLSTALTVAQVCG VQRLCNYYSARLTPLPGPDSTR ESNHRLAQITQYARQLASSPSII DNRSRQHLNDVGLTAWDCVIIS QIIGFIGFQARTIATFQAYLGHP VRWLPGLIQNYADASLFADES LRWRSSYEVEKLPEEHTKSSTA
25740	56108	A	25881	71	3478	CCLSSHPSATTATLRSLSPVRK WPKISALIPWEWAMCSLLSHGL MLSGRSLVAVCWTVI.VQNAS TSGRSLSGRCLPCKKASSISLVD SALSFLFLTLRFLVGLAEAPSF GNSRIVAAWFPARKGTGHNEIS PLANTALEGLGGSDALCTQC EAEGRHITYYLDRLPDVLARFT TKIHADKIKYPFLLSNGNRVAQG ELENGRHWVQWQDPFPKPCYL FALVAGDFDVLRTFTTRSGRE VALELYVDRGN

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25741	56109	A	25882	90	629	PGDWGRRQLIGS*KTPGSVFKK GKSSTPNDFPKDKTKQDRSGL ATFTMDGQIRLFYQDISGNHS GKQSLPPAQVIVSNSVDHLKIT GVEDHKPIFAGAGKPYQNLRFQ IDEGNYTSGDNHTLRDPHYVED KAHKYL/FEANTGTENGYQG EESLFNKAYYGGGTNFRFGSSR VDLQAC
25742	56110	A	25883	1	3066	
25743	56111	A	25884	104	547	LFPRLLSCLTTPPHCSFICFVIC SRTLILKGSSLMYVFLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLKFLKNGLNFLLLISVGTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLADDDVLSTEVKRVITS SASNITPAFFCS
25744	56112	A	25885	3	4288	
25745	56113	A	25886	2	2222	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSLP QHTIPDVFIWMLSNRRVAYA RIASKDLLYSPVAGQMGKHCG KIKTHFLKIPKQQNEKYQVPQ FDQSTIKNIESAKGLDVNSWP LQNAADGTVAEYNGYHVYFALA GSPKDADDTSIYMFYQKDFRLL GQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLMSWHD RFPDWKAG RILPISEPPSNRIFACWGKPAWT ACCNLSLRARR*RAISCCPSHW* KEKPPWRPIRKPLPARWPIH*C SWHDFRFPDWKAGRKGS DAHRF GSWKFLQQRVSGISATFTWGG KIRLYSADYSGNHYGKQSLPS GQVNGSNSDDTLKINGVEDIHK TILDGDKTYQNVQQFIDEGNY TSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFRKESQKLQQA KKRDAELANGALGIIELNNDYT LKKVMKPLITSNTIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSLKIDWIIR YQLPQSYQRMDFRRRLQVC VNEINSRTPMRLSYRMGVRGK
25746	56114	B	25887	1	2640	

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25747	56115	A	25888	1291	1629	
25748	56116	A	25889	1187	2925	NSLQRSHPNAAANS/WHNKL.WR SHSDSDLSDHHEPICKPGLLELN KKDITTSADQIAEVKTMESHPPPI PPVFVEHMPVQDANQKGLCTK ERMICLEFTSREFFHAGQIEDELN LNDINGCSSGSTLEDPPQFNDDSP EARKITRRWRIGEAADLVGVSS QAIRDAEKAGRLPHPDMEIRGR VEQRVGYTIEQINHMIRDVFGTR LRRAEDEVFPVIGVAAHKGGV YKTSVSVHLAQDLALKGLRLV LVEGNDPQGTASMYHGWVPD LHHIAEDTLLPFYLGEKDDVTY AIKPTCWPGLDIIPSCALHRIET ELMGKFDEGKLPDTPHMLRL AIETVAHDYDVIVDSAPNLEDP RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLTGTQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFDKKEE LLKQQASNLHEQKAGVIFEAE EVITLLTSVL
25749	56117	B	25890	1	1954	
25750	56118	A	25891	1	454	MERRNRRTGRTEKARIWEVTD RTVRTWIGEA VAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSSISSTEYTK VFALDVAARHRAIRVPRQQGD YRTRIWKFEGLSNVLVIQLNK LIICVMCLVRDCDVLKTYFHL
25751	56119	A	25892	10	144	FLFIGKGFLKGIT*PGQIVORG*E KKSNT*FRQFGGVDTAGNNLT

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25752	56120	A	25893	888	892	TVDLDACTKGVLTFTTALLAG GANQAFAKENTKKA YKETYGV SHITRHDMLQIFKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGR VFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTSGDNHTLRDPHYV/EDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLF TDSRGSK MTIDDLWKFELEND DLEYLVE ENSKQKTIQDVIWLF LTAYTHI RGATQAFAKENNQKAYKETYG VSHITRHDMLQIFKQQQNEKYQ VPQFDQSTIKNIESAKGLDVWD SWPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGR VFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTPGDNHTLRDPHYVKTAMR

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25753	56121	A	25894	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAFA KENNQKAYKETYGVSHTIRHD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNIDS WKNAGRNVFKDSKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGD GKTYQNVQFIDEIGNYTGDP EAETA VINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHYA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIERYQLPQSYQRT PDFRRRLFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIIKAWIERY QPPQSYQRMPPDFRRRLQSRPA CMHDWLCAEALAWSIQTASYL VTMQVNLTSLSSDTRDL SVVS NSGWVSSGSLVRFNITKTSSEGEI KRTVPRILPDPDDPRSAIEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLLPKAVHLA
25754	56122	A	25895	3	2356	
25755	56123	A	25896	1	2610	
25756	56124	A	25897	1	2496	
25757	56125	B	25898	1	3198	
25758	56126	A	25899	1	5274	
25759	56127	A	25900	1	585	
25760	56128	A	25901	1	2469	
25761	56129	A	25902	1	1914	
25762	56130	A	25903	1	2259	
25763	56131	A	25904	1367	1959	KLVTLMHDLWSRWNSGYQSQE T*K*PANRPVKRPH*GGI*FSRD QKRMLYLFVDQIRKSDGTLQEQ HDGICEIHYAKYAEIFGLTSAEA SKDIRQALKSF/DGEGSIYSR*A HGAA*PSHRKDRESADLGSDG QNDKGHWYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESHKLQSAKKLDAELSNGA LGFIE

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25764	56132	A	25905	1	2418	
25765	56133	A	25906	3	1918	
25766	56134	A	25907	1242	1463	
25767	56135	A	25908	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETYGVVS HITRHDMLQIPKQQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVGVD NSIDSWKNAGR VFKDS DKFDA NDPILKDQQTQEWSSGSAFTTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEQNEGI LPISPPKQDFRLLG
25768	56136	A	25909	610	2303	SLPNLDNAAICSSSSSPTRTR*SL SEGATQAFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNIDSIDSWKNAGR VFKDS DKFDANDPILKDQQTQEWSSGA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVKSDDTLKINGV EDHKTI FDGDGKTYQNVQQFID EGNYTSGDNHTRDPHYVEDK GHKYRGPLESPSTHQAEFNPT CVSSLGTLQGFAPAWLALAH VHPLKHKSGGSNRLSAAIWGK RKPARVCPGTGIHASSQIQGEW RTECAVGPKAKAKATAGWRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNQSEHQTY ESIVDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLKKNVDLKGFEPPDRILLT KYSNSNSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTGAWRNA LSIEWPVCNEIFDRLIKPRWEIR
25769	56137	A	25910	1	2103	

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25770	56138	A	25911	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDTSIYMFFKR GAIFRVHKKHAVNPMSPKCRPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFKENNQK AYKET/YPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKADDTSIYMFYQKVGDN SIDSWKNAGR VFKDSDFDAN DPILKDQTTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTFDGGDKT YQNVQQFIDEGNYSNDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFRKESQKLQQSACKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGINSNDI YMLGYVSNLTGPYKPLNTTG LVLMGGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ MNNASTMSKRTSAGCHCWQG
25771	56139	A	25912	1	3987	
25772	56140	A	25913	1	2235	

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25773	56141	A	25914	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDDTSIYMFYQ KVGDNIDSWKNAAGR/VFKDSD KFDANDPILKDQTEWWSGSAF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDDTSIYMFYQ KVGDNIDSWKNAAGR/VFKDSD KFDANDPILKDQTEWWSGSAF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGGDKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL/VFEANTGTEHPQPERP RTQSFSAFAERRECPNVPADT KLSKIKTLRLATSIAIYMLDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLT VTASQHA PPPPTHEMEGFEL FHL PDLCSPSQDAQT TGR TQMK PDHSPRPSHRVPQAKGNVVT SYM TNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQQQLTV
25774	56142	A	25915	1	2448	
25775	56143	A	25916	1312	1974	
25776	56144	A	25917	2	1778	
25777	56145	A	25918	1366	2673	
25778	56146	B	25919	1	1938	
25779	56147	B	25920	1	2262	
25780	56148	A	25921	1	2100	
25781	56149	B	25922	7145	7154	
25782	56150	A	25923	2085	11232	VNSEGSEPADRRKKPVHTEEAM NMTIKKIVKQATVLTTLTALLA EGATQAFAKENNQKAYKETYG VSHITRHDMLQIPKQQNEKYQ VPOFDQSTIKNIESAKGLDVWD SWPLQNADGTVAEYNGYHVVF ALAGSPKADDDTSIYMFYQKV GDNSIDSWKNAAGR/VFKDSDKF DANDPILKDQTEWWSGSAFTFS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KPILDGGGKTYQNVQQFI
25783	56151	A	25924	153	293	

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25784	56152	A	25925	420	687	
25785	56153	A	25926	242	491	WLHVQPLHDEHHCW/I*YPADT DGVRFPAFQRSPALSPHEGCVPY TPARQGSVRSKGPCTSAALLYVE CSIAAPDRKHSCHKSDQS
25786	56154	A	25927	2	113	
25787	56155	A	25928	779	862	NSTLPRCASTTFARY*AIPKIVFS ILP
25788	56156	A	25929	282	443	FSAGFLNLRYAQKFPSSYPV** CYRPIYYPASDPCRNL LYPAD VPYQALLD
25789	56157	A	25930	3	89	
25790	56158	A	25931	614	823	
25791	56159	A	25932	1229	1427	
25792	56160	A	25933	1965	2682	FAVPCRTSFGSIETVSHPGRDT* SA*AYRVQVDSHRPLAHNVQ HRT*RGEVLLAGVPRHVAEREI ATLAGSFSLEHQNHNLPDQD PGNTVSLEVESENITERFFVVGE KRVS AEVVAQVLVEVKRYLA STAAVGEYLADQLVLPALAG AGEFTVAHPSCHLLTNIAVVER FLPVRFSLIETDGVTRQLLGVS YRILAMGHAFLIQIADMRNDGG WRDFQFSGNLVMDENRNSAQT YIKLVKSRLGTTKR
25793	56161	A	25934	261	563	RHSRGRSALRQISPEC*IHVCSPP PVQQLHPGYGNAIPLSYGHRNQ PDESDDAPVPPGWCQRYNLHQ KSTAHCGGYTIHADLVKTRCW LAPHRLPPGPGR
25794	56162	B	25935	1	1329	

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25795	56163	A	25936	761	3224	RGGAVTAKAPPDISAISALTAV KHGNCSSLTPLLNP GSDVIVC AEMDEQWGYVGAKSRQRWLF YAYDSLRTVVAHVFGERTMA TLGRLMSLLSPFDVVIWMTDG WPLYESRLKGKLHSENGDAVL LEIEQEVSSVDSSFNTLGPTFN TRTIQNAVLVKTGTVVLGGLL DDFSKEQVSKVPLLGDIPLVGQ LFRYTSTTERAKRNL MVFIRPTII RDDDDVYRSLSEKEYTRYRQEQ QQRIDGKSKALVGSDELPLVDE NTFNHSHAPAPSSRWALAQRIQV SRVDMQQHVRPPVNLSPKRE NVIAGVLSNSVARKORHIQTGT VFHQLMNLRLDGINIIFMNFKY QFIVYLHFLSPKVVWMYNRKC VNGMLLIASVPATWMLSRYS SHRWIAKEIPMGKTQPLPILLG /GGRRIGLALA\WHFIIQKQPVIV SYRTHYPAIDGLINAGACIQQA DFSTTDGVMFADELKSTHG LRAILHHASAWMAEKPAPLA DVLACMMQIHVNTPYLLNHAL ERLLRGHGHAAADIIHFTDYVV ERGSCKHIAAASKAALDNMT RSFARKLAPEVKRQTATRAGH RGINQLSRYYRRALARQNR MVELRSLRFMYRHRPRSFVLW QATRLHRLNIARHRKPDARPL PAIQRTNDIAIKQPKRAVITGNH HRSTFVPTRLAQQTGEIRRHAM
25796	56164	A	25937	3	543	
25797	56165	A	25938	209	343	LSPPMSSFLATVFRSIAWLLTAK SIRYRTT*RWIRCAAVWLTMD
25798	56166	A	25939	547	640	
25799	56167	A	25940	174	583	
25800	56168	A	25941	2001	2610	DVLV\RKHNGHWTVELYSDSIP RLQINQHYASMCNNARNNDGDS QFIRSNLQDAKWLKSLERND TLRLVSRSCIVEQQAFFEQGEE YMKPMVLADIAQA VEMHESTI SRVTTQKYLHSPRGIFELKYFFS SHVNTGEGGEASSTAIRALVKK LIAAENPAKPLSDSKLTSLLSEQ GIMVARRTVAKYRESLIPPSN QRKQLV
25801	56169	A	25942	329	484	TRQLSLVRMTL*AFVRKRKRS LA*KPLWSWLSVKSQPGWKL MLARWKSF

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25802	56170	A	25943	1	1785	
25803	56171	A	25944	2493	2696	
25804	56172	A	25945	1	1861	
25805	56173	A	25946	456	700	
25806	56174	A	25947	1	2413	MPVIKVVRENEPFDVALRRFKRS CEKAGVLAEVRRREFYEKPTTE RSRYDLVDRNNNIVLEYRKKE VRLTLTDPVTGKSGEVKSLVSS LQTKYALKGYNVEATALEAAG GKVVTGKDILVRKPTLDLPLE VRRKMWFKPFMQSYLVVFIGY LTMYLIRKNFNIAQNDMISTYG LSMTQLGMIGLGSITYGVGKT LVSYADGKNTKQLPFMLILS AICMLGFSASMGSGSVSLFMI AFYALSGFFQSTGGSCSYSTNT KWTPRRKRGTFLGFWNISHNL GGAGAGVALFGANYLFDGH VIGMFIFPIIALIVGFIGLRYGS DSPESYGLGKAEELFGEISEED KETESTDMTKWQIFVEYVLKN KVIWLCFANIFYVVRIGIDQ WSTVYAFQELKLSKAVAIQGFT LFEAGALVNGCSYAQGMWG KTAETSDLODLIAALQGLSAW AVKAREYGIINHVDVSFAPRAF FSTLTNNVNDSPRIVGYAREAIA LREALKAQCLAVDANARVDNP MADLQLVSDDLGELQRQAAEF TPNKDKAAIGENILGLRLCLLY GLKVFNGREDQLDSCYHGNNRQ LRGSLRLFLAFIRQLRDLIITA HRVIRVNRQHAALGVKHCRLP GITGNRIQRQATQYDRRRGTGQ NQCMRGDMQQLFADIANVAN TFAQIIAGRGKRFGANLLHIAD
25807	56175	B	25948	1	3738	
25808	56176	A	25949	1518	2124	DCFCGRSHDKLPSAHQCSAKPG SDRFWRSHADAAVAHDGGIOP VLCASTRSNGCLQKPKCHTIVSG RCPLQQIGSVFPSPGDAANVAS FSCACDNAGSAQHRTLGLGKQ FFNCRNAFHFNRSRQTALKSG ISWVTFQLILKQPRPVIMTKM AIGFRKV*SQRNIRHLLVYIFKF ADGGCFVVFILCLQRFIETGINN KMG
25809	56177	C	25950	1	747	
25810	56178	A	25951	168	332	CAWRVCAAW/PTGASC/CNN DRFVFQILRSFEHDNSDEKPGP GMPPHGWRTQFWGG

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25811	56179	A	25952	1	2706	
25812	56180	A	25953	1	1062	
25813	56181	A	25954	1	855	
25814	56182	C	25955	1	2412	
25815	56183	A	25956	279	713	RCDAAGAVLHLSAGLLRHCGY WQRGKPDWRSSRRPGNYADRIC RRWFCAGGVGDRQYELCQLLA YTVSATRRGTGYCLYRDSRGR TGLPVV*HLSAGLYGRCRFAG VRWCVRHYRRRTATSGIPAGDY GGVRVRGRNAFCHPAVAP
25816	56184	A	25957	1	769	MDFAETELEFIKFWGDIITNKLN EALAAQGDNVVINLASDEYFKS VKPKKLNAEIIKPVFLDEKNGK FKIISFYAKKAGLMSRFIENR LTKPEQLTGFNSEGYFDEDESSS NGELVFKRYEQRAECRIVTRHL SFGSDVCLDHDRRDDHEELSY GGAAVAVALVIEPNKLAFDGS GYLAWEGLICMQEIGKC/YRRT SGDCA*VAGRAQTG*VSGWAL SRGKNQPGVGCAGARRHARE ARIGDERHRLAPRMDL
25817	56185	B	25958	1	2472	
25818	56186	A	25959	4300	4492	DCGGVRSQRPDQR*DWNR*GA GGESDS*SLATGGQAAEGVAV WRY SARWR*PLFAGRCARAGG D
25819	56187	B	25960	49	3000	
25820	56188	A	25961	266	812	LLRWRPGALALGHKL VAGEIR QQRMDA WRAACLQNPQILCC ARGGQRSHIVQSWLHAAAGIDY PLVEGGYKALRQTATQATIELA QKPIVLIGGCTGSGKTLTVQQQ ANG/VDLEGLARHRGSFGRTE DELGKLAQTSTSSPAHWRETSK CGGFLCPILFTNMRTPLPVCA T VLPYLAITV
25821	56189	A	25962	761	874	
25822	56190	A	25963	2	304	MAAYGSGIFAQTYIEAFGISTIQ PASCSPVNQYITAAVFLGNVA HALLIALQRRNRHLQRRKGGA VIVIAFNTSQGA/VPAFCCQP*S RYASPPCCSFSTA
25823	56191	A	25964	109	777	
25824	56192	A	25965	5	187	ITHKKPPSWRSALLPAAGVFS RRYMPALCE*HWAS*RMRAEA TETFSDCITMPIGMMMS
25825	56193	A	25966	1	711	
25826	56194	A	25967	757	1026	
25827	56195	A	25968	1	750	

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25828	56196	A	25969	1	1065	MKVLEKRNNASSEPEEKNEIRA AREHAGFTLQELVCLGASGRK VQGEAANAEEVAAAGELDANIA KITNEGSYTEQQIFNEGYMWLS TLMKIKENKISCSWATQSHFQG SIDAGEHLTPERVVKETESA LTTRNPQVFFQVLRDCGALRVL FPEIDALFGVPAPAKWHPEIDT GIHTLMTLSMAAMLSPQVDVR FATLCHDLGKGLTPPELWPRHH GHGPAGVKLVEQLCQRLRVPN EIRDLARLVAEFHDLIHTFPML NPKTIKLFDSIDA WRKPORVE QLALTSEADVRGRTGFESADYP QGRWLEAWEVAQSVPTKAV VEAGFKGVEIREELTRRRIAAG LRG*VSRSHPLPNAEPKNH/AS NYLIPSMPGVNRSVSSNWR*PA RLTCAAE/HGFESADYPQGRWL REAWWEVAQSVPTKAVVEAGFK GVEIREELTRRRIAAGLRGMPT
25829	56197	A	25970	2373	2597	SADDKADSV*YLRLASA*TN CRPYRRPSAPVCRRAPI*G*TP QNYGPPSSCPAGGFWRYPVDP RFGSGFVH
25830	56198	A	25971	2616	2777	TSVRKRFTSLSGKPVAKAGRKR PPPCR*TPTANGHPKPCRPVW CHPAPVARP
25831	56199	B	25972	1	1449	
25832	56200	A	25973	1076	1477	CAVRRSITWCKLSSKTPVRPLR PSTYRDCLTVSIALTPPASEKVK RRPVPAVKSAAMKVPPGAQSR KRVLWVSPFPTCEFLASNSRGK KISVLSALSPPRWTS*PKARWA ARRLTTNLVVRH*TATSVLMK KK
25833	56201	A	25974	1	3552	
25834	56202	A	25975	196	493	KRCRFADRPDGPGRQGTAAAT FGGMSFVTILPAPIELSPMVT GLITT*LPIQTLPIVIGKEYISPF FLNSWCTGCPVTERVTLAGIST LSPITV

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25835	56203	A	25976	1	3917	MTDKHQQHRYVAAPGPFVGD KCQVAGDPLMLRRALSNLLSN ALRYTPTGETTVRCQTVDHV QVIVENPGTPIAPEHLRPLFDRF YRVDPSPQRKKEGSGIGLAIVK SIVVAHKGTVAVTSDARGTSG DDFFIDVVYVWRRIKRLSVYR RIPRMSYRELYKPDQPLAIMV PAWNERASSAIWRAGGTTLD KFLFVGLPGPILGCKVPFEFLE VACPPSGGPVGPWRRCRGA AAACASPAAILAPT
25836	56204	A	25977	3	292	GDMQRLNSLFC/SVAYSVLEQ DEDEGRDSINIVNPSGRPIVSSG ATPAVREYAAHGFLHYGLRQR VGEVRVDLQREQIYASKPCGST IGISLVVR
25837	56205	A	25978	2	181	SARRLR/RSKHRFRJLNRRYSHA HSVMLGDMQRLNSLFC/SVAYS VLEQPDDEGRDSINIVN
25838	56206	A	25979	1	2781	
25839	56207	A	25980	1	2554	
25840	56208	A	25981	635	741	
25841	56209	A	25982	91	501	LWIRLAKRSGKAIKERRDFIRL CTHRVRQGTALLRLFQHSNGN RLMKLDNQHLRLRISNHRAFHF RHRTTVKQSQQTFRYPWLYRV RHWGQKPKTDNFWHGLLARIFG NSRSKTWGENR*EHSVLEQPD DEGRDEY
25842	56210	A	25983	2153	3062	APVMPPERLPVIAVRQYPTANC CSDCLAAASRFFLASVAAPSEQ DADTRRSRVAVGRRKTRNSNA NQPRPRRDWRELQMLMDRLARV AQARASFAARETLRIGDAMEQ MMEGLNKVMHGEPQREKELR KLADDINVLTAIKLYLAMPK EELAEESRRWAEIHEMSLNLEQ ASDIVERMGI/ELVDKSWAAR RAFSLDGLKELDALYEQLSNL KLAMSVFFSGDVT SARLRRSK HRFRILNRRYSHAHVDRLHQ NVQSIETSSHLGLLGDQMRLN SLFCSVAYSVLEQPDDEGRDE
25843	56211	A	25984	135	308	KLSLRLGIFRPSLFRPTPTSPST PAPAS*PAPS*VSPSPRTATPSCP TSYSSFFCH

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25844	56212	A	25985	3	663	ARGKKPPRRGKEDFDLSIATR VSVNPIKFPVEA*PFLKPLQQV SVGPLGGRLPLPIPGNLLQQVAD GTLSTGTDLLEMVMVARVALV QPHEPGATTVPARKFFDICRGL PEGAEIAVQLEGERMLVRSGRS RFSLSLTPAADFPNLDWQSEV EFTLQATMKRLIEATQFSMAH QDVRYYLNGMLFETEGEELRT VATDGHRLAVCSMPIGQSLPSH
25845	56213	A	25986	1	1077	
25846	56214	A	25987	1	1323	MHSGTFNPQDFGWQGLTLTPA AAIHIREILDEYGIPNAWQGE TNFWGSTAVSIDRLAAYKDVD VLCFDHDSKMDALMATPL WQAMPFVRAGRFRQVPAVWF YGATLSAMHFVRVLDNAIGVIV ATALTWMNFSQALPRSQAQ AAWSPDIDVIEQMIFHYSLLPRL AISLLVGAGLGLDVRYYLNGM LFETEGEELRTVATDGHRLAVC SMPIGQSLPSHSVIVPRKGVIEL MRMLDGGDNPLRVQIGSNIR AHVGDFIFITSKLVDRFPDYRR VLPKNPDKHLEAGCDLLKQAF ARAAILSNEKFRGVRLYVSENQ LKITANNPEQEEAEIILDVITYSG AEMEIGFNVS\YVLDVLNALKC ENVRMMLTDSVSSVQIEDAAS QSAAYVVMRMRLEGSPPLGNP EFQKISSPCALYIALCSKARHHT GRYLGLCGL
25847	56215	A	25988	211	475	GAIGVFTAGKLTRASVYHQAR RFMQRET VWLVEDEQGIADTL VYMLQQEGFAVEVFERGLPVL DKARKQVPDVMILDVGLPDISG FELCROLLALHPALPVLFTAR SEEVDRLLGLEIGADDDYVAKPF SPREVCARVRTLRRVKFSTP SPVIRIGHFELNEPAAQISWFD PLALTRYEFIVLKTLLKSPGRV WSRQQLMDSVWEDAQDITSH VVAFATILQGSRDLRRRILPYCI RCRRERCTGTALWQ

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25848	56216	A	25989	1661	2499	QMAHDEQWLTPRILQTAATLC NQNA PRDGSPLWLGVDLGTCD VVSMVVD RDGQPVAVCLDWA DVVRDGI V WDFGAVTIVRRHF DTLEQQFGRRFSHAATSFPPTG DPRISIN VLESAGLEVSHVLDPE TAVADLLQLDNAGVVDIGGGT TGIAIVKKGKV TYSAD EATGGH HIFLTFAGNRRISLEAEQYKRG HGEEIWPAVKPVYEKMADIVA RHIEGGITDLWLAGGSCMQP GVAELFRKQFPALQVHLPQHSL FMTPLAIASSGREKAEGLYAK
25849	56217	A	25990	915	1518	PSGHAPDLNGAPATAHQPGGR YPAPRSVRRATDNGYPAGDPLE WRSTAQVFVSSRRRVSLPNDRK TVLTRCWSAAH*FALPAPLCRD RTGERKNRRFHTPTRCGRGFCP APAASRRCAGRRRGDASGRAY RRPAPSHCPVQ*RGHRKSTTTSS TSRRRPGQSARPYSGPEYRE*Y CSAQRFFHNDGSRPPVVRQAGR AQFP
25850	56218	A	25991	1	1254	
25851	56219	A	25992	675	835	VRWCWIFPSQ*TLFQKRAGHA APSADVLHESQHFLLNLLNRLG RHYDFGEGEP

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25852	56220	A	25993	1	2255	MRESPTRRDSDKNTVNTTIRIRIH NSYTEQLQIVTNSYCTKQWHV HHTAKPYAHIQRPATPDALQTK MQEEEEVEPEPEMAEAEVEPEPN PEEAETESSEMNQRDVRGTVRI VLKTFNNCRD TVFVAFEVNTN VSLLVATTDMTSGDTAIVVTTT GFVAVFFQQRKSAANEVQILAF FQGDVSFFPVATTTDTLSVTFN FPFNYQGVNDFDFKQFLHSS FDFCFGRVFSNFEYLHGARAHA CIPPSACIGEVLETSSFDIRVS VY RSSCVCVRLRESSGDRYFGGL SLQMMRKATGLTDITSDTPGNT DDQRWHPEHGLTQRMQKEQE LVKEPEGAARDGDGEAEAWGE VKAKSSGCGVTRASSHLFRCNV CELHFKESSELLQHPCTPSGERP FRCGECQKAFKRPSGLRQHER THSAERPFKCDLCPMGFKQQY ALMRHRRTHKTEEPFKCGLCE KGFQGPSHLLYHQHVHTLETFL KCPVCQKGFQDSAE LLRHKCLP GA AERPFKCPVCNKAYKRASA LQKHQLAHCAA AEKPLRCTL ERRFFSSSEFVQHRCDPAREKPL KCPDCEKRFKYASDLQRHRRV HTGEKPYKCPNCDKAFKQREH LNKHQGVHAREQQFKCVWCG ERFLDVALLQEHS AQHSA AAA AAEGAYQQT LHHPRRQQQQY WQLLCARNNVKLCMHILFSPH
25853	56221	A	25994	98	596	YSGIIMASQSKLYPVVMAGGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTITICRLNGVECESPVVICN EQPRFIVAHQMRQLNELSENIL EPAGRTTAPTIAPAALAA NRHS PESAPLMVLATDHVIANEDAV RAPVKNAIPYPPKKGKLVTFGIG LDGRVPRYNM
25854	56222	A	25995	3	554	
25855	56223	A	25996	1	222	

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25856	56224	A	25997	1	1043	MKVKVLSLLVPALLVAGAANA AEVYNKDGKLDLYGKVDGL HYFSDNKKDVGDDQTYMRLGFK GETQVTDQLTGYGQWEYQIQG NSAENENNSWTRVAFASLKFFQ DVGSFDYGRNYGVVYDVTWS TDVLPFEGGDTYGSDFMQQR GNGFATYRDTDVFGLVPTRLHP ARVCCALRELKDAGADRIWYI ADAFRAGLSVDGVFNLTNIDR WFLHINRAKDKNHMIIISDAEK AFDKIQQPFMLKTLNKLIGDGT YFRIIRAIYDKPTANIILNGQKLE AFPLKTGTGQCPLSPLLFNIVL EVLARAIROKEIKGIQLGKEEV KLSLFADDMIVYLENPVSAQN LLKLISDFSKVSGYKINVQKSKQT FLYTNNRQTESQIMSELPFTIAS RRIKYLGIQ*IRY*WDFQNNK SYL*QTHSQYHTEWAKTGSIPI ENWHKTGMPSLTAPIQHSVSGSS GQQNQAGEGNGKYSIRKRGSKI VPVCRRHDCLSRKPRLSPKSP
25857	56225	A	25998	1	3339	
25858	56226	A	25999	1440	1880	AAQHASVYLYQNRRIRGAVPPV RFFHADQRTRRDGDGKQRHA TETLCRAEKISSREQDWLHCD ERQSLYEWTW*PYSPHSGRSQK EKROT*TAILDAYCADCFRCGR GVFARRRRTKRDRPGNAGTG GDCPCWLRROQYECVRL
25859	56227	A	26000	1	2277	
25860	56228	A	26001	1	1845	
25861	56229	A	26002	56	113	QQQPNPTRDQLQLAILHNIRGIR KIYG*IQSATREAG*GHSPQY
25862	56230	C	26003	1	2317	
25863	56231	A	26004	3	2168	
25864	56232	A	26005	670	2541	
25865	56233	A	26006	98	944	YSGIIMAQSKLYPVVMAGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQHRFIVAEQLRQLNKLNTNII EPAGRNTAPAIALAALAAKRHS PESDPLMLVLAADHVIADDAF RAAVRNAMPYAEAGKLVTFGI VPDLPETGYGYIRRGVSAGEQ DMVAFEVAQFVEKPNLETAQA YVASGEYYWNSGMFLFRAGRY LEELKKYRPDILDACEKAMSAV DPDLNFIRVDEEA/FLACPEESG DYAAMGRTGDAVVPLSLGAH

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25866	56234	A	26007	3	417	
25867	56235	A	26008	507	717	WPEAEYLDNADAVLAMYYHD/Q GLPVLKYQGFGGVNIT/LGLPF IRTSVDHGTALEWRTCKPMVP DSIVSCIL
25868	56236	A	26009	5	378	MAVCSSLSPRRSPAFL/HDFTDV WTHHLVFGVNP*RLIHHGTALT DHVG/ENGNYSSD*IHGTALTD HVGKTETILPTKYANIYSINTSK DRFLTKPAFAEVVLFHLPRELQ TCSFFLSQNMLVKVGHQRHWF TEVDVTLTEITQLA
25869	56237	A	26010	1	469	MQKEYAYWMDGLKTCKPDNR KNALSNGWYPSQPLLGRSRY ATTESWVEDIATAKSNPNRLPL KFTATCALPLRLAGFQ/PRWMD NPQQLNTLAPPASYRSI*TA*CL K*KNPRPRQQSCRR*RDGNQYE TLANARQKGIEKTCGTINKAG MPITT

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25870	56238	A	26011	2	1854	CGGTLARACDGLNGEFAA/LI TGPVHKGVINDAGI/PFTGHTF FEERSQAK/VVMMMLATEELRV ALATT/HLPLRDIADAITPALL/H QPKYLDNADAVLAMY/HDQGL PVLKYQGFGRGV/NITLGLPFIR TSVGHG/TALELAGRGQ/ADV SFIRPYSIAIK*L*NAGASVRWLS ERRICRAITGPVHKGVINDAGIP LPVIPSFSKSVRRKRCDAGD RRTSRGAGNDALPLRDIADAIT PALLHNRNILITPTPCWRCTRSG SSRAKIPGLRARCITLGLPFIRT SVGHGQPLNWRDVANRCWQF YTPLFCHQMIVKPMHNRIPRAT YRGAVKSAIGLGCCCLKASATR CAYRWRRSGRDQSRFRYFEIA GIRSRGINFIACPTCSRRNMLS VRLTRWSNAWRYHHS DGRFD YRLRGECPEALVSTLGVTTGG NKKAA SMKMGAQRPSGQQDM IDOLEARIRAKASQRTKRVLT FSRLKNNNVEKQDTALFALYQ RRLRCVRKVRRYVMAAVSAGC GGGVCAVSA YMPLNRLPNAQE ANNEYTSFENCICKTVCTTACR VTLRNNDPKLPYL VKAGLKMK RVTRSPRRYCAAA SATHRFNDE RAGKVQGM PDINKLPADRETC STLTCARSQNTNPYPANRAA NAYQVVLATKALEKVS MKSP WQHKVSSPAAVRHLPSITQRR

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25871	56239	A	26012	1	1504	MGIVASASVQAAEINYKDGNK LDVYVGKVKAMHYMSDNASKD GDQSYIRFGFKGETQINDQLTG YGRWEAEFAAWTDMFPEFGG DSSAQTDNFMKTRASGLATYR KTTSSAYRWPELNLYHRCTS AARAMLLSGRPVMQINERTAV RRQMTVYLRVERIHEIDPLVSL SHSMSVIPIDVERPIAAAPCTPG I.WRTKTPLRVPSTYPLRLPGRA RVVCHRTFRLHLCKDWVFMFS GLLILVPLIVGYLIPLRQQAAL KVINQLLSWMVYLILFFMGISL AFLDNPRPYLADSVPRQLLAP VNSISRYKTIEWLNYIATLHK GFTPLFRPDTPEEYKPTVRAHSE KKLQYVNEALKDEHWICGQRF TIADAYLFTVLRWAYAVKLN EGLEHIAAFMQMAERPEVQD ALSAEGLKGSRLHAGARRLIL GIIVTFSLLALICVTQPFNPLAQ FIFMLLVGVALIVRRMPGRFS ALMLIVLSLTVSCRYIWWRYTS TLNWDPPVSLVCGLLLFAETY AWIVLVGYFQVWWPLNRQPV PLPKDMSLWPSVDIFVPTYNED LNVTPDELKQVLDVAAALKAL RAENISTKVFNLSGLGISVFRDMS TRTRFSYASALNLLGLAQQLD EGKSQIAHGETVRETANMISFC ADAIGIRDDMYLGAGNAYMRE VGAALDDGYKQASGFSEPMAR
25872	56240	A	26013	2903	3024	
25873	56241	A	26014	123	335	
25874	56242	A	26015	2634	2787	
25875	56243	A	26016	1477	2485	NPEQLMVYKQTVVITGPAGI GPDLVVQLAQREWVVELVCCA DATLLTNRAAMLGLPLTLRPYS PNSPAQPTAGTLTLLPVALRA PVTAGQLAVENGHYVVELLAR ACDGCNLGEFAALITGPGHKG VINDAGIPTGHTTEFFERSQAK KVVMMMLATEELRVGLATTHLP VRDIADAITPALLHEGIALHHD LRTKFGIGEPRIIVGGLNPHAG EGGPMGTTEIDTIIPVLNELRA QGMKLNGLPADTLFQPKYLD NADAVRPMYHDQGLPVLKYQ GFGRGVNITLGLPFIRTSVDRGT ALELAGRGKADVGSFITALNL AIKMIVNTQ

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25876	56244	B	26017	1	3432	
25877	56245	A	26018	1385	2536	KSSQSHLITGMLEHVFKSGDTPSR/LPELMNGA QALANQINT/FVLNDADGAQAIQLGAN/HVWKLNGKPDORMIED/YAGVMADTI RQHGDGL/VLLPNTRRGKLLA AKLAPDASRTGETH/TVEWQAP AVAITRTATQARQSNVLDLDA RLVVSVVGRGHTDSQTLRLYYI RLPPSLMGMRLTVFLPICGFH RVGPPTLLSVLATNRNRNAKVFAHKNAPKFRSHTASEQWKSSIA HNKGVHPRVTSHTHARHSLMETDIPHNIHSGHASPADITRHRAQVFNSVPKMASPIGDRVPTLHTQHNSPANTGKAQSLTTCGPAAESCCRLIPRQMVSLVRLKARLLITTELPGGLVPVATISGTGNFGNTQSANPYRPSENTDLSLS
25878	56246	A	26019	926	1293	LSPNPKPEPCRTRLKKSGFFTRI SAGAEPLMAIPARLSNSLACGARDSAAKE/GFVVVPVCVAVEADIAELDDDEERDEFMADVGFTVGVKEVRAWTIPVGATAPQAAGKIHTDFEKGFIQAQT
25879	56247	A	26020	1	1278	
25880	56248	A	26021	678	1526	ERNTNTCEVVPNRKRAYASHDMELSISVPVKGASKGEVNPADDIEVINTELALADLTCERAIHRVQKKAKGGDKDAKELAVLEKCLPQLENAGMLRALDLSAEKAAIRYLSFLTLPKPTMYIANVNE DGFENNPYLQVREIAAKEGSVVVPVCAAVEADIAELDDDEERDEFMQELGLEEPGLNRVIRAGYKLLNLQTYFTAGVKEVRAWTIPVGATAPQAAGKIHTDFEKGFIQAQTISFEDPITYKGEQGAKEAGKMRAEGKDYIVKGDGVNMFLFN
25881	56249	A	26022	1177	1605	
25882	56250	A	26023	1	644	MDNHIALDFLLASECGSVYYVATTTHGRNMAGARALWRATGMTDADFQKPHIAVNSFTQFVPGHVHLRDLGKLVAEQIEAAGGVAKFENTIAVDDGIAMGHGGMLYSLPSRELIADSV EYMVNAHCA DAMVCISNCDKITPGMLMASLRLNIPVIFVSGGPM EAGKTKLS DQIKLDELVDAMIQGD PPKIN/DYQSRGRRCPNRCFRCKNQAGS
25883	56251	B	26024	1	1944	

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25884	56252	A	26025	1	1488	
25885	56253	A	26026	1	1919	MNKAHFVSNLGATKCCPLSFLP YRWRRVIAFVVAFYFRHLIDLL VVQMHFKLKGNVDVVFATAQ LIDSTVQLIDSTTTVTQFTHIQT QLMIQRAGTKCRKEDFRHCVGI LEPEWYPIIVRVVVVDVSQFEV RSQSLIFAVGEGITCIYTQFITHA VVRLTVNFHVVAQLSSPDWNR PETLPVRSHVTSITQFEVVTFGFQ TEAPSVGVGATVNVSTVAHGC RQVVVEVRVAQATINKDVVRE VSRRVDVGS LAVLIHLTRTVIH VTFSEACSRDDPLSVVTVNFGE NTDHD AVNIIIVDGA VVAVEV TTEVAYPCA AVISQAMTRVGQ TSTNGVWTISSVNAFQIRTGAA RSLAPPWSLTEKVFCGTTMER MRAALEAIMPFTESSATQAPY LPCGREGLAVRQFFGRGEGIE TVAYLFRIRVVRTRVL SIGGFS RTRISSTPVKIATLRQNRSDCHA AMIADTYRQVTPDPFSRHPFS RVI.RGLFFIIFKDKAHNGIGMI GGVNRRADYLNLLKVFVGD RV SSPQWQATLKAIVPSYGRKLNG DVAATERELQYTSEVVGLNYD KPQAADNNRQHKVRAARSRRQ NRPD RGSQIADSTAGARCRFQT PTAGDGA*SAASTAAPI/MLNLL EKVFGDRVSSPQWQATLKAIVP SYGRKLNGDVAATERELQYTS E VVGLNYDKPQAADNNRQHK
25886	56254	A	26027	1	2130	
25887	56255	A	26028	1144	1309	PGGSTPMAVEDPDRSSSERVLR FQPAVS VYGPEQPAV*DYA QTS YLRT RPRRSDP
25888	56256	A	26029	1	3546	

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25889	56257	A	26030	1097	3332	TRVLVDHRLRLCLYATVCAG ASWGMNPPVCSQQIDPQFHTM LMICASEEAQRMQQASEDEFN RALNIAFDNRLGLCKVESARQV FPLTGRYARQFASHRLALVGD AAHTIHLPLAGQGVNLGFMDA ELIAELKRLHRQKDIGQYIYL RRYERSRKHSAALMLADSFVR TTHALRRSHGGFPRLDDAAAL RFANRRTSCERNDDNTWSRL YADLKNGTAQNIKAKFVFIGAG GAALKLLQESGPEAKDYAGFP VGGQFLVSENPDVNVNHLAKV YGKASVGAPMSVPHIDTRVL DGKRVLVFGPFATFSTKFLKNG SLWDLMSSTTSNVMPMMHV GLDNFDLVKYLVSQVMLSEED RFEALKEYYPQAKKEDWRLW QAGQRVQIKRDAEKGGLVRL GTEVVSDDQQTIAALLGASPGA STAAPIMLNLEKVFGRVSSP QWQATLKAIVPSYGRKLNQDV AATERERKTLHVFINDRLPEQC EAGKSPSRVQLQWTNNGMLN APLSRLTLVEKLASMLDPGHL ALTQIAQHLALLQKMDHRQHS AFPELPQQAALYEWFSARCRW KEKALTQRGLLVQAGDQSEQIF TRWRAGAYNAWSLPGRCFIVL EELRWGAFGDACRLGSPQAVA LLLGDLEKATQHLAESINAAP TTRHYHYHQWFASSTVPTGGEH
25890	56258	A	26031	115	654	HATQTMTPWFLVLRITADNKL YTGITTDVERRYQQHQSGKGA KALTGGSARSPLIKKALAEQLP GIPIAGGDDFGSVTAGLAR*RF HQRHGPCWSMKAESLQLCRAD CQRRFQPMSPFGGHRHYRLSVC WRYRFRIRPEHKTAFTARFPVDN RLGQMVAKPFHLLNATTGNIC GCFNTRKP
25891	56259	A	26032	1	348	
25892	56260	A	26033	1	906	
25893	56261	B	26034	59	910	
25894	56262	A	26035	1	3684	
25895	56263	A	26036	1	2634	

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25896	56264	A	26037	1162	3478	LVRFGLLPLAYSARCFARSERD RPKDECETCCIKYPNGRNVLSQ EIHQVFVLNGIQSMGYVYNLGG NELASMQGLVDVVRVLSPOGSS AREAFSHSLDLARLAEKRGYH RYWLAEEHNNMTGIAAATSVLI GYLAANTTTTLHLSGGVMLPN HSPLVIAEQFGLTNTLYPGRIDL GLGRAPGSDQRTMMALRRHM SGDIDNFRDVAELVDWFDAR DPILEPTHNGRRLCSTVRHPRM GYTPGVPEPTGPLGQGLANAV GLAIAERTLAAQFNQPDHEIVD HFTYVFMGDGCLMEEGWFTD DTAKRFEAYHWHVHIEIDGHD PQAVKEAILEAQSVKDKPSLIIC RTVIGFGSPNKAGKEEAHGAPL GEEVVALARQKLGWHHPPEIP KEIYHAWDAREKGEKAQQSW NEKFAAYKKAHPQLAEFTRR MSGGLPKDWKETTQKYINELQ ANPAKIATRKASQNTLNAAYGP MLPELLGGSADLAPSNLTIWKG SVSLKEDPAGNYIHGYVREFG MTAIAANGIAHHGGFVPTATFL MFVEYARNAARMAALMKARQ IMVYTHDSIGLGEDGPTHQAVE QLASLRLTPNFSTWRPCDQVEA AVGWKLAVERINGPTALILSR QNLAQVERTPDQVKEIARGGY VLKDSGGKPDILITGSEIETL QAAEKLAGEGRNVVVSLASS
25897	56265	A	26038	1	1033	MNKSPTKTRDIQEELEVLLEE AAGGDEDREKEILIERIQSIKEE KQKGLGLAAGWTADVSSRRPG ASQLPPPTTHPIQYRGWGPPD QHLLSTLWTNVSYSKSGSFLQL GGWCMNLDMDLNSESRWLF RRHWDGTGGIKPHERKRAVAHL TLSEEEIRAGLSAKMSIRAIAT ALNRSPSTISREVQRNRGRYY KAVDANNRANRMAKRPKCLL DQNLPLRKLVLKLEMKWSPE QISGWLRRTKPRQKTLRISPETI YKTLYFRSREALNHLNIQHILA RSHWLWPGERYNRNGERGPV TLWTG/TPISDGSRTSVKRALGQ WGEHLSSRNAFFPLCATVV

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25898	56266	A	26039	797	1440	PAMRLTAMRCISMKSRLPASR MQFCATVRWKYRCHREPTLSA QHGAFRSINPTPRNSRGNCWKK REMKWANWPIWCR*KN*RERS LSAICCASRK/TGQFVLPARYH LRRSHSLRHGRRHTRKGERGTI NIVNGTPIHERSRNIDNRRSLGH WEGDLVSGGVGTIVGVVTGVII FTVINYGLTYIGVNPYQWYIK GAIIIFAVALDSLKYARKK
25899	56267	A	26040	687	1106	GSLSLTALLPDTAEREERAGLS AKMSI/RAIATALNRSPSTISRE/ VQRNRGRRYYKAVDAN/NRAN RMAKRPKCLLDQ/NLPLRKL LEKLNIOHLRRSHS/LRHGRRHT RKGERGTIN/IVNGTPIHERSRNI DNSALVTVL
25900	56268	A	26041	1	2851	MKTLIARHKAGEHIGICSVCSA HPLVIEAALAFDRNSTRKVLIEA TSNQVNQFGGYGTMTPADFRE FVFTIADKVGFAERIIILGGDHL GPNCWQQENADAAMEKSVEL AVVIDLWSRAVIGWSMSPRMT AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK RHNLRGMSAKGCCYDNACVE SFFHSLKVECIHGEHIFISREIMR ATVFNIECDYNRWRRHSWINS LLSQKRNTQGRIEDGRQH
25901	56269	B	26042	1	1048	
25902	56270	A	26043	323	1290	GTSMTNVGTPLLWGGFAVVVA IMLADILLQRRGAHAMTMK QAAAWSLVVWTL SLLFNAF WWYLVQTEGRAVADPQALAF LTGYLIEKSLAVDNVFWLML FSYFVSPAALQRRVLVYGVLG AIVLRTIMIFTGWSLISQFDWIL YIFGAFLLFTGVKMALAHEDS GIGDK/RWCAGYA/VHLRMTDT IDNEHFFVRKNGLLYATPLMLV LILVELSDVIFAVDSIPAFAVTT DPFIVLTSNFLAILGLRAMYFLL AGVTKRFSMLKYGLAGILVFIG IKRLIVNFNLLQTRACLGCGWA FGETLIKPGEYRMKTAGG
25903	56271	A	26044	28	96	
25904	56272	A	26045	1	777	

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25905	56273	A	26046	77	532	KPSRPEISKGKSVKPAASRRARE CAVQALYSWQLSQNDIADVEY QFLAEQDVKDQDVLYFRELLA GVATNTAIVLDGLMKPYLSRL EELGQVEKAVLRALYELSKRS DVPYKVAIKEAIELAKSFGAED SHKFVNGVLDKAAAPVIRPNKK
25906	56274	A	26047	3	175	YSSSSLWAARKRRQMVLSARR FATSDRVRCRVLVWSAGTSRA KSKSTGWLSMASKAIGVSS*TK TPTARRVSSSLPCGMAIPLPIP VLPIFSRVRIASKTT*GSSLSCFA ARSLMTS
25907	56275	A	26048	85	440	
25908	56276	A	26049	80	706	KLIQVAVVIGGGQPLGAFLCHG LAAEGYRFPVVDIQSDKAANV AQEINAEYGESMAYGFGADAT SEQSVLALSRGVDEFGRVDLL VYSAGIAKAAFISDFQLGDFDR SLQVNLVGYFLCAREFSRLMIR DGIQGRJIQINSKSGKVGSKHNS GYSAAKFGGVGLTQSLALDLA EYGITVHSLMLGNLLKSPMFQS LLPQ*KTKLGK
25909	56277	A	26050	741	893	TGCSGKRSLQQRRREERRRNPVQ KIRCTV*RVRNGRIRYCSPRAGF YSRYR
25910	56278	A	26051	269	987	MDAKCDRSRFPWLWPTKRPRG CFATFVPIGIPYDQTKTHLHTLS LVAKRLADKTCRRLRAAQSDSE ELYQIITDTEGTPDEARCEEKQY MVLMIVSGRSGSGKSVALRAL EDMGFYCVDNLPVLLPDLAR TLADREISAASIDVRNMPESPE IFEQAMSNLPDAFSPQLFLDA DRNTLIRRYSDTRRLHPLSSKN LSLESAIDKESDLEPLHGFPDY DTVGFSCKRRIIDYVCRKHSRR RQVLLNFAKSGAFSTTRGTDD KTRRSLVTL/VAYFLCAR/EF RM/MIRDGIHVRIQINSKSGKV GSKHNSGYSAAKFGGVGLTQS LALDLAEYGITVHSLMLGNLLK SPMFQSLLPQYATKLGKPDQV EQYYIDKVPFKRGCDYQDVLN MLLFYASPKA/SYCTGQSINVT
25911	56279	A	26052	1	1268	
25912	56280	A	26053	1	168	LKVFILVIFTLRE*EHAMFGFL FLC*FAENDGFLHPCHPCCKGHE LILFYGCIVFH
25913	56281	A	26054	2	253	

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25914	56282	B	26055	319	3780	
25915	56283	A	26056	513	762	
25916	56284	A	26057	375	550	GVGLCGRSSIRRNM*CK**G*/L SPKIALMACGRRHTRSLFMTSK DLRMMRLQKEIRL
25917	56285	A	26058	662	1033	EPKRASGCMWPVGAHCHPLP LLACQKQLGPPSHQASSR*NIQ TLDRLCMSSWIPQEHSSSQSWH RSCFLNVTRPWSFYSPVGKNR WMGPFWSFSLDALLFFTLHSY VAWVPEMMALNLLG
25918	56286	B	26059	1	2034	
25919	56287	A	26060	369	515	HAKPPGGLGHCSLCPSHYSCIH G*KGPRYVSVCSRGWKPEAT KAFMW
25920	56288	A	26061	352	2631	
25921	56289	B	26062	10	351	
25922	56290	A	26063	321	537	EPLDTGRGTSHTRACHGVGYW GRDSVRRYT*CK*RINGYSTPT WHMHEYVTNLHIVHMYPRITYS IIKKMSD
25923	56291	A	26064	788	912	VHTHLSERTRKCLPPAPS*WV TCHHGDCCLPTRLRAPQGP
25924	56292	A	26065	1348	1799	
25925	56293	A	26066	606	2219	ATYPSAHYPDHNREGFLWPSL GLGKELDTFWSSLRVFGSPVSA VSRELVRKFSLGTVDTSGSLP VCGDISPVSDVA/ACTREPLRFR LQVGDRYITLMDLPGVGESGA RDTEYAALYREQLPRDLVLW LIKADDRALTVDHFHYHQVIGE VYRHKVLFVISQSDKAEPSSGG GQLSTAQKQNISRKICLLHELFO PVHPCAVSRLQWGLKVMA ERMIKCLPREATSPVVSQHLPSF RTTVVREQARSDFGETVGAVL DSISAFPLIPAPRAVIAQVVRTT VVSFAASVTLLLLPLRSTPVEKS PTCILPASETFPLLVMMLNPVAS LLTLTSPVLDTSCPTHLSAAQP NLIQLSGNNNISFVNVRAVVTN VLNMTMTACNSQATIQIYNADI ARDFGTRGIFSINSGFSTVYSRRI GHQSPEVTGEAMALTLSSQPSC IDDGLVAVNLDTDGLRIGDARQ KAITAGYPVVDTDKCRIRRLR RIRHEQCADENSYQAYNYCRP VGRIRHLCRIRQSMPPDATLSRLI
25926	56294	A	26067	543	741	

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25927	56295	A	26068	3	373	VYTGLKPRITDAQYTPINVV/W KFLSLTHHAYSPLL VVINKAKF DGLSPEFQQALVSSAQEAGNY QRKLVAEDQKKIIDGMKEAGV EVITDLDRKAFSDALGNQVRD MFVKDVPQAGADLLKAVDE
25928	56296	A	26069	1	1107	MGAFITGKT VILGGSRGIGAAI VRRFVTGDGANVRFTYAGSKDA AKRLAQETGATAVFTDSADRD AVIDVVRKSGA*ILILKRRSISA FNRSRSPKTPIPAFTRISNAPLL RTTSMATASLSAVNTAVAPVS CARRLAASFDPA
25929	56297	A	26070	39	254	
25930	56298	A	26071	1432	1845	
25931	56299	A	26072	674	1614	AIVIVAILVSKSTGAWVAFSIR MPSITFSHNSVAVAGVASARKDS SPSYGDPLESAIPKLNVRKRSRG LSKSLTLTSCSTIWINWITGQT PLKPCSVTGSVVPKAWRSPSTL TTMTTR*PFTLPA/LDTFISRPAG CTYANECHAPESATIRNDVAAR PCNCAQCAALDCVSVFVTIRHS CSSVYSAPGILVAALQAGHKPV ALVGGATGLIGDPSFKAERKL NTEETVQEWVDKIRKQVAPLP DRKNISPADSRLSPDGRYRGYV HPAPPIDPSHLIRHRCVYQWR QCLAQFRLNGWAASRSQSICRI GCD
25932	56300	A	26073	1	3476	MSSSCIEEVSPDDNWYRIANE LLSRAGIAINGSAPADIRVKNPD FFKRVLQEGSLGLGESYMDGW WECDRLDMMFFSKVLRAGLENQ LPHHFKDTLRIAGARLFNLQSK KRAWIVGKEHYDLGNDLFSRM LDPFMQYSCAYWKDADNLESA QQAQKLMICEKLQLKPGMRVL DIGCGWGGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGL DVTILLQDYRDNDQFDRIVSV GMFEHVGPKNYDITYFAVVDR
25933	56301	A	26074	200	1100	
25934	56302	A	26075	1	2061	
25935	56303	A	26076	1	3294	

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25936	56304	A	26077	1	2064	MNYSLKQLKVFVTVAAQEKFSF RAGERIGLSQSAVSHSVKELEN HTGVRLLDRTTREVVLTDAGQ QLAFRLERLLDELNNTLRDTGR YGATTERSARYSASLPAPTSGR SEPAALVQNSSSQPSSLKENIM KLRSVTYALFIAGLAASFSTFLA IAQSIRCGYETSQADSQHSQAK KFNDLLQERPKGELKLLFPDS TLGNAQAMISGVRRGTIDMEM SGSNYFAGLSPVMNLLDVPFLF RDTAAHAKTLDGKVGDDLKAS LEGKGLKVLAIWENGWRDVT NSRAPVKTPADLKGKIRTNN PMNIAAFKVFGANPMPFAE VYTGLETRTIDAQEHPIVNVWS AKFFEYQKFLSLTHAYSPLLV VINKAKFDGLSPEFQALVSSA QEAGNYQRKLVAEDQQKIIDG MKEAGVEVITDLDRKAFSDAL GNQVRDMFVKDVPQADLLK AVDEPGWAERDIWAFAPAFFY PLFISDFNVRLEFVGHYQDVC EKPASTTLWLDVGRSSGLDLTY QTLNVKNDLSHFVPFFDPSDN RTNTLPMVFAGAPDVGLQOAS AIVASWFGSRSGWRGQNFVPL YNQLPDRNAIVFATNDKRPDFL RDHPAVKAPVIEMINHPQNPVY KLLVVFGRDDKDLLQAAKGIA QGNILFRGESVNVNEVKPLLP GSQPVVSSASERCCFYA
25937	56305	A	26078	1	480	LGNTKTIVKGWLAQLPAKYHQ RATCMFDRHGLLALLAGRFLA FVRTLLPTMAGISGLPNRRFQFF KAKLR/WLS*PTRIAAALAFMP/ FMDDHHPRLMQTVILQILQRRG TGDRLKIMVERRYAHVGFRCRQ LLDAQVFGVFILNPFQHAANQT EVSLATDQRQ
25938	56306	A	26079	1	2184	

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25939	56307	A	26080	1429	2152	NLFREVVPFTHCPVCGSDVERY EGEAVARCTGALICGAQRKESL KHFVSRRAMDVGDMGDKIIDQ LVEKEYVHTPADLFKLTAGKLT GLERMGPKSAQNVVNALEKAK ETTFARFLYALGIREVGEATAA GLAAYFGTLEALEASIEELQK VPDVGIVVASHVHNFLLPKKAT AMSSASCWRKVFTGLRRSLSTR KRLTARLLVKPWCLRAASGTP LKRAALLMFSGCFSHTSGLAMY
25940	56308	A	26081	1	2448	AHLNRTRWKVCWIR*RKISPW AKRNTKTVKG\WLAQLPAKYH QRATCMFDRHGLLALLAGRFL AFVRTLLPTMAGISGLPNRRFQ FFNWLSGLLWVSVVTSFGYAL SMIPFVKRHEDQCRNGVFGKR KGGIAAAILTRLRRRFVSSWK RFRELRRKSSQADDMNVFGILE DFTHQFIGGAFLRADISGAAKM SCLAKAQASSSMH
25941	56309	A	26082	125	741	
25942	56310	A	26083	1066	1359	RLKRCSTGKSMVQIDIIAALW QHDFAAALADPHIVSVVYFVMF ATLFLNGLLPASFLPGDTLLIL AGALIAQGVMMFSGRLRIAVLDP RNQVRGGGLSIFKGRWLGPNK TVKG\WLAQLPAKYHQATCM FDRHGLLALLAGRFLAFVRTLL PTMAGISGLPNRRFQFFNWLSG LLWVSVVTSFGYALSMIPFVKR HEDQVMTFLMILPIALLTAGLL GTLFVVIKKKYCNA
25943	56311	A	26084	256	952	
25944	56312	B	26085	1	1290	

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25945	56313	A	26086	1	1839	MRCQNAWWMQHSSGSERLSS VLLHFRRTNLADSNDRIQYHSL RFFDEDEGAQWLVLGDLVNHG PRNALPDGYAPRKVAERLNEV AHKVIIVRGNLRQVRDQMILLI SRAINRLVASNNRRSAQMRC PISGKNLAWIPVQLPVYQNN CRRLLMRSHRKHGSGTNLPGE LMAIKLIAIDMDGTLTLLPDHTIS PAVKNAIAAARGVNVVLT GRPYAGVHNVLKELHMEQPGD YCITYNGALVQKAAD/GYDDY/ RF/LEKLSREVGSHFHALDRIT/ LYTANRDISYVTVHEFLRCHQ FPLVVCDDGGRMTPRAMFLSSA HILMPLNYHNSHINTLFPVAGT LMVEPTSESEKVELDRFIDAML AIRAEIDQVKAGVWPLEDNPLV NAPHIQSELVAEWAHPYSREVA VFPAALVTGSGRGIGRATALLL AQEGYTVAVNYQQNLHAAQE VMNLITQAGGKAFVLQADISDE NQVAMFTAIDQHDDEPLAALV NNAGILFTQCTVENLTAERINR VLTSTNVTYFLCCREAVKRMA LKNGSGGGAIVNVSSVASRLGS PGEYVDYAASKGAIDTLTTGLS LEVAQAQIRVNCVRPGFIYTEM HASGGEAWTRRSR
25946	56314	A	26087	2	1275	VNFSPKSSQIHHLRTVAGRFA VKSIDYFWHDSNASKRFHIWE SIMLELLFVIGYLVMLMVTGVS LLGIIAALVVATAIMFLGGMLA LMIKLLPWLLAISVVVVIKAI KAPKVPKYQRYDRWQLAVRRS PLLPDHTISPAVKNAIAAARAR GVNVVLTTRGPYAGVHNLYKE LHMEQPGDYCITYNGAL/VYRK AAGWLAPLAAKLLKLMDIELI GFLEKLSREVGSHFHALDRITL YTANRDISYVTVHESFVATIPLV FCEAEKMDPNTQFLKVMIMIDE PAILDQAIARIPQEVKEKYVVLK APNLQOPHSGSGSFHREIFFSS RSEDKRRGGLVVSIGSLVVSVA GPWVRNANEPLGQLKTWFSLS HTLTLTYTRAPACRLTSTQTEP RARPCLSPLSSEPRDRSLTPRLG QRFIYLA VQ
25947	56315	B	26088	1	1509	
25948	56316	A	26089	1	1323	

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25949	56317	B	26090	1	5073	
25950	56318	A	26091	249	531	CWAMRMDSKVGVTPIRMWSA SGPFAMGTLVPTFAAVTDIPTK SVTTCRLQICERWQAPSTR*SRF ASLSQAPRFTPSPIITLALVLLP ARRC
25951	56319	A	26092	3	1038	LVLFGVAETYPVANDFAAGAG AYVRGRYAAGVRAWPTIITRK TMKTLVVALGGNALLQRGEAL TAENQYRNIAASVPALARLARS YRLAIVHGNPQVGLLALQNL AWKEVEPYPLDVLVAESQGM GYMLAQLSAQPOMPPVTTVL TRIEVSPDDPAFLQPEKFIGPVY QPEEQEALAAAYGWQMKRDG KYLRRVVASPPQRKILDSEAIEL LLKEGHVVICSGGGGVPTVND GAGSESVIHKDLAAALLAEQIN ADGLVILTDADAVYENWGTPQ QRAIRHATPDELAPFAKADGSM GPNVTAVSGYVRSPVQMHHRQ FQPVIIHIATNQIDHHRJIIHHL
25952	56320	A	26093	1	3639	MKRLIVGISGASGAIYGVRLQ VL.RDVTDIETHLVMSQAARQT LSLETDFSLREVQALADVTHDA RDIAASISSGSFQTLGMVILPCSI KTLSGIVHSYTDGLLTRAADV LKERRPLVLCVRETPLHLGHLR LMTQAAEIGGNTGEIDEEEL LLYAIAGNVNFQITLHLPVA VQNDTIDFYQMFARIWSSHPQ WL.TLYLAQHRAVIIPDDAKLHR NLLRWYSAGRLDIPPELLDYAQS WRETEPDNEDAPY

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25953	56321	A	26094	1	1260	AWARQDRRLSVKQWGKPPVD ETIPAKEQVRILRKLFDRYYGE VAGRGDGFCSPHVARYVGRVA G*RPCRLGPGHPTNRTPFVAPL LEALDIKYSVSVIGDDVQNK KPHDPDLLVAERMGIAPQQML FVGDSRNDIQAAGAAGCPSVG LTYGNYGEAIDLSQPDVIYQSI NDLLPALGLPIAKIRNRKMTKPI VFSGAQPSGELTIGNYMGCTEA DRQFAFNFNFLIQLLTNGGP DRLGTTTPAGYTDLLVNYTYRI AFEGGGGQDFGLAAAIATLFL LVAIMFLLMVVAISLRQGNFA TGS�IPEQISWDHWKLAGFSV EQADGRITPPPPFVLLWLWNSV KVAGISAIGIVALSTTCAYAFAR MRFPKGKATLLKGMLIFQMFFA VLSLVALYALFAPRVRAALCY
25954	56322	A	26095	1	3240	
25955	56323	A	26096	494	792	ATRLRHGVTSVGGDGGGLQTV MDKLDVILLMSV/NPGFGGQSFI PQTLDKL/REVRRRIDESGDFIR L/EVDGGVKVNNIGEIAA/AGA DMFVAGSAIFDQPDAR
25956	56324	A	26097	1624	2390	RTSERRWHAKALLKLSAHHA GFVCKEERLATGKVGWLP VETLLAQQHIEGHYQVDPFLFK PNADCPVRVSGMSMKDIGIMD GDLLAVHKTDVVRNDPLLVP FTLIREGKLAANWPLEQDELLT RLQKSCDMTQVSADYNALFIG DECAVPPYRSAWVEGATEAEV RAFLSERGMPLADTPADHIGTL LLAASWLEDQSTEDSEAELET FKRGA/LPKSLCLWGKAPAPHG SPVGGFSKGPKTWAPHEGAS
25957	56325	B	26098	1	534	
25958	56326	A	26099	67	399	

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25959	56327	A	26100	8	1016	PESRRKAVMTQPVLDIQQLHLS FPGFNGDVHALNNVSLQINRGE IVGLVGESGSGKSVTAMLIMRL LPTGSYCVHRGQISLLGEDVLN AREKQLRQWRG/ARVAMIFQEP MTALNPTRRIALQMMDVIRHH QPISRREARAKAIDLLEEMQIPD AVEVMSRYPFELSGGMRQRVM IALAFSCEPQLIIADEPTTALDVT VQLQVLRLLKHKARASGTAVL FISHDMAVVSQCDSSVYVMYA GSVIESGVTADVIHHPHPYITIG LLQCAPEHGVPRQLLPAIPGT PNLTHLPDGCACFRDRCYAAGA QCENVPALTACGDNNQRGAC WYPQQEIVISV
25960	56328	A	26101	3	102	ISRLNTQHFQ*RTQISPHSPQ GCSRCLHS
25961	56329	A	26102	290	490	SSLNSCMAVWDKTRLIRQ*LV MWSY*SPSPCR*PAGYRHMKL RSTSLVLSTPSRLFLAVIPPVVVI
25962	56330	A	26103	1	3255	
25963	56331	A	26104	119	634	
25964	56332	A	26105	1640	1770	HLDSNRRVHDSTCNWCCNLS* QRLWSG*WSELCCSVPRQKR A

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25965	56333	A	26106	281	2108	RESLKQKVGGRPQLSPFPPPDS WALDPGGGRARETPRGVSNAT KEPISVAQHGN/GGDKEIRRELK YYAHLGRRLKDWSGIPRYHGT VETDCGTGYVYDVIADFQKGP SITLTEFAEQCRYEEDIAQLRQL LKQLKRYLQDNRIVTMSLKQP NILCHRISESEVIPVVCNIGEST LIPLATWSKWCCLRKQERLWK RFIAQPALAIALQKDLQPQATE ASGAENMASIASGNIARTDPDM LSIPLSKKICCGDRIIEIPETIDQ PVRFWVLTPGVVDMGIYACYL SSPQWGWY AERDAEINETVR REVEELRQASETDLPQGTIEYE RHRLTRAQADAQELKNARDSA EVVETAFCTFVLSRIAGEIASIL DGIPLSVQRRFPELENRHHVDFL KRDIHKAMNKAALDELIPGLL SEYNRADRQYAGGSRVAARFA ASPRVALSVITGLIPRHVCAPY LLCGDPCCLSTPDEMTPRFRRY AVRSGNRSTPGLDHRCDACQR SAYELADLCRPPPTLFLPEA DKNDFSDALPAVADAMYAAP RRKAAPSKPEKAVVSPRSVRK ARHGSVCSLRPDQYAVRNLP YRSCSPDLQFMVWCALA
25966	56334	A	26107	1	2880	
25967	56335	B	26108	61	5101	
25968	56336	A	26109	80	561	IRPLPPRFKTESRSLPGCLQPGT FLWSRNRVLGFPMSNGEDMG LLFLCSEWERSSEGWLNCNREGG SGHSIEPHCCTFLHLTHRSLAFS LLAGVSTCASSCKCKE/CKCTS CKKSECGAISRNGLWLKVGRR EPKAVPEVRASGEPAFLCPCRL SLPV
25969	56337	A	26110	1	277	
25970	56338	A	26111	902	1006	
25971	56339	A	26112	2	1265	
25972	56340	A	26113	409	525	
25973	56341	A	26114	91	431	NHKPGNIDVARRIQRGFAGDQI GHLRPVERQCSPKRRFIAADG REIRGKQRAGHIFQLSRCLLQI LNHCQRRAAHFRFQLSNQRHQ QLLPV/HYHAAEREYPAGACLV RWLL
25974	56342	A	26115	3	71	
25975	56343	A	26116	1	1212	

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25976	56344	A	26117	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVDIVWNATAAFIAVIII SLLLDSEGGFEWAALHVLRWG YGPGRLPFNRIQLIRITRRIRQR LLFGLVTFILLNRSQNPQADIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAADGTLD DFIVARETEGQSGLKRVIHSPG APDIREFTRDAIP
25977	56345	A	26118	5	402	EIFSVVVIIMTRGDVVVISRW VSSSPLETWNKRWAKISPAF LLPISRLKESGDWLPETVISAF NMPSSLSLISSL*FKVRDV*HFF /RI*TLRGHYRVINWPFNIVVS QGIGKRLANSWLVFRLFHRI
25978	56346	A	26119	48	219	PETCGHLWAYVWPSCAAVGL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25979	56347	A	26120	1	912	

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25980	56348	A	26121	1	1857	MRVCARACVTRTRMCVYAH TCVCVRYAYVRRVRVRHVR RVRVCAYARTRVRNSLSILPFIQ LTLATPIHHIQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLIRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPALLALFLCSTSPGF GDPDGLGVIAVYQDTRVRPNAAT AISELNALAVKGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIAGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTLDDRVRVAGSAGRYGGDGA GDSECVKIVAQEIRQTRDNIER DRSPRPSGERVRVRGKGGIEAN QPLSTAFNTQITIRQSIRLFSNQF VFHKGISRVVAGSSAHSNVSPG CILRTPNCRGFPISCTGEGKAA YGWQRDDGGHAEYLLAEKDLI LLPDALSYEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY* LPDVVY*IGVARVSWMNGRID SELRTVRVAYAHTRTRARTCTR TRTRTYAVVRTHTHVCAYTHM RVRVRTHARAHTR
25981	56349	A	26122	3	1180	SKLGTRRSVVWA*SPSTPTLW CSTFSAAGHSSMKRMNEFDL LPAQQRMKGENVYRGADAV TQNLDIIRRYKAEYVVLADHI YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIIEFVEKPANPPSPNDPSKS LASMGIVYFDADLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHPPFLSCVQSDPAEPYLAR CGYAGNFMESSEPRSGILRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRVPDPVELVLV AAEFITPGDPTRLHSGSFDIR QIIHQTRSHLEGVKTGIRFLNH FSGNPOGGIAHVNGVARFQVK QCHQAWGQQYAAARLRFQARGI SLQIAIHRVDIIHRFVRQL
25982	56350	A	26123	16	543	
25983	56351	A	26124	1	3387	

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25984	56352	A	26125	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTSPILALPSYSTTFFGVC TSASMNVPVLTLRIRTRVTEGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*ITTCANR*STSARGSL ERLIMATLL/VVAGTFD*SVWF GHDTDVVTLRYFHEALCYSVT LRTPHRRVLRFKSHQHPGELACFI SPVA
25985	56353	A	26126	905	4761	PPHNWMPNSATPGIAFVWCAY GAILPGDAPVPVDDYRKVVR KDTKGLIARWKYFWMVSIALG VAFALYLAGKDDPATQLVVPFF KDVMPQLGLFYILLA YFVIVGT GNAVNLTDGLDLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAALLRQEFLLVIM GGVFVVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25986	56354	A	26127	1056	1373	
25987	56355	A	26128	1	301	SSGTDAGRRYRPRQRPSPKSRNN RRVNRQAPQQSSRN/SLRPSTT SSPFSLPVAVKLPSP/V* LAEVRRVDSAISTVDSR* CPTAS SFSTGSTITVL
25988	56356	A	26129	362	595	
25989	56357	B	26130	1	1305	
25990	56358	A	26131	1	2022	MISKRSERSFGYGVGLVRRQDF SSSEGGFNLHSLRIDINKCLGVRI STATSTMGIVLPEQIKLACNGIQ RVALCGGDDYLTSDVSFDMVF CSRFGWQVRPSSFCSPVFTWVT ENQQLHHRGKDNLSLKNNSA CGAACGSLRGEKSDPPSARNNP SSQGGKKESGQPSLKDPHIL RHDSAHRPRKEKPRQPVNASLV VKFVRWKCVCVHNDHKRPACS VVCVDGDTYCWTEAYPAMGL PTLRGPDSALGERPE
25991	56359	A	26132	3	236	
25992	56360	B	26133	1	4638	
25993	56361	A	26134	1501	1914	SAFSRALTGROHFNNCAFTFRS NGAECLLYHVCQTAFVARRR VGAAVGFSGHIEIVPLHLLQPP LADLFVHVVARLSSTMGIRDQR PLPG*LLNNITRWRSSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
25994	56362	A	26135	561	698	

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25995	56363	B	26136	4	2040	
25996	56364	A	26137	804	947	LPCHCSCPWDGVDVQSPSTPRQ WT*GERLH*QSEALPGVCCAPG HGPL
25997	56365	A	26138	1	734	SVHIGHQFFQFQSTSLNICPPLH RLFIAPQMNIRRNAAARHAKFQ RLQAQVSIFEDDMSRKIANRQA TAMLNAPPEANIGIHNVPIGIF EAVIRQHFARLNAFFALLFR PFRLFCPPGINANQRSQVRQPQ LPRLDITFQFWSWLSGGVDQRT VDIVCHQWRSALDRKEYYPAE TTMPTALHSRLCIIVGKIKRPVI VLFREANQARVGLFE/H*STAA RPFWSAAPAGPALPLRVANAPS
25998	56366	A	26139	2	309	
25999	56367	A	26140	472	885	SAFSRALTGRQHFNCAFRFS NGAECLLYHVQCQTAFLVARRR VGAAVGFSSHIEIVIVPLHLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRSPVVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
26000	56368	A	26141	1	2469	
26001	56369	A	26142	1175	1435	
26002	56370	A	26143	218	443	AMARWKMLCTKSPPCVCLPGY P/G*RLAGPHHHHEFPPAGAAAS TGPPIVQDHQSLAGRSRRHDDS RHLGRCHHH
26003	56371	A	26144	1	2031	
26004	56372	A	26145	1419	1875	TFCSPRSQPSGLKRRRLRAGAGN CPLYSTGNGLQRAICCAQPT*L HGRVPSHVPAFTSSFQLWSFTV GACIHRSMYIISRSRCPDPKTK TATMLGITSFVMERCQLFILSRA FTSGQPTCYYPASSNTWFSST RHCQVINLHSNSMHISL
26005	56373	A	26146	218	441	AMARWKMLCTKSPPCVCLPGY P/G*RLAGPHHHHEFPPAGAAAS TGPPIVQDHQSLAGPRRHDDSR HLVRCHHH
26006	56374	A	26147	1196	1462	LNTLVVAVRDGLKMTTVIANN VTSVSVLKIARNVTRKTILPPAA AANVTYPWLIRTIC*KRRYD*K TRWYYAVAACLNCNMGTTRKA NG

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26007	56375	A	26148	45	443	APSPDKRDFPLPHGADSAMAE YDRCHRAVLSSGGQWPTALSA GDHAAAYSLHAALVQPERRCHG RCPVRNRLHAPVCPPIPG*RPAG SHHHHEFPPPARAASGPSIVQ DHQSLAGRSRRHDDPRHFGGC HHH
26008	56376	A	26149	581	957	TSWISFSRTTPSTVSPYSTVDAN GIIWSARNRLASVNNIASWLSFF SNPLYLAITKPNCLMMNRNGCS TPGPGCWLSCIRC*WAVCSCVD AASRFLPCRGARRSASPHPRQ APRRCGALW*PASAETNCSSPC SRLPS*LRGCCFKVLTLPGRSAI SQSTSTSASSSALWRPLVAGIG
26009	56377	B	26150	1	3924	
26010	56378	A	26151	597	856	
26011	56379	B	26152	1	2781	
26012	56380	A	26153	2809	2989	RCGYVRE*LAKSLQSNHFQWR MPQHQTAYCRS*AWYRHVAH ERLPAQTDNRHQHADRWNQ
26013	56381	B	26154	1	2802	
26014	56382	A	26155	4493	5470	IQRRNHRRDGWCLASLPGTGD HAGARAEAGSWHSGGPHRVR ARSVSTPFAPIVNTATSLKPRV QLLDAALKIDHRRTLPKYSFGT FRRWYRSVAAQQAQYKDQVA FFHGCNVNYPQLGQDLIKVL NAMGTGVQLLSKEKCCGVPLI ANGFTDKARKQAITNVEISIREA VGVKGIPVIATSSCTCFALRDEY PEVLNVNDKGLRDHIELANRW LWRKLEGGQTLPLKPMTLKVV YHTPCHME*MGWTLY/TLELLR NIPGLE/LTVLDSQ/CC/GIPPIRV VIHMFRIEESGADLVVTDCE CKWQIEMSTSLRCEHPITLLAQ ALA
26015	56383	A	26156	2467	3465	

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26016	56384	A	26157	5758	7019	LKEGLLEPLAVTERLAHRRWRP TMNDTSFENCICKTVCTTACPV SRVNPVPGPKQAGPDGERLRL KDGAlyDEALKYCINCKRCEV ACPSDVKIGDIIQRARAKYDIT RPSLRNFVLSHTDLMGSVSTPF APIVNTATSLKPVRLDALK IDHRRTLPKYSFGTFRRWYRSV AAQQAQYKQVAFHGFVNV YNHFPQLGKDLKVLNAMGTGV QLLSKEKCCGVPLIANGFTDK ARKQAITNVESIREAVGVKGIP VIATSTCTFALRDEYPEVLNV DNKGLRDHIELATRWLRKLD EGKTLPLKPLPLKVYYHTPCHM EKMGWTLTYTLELRNIPGLELT VLDSQCCGIAGTYGFKKENYPT SQAIGAPLFRQIEESGADLVTD CETCKWQIEMSTSLRCEHPITLL
26017	56385	B	26158	1	2247	
26018	56386	A	26159	882	2372	HAVHESPPCECRSNQQRPTRTCR TIIDIMEMYHALHVSWSNLQDQ QSIDERRVTLFGDAATEARYL GYVRFMVNVEGRYTHFDAGTH GFNAQTPMWEKYQRMNLNVWH ACPRFLFDLDGTLVDSLPAVER AWSNWARRHGLAPEEVLAFIH GKQAITSRLRHFMAGKSEADIAA EFTRLEHIEATETEGITALPGAIA LLSHLNKAASGVTNKGFLTVD EIRRVTRAFLRGTEKVRLTGG EPSLRDRDFTDIIAAVRENDAIRQ IAVTTNGYRLERDVASWRDAG LTGINVSVDSLDRQFHAITGQ DKFNQVMAGIDAAFEAGFEKV KVNTVLMRDVNHHQLDTFLN WQHPRPQLRFIELMETGEGSEL FRKHHSIGQVLRDELLRRGWIH QLRQRSDDGPAQVFCHPDYAGEI GLIMPYDKDFCATCNRLRVSS IGKLHLCLFGEGGVNLRDLLED DTQQQALEARISAAALREKKQTH FLHQNNTGITQNLISYIGG
26019	56387	A	26160	68	399	NKVKPRGDSV/PGSPHSRLLSP PPLPGLLLWR/PLEEPFSPPLHC GSPFLGWPRPGGRGLGG/PPHSE QPASLSLPPTPRAPVRPEPPRA PPAPRRPVPSITQGLRNASAP

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26020	56388	A	26161	207	479	PWSDGAGPLPSLPHPDGRG*SV NSPQVLL**GSGE/PRASDSPLP QLCGVSPHRPTWGSALWGGEQ CTSEMGETIDPPGPHTFSKNFCF ELQ
26021	56389	B	26162	1	453	
26022	56390	A	26163	1	379	
26023	56391	A	26164	1	1054	MFLQAAQKAWNPHLLLVRTQ AASTHGRRADPHVGRGCTETPQ SWGKGESLALAPLSLTKAALED CSQISPSHQGTLLCLLILDRLTG KLSLEHTEEPSDVPSHLLYRWSI SSAITEVFQALASSDSTSQPVNV IITKEDMKVQDIALVLPKRKR NACRTTTSTCKALLMRQLAAR VILQNCVSKSSRGHVPQKNLT LPVRGDSVLAGSPHSRSLSAPP LPGLPLWRHLKSPSAHRCVTGG PFLGWPRPEPAPSACREALAAF P/PGQSGSPAAR/QPEPPPPWA PVQPESPRQAPPPAPRSPVSTT QGLRSTGTKHRDWQAAPPAAP VRDPLGEASWAPESGGDVENL
26024	56392	A	26165	2	362	EMSRLYRSRDRD/GVCLQ/IEVK MVSRTANIDDSLIGGNASAEA PEGEGTESTVTGVDIVMNHHL QETSFTKEAYKKYIKDYMYSIK GKLEEQRPRDVKPFMTGAAEQI KHILANFKNYQ
26025	56393	A	26166	35	359	
26026	56394	A	26167	22	459	
26027	56395	B	26168	102	431	
26028	56396	A	26169	85	674	RRRLPSVAIMIILPGPSSSHDE MF/DSKIR/EAIDGVCAWKVE G/KMV/SRTE/GTID/DSLIGGNA SAERPRGAKGTERHQLITGV/DI VMTPHL/QETKFSQKEASKYI K/DYMYSIKRET*KNRRPEKSK TFL*PGA AEQIKHILANFKNYQ FFIGENMNP/DGMVALLDYP*D WVVTYPMIFF*GWV*KWEKC
26029	56397	A	26170	1	1640	
26030	56398	A	26171	1	1527	

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26031	56399	A	26172	61	2560	PGFCHPRKAYSSYGQRSGQSK MKASSGRGCLVRWLQVLLPFL LSLFPALPVQIRYSIPEELAKN SVVGNLAKDLGLSVRDLPAK LRVSAEKEYFTVNPESGDLVLS DRIDREQICGKQPLCVLDFDTV AENPLNIFYIAVIVQDINDNTPL FKQTKINLKIGESTKPGTTFPLD PALDSVGPNSLQRYHLNDNE YFDLAEKQTPDGRKYPELILKH SLDREHSLHQLVLTAVDGGDP PQSGTTQIRIKVTDANDNPPVFS QDVYRVTLREDVPPGFFVLQVT ATDRDEGINAEITYSFHNVDEQ VKHFFNLNEKTGETTKDDLDF EIASSTYLSEAKDPGDAAHCS IQVEILDDNDCAPEVIVTSVSTP LPEDSPPGTVIALIKTRDRDSGE NGEVYCVLGNAKFILKSSSKN YYKLVTGDGALDREEIPEYNLTI TATDGGKPLSSIIIVTLHISDV NDNAPVFQQTSYMVHVAENNP PGASIAQISASDPDLGPSGQVSY SIVASDLKPREILSYVSVSAQSG VVFAQRAFDHEQLRAFELTLQ ARDQGSFALSANVSLRVLVGD LNDNAPRVLPALGPDGSALFD MVPRAAEPGYLVTKVVAVDA DSGHNAWLSYHVLQASEPGLF SLGLRTGEVRTARALGDRDAA RQRLLVAVRDGGQPPLSATATL HLIFADSLQEVLPDLSDRRREPSD
26032	56400	A	26179	47	325	ATMRLSVCLLLTLALCCYRA NAVVCQALGSEITGFLLAGKPV FKVQLAQFKAPVEAVASNMEA INCVDTMAYEKRVLITKTLGKI AEKCDR
26033	56401	A	26180	1	3747	
26034	56402	A	26181	2776	2874	
26035	56403	A	26182	89	369	
26036	56404	A	26183	382	555	
26037	56405	A	26184	2	67	
26038	56406	B	26185	1	444	
26039	56407	A	26186	1129	1275	
26040	56408	A	26187	61	313	WIPHQGYRWSCLPVPRCALAFL SPWVVDGTGHRGAGGGAGWG GFGRTGAHGIVGSGSGMAGCR SRAHSGGVGMTMTWQIPEVP

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26041	56409	A	26188	61	433	WIPHRGCRWWSCLPVPRGALAF SPRVVSGTGRRGAEGGARRGG SGRTGAHGVGGRLRHGGLQVP SLAPREGSCTCGGSGSAREEQ NLGFPREPRSGGGARGSDGICG MRVMFRKWILFCPSRR
26042	56410	A	26189	297	599	
26043	56411	A	26190	370	585	
26044	56412	A	26191	222	799	
26045	56413	A	26192	346	634	
26046	56414	B	26193	206	955	
26047	56415	A	26194	281	549	
26048	56416	A	26195	1981	2337	
26049	56417	A	26196	267	770	TRVDMIHVGLRKGPGETPS*SL RSFRAGQGTGASRARGLTLLSSH SSALRKGSPPKHFTCLCWQTF LAWCVWVAFSPSRCTQTFDLGK STQWTLLEILTDPKSHLFSRKQ PQARAPAVFPAPLKGCHVGAR GSHCCQFGQCFRPSVAPLILGT DGFSLLEKLWTFKTC
26050	56418	A	26197	165	374	RVTVQWL*YLRPRMP*N*PRPR SGKPFIDSTHSSHR*RQRNAVSL FSPVMSALRRCSVHRRLPDGGV VA
26051	56419	A	26198	357	981	HWRGDVLRSHRRTALQSRYF CGIYRSP/YKAR/MQIQFFDPQQ MEAAQKRLTEESDILNALENHQ FAIWLPQVEMTSGLRGISKQ LVGFTNRQNGATKLLVQYFTH RQIDCAGTADQPNPAGKVDDC GVTGNVTDROQKQKHGQAKE NELQNAACAFQRAECHKQRKYA PQTQVDTKELCIWRIGQTQFRH QQNRNRQAERTNHFQVR
26052	56420	A	26199	1	2601	

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26053	56421	A	26200	1	1236	MGPGLDLPRLATFWTELGLLS WARELARMPAVEMPPRSCPGR SRLSCSIGVAMFYGDLTAEQLY SRAISAAFTARHKGKNQIQFFD PQQMEAAQKRLTEESDILNALE NHQFAIWLPQVEMTSGKLP KSAAILPLSVNLSALQLMHPN MVADMLELLTRYRIQPTLILE VTESRRIDDPHAAVAAILRPLRN AGVRVALDDFGMGYAGLRQL QHMKS L VRLTKSEVSSETDQDE LPLAKVSEVDEAKRQWLQGM HPVDVTVEPEPAEILAEFIRQHS AAGQLVARAVFLSPPYLVAEEE LSVLLESIKQNGDYADIACTG SKDDYYSTQAMSENYAAMSL QVVEQDIFSPIAHAVRFECQTY PRPYKVAMLMQAPYYFQEAQI EAAIAAMDVAPEYADIRQGIVG
26054	56422	A	26201	1	1161	
26055	56423	A	26202	1	1038	
26056	56424	A	26203	1	1472	MVRLCIRLPVYAKVVDKNAL SLWMRERSDLWVQPKVDGVA VTLVYRDGKLNKAISRGNGLK GEDWTQKVSLSIAVPQTVSGL ANSTLQGEIFLQREGHIQQQMG GINARAKVAGLMMRQDSDTL NSLGVFVWAWPDGPQLMSDRL KELATAGFTLTQTYTRAVKNA DEVARVRNEWWKAELPFVTD GVVVRAAKEPRIPPLATGPGRV AGGLEISTCSSGCRSEGNEPGKI SVVASLAPVMLDDKKVQVRNI GSVRRWQEWDIAPGDQILVSL AGQGIPRIDDVCPSPAILSDIVP SW/VTITQW/LKKRAVSSRMK NQ/VKKGSETGYFDKDEARFQK EGFRVVPAAALRQGAFIARNT LRPSYVNI GAYVDEGTMVDTW ATVGSQAQIGKNVHLSAGVGIG GVLEPLQANPTIIEDNCFIGARS EVVEGVIVEEGSVISMGGVIGQ STRJYDRETGEIHYGRVP/AGKV DAKTRGKVGINELLRTID
26057	56425	A	26204	240	455	RLHPYPYRGWIFEVVPVISMGV YNGQSTRIYDR/ETGEIHYGRVP AGSVVVS/KVDAKTRGKVGINE LLRTID

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26058	56426	A	26205	197	1043	YEKSLTMQQLQNIETAFERRA EITPANADTVTREA VNQVIAL DSGALRVAEKIDGGVWVTHQWL KKA VLLSFRINDNQVIEGAESR YFDKVPMPKFADYDEARFQKEG FRVVPAAVVRQGAFIARNTVL MPSYVNI GAYVDEGTMVDVTW ATVGSQAQIGKNVILSGGVGI GGVLEPLQANPTIIEDNCFIGAR SEVVEGVIVEEGSVISMGVYIG QSTRIYDRETGEIHYGRVPAGS VVVSGNLPSKDGKYSLYCAVIV KKVDAKTRGKVGINELLRTID
26059	56427	A	26206	1	406	MGKKNWNTLGEVGCSCRMFL PDANTLAKNSACSAASAVQAA DRPDSQEA EALEHMAHSRCAL RCQTLVIVHSLMRVSWYHSLVI IVVPLTEPLESLVRCRLRSRRD DVPVAPAVSATPRREPISVLRIA ERTNA
26060	56428	A	26207	1	2574	MWAFRGKRPVTLKILHVPITNL RKNTSTRGLTKESSQGLVRA QEEYTPAREIAKMG/GNPCRPG GIVFAGER*DVTSPPYV*TSRGL TKESSQGLVRAQEEYTPAREI AKMGWQSLPARRYCLCWRKIR RYITLRLNIAYAGGYKAPVEDI ALWMETDGACDHVDFWTNIPS KCQGPMDIVSRPVFWAHGIV LFAGARNLNPTRLTRIPPYLWLL TLRTGYAAAGMQALALDSRGS PDVVVLSTQHSSEIDQ
26061	56429	A	26208	1	3771	
26062	56430	A	26209	239	451	LPPTAWMSTTNLTSA MLSVRG NVPMTLPARRRVNLPSSLICTCF HKPA*RI SMPKPWW*KARIISGN STS
26063	56431	A	26210	1	2079	
26064	56432	A	26211	1573	2562	
26065	56433	A	26212	275	643	SSRTALFTGSAVPGCAPPSSGRSL FPQCLQSKLARSFPICRSRGAA ILFRRLSFSPTLILEDRIVKRF MRENSRGPQVPAGLPMTTEEQL KKLGGRLRALGKMPGEEES VLRIAERTNA

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26066	56434	A	26213	1	899	MGRTRRRDAAQAPGTRRSODS RGYPYVTRPEGTDADDPQKDK AALGSHRVAGQPELFSIDELTR RDPHSASGAWTARYTVSTIAAF ALVIANRLYTIEEEATTPSGCGP ASSSTSSRGVDMCLRLNLCMHG YDATIPLTLIAADSMDEYNKPD LSHVISQQRADDLTRQTAGEF AEQFNHLHFPQTWVTDIDAEAR VVKSQNNQWQYDKLVLATGA SAFVPPVPGREMLMLNSQQEY RACETQLRDARRVLIVGGGLIG SELAMDFCRAGKAVTLIDNAA SILASLMPPEVSSRLQHRLTEM GVHLLLSQLQGLEKTDSGIQA TLDRQRNIEVDVIAATGLRPE TALARRAGLTINRGVCVDSYLQ TSNTDIYALGDCAEINGQRD*SS ARRVVPGRFPGAVRWQLPHP LRYCAGGPALPECQNPFPPAPV TEISTADERPSPTDAAASGCLLP VALTTPEYWQRCRLA
26067	56435	A	26214	1	1264	MDYMPVPGMDWLCRETAGM RVSIGKSSVFPNPELVMKVV RQRSTIVTPSGFKAGAFNFERFK EASNQTLGSTFLYSLCPKNL GSQPLDFDTKKSYTLKVEAAN VHIDPRFSGRGPFKDATATVKIV VEDADEPPVFSSPTYLLEVHEN AALNSVIGQVTARDPDITSSPIR LYRIPGDDAKCVQFNREGVKA LKAKPVEKAAPAPAAAAAPKAA PTPAKPMGEQLALYRMAGSNA DRIQGRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPMTRTKELAEV VAAATPVKDKFKHPATRTFQA VRIWVNSELEKIEQALKSSLNV LAPGGRLSIISFHSLEDRIVRKF MRENSRGPQVPAAGLPMTEEQ KKLGGRLRALGKLMPEEE/S VLRIARTNA
26068	56436	B	26215	64	663	
26069	56437	A	26216	27	791	
26070	56438	B	26217	1	1638	
26071	56439	A	26218	1	375	STKKQRGEIHHPDGHGIAQDRH LPRTSVDQRLRQTNNHAGL*Q ANG*GVFKRCRAHSATT**KDD E*NESAENAA*GGKVEGTDVT GDLLHENPAITPDKCEHNQATD CQWVALSCGRHERSSV

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26072	56440	A	26219	213	407	TTCCCTNL SIPLANKYRSLSPQS DWRLSMPR*NRVYVQKAPARAN KTSPMKAPPANIALGVNVAR
26073	56441	A	26220	1	1179	
26074	56442	A	26221	176	569	WPMRHTFSEAHAAQRAGGKNP GHDTADYATNAVHTEDIAGIHH PQQA FEHGNAPQARQTSYHAD NQRAANPNVAAGWRHADQGTG NRARTRPQQ*RLTTQRPFTEDP AKNCRRRCDHSIHKCCQCRDFIR RAR
26075	56443	A	26222	1442	2309	
26076	56444	A	26223	155	2929	HLHWVFVSGWFTVTRLAFGEG NNFFGNINWMLKNIETAYVM GSIYQYIHVAFQGSFACITVGLI VGALAEIRIRFSAVLIFVVVWLT LSYPIAHMVWGGGLLASHGAL DFAGGTVVHINAAIAGLVGAY LIGKR VFGKEAFKPHNLP MVF TGTAILYIGWFGFNAGSAGTAN EIAALAFVNTVVATAAAILGWI FGEWALRGKPSLLGACSGAIAG LVGVTPACGYIGVGGALIGVV AGLAGLWGVTMLNAC
26077	56445	A	26224	2	1064	
26078	56446	A	26225	1849	2515	MEGHLWIRIDLSQSAVSHSVKE LENHTGVRLDRITREVVLTLD AGQQLALRLERLLDELNSTLRD TGRMGQQLSGKVRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQVVMESIRQGDVDFGIVI DPGPVGDLQCEAILSEPFLLCH RDSALAVEDYVPALPLPEGSP VVKRITPVVERQLMLVRRKNR SLSTAAEALWDVVRDQGNAL MAAA

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26079	56447	A	26226	102	1655	RKQMNYSLKQLKVFVTVAQEK SFSRAGERIGLSQSAV\SHSVKE LENHTGVRLLDRTTRAVVLT AGQPLALRLERLLDELNSTLRD TGRMGQQLSGKIVRVAASQTIS AHLIPQICIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIVI DPGPVGDQLQCEAILSEPPFLLCH RDSALAVEDYVPWQALQGAKL VLQDYASGSRPLIDAAALRNGI QANIVQEIGHPATLFFMVAAGI GISILPALALPLPEGSPLVVKRIT PVVERQLMLINVIQTLRF AFIFR LSRRQHFAKVTPLLHRHGDYF VFIFGFDYGTANCSVAVMRDGK PHLLKMENDSTLLPSMLCAPTR EACGRVDVIEVSKSKVRKNTY AMRYVAGQPAERILPPGSFASI GQALPPGEPLSTEERIRILVWNI YKQRAEWL SVLKNYGKDAH LVLLQEAQTTPELVQFATANYL AADHVPAPVLPQHTSGVMTLS AAHPVYCCPLRERKPIRLAKS ALVTVPYPIFYLSNS
26080	56448	A	26227	159	290	
26081	56449	A	26228	562	774	VLRMIT*SKSQFAQDMCRNVLL INNFGRIQHDP AIFHFQORNEAVP LWTVSAQEVKKDFTSGLRHGS VRGDL
26082	56450	A	26229	50	409	GYASQALILASIP AASRPSSARIS S*VPCGIKKSGRPFMFSTGTGLR WAISTSFTPLPAPPIMAFSSTVTS ASWLA AISRINASSSGFTKRIST SVAFSDSATFAASSTNSRNAPP VEM
26083	56451	A	26230	405	626	
26084	56452	A	26231	1	1528	
26085	56453	B	26232	1	1755	

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26086	56454	A	26233	152	2099	GNRLLVVSFIASFKNSTHFKGIF AMRIILLGAPGAGKGTQAQFIM EKYGIPQISTGDMRLRAAVKSGS ELGKQAKDIMDAGKLVTDELV IALVKERIAQEDCRNGFLLDGF PRTIPQADAMKEAGINGHYVLE FDVPDELJVDRIVGRRVHAPSG RVYHVKFNPPKVEGKDDVTGE ELTRKDDQEEVTRKRLVEYH QMTAPLIGYYSKEAEAGNTKY AKVDGTKPQIYRGS LYSDQIG HTIVNPDGVVDCGRYGCLET VASLSALKKQARVWLKSPVS TQLDPEKLTAAQLIAAWQSGEP WITSWVDRSANAIGLSLYNFLN ILNINQIWLYGRSCAFGENWLN THIRQTGFNPFDRDEGPSVKATQ IGFGQLSRAQQGVLDGNMIITS GQIPVNPKTGEVPADVAQAAR QSLDNVKAIVEAAGLKVGDIV KTTVFVKDLNDFAPVNATYEA FFTEHNATFPARSCVEVARLPK DVKIEIAIAMLYTYGHHNDAP SAVRYPRGNASGVLETPLEKLP IGKGIVKRRGEKLAILNFGTLM PEAAKVAESLNATLVDMRFVK PLDEALILEMAASHEALVTVEE NAIMGAGSGVNEVMAHRKP VPVLNIGLPDFFIPQGTQEEMRA ELGLDAAGMEAKIKAWLA
26087	56455	A	26234	935	1020	
26088	56456	A	26235	145	373	

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26089	56457	A	26236	530	1865	RGNKRLDLMFKQSHASMYIKQ PEQLDYQLNLKEVITAVFISMV VLNISPSTLY/PDKPSPKDKYVAY AINIPDYELAADVYNINVTSPSG QQETFKILINLEHLRQTLERKSL TAVQKSQCEITPKKPGEAILHA FNATYQQIRENMSEFARCHYG YIQIPPVTTFRADGPETPEEEKG YWFHAYQPEDLCTIHNPMDGL QDFIALVKDAKKFGVDIIPDYTF NFMGIGGGGKNDLDYPSADIRA KISKDIEDPVTKERKQIHPEDIH LTAKDFEASKDNISKDEWENLH ALKEKRLNGMPKTTPKSDQVI MLQNQYVREMRKYGVRGLRY DAAKHSKHEQIERSITPPLKNY NERVHNTNLFNPKYHKKAVM NYMEYLVTCQLDEQQMSSLLY ERDDLSAIDFSLLMKTIKAFSFG GDLQTLASKPGSTISSIPSERRILI
26090	56458	A	26237	14	2031	LIVLS*QHG/DLRQNRSGAEHFG LQRLMLHASQLSLTHPFTGEPL TIHAGLDDTWMQALSQFGWRG LLPENERVEFSAPSGQDGDPTL GLIKEVACELSGMMRRSQPWE EAEESIPDRGESLLEVSGTPNAG WGAEGLAEREALLCCCCGPM GPDPLGLGSPGSGVRGRSRLIHH AISGEALWEVTSEGLDMAAAR QFAIEKGAPALRAMTFIERAAM LKAVAKHLLSEKERFYALSAQT GATRADS WVDIEGGIGTLFTYA SLGSRLEPDDTLWPEDELIPLSK EGGFAARHLLTSKSGVAVHINA FNFPWGMLEKLAPTWVGRNA SHHQTSYRDGPLTQAMEFEDK AQQRDVETARHFTFFRIANED KKTGFPRFQTIVITASHKTIDRT RYTYGAWRCYRPLLTVEEYRA TGSLITQPKFPPHKSSEVHRVPR NQGRFVAVNSTLPTEPATVAPV RNGNASRDTAKTQTAERPSTTR PARQQA VIEPKKQATVKTEPK PVAQTPKRTEPAAPVASTKAPA ATSTPAPKETATTPVQTASPA QTTATPAAGAKTAGNVGSLKS APSSHYTLQLSSSNYDNLNGW AKKENLKNVYVYETTRNGQP WYVLVSGVYASKEEAKAVST LPADVQAKNPWAKPLRQRHRD LRGDERRDDRRSEYFNQOVIS

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26091	56459	A	26238	732	1025	HEAKRTGRSYWFTAV*WLRG WRRMVARQNAKNCWHGTFFR VARVSLPISAHASSTHLSGSAH YVPPSA YRNSRRYSRGLCRCRV SSCDAATGVVVVQ
26092	56460	A	26239	1905	3087	RVCSCDAGTLHWLQNLRCGLP VWCDGSGGTSGDPQQRGSEC TG*QSRSQ*MRPVQPS*RRPGV YGGLPDS\WLICVDRNKLEQLT PEKRRQAKLRAMKPDEFAQIQ QAVITQMLQHPQTLGEEASKLS KDFDRGNMRFDSRDKIYAQIKL VTPQKLADFFHQAVVEPQGM ILSQISGSQNGKAEYVHPEGWK VWENVSA LQQT MPLMSEKNEQ NL YDCGALFAPVTWTS GSAAF PRPLTVEELLVVTTEAA TAE RGRIRSN IHELRIACLRETTDNP LYERLLEEIDDKAQAQWLLL AERQMDEAAVFTIHSFCQRM NLNTNECCFQRTTKTIHRDSFK STPRAAKSCSGLLPALAPSQISS NTPIQLSRFKFSGVTSPTSAAAS
26093	56461	A	26240	1	2235	
26094	56462	A	26241	166	416	CHVVGPFRRVRRNLISAQHPLTL NSRHHTTTAARRLLRYFGTPR YRHSIDIHMLQDMTTSRSLSSL RDQLHCRWLLPAERQAI

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26095	56463	A	26242	1	2084	MLFPLATSGAMEPPFFLAGTAG ALVGGGLQNGISGVLASLSAML QTGGQPGVVDNLNGIVDRAVLA AAGDADVASGAARLSARHRSI VISSMGERCCFIRSRITRICGHWI CPQGNEIPVVAVASHDTASAVI ASPLNGSRAAYLSSGTWSLMG FESQTPFTNDTALAANITNEGG AEGRYRVLKNIMGLWLLQRLV QEQQINDLPALISATQALPACRF IINPNDDRFINPETMCSEIQAAC RETAQPIPEDAELARCIFDSLA LLYADVLHELAQLRGEDFSQL HIVGGGCQNTLLNQLCADACGI RVIAGPVEASTLGNIGQLMTLD ELNNVDDFRQVVSTANLTTFT PNPDNSLYTTDKGALRMTTQL EQAWELAKQRFAAVGIDVEEA LRQLDRLPVMHWCWGDDVSG FENPEGSLTGGIQTGNYPGKR VMPVSYVPIWNSTLSLGSNWF NRKALGSPARYDVLPKWWRN VVKPTRTRYIGIAFYKVGEP KIEPDWMINGGVPELKKQLDL NDAVPEISGTLFREDYRNKPQT QQAADPPIRAKAAEIAVAHAH YLSIEFYRIVRIDPHAEFLSNEQ VERQLKSAMERWIINVLSAQIR PQPAVTHYRGLATVEMPVATG RYPTRYVGLVEPKTGRKHQ LRRHLAHLRHPIGDSKHGDLR QNRSGAEHFLGQRMER
26096	56464	A	26243	1	2871	
26097	56465	A	26244	690	824	
26098	56466	A	26245	950	1484	

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26099	56467	A	26246	1	2625	MVAFYRHAGRMWPGIALSCSL GNIAASILLFSTSSLNMTWTTINI VEAVVGAVLLRKLPLWYNPLQ NLADWLRLALGANSAGVNIS TATVCRQCEDAPCANVCPNGAI SRDKGFVHVQMERCIGCKTCV VACPYGAMEVVRPVIRNSGA GLNVRADKAEANKCDLGNHRE DGPACMAACPTHALICVDRNK LEQLSAEKRRRIPGNIRIRSGR YRRPVTAGCDVVSGRAGYAI HDGNNNSMAKNTSCGVQLRIJ GKVGQVGRPFVWLAQQLSH GSRMRDGTCLNKYDEYSRSGS MQYNPLGKTDLRVRLCLGCM TFGEPRGNHAWTLPEESSRPII KRALEGGINFDTANSYSDGSS EEIVGRALRDFARREDVVVATK VFHRVGDLEGLSRAQILRSIDD SLRRLGMDYVDILQIHRWDYN TPIEETLEALNDVVKAGKARYI GASSMHASQFAQALELQKHG WAQFVKSDENDAPDRQSGSTG SQCKNCGADTEPQVAAGPGLS ELNPVHCPHLHYRAHFRADRH SVACSLDTPVTGHQVAPTYRQ QVPRAGQVHDPSKHTRMPCEN IDPVRTIIRISDPPVPASATLGA SKASRIRPRRSHIPEITAKSRKP GGQPKWQVICWLDREKVVV MQTVRDOIQGHVFTAHRLDRP TSGVLLMGLSSEAGRLLAQQFE
26100	56468	A	26247	1	1833	
26101	56469	A	26248	1	517	MRNKL SFDLQLSARKAAIAERI AAHKIARSKVSVFLMAMSAGV FMAIGFTFYLSVIADAPSSQALT HLVGGLCFTLGFILLAVCGTSLF TSSVMTVMMAKSRGVISWRTWL INALLVACGNLAGIACFSLLIWF SGLVMSENAMWGVAVYTAPR AKCIIHLLNLSASALCAI
26102	56470	A	26249	3117	3527	EA VHLRLARYRDAPRRS**SPLL CASVYP*LEQVPLQAQAVVPLR VLQAGKPVVPVAVLNAQAAAL ARPVAKLAAATAVQAAADRQ AAAPALDAEHVAAPALQAA AGPVDAAAQTHKAVGTGVAA TDEQHPAPER

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26103	56471	A	26250	2	563	STTSITAFSATTAGTPTSGNTP SASPIWRRPNFWARKVYLLHW FCHRQPSKEVLFHLALYRNNPR CKAVVHLHSTWSTALSLQGL DSSNVIRPFTPYVVMRMGNVPL VPYYRPGDKRIAQDLAERETH/ NHAFLLANHGPPVCGESLQEA ANNMEELEETAKLIFILGDRPIR YLTAGEIAELRS
26104	56472	A	26251	2	1481	PENQINKLKQAIPADYRSHQKC VNQPSPTITPRLFAITVITDERG YATGSAGNLSL/LLPDGNLLAT PT/GSCLGN/LDPQRFKVAADG EWL/SGDKPSK/EVLFHLALYR/ NNPRCKAVVHL/HSTWST/AL.S CLQGLDSSNVIRPF/TPYVVMR MGNVPLDLAELAA/DNQAFL ANHGPPVCGE/SLQEAANNME ELEETAK/LIFILGDRPIRYLTAG VCP/LAKMLNGTGQYLSIKRCT NNRSVRGTCSAPRAGPKGYGL MMMIDVLSASYSAYRSGDRTL LYSYHRASACADSTTLTVLISY TFHLVNSYSTVPPLESGTQPA SPSFPTRVSDDHNRDFFLLSPC GLLQNLAQCIQVGIQLDFGCV IISAQTETDGPLVCGRFEEGTPF SPQTPRDCDPNRSYSGNTQGVR GATSSPGSAISFEQTVNARSHVL RVTLTLGLTRPMLVYTGSLKWI NICILPISLKPLRYIHLAAQFPT APISLGRSLHVVVPHEEVAM
26105	56473	A	26252	1	413	
26106	56474	A	26253	3	247	
26107	56475	A	26254	300	665	
26108	56476	A	26255	1	1854	
26109	56477	A	26256	1	1611	
26110	56478	A	26257	942	1040	

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26111	56479	A	26258	1616	3678	PLAKTGRQREQLAGLAK/AHPS LTLHQDPVYVTRADAPVAGKV ALLSGGGTEHEPMHCGYIGQG MLSGACPGEIFTSPTPKIFECA MQVDGGEGVLLIHKNYTGDIIN FETATELHDSGVKVTIVVIDD DVAVKDSLTYTAGRRGVANTVL IEKLVGAAERGDSDLACAEELG RKLNNQGHSGIALGACTVRSR GKPSFTLADNEMFEGVGIHAIL KGDIPAEAILASIKPAGVVSRA DVLVLPNQFQALRKSFIPERPVP VMVIRLFELPVQISLGVYSLER PANPQPIAYLVLPQRRKANNQN ASTSAIIRATIGEPISCSVPSRGC EGGISVAETVPAMIIAIGITISEG LDARYRHVNSEHDPDRQAKF EWRYFGNLGKTVNDWRKNNK ADIKEDGNRRCRHTNQPHCRIE AVEYDDGRLCPLHGAHRGQSS DGELVKPTVKQSLAVHYSIGK LRHRPNHGAVVYQRLRSGMGL MNAFDSQTEDSSPAIGNRLRSR LARKKLESEMVEEELEQMIRRE FGEQEQLPSERELMAFFNVGRL RAGSVKTRQSGANKQRRTRCV SRPSADTIIGELSGMAKDFLSHP GGIAHFEQLRFFESSLVRYAA EHATDSRDPYRYPKFYSISRVP VSDNITLQQLLSLNDQPARCK PSARCRLHGSHTSRYEENHRHG
26112	56480	A	26259	185	775	IPEIFSGETHLKVSTLSKPTFSISS LIRCTTRFSSQLSLGIATMSHRK RVISALKSLRSLANSLSVFANQ VERSSLTNLGCTRCSG*SLFWQ RPALR*PFGLCPTVALTLYLVSP EW*KAVSVKCRNRRLTLMTS PICTNSGTLTTAPVDRVAQVTF QSPECLQHMRLTIALRYFRVAL SRLLLVYASVCFTFSG

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26113	56481	A	26260	301	1313	RLEHDDGVCLHRANHRYPGCRLLHI.DYVEPQLQHDDALRAAVMMFKQYLQVTKPGIIFGNLISVIGILLASKGSIDYPLVIYTLVGVS LVVASGCVFNYYIDRIDRKMERTKNRVLVKGLISPAVSLVYATLLGIAGFMLLWFGANPLACWL GVMGFVVYVGVYSLYMKRHS VYGTLIGSLSGAAPVIGYCAV TGEFDSNAAILLAIFSLWQMPH SYAIAIFRFKDYQAANIPVLPVV KGISVAKNHITLYIAFAVATLMLSLGGYAGYKYLVAASVSWWGLMALRGYKVADDRJWAA QSCSGFSIIPITALSVMMSVDFMVPDSHTLLAAVW
26114	56482	A	26261	3631	4078	CFLNFKTLLLVHLFRVRFLRRLRHRKLHPVGLGGPVNKAAYAFCLGAMANGVYGPYAFASVKMVS AFTVTASTMLAPRWLLGLA GITEGAIPMAIEDPLRVIGSFVL GSMVTGAIVGAMNINRTRLRVEASVTSAQIVQTIIRLRR
26115	56483	A	26262	814	2126	CTGCRKQRLPVVQGFAGLAA NMIGSGFLGAVVGGIAGYLMRWVKNHLRLSSKFNGFLTFTLYPVLGTLGAGSLMLFVVGEPVAWINNSLTAWNLGSLGSNALLGAILGFMCSEFDLGGPVNKAA YAFCLGAMANGVYGPYAFASVKMVS AFTVTASTMLAPRLFK EFEIETGESTLLGLADITEGAIPMAIEDPLRVIGSFVLGSMVTGAIVGAMNIGLSTPGAGIFSLFLLHDNGAGGVMAAIGWFGAALVGA AISEGKRIFRYRDLIIVNSNQLFLHDHFRFPRWEGLESVFLLAA FQQDVGIVPPLGAMLGLATAVVLGFLLYWGGIRLNLGAFFKW TSLFILFVAAGLAAGAIRAFHEA GLWNHFQEIADFMSAVLSTHSLFGTLMGIFGYQEAPSVSEVAV WFIYILPALVAFALPPRAGATAS
26116	56484	A	26263	1	525	
26117	56485	A	26264	1	700	
26118	56486	A	26265	1	1428	
26119	56487	A	26266	254	475	RDQLVSELNQMLV*KSAFRMALITSRWPMVTHWFREVRRGNWRQFLPALTLVRLSLMLMGRQAILRSRRNY

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26120	56488	A	26267	1	1657	MLIQRRRLAFDRAKHRRRAEML AQRARGEEEAHHHSSPEGAIEV DESEVDLDAISAQSLRLVRSILM LIALLSVIVLWSEHSAGFLENI SLWDVTSTVQGVESLEPITLGA VLIAILVFHTTQLVRNLPALLEL AILQHLDLTPGTGYAITTITKYL LMLIGGLVGFSMIGIEWSKLQW LVAALGVGLGFGLEIFANFIS GLIILFEKPIRGDTVITRDLTGS VTKINTRCHTHRRQQLLQQA ATSSADVIYLGAEVCSKRRATK VGDWLEMAKSLAGSGKQIVLS TLALVQASSELGELKRYVENGE FLIEASDLGVVNMCAERKLPFV AGHALNCYNAPLKILLKQGM MRWCMPVELSRAWLVNLLNQ CDELGIRNQFEVEVLSYGHLLPL AYSARCFARSEDPRPKDECETC CIKYPNGRNVLSQENQVVFVFN GIQTMISGYVYVNLGNELASMQG LVDVVRSLSPQGTDTFAMLDAP RVNENGAAPLPLTANSDCNGY WRRLAGLSLRQIKTCLIFLLCQP RGRRPYRTRAMPPLTMPANSP
26121	56489	A	26268	482	605	
26122	56490	A	26269	1	298	MWPGMVTHAVRIPLHNDTVTL SDNFQPFAGTDAMTITRPLEML RDGKCPQPDWISSEGACAGNA TDSPPHFELKAGKTITLEDGRQI NGADYLAAPVPGKALAIIFGDT GPCDAALDLAKGVDMVVEHA TLIDITMEAKANSRGHSSTRQAA TRESELFRYTVKHSILFASVIGII TLLQASTKIYTPGRKEQGEPM PRRTPARF*IKSGQNNHAGRWK AD*RRRLSCSSAR

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26123	56491	A	26270	1	1707	MTRDGLANKALAVARTLADSP EIRQGLQKKPQESGIAIAEAVR KRNDLLFVVTDMQSLRYSHPE AQRIGQPFKGGDILKALNGEEN VAINRGFLAQALRVFTPIYDEN HKQIGVINDSRWSIHSVLFMG LVGLIGTCLVKVKKILFGLPE YEISTLFEQRQAMLQSIKEGVV AVDDRGEVTLINDAAQELLNY RKSQDDEKLSTLSHSWSQVVD VSEVLRDGTTPRRDEEITIKDRLL LINTVPVRSNGVHGAISTFRDKT EVRKLMQRLDGLV/NLC*RTS* TIPLRAHSPQSKSAIYHEIAP*NA PAFYRRKCHCADIFLPYF*TCR\ RDRAMSAYLRYIVQKADSSFL YDKYQNNQIAAHVMRALAAEQ SEVSPEQRRAICEAFESANNTH GLNLTAHKYPGLRGTLQTAST DCDITVEAAALLPAFDQAVEGN RHQDDYGSGLGMAEEKFHYYL DLFRAVGDGHNSKEDATFGLG WRVNGNATMTPTFGTLASPQT YGHGTWGTGTVIDPVNHMTI VMLSNKPSPVADPQKNPNMF ESGQLPIATYGVVVVDQVYAAL
26124	56492	A	26271	257	817	TSSRCISLRTSVLSLKVEMAPMI TPLRLTGTVLISNSRLIVISSR RGVPSRNTSETSTTCDEWLSV DSFSIVLRLTVIQQFLCGIVDQR DLAAIVHGNDAFFRLQHGCLA LLKQRGDFVGFQAEKDFQYL NQNAGANQSDQHAK*Y/LTR*C SSDCH*SVGSHGLTQGRSPPRQ FVYDFHRRWG
26125	56493	A	26272	I	2700	

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26126	56494	A	26273	1	1038	MGCLDLGDGRAGSVARYFRRY RPPCDAALDLAKGVDMVHEA TLDTMEAKANSRGHSSTRQVL KKILFGLEPYEISTLFEQRQAML QSIKERSRRHRLPKEKIMTPTI ELICGHRISIRHFTDEPISEAQRE AINSARATSSSSFLQCSSIIRITD KALREELVTLTGGQKHVAQAA EFWVFCADFNRLHQLICPDAQLG LAEQLLLGVVD TAMMAQNALI AAESLGLGGVYIGALRNIEAV TKLLKL PQHVLPLFGLCLGWPA DNPDLPKRLPASILVHENSYP LDKAAALAYDEQLAEYYLTRG SNRRDTSWDHIRTIIKESRPI LDYLHKQGWATR
26127	56495	A	26274	1	1338	
26128	56496	A	26275	2	375	HSDPEASGLTRLRAMEQRRT DFFARRRTPGSVPTDRR*TIIVR MIPCTSSGRRTKAMVILRTSLV NPASNE/CATELFNALDVSIQNP RMIIIS*IQHRTLSGSLVAVG RMCSTLTPRVIFEH
26129	56497	A	26276	219	767	RFTQGGKPINNPAVIRPLDFPQN GSRPLANQIFTSLKVGDFYFGK RHKDVLRAIRNLKCSDDFTQRN FAPIDFIDKNGDVQPMYNITRD GCMMLVMGFTGKTA AAVKEC YNAFNWM/AEQLNRRMAMGE ELQHRYAIKETRSKLKGTIG/IR LMNERKKEKRVLELEHEHIMQ VTQPELLIG
26130	56498	A	26277	16	104	HICQSAPL*RGSSGLNGYGQYR PAGFLDG
26131	56499	A	26278	3	399	
26132	56500	A	26279	1112	1831	TGIRNCAPLSLTWKSCTANKV RCGHIRYPLADGAKTSDGKDY LVVATTRPETLLGDTGRSRLTR KIRVTKELIGKYVILPAGTAPGV RQGPVWMPGDEVKVTCKNG VVNEIWTRNHADIPLRPRFAVL ASGFFSVGLVAERNGIREPILG LDVLQTATRGWEWKGDFFAPQ PWQQFGVTTDET/LRPSQAGQT IENLFAIGSVLGGDFPIAQCGCG GVCAVSALHAAQAQIARAGGQ
26133	56501	A	26280	3	790	
26134	56502	A	26281	334	609	

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26135	56503	A	26282	1	1338	MTRHYGAEATNALLPGKASKH QIVGCGVNALSDLDPRRPDKTR SVASGIGAALLRLIKTLADDL QNLTDLSVFNGERYKDAQHV IRAAAGEKNQAFIAGARHDLGGE LGVGLVWIPASKVNGIMGPSVP WLTFRVSNIAGESAEGLLVTKP KNYDQVPANKPIVDAIKAKKQ DPSGAFVWTTYAALQSLQAGL NQSDDPAEIAKYLKANSVDTV MGPLTWDEKGDCLKGFEFVFD WHANGTATDAKRYCANVKGV NPDTQEPSPSGVKVNPKVDER LIRQEAGMVFQGFYLFPHLTAL ENVMFGPLRVRGANKEEAEL ARELLAKVGLAERAHHPSELS GGQQQRVAIARALAVKPKMM LFDPTSALDPELRHEVLKVMQ DLAEEGTMVIVTHEIGFAEKV RSRLIFIDKGRIEDGNPQVLK NPPSQRQLQEFQHV
26136	56504	A	26283	1170	1575	DPPVLVQRDANSTVRFPHASAS ADPAGDIPPIFAQAAGADLVY VGVEPPKPKAEVILVAEYSPKPT VADLGCPHVKVSRYPPEFTQ VITPVQCYVTIDALGQYAAWT RANMTYRPGSNIIQNLGNDIRL RTVQ
26137	56505	A	26284	3	1351	RTAPETPNQRPATLDSGILGGYI APDNLTTTFIGGHSFLDERFCLA HRCQKAAEDDAFPHDSLDAAS LLEYAREKLNGLDVEVYHWN QNFAPELDLYARFDSALKTFT EQLQQADGLIVATPVYKAAYS GALKTLDDLPERALQGVVLP LATGGTVAHLLAVDYALKPVL SALKAQEILHGVFADDSQVIDY HHRPQFTPNLQTRLDTALETFW QALHRRDVQVPDLLSLRAPKP KAEVILVAENSPIKTVADLKGH K/VAFQKGS/SSHNLLRLA/LRQ AGLKFTDIQPTYLTPADARAFAF QQGNVDAWAIWDPYYSAALL QGGVRVLKDGTDLNLQTSFYL AARPYAEKNAGFIQGVIAFSE ADALTRSQREQSIALLAKTMGL PAPVIASYLDRHPPTTIKPVNAE VAALQQQTADLFYENKLVKK VDIRQRIWQPTQLEGQL

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26138	56506	A	26285	364	1937	KLSGRHCTAAMFRFLTFCLEGM MPMRNIKLALAGLLSVSTFAD AAESSPEALRIGYQKGSIGMVL AKSHQLLEKRYPEKISWVEFP AGPQMLEALNVGSIDLSTGDI PPIFAQAAGADLVYVGVEPPKP KAERILVAENSPKTRTDLKGH KGAFQKGFSSHNLLRALRQA\ GLKFTD\NPTYLEPRWRPRAA\ FQTRGTVD\AWIWDPPYSAA LLQGGVRLVKDGTDLNQTGSF YLAARPYAEKNAGFIQGVLATF SEADALTRSQREQSIALAKTM GLPAPVIASYLDRHPPTTIKPVN AEVAALQQQTADLFYENRLHY SEYCRPMVSVGNWFLDGSHSV FSYDALDRLVQGGFDGRTQR YHYDLTGKLTQKQWQYDGHG WLTDISHLEGHVAVHYGYD DKGRLTGECQTVENPETGELL WQHETKHAYNEQGLANRVTP DSLPPVEWLTYGSGYLAGMKL GGTPLVEYTRDRLHRETIVRSFG SMAGSNAA YEMTSGETLIDLC
26139	56507	A	26286	511	1152	SVRFNIVFHFMRLLRFCCVLDH LICFTSPVNTFLRYNAFTLCNGE FGMSPAL TQLRALRYCKEIPA LDPQLLDWLLLEDSTMTRFEQ QGKTVSVTMIREGFVEQNEIPE ELPLLKESRYWLREILVCADG EPRLAG\RTVPVSTLSGPALAL QKLGK\TPLGRYLFSTSTLTRDFI EIGRDAGLWGRRSRLRLSGKPL LLTELFLPASPLY
26140	56508	B	26287	184	415	
26141	56509	A	26288	15	87	
26142	56510	A	26289	78	157	CKRYGKARDTG*QPRTQKCTC CELDE

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26143	56511	A	26290	1	1817	MTSAISLGSRCSGRIPSDIIGSNL DITAFNWQPDLLTIWHRQLHLH LTRLGGGGHYRQEVHLWRD KSGDKRRPQGDPKTTGITAKVI NVRSTKLVLPHRITATRWKR KRSRMLHTNTGKLVFNRRDQK RCTRKVMFDKALKLLDEAERL GSTSARSTIYQQCKRQGVITPHS ADFATTVRLLAHLRQERLGLKQ DSIYISLTDHCQFAIKRFQQNVL LPNPLLWDIQLRYPKEFQLGEE ALTIIDKRLGVQLPKDEVGFIA MHLVSAQMSGNMEDVAGVTQ LMREMLQLIKFQFSLNYQEESL SYQRLVPHLKFLSWRILEHASI NDSDESLLQAVKQNYPPQAWQ CAERIAIFIGLQYQQLGLTPQAV SKIINDIEDYFGVELVVRKNTG VTLTPAGQLLSRSESITREMK NMVNEISGEKNPGESEKELET VYVQAVGAHWEGNQVWLILA GGALFAAWPRVYAAAFSGFYV AMILVLCSLFRPLAFDYRGKIA DARWRKMWDAGLVIGSLVPPV VFGIAFGNLLLGVPFAFTPQLR VEYLGFSWQLLTPFPLLCGLLS LGMVILQGGVWLQLKTVGVIIH LRSRVRIPCDLHIYAQMA
26144	56512	A	26291	557	808	
26145	56513	A	26292	8	274	
26146	56514	A	26293	523	1851	
26147	56515	A	26294	1	589	

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26148	56516	A	26295	1	1848	MDLSTPERGSPYPRLLPCGDPL GETIVAIDQEAKPSTEDLGNKK ETKYIKLVIRWDNSDFNFLYS NYERIRARTTKKEDSATNPVT FEKHGSHAVVYARRSATVLT RNKEAPRVPPGGYMYSFVDIPE ALTQGETVAEAMEAAKDALLT AFDFYFEDNELIPLSPNLNSHDH FIEVPLSVASKVLLNNAFLQSEI TQQELARRIGKPKQETRLFNH HATKIDAVQLAAKALGKELSLE CLMDILNLNKHISGQFNAELES RTQVMTLGGMVDKQLSDAITA IHNQSDLAKRVIIEGHKNLNM MEVAIDEAR/C*AIIAKHQSTAS DLRLVMVI/SKTIAEMERIGDV GRNKICRTALEKLSQQHQP*VV SLES/SLDRHTIQMLHDVVKAFA RMDIDETAKCQIFVEYVLKPKV IWLLCFANIFYVVRIGIDQWST VYAFQELKLFKAVAIQGTLFE AGALVGTLLWGWSLDAANGR RGLVACIALALIIATLGVYQHA SNEYIYLASLALGFLVFGPQLL IGVAAVGFVPKKAIGAADGIKG TFAYLIGDSFAKLGLGMIADGT PVFGLTGWAGTFAALDIAAIGC ICLMAIVAVMEERKSAARKKFS
26149	56517	A	26296	395	1428	TSATATSTFALPRGGGYLVVSE WVVLRFTHDIFLRIFPCDNGRTILI RFGIFRMLMIVAIETQQFPVTAI FRVIGMVVINVNASEETNRRL HHRSLRLIQECVMDSLNLNKH SGQFNAELESIRTOVMTMGGM VEQQLSDAITAMHNQDSDLAK RVIEGDKNVNMEVAIDEACV RIIAKRQPTASDLRLVMVISKTI AELERIGDVADKICRTALEKFS QQHQPLLVSLES/GRHTIQMLH DVLDAFPRMDIDEAVRIYREDK KVDHVEYE/GIVRQLMTYMMED SRTIPSVLTALFCARSIERIGDRC QNICEFIFYVKGQDFRHHVGGD ELDKLLAGKDSK
26150	56518	A	26297	667	1002	
26151	56519	B	26298	1	1716	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
26152	56520	A	26299	1001	2193	LMAATKPAFNPPGKKGDIFSV LVKLAALIVLLMLGGIIVSLIIS WPSIQKFGLAFLWTKWDAPN DIYGALVPIYGTLTVSFIALLIA VPVSFGIALFTELAPGWLKRP LGIAIELLAAIPSVYGMWGLFIF APLFAVYFQEPVGNIMSNIPVG ALFSGPAFGIGILAAAGVILAIMI PYIAAVMRDVFEQTPVMMKES AYGIGCTTWEVIWRIVLPFTKN GVIGGIMLGLGRALGETMAVTF IIGNTYQLDSASLYMPGNSITSA LANEFAEAEESGLHVAALMELG LILFVITFIVLAASKFMIMRRIA LTLSMATMAFGLFWLIWLMST ITRGIDGMSLALFTEMTPPPNT GGGLANALAGSGLLILWATVY CGPLSDDRGGRPTI
26153	56521	A	26300	1	1645	MPAFPPYADYFSGLTATTAALA ALHKVRETGKGESIDIAMYEY MLRMGQYFMMDYFNGGEMCP RMSKGGKDPYYAGCGLYQCAD GLLSLDCVHRLGAIIDPILNECF KDIGLAHLGTPEIPEGTQLIHRI ECPYGPLVEEKLDAWLATHTIA EVKERFAELNIAKAKVLTVP ESNPQYVARESITQWQTM DGR TCKGPNIMPFKNNPGQIWRG MPSHGMDTAAILKNIGYSENDI QELRPNNKRTKMDRGAMDII GGQHLRQMWDLDADVYGHKT ALICSSGGVVNRYSYLELNQEI NRTANLFYTLGIRKGDKVALHL DNCPEFIFCWFLAKIGAIMHE AVIALASPDNMNAFELTP*SGK LITTFPHLPLAISA*ASPACSEK RWMALRGHSFQSVRSWAHFS IWNRLVTQEPIRR

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26154	56522	A	26301	2	1021	TPGNNVDSIFLAFFLNQFLTGLY IMGKTISIKVLFGIYLLMAAKV FAFSCNVGGINGAGTTSVYV NLDPVIQPGQNLGVDLAHHISC WNGDGGWYDTHMNLVQGS AFAGSLQSYIGSLYWNNTYYP PLTTNTNVLIDIGDKTPMLPFK LYITPVGAAGGVVIKAGEVIARI DMYKIATLGSNGPSNFTWNIIT NNNAVMPITGGCTVDSRNVTD LPDFPGSAEPLGVYCSSEQKLS FYLSGATTDSRQVFANTAPDA TKASGVGVTLMQRQLAGINDS HLLHYLDDEVWDNDYLATPHF LLKSAILRSMNDALMTRVTGE KNGQVRLIEIER
26155	56523	A	26302	522	714	
26156	56524	A	26303	1	976	STCSSRSHLHLIQASPILPNYVA TAVAARIADVQGISDTCVIAQP SPHPGALRTLVTTFDEPETPQP PGAAGFQLVQKKQVQLHNVLV VMTPHAFAGQTVIITLPGEQQT LSVAPLKNVQVLVTQQLRLDR LWWPGAFLLDFAAKVKALKD/ YPNHVMAQRASGEAEADDDV AATIKSVRQQLNLNITGRPLV KLDPDFVRVDENSNPLVGDYIT LYTVQRPGTEQGSFKVKRARA RVRQTRAPLFGPKSPAPEHMES ELEFELIGPSKSTSGNPRGLRSE RPVLFCLYPEMPTAAARAILIAE EQSREVKIALVVLDRLQRE
26157	56525	A	26304	1	1701	
26158	56526	A	26305	1839	2038	ARSGCFVRQSCPRGRCSKNRR WRDPYDHYPARPAYCP*R/WC M*LSTLATPKKVSCKPAPAAH RWR
26159	56527	A	26306	1	3270	
26160	56528	A	26307	1962	2049	
26161	56529	A	26308	94	942	
26162	56530	A	26309	1	4104	
26163	56531	A	26310	879	1367	TASELGKSCSRDHTPCTASVRA LYYARLRHAPANDPGEDGWAL AAKPPALPPRNSLSQAIIFRDKP NLPHRSPATYRQTERG*DTRSE FHA*TDIAPVATRARAGEFCRQ MFWGEDQADEQPA**ACCHRK *PVPK*DLAMLRAPPRMDSPPD ASRTSDLHN

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26164	56532	A	26311	1203	1911	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDHK RPREALLDSLKKLQLDYIDL LHAWNPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQG GKGVFQDKVIRDLADKYGKTP AQIVIRWHLDSGLVVIKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDQDQFGG
26165	56533	A	26312	3	793	
26166	56534	A	26313	181	336	
26167	56535	B	26314	1	374	
26168	56536	A	26315	591	679	
26169	56537	A	26316	937	1395	YRLAAGSCGIRRRNRHCQRRPG RNSKRLIALISAIGMSIFLQNYV SLTEGSRDVPASSVPLTPASLLI AGSPPH*TISRLSGPLREIMLK QLYHCGKSLTNLPREILRM*G* LTGEEIELARGDFHIDIWHRA VTNTAHKTGITQAQHRH
26170	56538	A	26317	627	878	VVEWFEPLICVNGWESKWPVL LSE**PETVGTNCDSSN*IPASLN TSYTGMLMAFDAIMVAVPTS*TC KIRRRVAGTKCGNPRA
26171	56539	A	26318	125	3078	IYTVIEIQLGFAFVTGENTTGIN SGTISLLQNGKDPAPSPVILLAT NGGSATNAGTITGKVTEQHSVF NKYSTGTSSNFIFNNDVSSITGL VAQNSNTIINTDSGIIDLYGRGS VGMLAIADSTAENQKGITLDSM WVDANDTTAMRDIASNSAIDF GTGVGVGTDRYRGRGRKNAPAF NQLGGVITINYAGAGMAAYG ASNTVINQGTINLEKNGNYDDS LAANTLVGMAVYEHGTAINDQ TGVININVTGQQA
26172	56540	A	26319	205	419	
26173	56541	A	26320	1829	2903	AWKVSHCAARPSFSRRWRGEK CTAGRRSQQFSARSTLKPMPSP R*SSMHR**MPSASCALRLPIP PAAAQSSHQSKKLRITSDNASPV AAARPVRPIRWT

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26174	56542	A	26321	402	1781	QRTTGAERYVPHIQCPCPASSL SAGPRGLHPAKVQEGVDIAIEN DVIVAIGDALTRQYPDA SFKEM HGRIVMPGIVCSHNFYSGLSR GIMANIAPCPDFISTLKNLWWR LDRALDEESLYYSGLICSLAIAIK SGCTSVIDHHASPAYIGGSLSTL RDAFLKVGLRAMTCFETTDNRN NGIKELQEGVEENIRFARLIDEA KKATSEPYLVEAHIGAHAPFTV PDAGLEMLREAVKATGRGLHI HAAEDLYDVSYSHHWYGKDL LARLAQFDLIDSKTLVAHGLYL SKDDITLLNQDRAFLVHNARSN MNNHVGYNHHLSDIRNLALGT DGIGSDMFEEMKFAFFKHRDA GGPLWPDSFAKALTNGNELMS RNFGAKFGLLEAGYKADLTICD YNSPTLLADNIAGHIAFGMG GSVHSMVMNVGMVYEDRQFN FDCSIYAQARKAAASMWRRM
26175	56543	A	26322	284	340	
26176	56544	A	26323	113	646	WTLVPWNWNTQPYLGLFF*FIR DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQRSDSSLR EKKITKHHTKRTASLILHAMI CCRSLSNKKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT EQ
26177	56545	A	26324	1	582	
26178	56546	A	26325	3	947	QTQEWSGSATFTSDGKIRLFYT DYSKGHYGKQSLTTAQVNVSK SDDTLKINGVEDHKITFDGDGK TYQNVQQFIDEGNYTSGDNHT LRDPHYVEDKGHKYLVFEANT GTENGYYQGEESLFNKAYYGGG TNFFRKESQKLQSQAKRDAEL ANGALGIIHLLNNDYTLKKVMKP LITSNTVTDEIRANVFKMNGK WYLFDTDSRGSKMTIDGGATQA FAKENNQKAYKETYGVSHTIR HDMLQIPKQQQNEKYQVPQFD QSTIKNIESAKGLDVWDSWPLQ NADGTVAEYNGYHVVFALAGS PKDA/G*HINLHVLSK

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26179	56547	A	26326	2	223	RIPKINIESAKGLDVWDSWPLQ NADRTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNISID SWKNAGRNVFKDSDKFDANDPI LKDQTQEWWSGSATFTSDGKIRL FYTDYSGKHGKQSLTTAQVN VSKSDDTLKINGVEDHKTIFDG DGKTYQNVQGFIDEQNYTSGD NHTLRDPHYVEDKGHKYLVE ANTGTENGYGGEESLFNKAYY GGGTNFFRGATQAFAKENNQK AYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFQDSTIKNIESA KGLDVWDSWPLQADGTVAE YNGYHVVFALAGSPKDA/G*HI NLHVLSKGRRLNRQLEKRG
26180	56548	A	26327	1	803	MLEDPRKGLTSPVSHNLHFQ FHLGPLLPGSPMKKWPAVLT GSKSPKLESYKHFQKIWDHMG EPSKREEGAGLTVNQHIPNGAS TCNEGPQRLEALGARIPMAAGF SSSKPTLVTPRRAYRADLRLEG YWGCGQVPGPLVAQGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDA/G*HINLVLSKGRRL NRQLEKRG
26181	56549	A	26328	2	439	
26182	56550	A	26329	1	1084	MVIAAMETQLSNGPTCNNTAN GPTTINNCSPPVDSGNTEDSK TNLIVNLYPQNMTQEELKSLFG SIGEIESCKLVRDKITGGATQAF AKENNQKAYKETYGVSHITR HDMLQIPKQQQNEKYQCDNLKT CHTSHGSMVMAETAVINHKRRK NSPRIVQSNDLTEAAYSLSRDQ KRMLYLFVDQIRKSDGTQLEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIRKGTQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTPERR**HINLVLSKGR RLNRQLEKRG

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26183	56551	A	26330	34	1949	MGYLNNAVGYREDLLANRAIV KHGNFALLTPDGVVVKNIIPGYE NCDATILSTPKLGASFVDYLV LHQNGGNQQGFGVEGIEFRY VISGNITAKAEGKTYALSEG LYCPPGSLMTFVNAQAEDSQIF LYKRRYVPVEGYAPWLVS SELERIHYEGMDDVILLDFLPKE LGFDMMMHILSFAPGANHGYIE THVQAEHGGATQAFAKENNHK AYKDTYGVSHITRHDMLQIPKQ QQYEKYQDTHDTPYCEPLPGET RLWGD TDVIGLFD AETDMNDV VAILENHPLLGAGFAHKIEQLE DKDWEREWMDNFHMRFG LWICPSWRDVPDENAVNVMLD PGLAFGTGTIQLSV PAMLDSS THTRRM RSTLNLYEITRMSTVS TSEHSMYTLVQVDMKEAQKP DTASYRTFNEFFVRPLRDEV RPI DTPDNVLVMPADGVISQLGKIE EDKILQAKGHNYSL EALLAGN YLMADLFRNGTFVTTYLSPRD YHRVHMP CNGILREMIYVPGD LFSVNHLTAQNVPNLFARNERV ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDES FVVG PVG DFELLCHGTVCVVGKMRDLIL QLSKSSIYSTKPPSRQVSVMLC
26184	56552	A	26331	1	145	LRLGLLYGRRFVPPP*YALLNK DSSPWYFSPVPLASKTRYLWL LSPT
26185	56553	B	26332	1	3090	
26186	56554	A	26333	3	832	
26187	56555	A	26334	1	3258	

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26188	56556	A	26335	184	2324	ENRVRLFVLIVFQDLPTCYVNH NFCVCTAADTFTTITPKAGDAR LIGIAQTVRHLEDPMRWAKSIH KSCEILDPHRAVPKENTHPARK INISDPAAGAVARIRYEGVLSVC RASASAYVSRSTITVACWYVS NTGVGTGATIGVKRQHRHARLFS GDGAPGFGTGKRDIRQLRLVR IQIQRTFFAAVLHVPTPWSRAID AAALLTVIDVKVLTACACQAC RTLALRVAQVIDRCSNPGDIMS SVARRYWFISWSAKRDCAVS YDQDPGQAQRSCRSCLVAVDR GLWLSAYCRSLMTQTLLPDDV PRILPNASSPSRLRCLQHLGNRY LLDLRKLWLHRSQFSLCGWEK RLVKDLTRIQDTGRAKEILGAT ATLEFRLVNTNVDAQAAASGR VPGDSEVKQTREGQPVVLYKR VILTGDHITDSTSSQDEYNQPO VNISLDSAGGNIMSNFTKDNIG KPMATLFEVEYKDSGKKDANG RAVLVKQEEVHIANIQSRLGNS FRITGINNPNEARQLSLLRAGA LIAPIQIVEERTIGPTLMQONIEQ GLEACLAGLLVSILFMIIFYKKF GLIATSALIANLILIVGIMSLPG ATLSMPGIAGIVLTLAVAVDAN VLINERIKEELSNGRTVQQAIDE GYRGAFSSIFDANITTLIKVILY AVGTGAIKGFAITTGIGVATSM FTAIVGTRAIYNLLYGGKRKVKK
26189	56557	A	26336	1	369	

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26190	56558	A	26337	1	1316	MNGLLSDSDLSLSSCQQRVKA RLHEILOKDRDFTAEDYEKVES RIYHFARLSVGGYTTADSSLT VYLQLMKAPKKRRGEVNVGT VVAFIGGGFPVVKDYFRPAA DGSSALCRFFPTGNVHDQSDPQ KVTGDGAVVPVQPTDGPGLRCL RRARGCGAGRQGREQAQDCG AEIQAEAAASRASRVQEGSYPRP PNGPFSTDLTGLMQFTKLLVLK VESQLTRRIRKCHNLREANIREE LRFNCTNVALRTGVQFNRRPD SPGYSRGVLSPERHVRTRLTYFT SESHVHSLLSILRYGALCNRRG TLCRAIHTLHRHTIVLVNGVT TLNLVQLTFYGNVSEIIRHQCC LTRHGNHPLPLTAIQGIALFSDN QAAYRFRADQRTLRFGLPVAR QPVRRGGFHIDIVVDFGTARQ QQE/LRLQLRVFSSFVLHEKKR
26191	56559	A	26338	2	1415	
26192	56560	A	26339	1434	1667	KRTDWRDRVAFRCRSIAESG*R QAIAKELELTASAEILLWDDYF APGYGVPNDEGMEAVKLLARL EGILLDPAVRLR
26193	56561	A	26340	1	1671	
26194	56562	A	26341	1067	3947	FCTVNPNAVYIGGPGFGARHNAS NSLKDIAELVPFAHRYGAKIFV TLNTILHDELEPAQRLITDLQY TGVDALIVQDMGILELDIPPIEL HASTQCDIRTEVEKAKFLSDVGF TQIVLARELNLDQIRAIHQATD ATIEFFIHGALCVAYSGQCYSH AQTGRSANRGDCSQACRLPYT LKDDQGRVVSYEKHLMSKDN DQTANLALIDAGVRSFKIEGR YKDMSVYKNITAHYRQMLDAI IEERGDLARASSG
26195	56563	A	26342	182	881	HAEPYPYRGLLLKLGESRGCLL PASLPFSLQEFFYSGPREELAQK TLLVSVWDYDLGTADDFIGGK CDPADQDVVHTALREVTREELG LAVPEEHVWGLLRPVYDPQKA TVVPVLAVGVLDPQSLRPNSE EVDEVFALPLAHLQTNQGY THFCRGGHFYTLVFLHGPFR VWGLTAVITEFALQLAPGTQYQ PRLAGLTCGAEGLARPKQPLA SPCQASSTPGLNKGL
26196	56564	A	26343	237	338	

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26197	56565	A	26344	279	533	IHLRRILQRGQ*PRQRWRERCC ESGRGTS GPGSSQ*LTGSPQECC TPAGETG PRAHSPQ*SCWCHCC TPOGRQSICRTTSHRTA
26198	56566	A	26345	126	303	LLLSYGVGASHQSLECHHRSNH GSLWMH SKRCAGGKIRVGTPE CQ*SALERPGLPLC
26199	56567	A	26346	368	746	SLHTTSRAPEGPSRYPGPGPPS AATKGQRTRRPLCARPP/PGLPD APL/SPAAPTTLPLPCPRVAQP AHGPPSASALSSWENRPCCRHE LAAKPPEQAARRGHARTPTAG PAPPGRRAALSGSQFP
26200	56568	A	26347	79	159	SFLGVSRRGFGFRVTGQ*WRE GQQINK
26201	56569	A	26348	1	3369	
26202	56570	A	26349	3	529	MELAKVVKSHPSAKMVLCIAT DDSHLSCLSLKFGVSLKSCR/T LLENAKKHHVEVVGVSFHIGR GCPDPQAYAQSIADARLVFEM GTELGHKMHVLDLGGGFPGTE GAKVRFEEIASVINSALDLYFPE GCGVDFAELGRYYVTSFTVA VSIIAKKEVLLDQPGMEEENC
26203	56571	A	26350	146	502	

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26204	56572	A	26351	3	2212	MKRSRCRDRPQPPPPDRREDGV QRAAELSQLPPRRRAPPGRQR LEERTGPAAGPEGKEQPALASQ SAEIAASARLPPRLGRLLGFQK ACRCWSLNPILMALRLSLVPP DKKHPQVWRGPPLHLAPNVG LFSRVKVRSSVIEDKSMRDSR RGLSQRRRRRKKKRGSSSKK KKRRKKKKKKKKKKRRRKN RKKKKKKRKNRKKKKRKKKEK KEEEEEERRKKEEEDDEGRGRGR RKRRKKKKKKRRSRKKKETAA AAAAAGERLGKWWPGCEPVEC VAYFLRRRLQQLRHPARQLLL QGMAGYLSSEDFVMVEEGFST RDLLKELTLGASQATTDEVAAF FVADLGAIVRKHFCLKCLPRV RPFYAVKCNSSPGVLKVLAL GLGFSCANKAEMELVQHIGIPA SKIIICANPCKQISQIKYAAKHGI QLLSFDNEMELAKVVKSHPSA NFHIGSGCPDQAYAQSIANAR LVFEMGTGLGHKMHVLDLGGG FPGTEGAKVRFEIASVINSALA DLYFPEGCGVDIFAEALGRYYV TSAFTVAVSIIAKKEVLLDQGR EEENGSTSKTIVYHLDGEGVYGF NSVLFDNICPTPLQKSSTKSLR TTIGEAFERLHRLRLRERQKAML EELEADTARTLTDEQKVQRYR QQLRKVQEGAQILQERLAETDR HTFLAGVASLSERLKGKIHETN
26205	56573	A	26352	1	860	MKKEDAFKAFYIVHGWNCV KGSLTRTPCCCTNCLAGGIWC MRVQIFQLENKVLPGFPWACR VDLYGQIGFDAAAQCLSLSVSK AEPLVKKAPPELREQLARKTSL SDNLKYLFDNKDIMVKQSKK KKEHSFRKNNGCIKIIAFSDHAE DFRKLGCVELGISVDSQFTHLA WINNPQREGDLGPLNIPPLAEV ASGLSEDYAVLKTDAGIAYRG RFISDGKGLV/SQITVNDLPVGR SVDEALRLVQAFQYAEHAEV CPAGWKPGTDITKLNVGDSKE

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26206	56574	A	26353	70	745	ERGSTRVIVRASSLCPRSFQSWP PVTRASESQPLTSRQQRWSDGA FKEVKLSDYKGKYVVLFFYPL DFTFVCPTETIIAFSNRAEDFRKL GCEVLGVSVDSQFTHLAWIT PRKEGGLGPLNIPLLADVTRR LSEYDYGVLTDGVIAYRGLFII DGKGVLRQITVNDLPVGRSV DEALRLVQAFQYTDEHGEVC PAGWKPGSDTIKPNVDDSKEL YFSKHN
26207	56575	A	26354	1	689	MAAEDELLPRLPMLLETGKQ LLDEVELAAETTYQIVQEKRA REHFINYLQCHYYHIAKFELL KTKNNSAENHTANSSMAYPSL VAMASQRQAKIERYKQKKELD HRLSAMKS AVESGQADDEHER PPVKSFILTRNTAQAKLFGASYP SLATMTVSDWYEQHRKYGALP DQGIATATPEKFRKAAQQQKY QEVKEGEDDE/ALYRVREWDN WKDTHPGGYGNRQNMG
26208	56576	A	26355	1	810	NYLTQCHCYHVAEFELPKTMN NSAENHTANSSMAYPSLVAMA SQRQAKIQRYKQKKELEHRLSA MKS AVESGQADDERVREYYLL HLQRWIDISLEEIESIDQEIILR ERDSSREASTSNSRQERPPVKP FILTRNMAQAKVFGAGYPSLPT MTVSDWYEQHRKYGALPDQGI AKAASSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSS KAAQQQEEQEEKEEEDDEQTL HRAREWDDWKDTHPRGYGNR QNMG
26209	56577	A	26356	223	359	RKQQDEPCGHLQSPGKPFLLS CRDPWGGLPV*LEKDRHKKS
26210	56578	A	26357	1	3855	
26211	56579	A	26358	1005	1293	SDRRYEWDCPR*LNGALLCLL LLEHPEGCPWHSVWSTGHSLEP MHFRFPSSQDLQLLLPLPGKLG YRARIRNHGHSCLQRRKTVYQ GDGPLREP
26212	56580	A	26359	763	978	

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26213	56581	A	26360	1	1217	MQRRLKRRNAGLPCCCEVPGYY REDASSPLLPKYKTNFSQCLVH FFDELRRHHLVKTRHVLFIPLNH DIMQAFTHARVIVGVKVPGIFS RHPHAVLHLGHSQIGLLMEYPD ELLWECKEDALALIRRDAPMLT DFTHINLLNAPLLDKQAEWCEV FDRGRTTSLLLFEHVHAESRDR GQAMVDLLAEYEKVLGLDCR ELPDYLLPLYEYLSVLPDDQAK EGLLNVAIPILALLGGRLKQREA PWDALLDALVQLGGSSLSND VKKQVNSEERDDTRQALDAV WEEEQVKFIEDNATACDSSPLN QYQRRFSQDVAPQYVDISAGE GQSSQLVSYWEKDVQTCLEFL PSGGFVVSLSGVKLQTFETD NLVKDITFFGKISTRSLKTYLKD VTEKREQSCVNLELK
26214	56582	A	26361	1	783	
26215	56583	A	26362	2	1646	PGSTISFRRVTQREKKQPEALC QGSTSNLQFIIHPLLSAQTVEL GLSKFVPPKMIITQTS/ICYMTS LGILFLINILPGTTGQGESRRQEP GDFVKQDIGGLSPKHADPIDDD STDNITIFTRILDRLLDGYDNRL RPGLGDAVTEVKTDIYVTSFGP VSDTDMEYITDVFRRQTWHD RLKFDGPMKILPLNLLASKIW TPDTFFHNGKKSVAHNMTTPN KLLRLVDNGTLLYTMRLTIHAE CPMHLEDFPMDVHACPLKFGS YAYTTAEVVYSWTLGKNKSVE VAQDGSRLNQYDLLGHVVGTE IIRSSTGEYVVMTTHFLKRRKIG YFVIQTYLPCIMTVILSQVSFWL NRESVPARTVFGVTVLTMITTL SISARNSLPKVAYATAMDWFIA VCYAFVFSALIEFATVNYFTKR SWAWEGKKVPEALEMKKKT AAPAKKTSTTFNIVGTTYPINL AKDTEFTSISKGAAPSASSTPTII ASPKATYVQDSPTEKTYNSVS KVDKISRIFPVLFAlFNLVYWA TYVNRSAIKGMIRKQ
26216	56584	A	26363	217	559	MKKALQVAMFSLFTVIGFNAQ ANEHPHETMSEAQPQINSATGV VKGIDLAEKKITIHHDPIAAVN WPENTMRFTITPQTKMSEIKTG DKVAFNFVQQGTLSLLQVIKVR KPAQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
26217	56585	A	26364	72	157	ERRKF**SQSSQKKNKERLQNAVILEL
26218	56586	A	26365	3	620	VSGGGWEPSGTLTAFKTASAIT TEMASRSQGIQQLLQAEKRAA EKVADARKRKARLLKQAKKEA QMEVVEQYRREREHEFQSKQQA AMGFGGNLYAEVEQATRRQV QGMQSSQQRNRERVLAAQLLGM VCDVRPQRPDLQKEEMTTTFSP SLIIPARACRFLVRAQQSSGHLH YRAKDPVGTSLRHRSSRIHG GVPTKTCVAKT
26219	56587	A	26366	28	187	TGTESGQYHCKRRKMGPPIIK SLWARSDEPVFWG/LFGAGGM WSAIIAPVMIR
26220	56588	A	26367	1	870	MAVWPTGALALTSPAGDAGA CSTAGGPCQGARGRGSGPPA WGPDAVLEPLRGQRKPYVRPM TSTWWKKLPFYRFYMLREGTA VPAVWFSIELIFGLFALKNGPEA WAGFVDFLQNPVIVINLITLAA ALLHTKTWFELAPKAANIIVKD EKMGPPIIKSLWAPEMINPNP KRSDPEPVFWGLFGAGGMWSAI IAPVMILLVGILLPLGLFPGDAL SYERVLAFAQSFI/GRVFLFLMI VLPLWCGLHRMHAMHDLKI HVPAGKWVVFYGLAAILTVVTL IGVCTI
26221	56589	A	26368	741	894	
26222	56590	A	26369	504	558	
26223	56591	A	26370	897	1097	RKWSQSTRLPWETGSPSETSPS GPVSPTRSHLASPRRPPPTPP*S SPRRLLGAIPFGVGPLNE
26224	56592	A	26371	200	657	GPRRLSFVTGHKAYRGLGIVSG PTVPLVCAVCCSYWDPGVPRV VRLVVRLWPLCRCGGRSGDAS VAAAPLVCGGGI*DWDHCPFV CGPSLICALRPSGCGSGMACRV VLLLRCLAMFAFTSFVTEV GKFSFPPLPEFFSGFALDLSLP
26225	56593	A	26372	196	404	
26226	56594	A	26373	1	3162	
26227	56595	C	26374	287	349	
26228	56596	B	26375	366	1637	
26229	56597	A	26376	365	604	VLAVSYPQLCLLL*KPIGPEDAI YALSSDFTCGSPTAAGRKQIRG EVCPRERCSVETCLSPNFHSLVS SFPFSLQGFK

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26230	56598	A	26377	1	1404	TLVRCFPPLKLIFSIFKKKAASL GSSQSSRTYAGGTASATKVSAS SGATSKSSSMNPETKAIPVSQ QMEGPHLPNKKKKHKQAVKTE PEKKSQSTKLSVVHEKKSQEGK PKEHTEPKSLPKQASDTGSNDA HNKKAVRSAAEQPSEKSTEPK TKPQDMISAGGESVAGITAISG KPGDKKKKKSLTPAVPVESKP DKPSGKSGMDAALDDLITLG GPEETEEENTTYTGPEVSDPMS STYIEELGKREVTIPPKYRELLA KKEGITGPPADSSKPIGPDDAID ALSDFTCGSPTAAGKKTEKEE STEVLKAQSAGTVRSAAPPQEK KRKVEKDTMSDQALEALSASL GTRQAEPELDLRSIKEVDEAKA KEEKLEKCGEDDETIPSEYRLK PATDKDGKPLLPEPEEKPKPRS ESELIDELSEDFDRSECKEPPSK PTEKTEESKAAAPGSCVGGCVS
26231	56599	A	26378	1	688	ITAISGKPGDKKKKKSLTPAVP \VES\KPDKPSGKSGMDA\ALDD LIDTLGGPEETEEENTTYTGPEV SD\PMSSTYIEELGKREVTIPPK YRELLAKPIGPDDAIDALSDF TCGSPTAAGKKTEKEESTEVLK AQSAGTVRSAAPPQEKKRKVE KDTMSDQALEALSASLGTRQA EPELDLRSIKEVDEGSLPDFQQQ SLSLGLPWPKMGQFLSSTFLEG SPATQRK
26232	56600	A	26379	199	384	VYKECR*GFSHESPSPKPS/HIE *KFCMCGENGQGLRKKSSKN SFFGTSFTWVGRENVKHI

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26233	56601	A	26380	166	2172	TYILRNLYKEVMLENYRNLSL GKAVFFPFLH*FSRDLIT*YVP QSQQFLSQHVLQIFLGLCAENH FHPGNSSPGHWWKQQGQYSHV SCWFENAEGQERGGGSKPWSA RTEERETSRAPSPLRQASAPR KGNMNVVETEPSSAQRPNPVL DKGLKELETLRFGAINCREYEP DHNLESNFITNPRITLLGKKPYIC SDCGRSFKDRSTLIRHHRHSME KPYVCSECGRGSQKSNLSRHQ RTHSEKPYLCRECGQSFRSKSI LNRHQWTHSEKPYVCSECGR GFSEKSSFIHQRTTHSGEKPYVC LECGRSFCDKSTLRKHQRIHSG EKPYVCRECGRGSQNSDLIKH QRTHLDEKPYVCRECGRGFC KSTLIHERTHSGEKPYVCGE RGFSRKSLLL VHQRTHSGEKHY VCRECGRGSQKSNLIRHQRT SNEKPYICRECGRGFCDKSTLIV HERTHSGEKPYVCSECGRGS KSLLL VHQRTHSGEKPMQTFSG VTPQLLERTVLLAEMHSRDAL RSGTHSQPGAACCTTGAMHL RGTFWQPLTQRGQLQKVIPDP EPIELKDHVWVADTLQVSFFLCP VLPSPSESSIFLCVVCINAYAV APQSGLMREKDVHVWECGPPP FARTAPITPSTQNWRLPREKY
26234	56602	A	26381	434	946	NTFCLTAMKILCMWFSRWHSR WVGMQGPSC*PQRTLWMTLS STGRSCVPAACTPAPCGRISAA GRLRCSQLLPHAPAPAACSC SVHISFQPL*QLRTSLWTVQMK SQVTQTQVGSHTSQAARALQG HQQVQKPGSRIRTTGGVKPQLEG PGRWLKIRLEGHSWTCRQ
26235	56603	A	26382	3	2119	

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26236	56604	A	26383	3	2237	NRRKFSVSIGFYTVMDAQYKIH TKTAHLITKESPOEEGKEMFAT MSKLKEQLTKVRK*FNALLYES QQLLIPLEELEKQMTSFYDSL KINEIITVLERAQSSALFKQKH QVRTILFKWCNSSQKMTLCLVL GSMISMLSTAKITAGYKSEVEV SVSHHCI*NCKKTLTLEKGSQS VQKFVTLSNVLKHFQDTRLQR QIADIHVAFQVICSPC*DWKKH VETNSRLMKKFESRALEKVL RIAQEGLEEKGDPEELLRRHTV SPPFRDQRVLNAFLKACDELTD ILPEQEQQGLQEAVRKLHKQW KVSQDRTAHYLLHLKIDVEKN RFLASVEECRTELDRETCLMPQ EGSEKIKHRVRLPHHSPHHL EKRLQLIEELCVKLPVRDPVRD TPGTCHVTLELRAAIDSTYRK LMEDDPKWKDYTSR*PQNGLW ISTNETQLKGIGEAIDTANHGE VKRAVEVSSGSLSKRGETLSWL KSRLKVLTEVSSSENAEQKQDDE LAKLSSSFKALVTLSEVQHLL THFGDCVQYKEIVKNSLEELIS GSKEVQEQAEKILDTENLFEAQ QLLHHQVKMPLSSAKKRDVQ QQIAQAQQGEGGLPDRGHEEL RKLESTLDGLERSRERQERRIQ VGAGS*ERFETNKETVVRYLFQ TGSSHERFLFSLSLESLSSELEQT KVVYGSLESIAVQEAENLVKEAS
26237	56605	A	26384	1	390	GTSLFDEEGAKIVKDLMSKAEK NGVKITLPVDFVTADDFDENAK TGQATVASGIPAGWMGLDCG/P ESSKKYAEAVTRAKQIVWNGP VGVFEWEAFARGTKALMDEV VKATSRGCITHGRSRYTKLIPI

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26238	56606	A	26385	1125	2228	NVMShLGRPDGVMPDPKYSLE PVAVELKSLGK*VPGSGAGRL CGGGSCQARCYAGSVILLENLR FHVEEGKGKDGASGNKVGPIVIL TLGLVRA*VCKRLWLNVNDAF GTAHRAHRYQEPCLPH*EQYS YLLE*PKYFAKALESERPFLAI LGGYEELFKIML*VLF**AIT WIGGGMAFTFLKVLNNMEVGN KCQVDVK*LSMIIAGCINEKNG VKITLPVDFVTADKFDENAKTG QATVASGIPAGWMVSHLSGLV V*VNRNSVVSFIHFVWNGPVG VFEWEAFARGTKALMDEVVK ATSRGCTIIGKRSYTKLIPI*AG RILIRGRCTGGGASLELLEGEGL LFFGLFGIRVDCAVRGG
26239	56607	A	26386	2	482	TRQAWHEGPRGVPHSASLRSRA RRQSAPSLTESPTSPSCISKMA LSNKLTLDKLD/VKGRVVMR VDFNVPMKNNQITNNQRIKAA VPSIKFCLDNGAKSVVLMSHL GRPDGIVMP*QVTPLEPVA/V VELKSLLGQGMFCS*RDCVSP VEKACANPPG
26240	56608	A	26387	3	378	
26241	56609	A	26388	311	578	LGIRQTLGFLSRARCGGSRRS LEMQNNAgefVDL*VPRKCSA SNRIIGAKDHASIQMNVAEADK VTGRFNGQFKTYAISYFLNLF HH
26242	56610	A	26389	3	333	DAWDLCRVTSCLSLSRVWV QQAQPSLEMQNDAGEFVDLYV PRKCSASNRIIGAKDHASIQMN VAEVDKVTGRFNGQFKTYAIC GAIRRMGESHDsFLRMAKADG IVSK
26243	56611	A	26390	23	389	LAASFLSRARCGGSRRTQALEM QNDAgefVDLYVPRKNSAS NRIIGAKDHASIQMNVAEVDK VTGRFNGQFKTYAICGAIRRM GESDDsILRLAKADGIVSKNFL TGEESQDVGIFCHK
26244	56612	A	26391	206	354	
26245	56613	A	26392	1227	1430	GSSSRPDQEEEDLKLKFAFSR GPPLSLVHPPLLSYPSARR*PQ TPRPPrRHPSLHLHPSPAQP
26246	56614	C	26393	17	319	

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26247	56615	A	26394	1	645	MIHEQENIKKNTKTIKKNQTEI LELKNTVTWEKNLLEVFNNNSFR QNEESVNLQTSYLSLSRGEKR KKKCEEMIRDLGQYQPGPYMH DGYSRRESGPNVPRRAQVDGG DARKGTHRRKRVLERGLWLKR EDKKAQGYKGR*KGPRV*GTD PQEEDLQRLSAETWLV*PEPR P*KAPAKKGEKVP*GRKGKAD AGKEGNNPAENGVDKTDQAQ KAEGAGDAK
26248	56616	B	26395	1	663	
26249	56617	A	26396	265	735	VMWLRYDTLSETHMHQLLGL NLLFLLSQD*VAEFHMELEWLP ATDTQTNAIKRPVSLPEPYLME GGYNKVFLLAKGNIPAKSYTFIHI LLDTRIDEMAGCIEKAYEKILFT KATWILFLNTPKQMMNDTKK* GWVLGPNNYYSFASQQQKLED ITIPS
26250	56618	A	26397	215	386	
26251	56619	A	26398	3	515	QLPESAYMHQLLGLNLLFLLSQ NRVAEFHTELERLPKADIQTNV YIKHPVLSLEQLMEGSYNKVFL AKGNIPAESYTFIDILLDIRDE IAGCIEKAYEKILFTEATRILFFN TPKMTDYAKKRGWVLGPNN YYSFASQQQKPEDTTIPSTELAK QVIEYARQLEMIIV
26252	56620	A	26399	423	4482	KLWVILFDFICLAFL*FFSTYMY SCE*ILVKLTLYFSFHVYLLIYC ECENLTGTLDLVFI*KCKSLLIW IA*TVYKKIHMEGEVKG
26253	56621	A	26400	173	174	AVSLLKHSNNDLCS/GFPTSRT ADPTSCGSH/WPWPQSLKQ*P ELYIGPF*PRLKQLGCCRAFP
26254	56622	A	26401	135	699	RDLVPCAAPAPAMAKRGQDVT WAMASEGASPNPCQLPQGVPE AGQCRKRMWG*SPHTEPLGT A*WESLELPRDLLNGFDQND NDMDNEIQAEVVSDEELVG NQSKGTWCPVPQLLQLWLKGA KIQFGPWLQVRQAPILASFHKV LSLQGSAGKCGVEAPTQSPH WALPSGAVRRGPSSRPQNGRS TNCLHCEPGKAADTQCQPVKA ARREVVPCKAKGAELPKTMGT DLLHQCDLGVRHGVKGDHFGA LRFDCPTGFTWYMGVPAPLVW PIFIWNSCIYMPMPVPIVSRR

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26255	56623	A	26402	27	264	RLVEWL*PRDLLNGFDQADNADMDNEIQAEVVS DGDDEELVGNQSKGTWCPVQLQLWLKGAKIQFGPWLQRVQAPILASFHKVLSLQ
26256	56624	A	26403	624	955	VPSLGSFHVVLVLSVHRRQELRFGNLHLDFRRCEMMPGPFGRSLQQR*SPHGEPLLQCCRREMWGQSPHTESPLGH*LMEL*HPPSPRMIDPPTACAVPLEKLQALNASH
26257	56625	A	26404	851	1387	PKIVELLKYSQDQLEKRLKKDKALMGHFQDGLSYSVFKITTDQVLMGVDPGRGESEVKAQGFKAALVIDVTAKLTAIDNHPMNRVLGFGTKYLKENFSPWQQHGGWEKILGISHEEVD*NIRFVIRNTLCLLWSCARWPSDGP TG DYNVQGRWSIDVFKTHIPTGEASGEVSFV
26258	56626	A	26405	1	229	LRLRGTHVLNASHSRWRGTPEAYEGLGIRYLGVAEHDSPAFDMSIHFQTAADFIHQNKRAISALHLCKRSGIRQA*MSIHQTAADFIHQNKRAISALHLCKRSGIRQA
26259	56627	A	26406	2	594	SVLGLTLPAFRFKTLRRRWVQGGKVLRLKAPFGKKPRGSLTFWRASTRVDRDMANNRRELRLRGITHVLNASHSRWRGTPEAYEGLGIRYLGVAEHDSPAFDMSIHFQTAADFIHRALSQPGKILVHCAVGVSRSATLVLA*PHAVPPLPFVEAIKKVKDHRGIIPNRGFLRQLLGLGPQLAAGSGSMRGGGEKLR
26260	56628	A	26407	605	1231	NCSNSGVWRISHKKERSIPDSKRRSRGNTKSSSPRPTTSLLEKLLTSGSPRIWVPRMS*LHDKARRASFSSSSSAIKAFSSASRSSNESVSSLSNSSLEGQSKMSISSSTGVGSRLLALGLYTSSEMVKGSSFILSSSLGLSSYSRAAFTGELEIKGAEMFSSLGNGTPVLRVLTLEP SLRRTNTLLQWFP MCNWRLLRRVWI
26261	56629	A	26408	771	1121	FSPKLLPRREGRKPCAPARTQTPRSKSTPFSQV***SVDSDPQKKGKQDRSRGGPLQERAQRESGNLLAATVVPRAERHPAISTEGPTGPPEGSAPSATSSVAAAGPAHSR

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26262	56630	A	26409	3777	4343	DQEEPFGNSSIIQSLFTIKLNPQ SSLQEVCSLDTHNSPVRFKNS CSAKFHFKFVWNVILLQLSSE ELILSFVIPGVGHCSWSSYCYILQ PRIFPLWSFYIVYVEDSSICVSS LFPSWR*RP*IIGSIK*CLSSQMG WNFQSW/NLPR/CVVLVLSIK KGL/HIWCMPDFPAFRKESLLN FRWLGHLLA
26263	56631	A	26410	473	667	PCSDWGWRSWPWNLQLEETWAL *CCSHSHKVSQEGTWMKLETI LSKLLQGQKTKHPMFSLTGGN
26264	56632	A	26411	1416	2108	QRANIQNLQRQTNLQEKRNPI NKWVKDMNRHFSKEDIYAAN RHMKKCSSLAIREMQIKTTMR YHLTPVRMVIIRKSGNDRCW GCGEIGTLLHCWWDCKLVQPL WKTWVRFRLDLQLEIPDPATP LLGIYPKDYKSCCYKDTCTRM FIAALFTIAKTWNPTPKCPSIMI DWIKMWHIYTMYYAAIKK DEFMSFVGTWMNLETILSKLL RQKQTKHRMFSLIGGN
26265	56633	A	26412	1	278	FRCCSYYFYKFFCFFLSLLF *IFFLFLSLLFASLLFLASPLCVC YFFFIIVAQFLNSLFHFFSLFVL CFSGLEVSIDISSVEILSSAMSIT LMGLSKAFLIT
26266	56634	A	26413	181	742	PLLKSGCISFLLRLLVKLYRFL VRRNNSTFNQVVLKRLFMSRT NRPLLSLWMIQNIKLPDRENR KAVAVGTITDDVRVQEVPKLK VCALRMTSQARSGLGAGGKIL TFDQLAPDAPKGCGLVLLSGPR KG*EVYRHFAGAPGTPYSHTKP YIRSKGRKFERTGRGLASRGYK NYRSYPLIKDCL
26267	56635	A	26414	368	675	SLSTLLSSRDCLPATISKQLRVL ARGCVVNNCFCKHLLNTCSLA GTVP*GASSGRQKFKLLAKFK VLARLCSSGSGRGEFSCFLFL GATGILRLMASSS
26268	56636	A	26415	40	355	LLGNPSPVVKGRCRHDGSEI/A PRVYFRGCS*SSHSWVSHFLSA PSHRPMLPTSRHRPPLRPLT*ER RGKRDD*PLHHP*P/CWSTCSP STSARATPTPPSGSGW

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26269	56637	A	26416	347	725	EAKRRRLPLSTLMEKRCFQPLWT RPSRKKPRGRTWRPPALNPTRI AGPPSPPAVSPFGPIPP* KGPFGSMGFLRLCFSAVQKVL APGSPA* PCLSCGPFRATLGD ARTPEKLCWLEERS
26270	56638	A	26417	525	708	IVAELIQHHQLPCHPLSGGKIK DQQVVFLSLSP*SSHNKTLTY* KTNQRQDYPEGCNA
26271	56639	C	26418	1	1050	
26272	56640	A	26419	934	1708	PQRGVVWVLSVILHFPWLWGSGL PNSAGD*AARYSWNQILKPD WKLSSAAGISFQRS* FCPKIPSGMYESKLSIITDKTP HFLPAQKTRSTPSPATAPLPGAT SPRPPRGRRRRRRCPEQQPPPL QAGPTAAARHRQDPLPRFSP FHHSPRASGAGSRPAPARVSPW TRRAPAPVSSGRGLAPKRSLS PRPPRPGQGGGRVAPRELPLA PRGLCVRLVYSLCSLCSGLPSF SLGSLVFSDDQ
26273	56641	A	26420	630	734	TAARSGYPGRAGTLTGLHPMQ VCCRRT*PYSRGT
26274	56642	C	26421	4	90	
26275	56643	A	26422	216	305	ICWKYFCAG*CGKYFTLGRSH SYRRSDY
26276	56644	A	26423	859	1248	CVISVFRASRKSXHNVI YCSVSVGQRPAPV/QH QGISGYPRAGTLTGLHPMQ CRCRR*PYSRGT* GSAPPKSVCPVW SSFSFPIKHAHACRVL
26277	56645	A	26424	132	548	SSGSWGFSGYQRCRES/CD YPPDMEIRGRVEQVGYTIEQ NHMRDVFGLRLRAEDVFPVI GVAAHKGGVYKTSVSHLAQ DLALKGLRVLVEVDHGPTR IVGLIISLGRSHSYRRSDNQTG TTVPLVSSV
26278	56646	A	26425	382	697	YAVKQAKTTFEDMTGRASLL LHKGYLEFLFLQTAAYQSGSP APQGTWSGTGSVCHCCSLAE* PFRITGACGLMARTGHARA SICPPDAVAPLSPSNWAF
26279	56647	A	26426	167	412	SYVKYFPHQPAQKYFQQIHCAI GLHNAGYPGRAGTLTGLHPMQ VCCRRT*PYTILSLQEQTDVVSL N

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26280	56648	A	26427	3794	4021	RGLCAPLPPLTPCFSPPLRRRAA SHLAPPTPLPTPQTPTTRALPS SPGLGRGA*RTVLPSPAPPEVPLA WGCRRA
26281	56649	A	26428	65	564	PHPDSGPQ*LQ*PHPDSGPR*LQ *PHPDSGPR*LQ*LQ*PHPDSGP Q*LQ*PHPDSGPQ*LQ*PHPDSG PR*LQ*PHPDSGPR*LQ*PHPDS GPR*LQ*PHPDSGPR*LQ*LQ*P HPDSGPQ*SDSGPRGHR*LQ*L Q*PHPDSGPQ*LQ*PHPDSGPR* LQ*PHPDSGPR*LQ*PHPDSGPQ *LQ*PHPDSGPQ
26282	56650	A	26429	184	438	DPAVDLCDLSSRRLIFS*RYVL VMLFSISLVSFVFSVHVICNYFP ALFFVCASFCCGAGGLVEFVL MIVGDASAALLCMRCEC
26283	56651	A	26430	524	1995	
26284	56652	A	26431	601	1058	LPSSGGRCSRSPKTR*SACLVSGS PRTPAMIRSGAGQPLARSPTPT PPFCRPLTRAPQASSMTWTGTS TTTWTLCAMRTDCTGLPSTST WCFCSTRSSWPAATSGSNSRAP ARSWTLCCLSC*SASTRPGPRGP CRRQWRRRATPSRPSAR
26285	56653	A	26432	1	371	
26286	56654	A	26433	71	335	
26287	56655	A	26434	2	416	
26288	56656	A	26435	60	370	
26289	56657	A	26436	466	1454	PCVFQIGPRRIHTVVRVGGNKK YRALRLDVGNFWSGSECE*GPL GVGGKTHLNGFKIHRARPALIF LNSAA*EIGAGKDCGLPNITRN VG*GVVEDELMPHGL*RLRVFP ISP*GPHGAEPPGVCGQHLSS LLDAKFLL*AGCTRKRTRIDVV YNASNNELVRTKLVKNCIVLI DSTPYRQWYESHYALALGRKK GAKLVRVTS*GLWGGQPDSS LLVMKTLSSSATEGREMRAF*A EEGQHWGVQGSRKLPGAFLP* AHIFVSPFQTPPEEEILNKKRSK KIQKKYDERKKNAKISLLLEE FQQGKLLGEKADELEVGSRRD

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26290	56658	A	26437	2	787	SQWLKLPSPHAGISRYNWD QAP*KTGGPRESYPHKKREVM KLGRPCPN/NPKIGPPAGIQHSP VCRGGYQEIPVPLRLDRGEFLP GGSECCTS*NGSSIVVLQCHL NNGAGFVPKTPGWKEFCIVASS DQQQPYRPVVTSSHLACPLGP QRKGAQAGLLEERRDF*TKKRS \KKLRKEI*LRKKKNCQNSAVL PGREQFPARGKLSRA/SRFQGP GQLWAEQDGFCA*EGQKSLEF LSLGKSKARKGQIKSFVLSPPM
26291	56659	A	26438	62	872	ANWTEPDDTKTMWRLSVPLDR SPQTQNTCTGEPLMPTGRQELPQ RGPEPMEAPAPARQSRVPAA GPVARQPHMRPPHSGQGEKQK MPGSRWPGQGRGRWGSPLS A**TRKIFTGIPILPLPGTGRP APEEGMQSADKNRVKRRGGTQ RNSALALEFCELLFVSSKWFCALP STLRLKALSAVALLAGDPE FGVRNVVWVWAGGVRCRVA HRTTEAGAFFPDWFWVFAAT KRGDGETSGCEHSEPVSGSSGG SPPRGQYLPGM
26292	56660	B	26439	1	606	
26293	56661	B	26440	48	381	
26294	56662	A	26441	16	209	
26295	56663	B	26442	466	1275	
26296	56664	A	26443	2	252	
26297	56665	A	26444	95	266	
26298	56666	A	26445	119	343	CTLRQESKLSRGDLTAPPVSSPR GHRSSKKGNT*LGSMQL*AES CRAEPPRPALLCPGRSVSACQW GPEGPF
26299	56667	A	26446	1	383	NTGLGRGKAMTPSMSCRISML LQRPGGVLVGWDPDAHPVGT *RHSVAQHN*MPW*GAEGMGQ PC*WHGMGTSDBGPLSDSERPE LS/HADSEGRVSKAKQSELAP GQKR*GQKPPKGYRFQERTQR
26300	56668	B	26447	430	540	
26301	56669	A	26448	111	591	PGAPSSHSGRLLAWEPVLP VASLGLGEAEDCSFLGRKAGV GPRHPR/ARRVHSGSRETRCG *QEPRPMLREPVCSAFLRTVKK LSGRVFPLAVKQVLSAAPAVP ALLRTAPKTPWDGPESAESQPP SLGPVAVLDISDRRKQETIKAT GGPGLRR

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26302	56670	A	26449	1041	1410	QEERGVVEE*ELEGRREEKRR GRGRRGSGLEEGRRRRRRGGG DETKDKR*RRGGHRRKEKKEE RRRRRRGGGAACKEEEDRLP TRAFSCVEQASASKSPLVELHP GPIPGPPLAAAGAC
26303	56671	A	26450	288	424	KRPAEGAPNP*GRPGIRPQA*K RPAEGAPNPRGPRRKEGRSGAK GSLDTGDDGEAWWAGSPHPS WP
26304	56672	A	26451	111	540	LPLALSNPKQEVVSGRGGQVDS QAGLMTGTRAVCCLQLCLNAS GAGDAEAMSAGPPGPGPARAD TEQLPSPSLPQVS*HWRGSASTS ATRTWPLRRRCSSMARSTCRAS ASASAGPWPWPAGAPVWRHSA EPSCSQLPGPSA
26305	56673	B	26452	57	558	
26306	56674	A	26453	804	1524	ARETSHGDFLHFPLIWLFLSKG NVPAARINIMNWNQGLISHVGE GNVNRKHDVIGNFPPWCLFN VSDLVMTIGSPRQRNHFGLVM VLGTIHTFHRHVGHCRGCPWS NQASHQKGDDEHEQNPTNNA QLLGAHVFNCPFLRPFFFS P*NKCFRGELFAPSSHSPFLA SFLGAACKLQRCWSAARMGPGR KAPARIPPAQPARVPPMPGAVI VAAPPVDAPIVRICVHVCLHH
26307	56675	A	26454	2	330	SCSRSGTALGVVPLAGPVRSAL TYLPAHSAGQRHQHDAGPTRG LGA1*DLPPVVTPEQSPSPCRGQ DQVPVAAAGE/PRCAPSLGSPPG LE/PVSLSSMSSPPRPPSCPLSG
26308	56676	B	26455	1	969	
26309	56677	A	26456	43	568	RSRLVFPLYFHASQGPGTASRE VPGGWA WGPVAQRINGICLLH STGPEAPSTMPPPTRLCGGPGCP ALPFSSQLAARGNPRSLPAAQL RALLSKISPPVVTPEQSPSPCRG QDQADACGKQVNMCSQAWG SPPGLELCPCHQ*AGPPRPPSCP LSG*FVLRGTGAPGAAPPSTV
26310	56678	A	26457	1	456	HEDAASSFOADVSLGNDAAVP LSGRGGINTYIPLIIPGFPYPTAA TTAAAFRGALRRGRRTVYGA VRAVPPTAIPAYPGVDMQPTD MHSLLLQPPPLLQPLQPLTVT VMAGCTQPTTmplPLPLAME LALWRVYTEVATADLPTEVT

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26311	56679	A	26458	609	1031	VCKSYPGHQGSSCLPDGQIQWL LHGYGGQEFQGE TH PF ^{LDG} *RG AESL*GHNSGHDQWCLGDGCC WG ^{WLL} TYERHEQLPALEAPG GWGKDGDSRGTESTC*EAGAG AGPAHPAPPAPAAEGEPDLFQL PGQGCSRIPCG
26312	56680	A	26459	1	393	
26313	56681	A	26460	357	843	QTEGGAQT ^{DG} QGSQTQSSENSE SKSTPEDNKICG*KPDHK* ^{TLF} YQEISISI*RCACFPFSRCMQGF GFVTFEKC ^{NFM} FPNVVHFFPAL FSPCYDMH*SSLSSNSLKLPSI VVT ^{VHLL} LNAS* ^{NF} CHILGLPL VPGFPYPTAATTA ^{AA} FRGAHLR VFV
26314	56682	A	26461	3	1172	GRAHG ^{EAAD} GGGGMQNEPL TPGYHGF ^{PARDS} QGNQEPTTTP DAMVQ ^{PFT} TI ^{FP} PPPP*NGIPEY GV ^{PHTQ} DYAGQTG ^{EHNL} TLTY GSTQA ^{HGEQ} SSNSPSTQNGSLT QTEGGAQT ^{DG} QGSQTQSSENSE ESKSY ^{RNGL} HVSYYFLSGFRD P ^{DFRQ} MF ^{GQ} FGKIL ^{DV} GIIFN* RGS ^{KVNN} ATARVMTNKKMVT PYANG ^{WKLSP} VVGAVYGPELY AASS ^{FQAD} VSLGNDAAVPLSG RGGINTYI ^{PLI} PGFPYPTAATTA AA ^{FRGAHLR} GRTVYGA VPPTAIPAYPGV/DLPGTDFTVL TSMVDMQPTDMHSL ^{LQ} PQPP LLQPLQPLTV ^{VM} AGCTQPTPT MPLPLPLAME ^{LAL} WRVYTEVA TADLPTEVT ^{VKPL} QMGPSS
26315	56683	A	26462	1196	1459	KQ ^{QRC} LETEV ^{WKL} SKLQIST KASNRQ ^{DRST} F ^{SAP} PRKSQ ^{LM} W* ^{TSLLSY} FQKL ^{QSP} QSATT ALISQ ^Q PS ^{TLN} PQ ^{WP} WGSCPGG
26316	56684	A	26463	2234	2702	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTAC ^{RRA} FGTKSIG* ^{GPTI} PESSRWQ ^{QKGG} VSGDGRSSCR RAVAPLEPV ^{PRAP} EAA ^{AR} PRPP SHGRDPP ^{PGDP} PP ^{PLR} TPASAM DKSAGTSC ^{RLS} PLKALGSARAE QTMGRPAAERSY ^{PLLR} AQYSSR
26317	56685	A	26464	70	398	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTAC ^{RRA} FGTKSIG* ^{GPTI} PESSRWQ ^{QKGG} VSGDGRSSCR RAVAPLEPV ^{PRAP} EAA ^{AR} PRPP SHGRDPP ^{PGDP} PP ^{PLR} TPAS

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26318	56686	B	26465	18	123	
26319	56687	A	26466	19	347	
26320	56688	A	26467	3	746	SRKLLSKSVP*LN*SR
26321	56689	A	26468	1705	2031	CDAPGDPQPGRLRDISWLGTTDR SASPQRLA AAAA TAGNRRCCSS GPRRRPPP*PLARPRQRQP QPVVWPPAFPARWAEHTCPLA PWQPRSPPTPSQPAAVTARAS
26322	56690	A	26469	1	420	
26323	56691	A	26470	65	330	RDCEARCARGPFWWSLSPRRK GKRQKSQLISQRLERHFLSGKN RQKRPSKMAGPDGAAPLEPGA VAAPMGPKSSRGSPGRAGKAA ETS*SPGRAGKAAETS
26324	56692	A	26471	327	981	ASYQKFFQLLPDCNLAPSPHPQ VPATPSTSWGHL SKPPGAFRRK HSSSRCPKAGHQWGGGQRNTP TAAHFRRLSAGSLQCPQLRVS PLTTGSLPPRSREPPRTAPPSPY PNCRLPKSTRTPSVGWSGPPSC GTRLQSHQEAEPAG*GSVRRPF LGP*RMPS*ALL*KHTGGL*GPP HPPMPTMCQPKQASKLQLLNC PQPSPSQGAGATMGNVG
26325	56693	A	26472	336	923	LKNIFSLPR SINIRFATLLDTPG VENLVIACLQKHS*PYF*GS*NI CLSFQDGTLYHKMHA VCLKCL *KPSLLSLL*DI EYIRSHYNIEDFI YFHHQREEGHMHFALNPIF RHYTKFFLKVYL* SGTQTSVLS LSDILSPKI*IAVFQFNPAHSL TSALHYLVVPRPRLLPGLDDQC PGHNTFPVVSIN
26326	56694	A	26473	97	298	DNLTLLPRLECGMIMAHCSLN LTFSSDPAAS*VAGTTGT*H HAWIFVLCNWLNRGVTVKK RS

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26327	56695	A	26474	1958	3269	KFTMSILKIHARELFDSRGNPTV EVDLFTSEGLFRAAVPSGASTGI YEVLELQDNDKTRYMGKGVSK PVEPINKTIAPVLVSKKLNVTQ EKIDKLMIEMDGTENKSKFGAN AIIIGVSLAACKASAVEKGVPLY HHIADLSGNSKVLVPVFNVIN GSSHAVTKLAMQEFMVLVPGA ANFREAMPIGAEEVYHSLKNV IK EKYGDATGVGDGGAFAFNIL ENKEGLELLKTAIGKAGYTDK VIVSMDVEASEFFRSRGKYDLEF KFLDDPTRYISPDCLADLYKSF I KNYPVVSTEDPFDQDDWGA W QKFTASAGIQVVEDDLRVTNPK RTASAVNEKKCNCLLLKVNQIR SVTESLQACKLAQANGWCV M VPHHSGETENTFITDLVVGL*PG QLKGTGAPC*SERLAKYNQLLRI EEELGSKAKFAGRNRFPNPAK
26328	56696	A	26475	2	684	HSGSSLLHFPILLINRKGFSP TGMISLMCNRVLSTHAKLQSC TP SNLPSQLPIGLSMSTPTKYR KLS FPGKTSQNITVPDSIVSPIFK ETL EFISKGGSSSTCIVSPGPA*SL SNA VSSSSMSSSLSNATNPQSSSH* KSCFPWYTPSVKP*PRPSSSN ST PKNIPETVLSANRGPLKRITP G NFSSPDLSCFTGQPPSIWRPL L KLVSQFKQAEPLLTIGNCQK
26329	56697	A	26476	1284	2339	APPSARGACAASRRAAVPALPT PPSVCSGSHMSTYWPAAAP**T PGSSTAASPSPAASRAPRAASPV LTASPPLPAAASPPAASHAPPA A SPVLTASPPLPAAASPPAASPAP PAASPVLTASPPLPAAASPALA AS PVHTASPPVHVASPPVHTASPP VHVASPPVHTASPHVHVASPPV HTASPHVHVASPPVHTASPPVH VASPPVHVASPPVHVASPPVHT ASPHVHVASPPVHTASPPVHVA SPPVHTASPHVHVASPPVHTAS PPVHTASPPVHVASPPVHVAYP PVHVASPPVHVASPPVHVASPP VSCSGDSTSCFFPQPGAVFPHS LAPSLGGWSHLVAALP

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26330	56698	A	26477	131	544	TGRPLRPLKQTQEIPSGCGVMG RATPGTSRGLGDSVRRVRGAIPA PRSSLGRGFTCV*LTGGAQLAPS LVPAAPRLPAALMDIQEPLAS AAPAATGPAQVTAATPLTTASA TPLTTETACSLGSSAASPLAPRA HCV
26331	56699	A	26478	1440	1877	PFQNLFRQNRNERTSCLCCLCMGA TWASLRALCCSPSP*HGWIW WWSTPTPFANGSVTSCSALTRS RWRPTWSEASGLWHAPAALL WKLRLPTPCFRSPISLSDDLTS HHQQGAPTMTHTCLGVGSSWE LQAFVLSYWFSPHLC
26332	56700	A	26479	56	345	ITWHLGLMMLSRSLGL*SGISFI NFPMK*EMIPY*KLS*IQNLQFQ PKVRPKGSQFGQVKH
26333	56701	A	26480	392	634	
26334	56702	A	26481	416	601	FLITDPRIWKASSDPASAKLFTFP SGFLM*AGTWMKLETIVLSKLT QEQTCKHCMFSLISGS
26335	56703	C	26482	34	279	
26336	56704	A	26483	173	307	
26337	56705	A	26484	196	527	SAVAAACSRPEEDAMELVLVF LCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLF VGILLISRRCKCSFNQKPSGPR R*GSPGGRTSSPPMQKPKAE
26338	56706	A	26485	597	797	PSNELKALGYTSSAWKRFSEQ QWGLSLGSSAPSRLPW*GDW ELPGEPPGDSSHRFPFGPIRAP
26339	56707	A	26486	3	184	
26340	56708	A	26487	256	635	GCVAPQIREQHAQSTENAAKPT RRIHSRQSEKPGRWHRGWVAG GWRRSKRAPARHRPCPAVCP RDGEDCSREAAGA*GLSGSSAC PTSTGASCCFCVPGQLNSVGF AVLGSKVLWTPGESPFQ
26341	56709	A	26488	1	378	
26342	56710	A	26489	1	571	

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26343	56711	A	26490	105	849	RRQDSGQSPAWPAGALLTLT HCAVPGSWAQSVLTQAPSASG TPGQRVTISCSGSSNIGNNFPVN WYQQLPGTAPKLLIYRNNQRPS GVPDFRFGSKSGTSASLAISGLQ SEDEAQYYCAA WDDSLNGSYV FGTGKVTVLGQPKANPTVTLF PPSSEELQANKATLVCLISDFYP GAVTVAWKADGSPVKAGVET NKPSKQSNKYYAASSYLSLTPE QWKSHRSYSCQVTHEGSTVEK TVAPTECS
26344	56712	A	26491	129	1191	RSRPQCLPGQGRRTVISTCGSSS DIGAGYDVHWWYQQLPGTAPKL LIFRNSNRPSGVPDFRFGSKSGT SASLGHHWGSRVEDEADYYLP VPIDSSLSGTVLQARGELRQEP TSSSARRSMKKGRDLGEAQLQ LRVEKTGLRTISSMAWSPLFLT LITHCAGSWAQSVLTQPPSVSE APRQRVTISCSGSSNIGNNAVN WYQQLPGKAPKLLIYYDOLLPS GVSDRFGSKSGTSASLAISGLQ SEDEADYYCAA WDDSLNGYVF GAGTKVTVLGQPKAAPSATLF WPSFEDASDDEAEL*CAIRDYY PKAVMVA*KTNITPLKQKGDTP SPSLLTPSSDEVKSYKNLLPGFP
26345	56713	A	26492	283	840	TLPAAGFTDVISIHKTGENFCLIC GINGRFAVHCITL EEAKEYKLCK VRKIWFHDAHTIHYLDSFVKVN DTV*TGKITDFIKFDTNLGRIG VITNRKKHRGSFDVVHVKDAN GNRFAPWLSNIFVTGKCNKPWI SLPRGKGIRLTIAFHSDKWFCSD ISVQNLCKRFSQGDGTGKINSEA RRCSNLQV
26346	56714	A	26493	1	843	MARGPKKHLKRVAAPKHWMML DKLTGVFAPRPSTGPHKWRECL PFIIFLRNRLKYALTGDEVKKIC MQRFIKIDGQVR\TDITYPAGFM DVISIDKTGENFRLI*LTPKGSAF AVHRTPEEGVQSCAK**RYI VGTKRNPFI*VTHDAR\TIR\YPR NPLIQGEMDTPFQIEFKKTWPR LT*FPSKVPNTG*PCVMVTWRC LTLGRIGVITNRERHP\GSFNV VHVKDANVNRFAITRLSNIFVI GKGN\KPWISLPRGKGIRLTIAE ERDKRLAAKQSSG

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26347	56715	A	26494	375	1327	QPYFPMETVMTLEGGQKPVME SYTLHYLPCLLCLPWRNPESSE WQRQLLDFPLASAPGSGLTQH MAAPKSGQNLEAKPKGQASLV LSSRKICGVLGACAAACPGGPA R*VDPAPFPPLAGEAGLEGRPRP QRCAAKWQSRDLIPGLPGSTGL PFFPY/PPCSPGALLSQSPQAAG SLLARTPHAQGCPPRLRPARIL PWPASSARRYTPQPSRKGTQRT PLFSLNLLLETTTASYSLDFLLTA PEGFSPLFTASQEHQDNQEQHD FLLQDEGLRSPVKTRARLPLGL HGDKVEKAGPWSLGARES NLC SATSQRSAVAAGVPRAQPLPPK GKGWLDPTWQGRDRTQRTLRL SIHHRFYGYSGARGWPGPLALLQ GFVRSLELPCAGSDQNRGQRLK GNPGAFAIPKTLDFSKAGKED KGGNGVCTTPSQAFDPLPRSSQ SPLGNMAVSGSSSSGWSKSSGT QEKKSLNQRKVDAAEKKEEK EKKKEPEPNFQLLDNPARVMP AQLKVLTMPETCRYQPFKPLSI GGIHLKDTSEDEELVEPVAAH GPKIEEEEQEPEPPEPEYIDD
26348	56716	B	26495	1919	2074	
26349	56717	A	26496	179	431	PPTS LIRVSTSTSTSLCTS WLCS SLSWLYSWAGPFFSGKMTASC RGSGQINREIVLMLLLRS*VFVV ISPLEGGSETSPFMDL
26350	56718	A	26497	37	199	DGLPGLALGLDAQASWSASVV TGHRRPAPPGLALGGCHGPAAP P*SGPAGSPCH
26351	56719	A	26498	3	224	TGHRRPAPPGLALGGCHGPAAP P*SGPAGSPCH*TA PRGAGTLP GSRRTGTSPWHPPLPHIPDVT GGHRH
26352	56720	A	26499	151	403	MPRHRRSASVV TGHRRPAPPGL ALGGCHGPAAP*SGPAGSPCH *TA PRGAGTLP GSRRTGTSPW PHPPGLPHIPDVTGGHRH

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26353	56721	A	26500	1	465	VSPKLLPSYASRPYLVPNALSSP SVPPALSAASSAPRPATRRRPP RGLSASWPLRRRSRQDAGAGS RRLRERQNRGRRRSDLAPTGLA GLRRDRPGRQPRPGKALAPFAV PRPRTNFRGRS*KSGSQRTTPP RREICRTHSRDRPKLVGRGT ANGARALPGRGWRPGRSRSP APSVGARSERRRPFRWRLRRR EPAPASCLRLLLSGHEADPRG GGLRRVAGRGGAEEAESAGGT LGDERALGTR
26354	56722	A	26501	1	1344	
26355	56723	A	26502	548	689	LGKFAPGLTASKAETAALCL KYPLEICTFL*GCVVCVVCV CVL
26356	56724	A	26503	154	476	TLA*AAAASTSCSPRPPSPAS TTTRWRAPWRTR*EPPELCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVL CMTVDL
26357	56725	A	26504	920	1420	TLA*AAAASTSCSPRPPSPAS TTTRWRAPWRTR*EPPELCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVL CMTVDL*LI PTSTPTT*PSELLAPSPNSPIDTT QMSGTATTSVPKCLAFSWQQL CYISLIQPLSL
26358	56726	A	26505	1118	1403	AGWDPSFLISFGLSNAISSSSS LSSQ*ESNASE*YSSATSGSSGIS WYPRSDVASSTIDSSSWRSMEG IG*DSGRFSKVGSSDSSSLPCHL SS
26359	56727	C	26506	29	379	
26360	56728	A	26507	3	948	GVSLCCPGWSAVVGSWLTAAS TFRAQAILSSSWAYREPPVRVG RRQPPLLLTRAQGRVISSFRH LHDFVWRTAGKESTSGANETG PLPERGRRPGRGPGSRSPRSH AVQREGAAGSVPAAGRDGGRA GHDVPHEGQRAEAAAGEAGGE FPLLLSDRRGRARRSPAAGALQ SRPGRARHLLHQLII*GP*EEVS L*VQQRGA VSGVDGGSASGQL RVHAEKAHLLQERNPEG*RAK DPLGTVSALSEEARFQLRWLAG VSAGHGGQRAAGRDWPCPAM NRLAMPGSVLFVFLVFGSGFH CVAQARVQWCHSSL

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26361	56729	A	26508	31	202	ILITYIKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQL
26362	56730	A	26509	471	1716	FKRGQYQGQLLRPRFHGGQILYA RRQGADAAGSDSFCTEWPAAAL DSDEKCEKHFPFIEDSTDYVHH GPSVRNPRARVVLRWLRLTLH ESAAVEGLAVFPARRHREPEY SIPSPSQAFTPAVLATRVGTQLG GHTQIQNPVTAPTILGNTPTFHL TCFRIFSLPRHLFPKDKWRTL APFLRTLVLVGTSSVHLSGIDP DLLVFEQSPTYLNTRSSNRWD RLRLKAMNLDKQTTINGMLP STEAPSSTHQDLVVNTNSTSY SKELTTDFWARFTSLNESITTKI NKVSPSTDIFISNPDKTISPFEP IDTKLSHMPVPPGLNSSKQLLN KTKGYNSRNHTSANEDSVST SKTWLVSVALCTSVIFLGCCIVI LASGCCGKQGGYKPGQRKSG SLQIKNRNHNKENS
26363	56731	A	26510	410	867	LLTLRSTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRVWTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISRFVFAA GQGLLGGYSNPRYSFSF
26364	56732	A	26511	135	756	VITILTPMLADTRRIERPPKKK GTTSLGQRKWLTTQDWPSVYP VA/HPFKPSAVP/LPVPNGLSK KRACPWQ*EGNLELLK/INPFS GF*LPVGN*KSTCEALKDF/CAL SGPAALGQWTRKC*GR/PFSI* QH*LFWHQDHPVRNPRARVSS LKSASFV*I*HDHAKKTLITLV GERYCKTPDVLTIKQNRWPLRS QITIMPVYL

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26365	56733	A	26512	161	2150	YLDAEKMGQKASQQLALKDSK EVPVVCVVSSEAIIVHAAQKLKE YLGFEYPPSKLCPAANTLNEIFL IHFITFCQEKGVDEWLTITTKMT KHQAFILFGADWIWTFWGSNKQ IKQLAVQTLQMSSPPPVESKP CDLSNPESRVEESSWKKSRFDK LEEFNCNLIGEDCLGLFIIFGMPG KPKDIRGVVLDVSKSQMVRSH LPGGKAVAQFVLETEDCVFIKE LLRNCLSKKDLREGGASPGSL RLAAGPPLTLNAAACPLRLAVL AAMAAAALPAWLSLQSRARTL RAFSTAVYSATPVPTSLRVDD LHLTEIVGMLDSVLTPESSGK YRFISGEVLCRITGCFTGVRVEA KDLFGGCCSNPNEMVTWIKVI VEKEVWLYLRYILKALPPRTEK MAVDQDWPSVYPVAAPFKPSA VPLPVRMGYPVKKGVPMKEG NLELLKIPNFLHLPVAIKKHCE ALKDFCTEWPAAALDSECKE HFPIEIDSTDYVSSGSPVRNPRA RVVVLRLVKLSSNLDDHAKKK LIKLVGERYKCTDVLTIKTDR CPLRRQNYDYAVYLLTVLYHE SWEYWKWEGKK*D*SRHGKSI YGENSSSERKYPGKRFSR*KLL RKNMGN*LKKSSLGTKEIEEYK KSVVSLKNEENENSISQYKES
26366	56734	A	26513	3	1186	PASTMSIRVTQKSYKVSTSGPW FFSSCYLSGSPSAHISSLFSRAG SSSFQGGGLGRGYGGASGMEVIT AVMVNQSLSPFIDKVQFLEQQ NKMLENKWSLLQQKMAQSN LDNMFESYINLRWQLETLGR KKLKLAEELGNMQGLVEDFKN KYEDEINKYTEMENEFVLIKKD VDEAYMNKVELEYRLEGPTDEI NFLRKL YEQEIRELQSQILDMS VVLSDMNSHSLDMSIIAEVKY QYEEIANRSWAEARMYQN*Y AKLSQLEAALQRAKQDMALQL HEYQELMNFKLAQDIVITYRK LLESEGSWLESGMQSMIHMK TTSGYAGSLSSAYGGLTSPSL YSLGSSFGSGAGSSSFHTSSTR AAVVKIEAQNGKLVKSSDV
26367	56735	B	26514	361	1215	

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26368	56736	A	26515	230	561	VRTRHLFCFAAAEETPVFTMA NEKPTEEVEKTENNNHINLKVAG QDGSVVQFKIKRQPTLSKLMK AYCEPRGLSVKQIRFRFGQPIS GTQRNLS*KKESVDAASFIVVL
26369	56737	A	26516	1242	1415	NSPSDSSLVWAWRRPQSRWS ERGGANNRGGGRLLGNSVFG RK*LPHRRVSRVPNTK
26370	56738	B	26517	1	585	
26371	56739	B	26518	258	1081	
26372	56740	A	26519	42	275	TFAWSEEGTSPSIQSSWDPRCP HRNTPAQTGKPKRAWPRHPV HH*EPHGDDQDDGPAVSP*SY SQYPWPEGLDV
26373	56741	A	26520	646	1905	
26374	56742	A	26521	6510	7361	
26375	56743	A	26522	1	879	DCQDKVPRRKEPSMCSGLLRV KSWVSLQTYWKPRATQGVYV LPLTEERMVVLGASRVGKSSIV SRFLNGRFEDQYPTTIEDFHRK VYNIRGDMYQLDILDTSGNHPP PAMRRLSILTGEAHWCLGWGG RARAWRVSLGT*QILEVKSCL KNKTKAAELPMVICGNKNDH GELCRQVPTTEALLVSGDENC AYFEVSAKNTNVDEMFFVLF SMAKLPHEMSPALHRKISVQY GDAFHPRPFCMRRVKEMDAYG MVSPFARRPSVNSDLKYIAKAV LREGQARERDKCTIQ
26376	56744	A	26523	2	478	
26377	56745	A	26524	120	1167	GHVGHMCTGQHMASAYVGRV NVLRLKEVDRACFGEKAKQ*VG S*EELWAIWGGQREVCLGIEEA GAIHSTRHCNSQNGVRVWAPYL WALEAAPV*VQDRSSPGSQACS LPSPCALTMGTGIMPLYQEA WKPRQRPGTSGGTVSSEPHC*D AGSGCWLCPGLREVAHVSAE ITYTSKHSVEVQVNVMSENIL GTSGSDSDVWSSKGRGYTAAS LLRAEDAPGPGPKVLEVPVVV RCFFYFSLGGRWQRSGHLT*LE TKWRNGDIVQVLPNGKSRGH QQQVPLLTGDA*EAGALHGFV HGGKKEAPWPLHSCPLAHCCFS GRYNRPGAVAHACNPSTLGDG
26378	56746	A	26525	225	438	
26379	56747	A	26526	216	364	

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26380	56748	A	26527	2	397	SCCSDWSAMA*SQLTAISASWV QAMLLPRRPE*LGGSNPEGTG* SERRLCHY A/HSLGDRARIHLH KKGRQEGSKEMSRAQTRRVW HATMETEQKQNYGRL*CCSPST NTRRRTSMRKNKAIAIEIERYS KGI
26381	56749	A	26528	312	1061	QQTLYSFGVSFYSSYCLIFSHG CSSSSICRRARLYHWAAPFRPP GRKRRDCTGQRKTSAGEPEIPP PLHHHHHHYSHHHHRHHHH HHHHGLQRSSKNFLLWPE*ILF CGSRRLGRAALFLLRSFSHPAK QGAESLLGKQS*KHLASTQCQGP RGRGS*EKWPRAQLGRKQPSSES AAGAAGLAHGPDQSLVLERAG EK*SGLRGEGNRPFGSSSLGG HPLLQRSPAESSPAGTGVRTSH LEGRPASF
26382	56750	A	26529	161	453	SSSLPCSPSSCPHTSFFLDARQEP RTCRVVLKEL*QKQGLPHCR* QEREKSCSPSGSPDLGAPQPR VTPSLGLCSSWHLQASRRHCTP RCPQWKR
26383	56751	A	26530	301	630	RWKPKIRGSEGSAS*PQGR*LLP SGRRGATGSAESTLPKAESSAG DGPVPYPSQSSSLIMPRPNVA ATSSTKLEDLSYLDGQRNAPLR TSIRLPWHNTAGGRAQEVKA
26384	56752	A	26531	1	1394	
26385	56753	A	26532	240	1150	LLLHVPSPSPASTGPPSCGPCWP PRSPAAGRGSSSGCLAGEDPA TTHKSAGTGECGRGPVGHCGQ AHTGPSYPSGPPASCSPAASAV TRGQSCRSLTFRPGRHQIPGAE* QLPRGQGETGRTGLGHYLLLS CSSRWPLPKSGDGSPSRWEYRD S*ERPGRRTPAPRCCSRSTGLGD GLKKFPSSY*GP*KCAPSGCGG QAPWSAGGSTCPDART*MPR ARARSWAHTGRPCFPRLLSIQA TP*RTGGRTCGFCLAS**GSRRG RPSSAESLPAPPGCGQH**PER SARLSWGGGMRGPR
26386	56754	A	26533	1463	1627	

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26387	56755	A	26534	1	1758	MHKYVRYSTVHNSEDMESTQ MSINDRLDKNIIHHRGILCSH KKKQDQHVLCNIGEAAGNHYPQ QRNTGTEKIQCVLTYKWKLN NKNTWTQSEEQYAVGPVGGRI GRLTNNRHTQDSSEWVRGVTA FWSRGANNALDIPAFHKFSEGR GSLHTHDGPPGPTSSLKLSFSHS FDSTGLCRPHDLVGLIIPMTVN ITSQLDWLEDAQMAGEALFLE GKLTTRKDIYTENPSLHHHHQR PKVDKTTKMGKKQNRKTGNS KTQASAPPPKERSSSPATEQSW MENDFDELREEGFRRSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERVSA MED EMNEMKREGKFRDKRIKNEQ SLQEIWDYVYKRPNLRLIGVPES DVENGTKLENTLQDIQENFPN LARQANVQIQEIQTPTQRYSSR RATPRHIIVRFTKVMKEKMLR AAREKGRVTLKKGPIRLTADLS AETLQARR/DVGANIQHS*RKE FSTQNFISSQTKLHK*RRNKILY RQANAERFCHHQACPKRAPEG SAKHGKEQVPVAAAKSCQNV
26388	56756	A	26535	620	886	INGVILSKPPLPPISTPIAGALL PLTKEQRGDF*KPSRNMRTSCW KTPESRANFLKFRPRSHCLTRM GSSCLLPSTCLSSSSSTFHH
26389	56757	A	26536	237	415	RCLQRPSAGTAGHPSPAGRPPL AAGLAG*RARHRSDLPGSAASS QESWCLRAALPEAPA
26390	56758	A	26537	373	691	
26391	56759	A	26538	2	233	
26392	56760	A	26539	5	68	ALQWEEKHEL*EQSLHRKPGG
26393	56761	A	26540	184	434	GRRRGCTVGEAAVTQSLSLCS HEGRAIRHQRDSASIVLLDQ*Y TRHPVLDKLLAW*ALAEKAT LGSAIAAEWKITPAFSFP
26394	56762	A	26541	466	683	GRPHSLPHPHADSSSLTTDCS* WRWIFKHKTDIRHQRVHTGQ KPFKC*Q*GKAFRHSFDTVTKHQ RTDAVGLHQVTCLGGVLLWGA HWRGHPSYSLWSAHCCQHGGE GASGGGLSLHLDRSLDAAGRP QPVLPTGQNILVGPLPQISLCS RSLCVLRDLGSLSPGEEGSH SQKWTSEQVKLFRSRHQSTSDV

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26395	56763	A	26542	194	558	GCDRPSRRPGAPRPPAATASC PPRSCWPLVPSHCP*PCRKRRY PGERRTSPAPPVPPGPGRPAG*T PPCELRPSSTHVALGLALPGSE GTGLRTSVRARDRLHRRTRERA AAGTAPGP
26396	56764	A	26543	1	248	MVAIHNDADAKCWGDVEQLE LSFTAALPVLPHPSLPGERPLQE AVAFLCWLLVDVLLKATVSKV GGGSALASVARVMKAQAFSPL LRILHKASTSSFRARKDSAHTPS CLLTSPGPERAGPLTQDSCQSPS HDSFRAPALLEPSSALSTAVASL RRREERLEPEQRVGELGSLGER QHEPSDNHDFQPKSKQEQLQK TLQPSGGPHCSSLLLMVFWWK QWRKTEPLKAERTGYKEKEIST KCSSPSGQLSQSSAAGPAWPE DARPEATWSATLLSFDPCKND SIEEPCSVHISCTAYS DPLKIHNS YRECGLCEPVNLEVADPSSSR ELWFRAGAQQAGAMQGVTEL RPPEFVKSRRKPQVSGHMGNC LSKGKRFLGHCQYKQGLPQRH QLQAEERESGMRTTGAYAV LTTGVSPWWIWIWERRWPCAF PGKNEEPAGKVPPFSELVLTQ RC**CQMLGGCGAIGALIHCCS ACAASPFSPWRKAPPRGCCFSL LASGRCAPEGNCLKGGRQRQT CQCQSGYESTGF
26397	56765	A	26544	423	621	LPSRGAGLGTCSPPCLSLPSPPW APVRPEPPR*SPPPAPQRPVPS TT QGLNCAGAGHGTGRQLHR
26398	56766	A	26545	1162	2027	MTPEPEWSL*VGNYKRTVKRI DDGHRLCSDLNCLHERARGV SRADPTMAGAE*PAASLPCTGP QYGTVEKAWMAFMSEAERVS ELHLEV KASLMNDDFEKIKNW QKEAFHKQMMGGFKETKEAE DGRKAQKPWAKKLE
26399	56767	A	26546	1	504	

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26400	56768	A	26547	3	1215	QTMVFLTPILVAILCILVVWIFK NADRSMEKKKGEPRTAEARP WVDEDLKSSDLHQAGAGGN AVEGVQSKVNGRATGFASKL DIGKRRREGLEGTGSPPKTHA YALKKSGPWNPGTWQHRKIVR GLQFYTVFFPHSSVLAFLAPVID PSVASSSLRSSTTDNELAESE FADADEWQESEENVHIFPSHN HYPEKEMVKRSQEFYELLNKR RSVRFISNEQVPMVIDNVIRVT GTAPSGAHTEPWTFVVVKDPD VKHKIRKIIIEEEEINYMKRMG HRWVTDLKLHRTNWIKEYLDT APILILIFKQVHGAANGKKV HYNEISVSIACGILLAVF*NAG LVTVTTPLCNCPRLRVLLGRP AHEKLLMLLPVGYPKSKEATVP DLKRKPLDQIMV
26401	56769	A	26548	3	263	RPGEMACKYPLRCSGARVERL AKKKAHAACLLWTATIKVITNSV KLRRSS*GNRLKPSILC*DMKA LRQYPMPLRAWLLPMVVWVM
26402	56770	A	26549	82	318	SGEAGKEEGTRMVRIRPEPKRS LLWTATIKVITNSVKLRRSS*GN RLKPSILC*DMKALRQYPMPLR AWLLPMVVVRVMV
26403	56771	A	26550	91	714	SESLVLVWCGRVSCVLFVCVD VCVLVGGSGVAVRCFGGRGCG PRRVGRRWSCWGWCGAVLIR RVCLAVMFGALCVHPLLYPR TLLLRGQKVDRFKTNLSSGESL VTLVIFPAHGLARSFNLNVL FGVHFIAVEFWHAGVIVNKQ VKGKILAKRINALIEHIKHSKSQ DSFLHCANEQRQT*QACAGPCM GPEPQOACLNTCIRS
26404	56772	A	26551	29	363	FAKMTNTKGKRRGTRYMFSPR FRKHGVVPLATYMRITYKKGDI VDIKGMGTVQKGMPHKCYHG KTGRVYNVTQHAVGIVVKNQV KGKILAKRINRIEHIKHSKSR DSFLKR

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26405	56773	A	26552	186	512	FHLSKHRAPPYPVTAPPRTSWG SLVKQVNESNGSRLRLRTSLVHE DLEGVSVVSGMNCDSALARYII ILETLIYLIISPRCWIIDSSGACSG LAMYLPLLGDDGVLLCTPNFM AWRSNRTQFMMRSSSHMVDAS PRGRHMSPREAFGYSSRAHSHM LLSLLAPPWPQLMGRGLGCQQ QERPQECVPLGMTRSPYSEIH GSSRALGSSPGSCAHEVLGPSIL TVNPFIPGSSVHVWPSNGNETN KLPHTRAGSCGSATCSVKRWG PQKPRPLPKPPLVPQALLVRG PAAAREEA VQPPKEEVTQRP HSSPGVFAHLKGPRSVVEIRME YGEE*PPGRCVTSSFGGWTASS LAAAGPLTSRRAWGTSGGFGR GRGFWGPQRLTEQVAEPQDPA LVCGSLVSLVLLGQTCTEDPGI KGFTVRMLGPKTSWAQDGPED PRAREEPKWISL
26406	56774	A	26553	1	382	FRTSCRQLSAPPARSLRPPG GG/EPAPGRTSRGHRPQM*SGT PAPRPPARSTVSPASPLPKPRAG RCGSRPRSACSTFRPC*SLASVS SAKTQGWKMWQPATERLQHF QTMLKSKLNVLTLLKKEPLPAVI FHEPEAIELCTTTPMLKTRTHSG CKV
26407	56775	A	26554	797	1213	AWLKFLLGTRRFLRFKSYFSID SARSLVPGRWPAAGRTSRGHRP QM*SGTPAPRPPARSTVSPASPL PKPRAGRCGSRPRSACR*GAPG SRGPAFPRRTPSVTRWALGLPW LQGLRTAFWCQILSRVTAATLP DKIH
26408	56776	A	26555	1002	1655	KEFCIYNRNPACSYGVAVGV LAFLTCLLYLALDVYFPQISSVK DRKKAVLSDIGVSGEPHPACTP CTESTEGCPGHRRRKDNPLNEG TDAARAAJAFSFFSIFTWVSTAT AHQPTLVPPH*APGWVVPFAS AQP*ASPACRGRCQPCITPGSEVA GAPSTLGGQGRHYMDPSQDSS MPYAPYVEPTGPDAGMGGT YQQPANTFDTPEQGYQSQGY

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26409	56777	A	26556	262	628	QHFQTPWPWPLCAAAGTSAGT SHSGSSSGAFSSWPCWTA AEPA ARKRGRPAGSWSSPATGAPGR CRHRILSRGAGGSA GFVCSGLR GIGPLGI*LSGTFPGLTAGPETPA TERAPGASQHFR
26410	56778	A	26557	1098	1599	RIRKSHHCINTVTLGRGNSLGG DFVRESPPGGDRLNVGQTHKHR GLGRFAQPHGTSAGTSHCGSSS GAFSSWPCWTA AEPAARKRGR PAGSWSSPATGAPGRCRHRILS RGAGGSA GFVCSGLAESGL*ES SSPGRSQG*PQGQRHPQPNGLP APPSTSVSVLVRISR
26411	56779	A	26558	440	698	IKLWAATFIKVCRLSFSCGMSIL *RCTGSKSCCCRRPLWAGPT SCAGGCGCCWGP GPPAELGPD TPAAEEAAEACCWDA AIFLA
26412	56780	A	26559	448	576	
26413	56781	A	26560	513	782	EIWWAWTKWCGCWVVSFC HLCGRHC*GTCWSSETWR*MC GTSGTAPPCECWREGKDDCGR DRPMETHGCCSSFSISSPRAGKD ATTGT
26414	56782	A	26561	798	1505	FLRATSPSGHHFSYHLWIWISLR SFLCNECSESCLLNSSMWQAP GLSHYSLLLIWLWLVFQTLNPR HLLHLLPSPLNVVDRLCSCQHH HHQ*CHHLHNNLH*NHSHHRH HHHQ*RLPLHYHLHQHHHHHQ NHCQQHHHRYHQHHYQHHDH HYRHHHPWLAGARALCDSND AGCPGSGDGDWRPYSADSDSL DALSFPRPLFPDCQSLRGLASA VIQGYNWLVLTENHILHFLF

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26415	56783	A	26562	1	1073	MHATNSSSVPEIQVEALCPLL TQPKSPSITSAMLCQLKKPQPS RSKEREADPISCGPECQGNWDL CVEAATGLYGDGHLRDSRTR VLMITIGTYRDLQGLEGRAGHV AELHVLVPVWAIQDRGYVLWC WTASLHPRDVAREQGFPNDCT WALGCTLTAESTHTHSAALAR QAYSQLSKKPTLLNEPEHITEK KFINLARFEALNSRTWLGVLV WIAQIQDVPVTVESTTGQRAAR ISPREADRTLKGVQVQGIQTVI MSVPGRKEGDKLKEVSDGRE ANQAGMKWKGCKSSSGTEN AMSGKEVGILQEEKGDWSHGV VRGWQEKWMTYNFWACGRG KNATCRLEMTRTSENDLKHQ EGLWHGRERAMLGDTHTLAW REEEMEQQALRIHSLYGKTSQ QRALGSWWVERFMGMRSGSS DCNGLVTEG*TLQSA CIPEPTCS H*GSPAP*LHP*GAEKQSTTEH SPCPGLPQAERGAQPRVPPCP QDPADPCKFQWS
26416	56784	A	26563	1	387	MESTEIGHIYEQFTLT KMTKRF NKEQLVLISLALLDSGHTSN SL AWPSCLVSGVGS CRWVCGLT D/CQE*SLRPSQAGV CRRSTPD PVCLGVTRGGCRTEKIA ACSFL WKLPRPGAPARCQPELSCM
26417	56785	A	26564	47	472	LLRLHFWQEERLKPSR KKITKK HTKKRTASLILHAMICCR SLNSS KTKNTKCLNSINQRLKIL SLQK GDPLESTCRH*CCHVHR RTKAP GQRRVGRQHVV SAGNHRHPHK GDPLESTCRHATVTGQ GLEFA GGPLQTLFA
26418	56786	A	26565	329	615	TKTEIGTRSINELRQQL FATTNT FFFP SIFGESNTTSTSLTLKNS AI WCPTGTKLPEGRGTGS NLCCSAA SAGDTQANRVWSG PSAN/C*QT CRRRSC

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26419	56787	A	26566	525	716	PTCLLTTPPSKGRQTPYATGELR LASDGCPSGTKLPEEGAGSNTQ ANRVWVSGPSANSSRPAAEGPDC CRTTCRTTCWKPTTVTCSST PCCQPACCVSSCCQPCCRPTCC VTSCCQPSCCSTPCCQPTCCGSS CCGQTS CGSSCGQSSCAPVYC VSSCCQPSCC*SGPSSAGLLEFA EGPLQTLFAWVLLPAPSSGSFV PDGHPSDASRSSPVA
26420	56788	A	26567	3	390	EGPCKCGWCC/RSPTMTL/CPT VFITCRPGDSLRLHHQGRPFQ AQNCQPFQGTSS*LQEFFPIQ WLECRRALAGIWQVPLWDEA SLPEEGAGSNLCCSAASTGDTQ ANRVWNGPPANSSRPAGEEAD
26421	56789	A	26568	658	1005	NSKYWTPSGPPRLASGAIYGN SLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGSGPHL GPDG*MVGQVQHDNELYFC/ APAGSYPLWVKALPQPPSQPL KPVASM
26422	56790	A	26569	1149	1715	VLQLNLPGPVASWCSRDVGPPL ARPIPPAPHTLSSAGPSAAAP GPARQLPHPRGDSRTARLLPGQ GSS*SWR*GAWQSGCQSYRKP GLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGSGPHL GPDG*MVGVGPSGAGAAPEPA PGLWDPPGHCSQASTPPGACKE RETLPTALPRLS
26423	56791	A	26570	32	335	LWSLFDHHVQRAVCDRAKYR EGRRPRAVKVYTINLESQYLLI QGVPAVGVMKELVERFALYGA IEQYNALDEYPARRLY*SLSY*I YELTKCKDSQEKNG
26424	56792	A	26571	407	842	TEPLITINRLQRRRSAPVAAAG PAGTLARRAPAVTAERAAGPG PASVHRRPGWRRASGPAQAQ ALRPPPPR*PRDSASPLSRKELL KLLGTKHYGRLTATEAQAPQG QHKLLCRETGELVPHWAGSHY RGISNPINNIDHIL
26425	56793	A	26572	409	614	GLPPPAVGDRQCLPVRH*RPS QTIRAEQEPRSAAPRRKPKG CRRSRGSSPLADNLGDLGSGGQ GG

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26426	56794	A	26573	3	266	GNHCRRQYRDAQ*W*EAGRV SSCAGSARLGKAKGRGPQGV MGNE/MRSRRAQEFKKYLHKS TSR*KSHTGPEALSTSPGAKKE GCSQ
26427	56795	A	26574	36	384	GWYCSSRSDVCSGGNSSAHSQ LPHQLPLRLRPGGCHPRESSSP SKQRGGPVGDRQCLPVRIH*RP SQTIRAEQEPSRAAPKRRAKE GTRRSRGSSPHEKLGDLGGSGG QEVVP
26428	56796	A	26575	101	334	CSTSKEK WQCGLRAECSPVFPA TEVPEYSC*GRKPSHLSCHRAP TLEEAA NRKWPCTQYDAIQNA CYNDLSLVRLS
26429	56797	A	26576	435	761	QGTNTWVPHVLRLLGLHTSP PEGIAELPRSLPSLTHQACQLD CVLVAIGTAILVAQTATTSPPIC GEADAH PASTPLPPSWPPQGRQ LSC*NPLGWPWPSGRVQTP
26430	56798	A	26577	38	236	RLLPLENCLSSASGTCAHQAP LLLCSCPNC*SCCCCHCCCP GCCWHCHRPSTKGN SATFTA
26431	56799	A	26578	1316	1548	FFSITGLSSVAGGQFVNLYLKR LNSNFIYLSGYVIVYINIVFIYC I*KFVLHVTLRTDCCKTIVKKH VFRLFLKAM
26432	56800	A	26579	1	272	RPVNSRLDDFVAACAAMAKIK ARDLRGKKKEELLKQLDDLKV ELSQLRVAKVTGGAASKLSKM *VRRPDHSPRGWGARVHRDRR RISKLA
26433	56801	A	26580	1	363	
26434	56802	A	26581	286	867	IYALSLGAGGAAAAGLCSNEP RFKARDLRGKKKEELLKQLD/ DLKGGSCPOLTRSPKVIETRCGP PKLSKIR/VVRKSIC/RVFSPIYYP DFRKENLQNSYKG/KKYKPLG PCGP*GRTRAMRPPGSKARRE NLEGPKEAGSGKGAFTRCGK *RGSRALRGRLCQLKHKENLKT KKQQRKERLYPLRKYAVKA
26435	56803	A	26582	164	346	LHPGRRPGLTHLGVPSPGPGPT EKLAPGKPSSAACAPSPALD* HIAFGVDALCPTFGLN

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26436	56804	A	26583	316	723	LVGGWGLWGGHLGPLYGQA QGASPLLPPPPPAHRPPPHRHST EHGVEHPLVT*TAPLSPCLGFR LGQALHRGASTKGLLTGGVW GLHSWPIGDGRATHEAVVRAS PWPSRLGTHGVRGGRDVQEG AELPAV
26437	56805	A	26584	177	418	RNPVVAQGLLACACRMFKVGNR TPSSSAEWPFSSAPPKKGPLPKA TSEPLFPHKRR/PLASVPSHREC RPPLGASKTAPRD
26438	56806	C	26585	149	277	
26439	56807	A	26586	1037	1455	EESYGLLSVPSVTGSLLLQDLH KLGCHQFGHKKRRVSGIWMMA VLPFFFRCPHILLLENPRAN GPARQPTNHQPP*KAGTQLPNS VAPVQSQTGFPPTPARKARAPT WPGAARPPGTASNKSPARSPCS SPSFSILP
26440	56808	A	26587	175	450	
26441	56809	A	26588	77	337	RDHEPTRRKKVTRHPNVRRNK LRTRRL*EL*HSLRGSAAFLKE GRPWRSGGGAQRR*KYWRKG KYSGKMQSWSRVYCSLAKVRA
26442	56810	A	26589	1043	1555	ALRQGPAGARAPNMDSSVSR QVPGPOVCRAVPTEILASPAVE RAPAAALSSTTIWMPMSLCPW RPVLAACSTMVTRGRSTMYLP TTTGNAGCTWPKASLATRWLS SPMGRQARSLMLGAQVTLSDW RSMPWRRRRGRSSGRNLSTI*WR LDWSLRRTWRSGRAWMSGIST
26443	56811	A	26591	313	462	VCFTPEPARPRIRQTRPDRRNSE HIRT/RRRKKLRTLNLNRRNKL WTRHL
26444	56812	A	26592	630	777	KERRGREKKKEEEKRRRRGRG GRRRKRRRRRGRGRGRGRGR* KERRGREKKKEEEKRRRRGRG GRRRKRRRRRGRGRGRGRGR RGSRRFL
26445	56813	A	26593	284	461	HSPGGSAAFLKSVRRRTHQFR TH*FHHKNRTFTSR*SH*RMQR WDQREVKVFL
26446	56814	A	26594	573	968	AQRFCBSQWRCSRRVLEENP APLDTTPLSGRSKSSGRGLVLS LGL**PPSTRRSSHL*QPSSP*AS TFLQVRMTAPSL*PQPPA*KL RSSPLLLTKNPFEEAAAF*SRGP PVSLKDTASLQAFLGW

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26447	56815	A	26595	3	699	RGRSRANS PQLLEGGADPTVG DIGHLSVGVGPVHNNAVGCQP DQTTPKHLADNPGPWTLDALT YQPHAANSCHKRGIAAS*SLMII MVIIIFLVLLFWENEVNDEAVMS TLEHLHVDYPQNDVPVPARYC NHMIIQRVIREPDHTCKKEHVFI HERPRKINGICISPKKVACQNLS AIFCFQSETKFKMTVCQLIEGTR YPACRYHYSPTEGFVLVTCDDL RPDSFLGYVK
26448	56816	A	26596	2	483	
26449	56817	A	26597	2	1041	WPQDGSCTWLAVAMGCWLAT QQGSLTRVPVATSGIQGCQAAP SPMWAAWTHGWASCYFRAAL QLPLPPGSTGNGSMSTSTAYSA SSPGFM/YTKAQGERSDHKENV FYVQHQQYVGGATQAFAKEN NQKAYKETYGVSHTRHMLQ IPKQQNEKYVQPQFDQSTIKNI ESAKGLDVWDSWPLQNAAGT VAEYNGYHVVFALAGSPKDAD DTSIYMFYQKVGDNIDSWKNN AGRVFKDSDKFDANDPILKDQT QEWSGSATFTSDGKIRLFYTDY SGKHYGKQSLTTAQHLQYQYLT YKRSFSIVVDAILPPLKRAAW PKSRHPPQVGLMEVQHLFPIN NFEEHV
26450	56818	A	26598	116	338	

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26451	56819	A	26599	971	2485	FISSCFVRACGTLNPGVTMFYVI LGKFCDAEPWFPHVMEQQLR VVGKGLWGFVRVSLSGFRIHGP HQKTASLAQVHKAVLHDGRTV AVKVQHPKVRAQSSKDILLME VRALPFSFLCPQSTFMWLVDEA KKNLPLELDFLNEGRNAEKVSQ MLRHDFDLKVGGMQCRVWW SGGLMEFVDGGGVNDRDYE RNKIDVNEVRSRAQGCCAGER GVNGFVHCDPHPGNVLVRKHP GTGKAEIVLLDHGLYQVEEAFV TQPWGLWGQSLIWTDMKRVK EYSQRLGAGDLYPLFACMLTA RSWDSVNRGISQAPVTATEVG GPSRPCLFLNAEISHLNHNVP MLLILKNTDLLRGIEAALGTRA SASSFLNMSRCIRALAE*VWA PPSPPLLA*ISFSEAFNLWQINL HELILRVKGLKLADRVLALICW LFPAPLCTVHVITILLWNPLRT LWPLSQGGQAEALWHSSLFFSKK TQQTFFFLVCAIGLDVPTTSVK
26452	56820	A	26600	831	1205	RKEGQGPSVHPLGSGCFPPGHA FWEALEANTWVPCVRL*RTVP SAELLGLAPGGRWRVNRDRG RVAAASSLGEPYSSPADASFP RSDSGGLDRQGGSCRYPKELFG SHPQARCTEGSLQVL
26453	56821	A	26601	377	962	LFSIFTQDPKRELLDVGNIGR LEQRMITVVLKACV**LCSI*AN ASVIYIFQEWTDHLLVL*SMC HLNLSPLCSLHSIYRNREGGS WGRKKTIC*LRCFISQNDISIPQE DFTPEMQILE*NLV*KILIAWFI VFSGAKSKPYLTVDMQMMDFIN LKQRDPRLNEILYPPLKQEQVQ VLIEKYEPNNSLARK
26454	56822	A	26602	1	810	MDAKKRKLYKYSTDSPAFAI TFIIMPYMENQAAKLAERLSL NELVFSSEALTHSETFLPQPDNR HQNMSSTIHTAPIDTALGGNPA FLYLFLQDFQPTQDNLSASVTP SAGV SARLAPPTPGPFTDVVV LDVLDEVGQGGVEESAAPESA GIGEEGGGDACHGATSRA*P*Q ASPPPPSSPIPADSGAADSTSP WPTSSSTSRTTTSVNGPGVGGG ARRAETPAEGVTDASELSCVG

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26455	56823	A	26603	28	457	GGIPDSTARLSILTPRHHLQRSC SCNGTATRFSGQSYVRYRAPAA RNWHIHFYKLTLPQQAILLFTN ETASVSLKGFEGCLDAVVVNEE ALDLLAPG/NDGGRLAGDTSPLH PVLPPQ*LLQPEHMPQWWEVL MDPRGRRLCLQMS
26456	56824	B	26604	205	1722	
26457	56825	A	26605	11	374	VSPSRSGIPGTHASGQL*TGDR S/GPMGPPITATQ*DGSDSAYH GLATLHALLPALPGAAGF/PSGT SEPCPSSPC/GQHHHAGQLGHD LPVHCSEDP RPQPPPLGGPLEDL PSLLWHSDFFI
26458	56826	A	26606	69	551	QSGRSPQHVFPSVRGSGARSRG WILVHPSQYHHNPQRIYSACGR SGEHISPGYPCS/DGHDAVDQ ADGTHHDACIFH/PRGSPRSP/G QCCLLTGGSRSRGTSGASATPG GRRGGPAQGGG/PASRNSVVEE LTARVLAPAPALASAPQTLPL GFSISPSTK
26459	56827	A	26607	476	1016	CLWLLSCLYCSLGDCCLLWVAV SVLCQVSAPRQALCFAPGENGD GGQQGLRGAPP GPGRGPAPQP GPGYPGARQRGSPQP*LSSEP GPYLRLSRSGGR*GPGRCCSRSP PGR*PVQAGDEDDQDAGSHI*T QPRVSEEGTDEDQWSLPQEV SASVPYQPLSHCQTVPASLQPH CLFS
26460	56828	A	26609	247	342	RSIMPWLPKSGGWEVSSIPP*RC LHQLWSTSRNMAL/HVRVLQT EQAVKEYNALVAQGVVRVGGV FHSTC*WSLKRRIH
26461	56829	A	26610	129	272	NDTVSGLGRLESPTLMRQRNV CSHCYPGSAK*GYMIYKDALPR RTSL
26462	56830	A	26611	133	453	QVDNTVLRNAVHTNTYLQGL THPSANHKSLYTLNNFLHICR LHTRRMHGKTGRVYGITQRAV GIVVNK*VTGQILAKRIVPIEH KHTKSQ*SFL*ELRSPVAS
26463	56831	A	26612	352	543	VPSINCGVPQGNMMLMCRVLQ TEQAVKEYNALVAQGVVRVGG VFHSTSDGSLKRRIH*VPKKK

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26464	56832	A	26613	576	927	FAERTRTHH*PKPRWKALGC RARTAVTSRGCLAPSRRRRLP GRRAASQPGPNADPKACRPWN PRGSQVHAKRNALCFRSADAP PRPDASPGQIFPGRRRKECQTC KTRVRLGCL
26465	56833	A	26614	67	415	ALARKLPTNFQWVKKIDASPGS PIPLNAP*PSPSVQTTPTTGHG RALSTVSEVPAGARLTYRVFP TRCKRSLILPSPVWVSRIPTAK SPILISSPGGAHAASVSALT LVS GYE
26466	56834	A	26615	87	347	GIRY*LCHGFYHAYLGFRRTS SPLQVSRPPRGQTQSEP*AQSP RSPLELGLHTASHRAANAAS SFHLRFPGFHFHPRPSPLF
26467	56835	A	26616	3	175	GFVTSSFFLGCLSPFDA YDLVFL LARE*HWKH*TQSILTLIAQCVF PEQPKRLCWVS
26468	56836	A	26617	539	788	EKEVPTLLDCCALGQ*KCKMI QLLWKMV*SFSTKLNLLPNNP AVVLLGIHLKELKTYVLTTCT LMFIAGSQRNLRDYFRP
26469	56837	A	26618	843	1136	VKEQVYRRIASRSVRRCSYQS RPGLLPTAGHHPQHLYSDCHG NDIYSVYYQCEHGAHSSSETG VPRFPCPWVSETAQ*TCASHP GPSAQRSAL
26470	56838	A	26619	2073	2329	LVQTSRPPDPSWA*SATVTRPE QASWARNLSRFLLGMATVSG RGLPSGPGRAMPAGEPAPGA AEPAPGSAIPIHRRPLLGQ
26471	56839	A	26620	723	1023	ITLLGLSLIPLISRLPWTQSWGFL SFLSTPTSLISSTPLILNTINSML TLRFLPPGGAFF*TPCIPPTQH PHLDVSLTGISNLRPQSCFHCL HLS
26472	56840	A	26621	99	288	CLCQNKLGEGRDDNFTSQWSS AC*TFCLLAVDSAETTAES*C CCCCCCSAAGGWRLVH
26473	56841	A	26622	130	450	RQLKLTAGCAKSPWFLWLKSY HSLYLAAACLLGLTYTRLGRSQ SSPPIHSHFPPATSL*QQLHGQ PA*WLYDGPATP/SIAPPAHLLP PPWRGGTSPWLPSPPLQE
26474	56842	C	26623	1	672	
26475	56843	A	26624	408	581	LIKDESAPRTPQTVLASAQFCLL CR*ARCCRGSCCCCCCCCCC WWWCCCCYFGND
26476	56844	C	26625	66	264	

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26477	56845	A	26626	70	551	AAEDVWVVPSELYWPGPHGHC ETPRAGVFVVTSHHEEGPGAGTA SSSSKGPSPWARWGLEVSPPLRW SGQVGGAGSAESGQPLGSGFTF KAMGNLGESEARQAQLIHDRN TASHTAAAARTQAPPTPDKVQ MTWTREKLIAEKYRSRDTLSLG FKDLFSMKP*VSPPLRWSPGQVG GAGSAESGQPLGSGFTTKAMG NLGESRARQAQLIHDRNTASHT AAAARTQAPPTPDKVQMTWTR EKLIAEKYRSRDTLSGFKDLFS MKP
26478	56846	A	26627	479	961	PQSSLQGNLQMPWGSCLDST HYRPSLVGVDFQLPSFWLVICG TCKHCHRMHLHSVALFWVPLHC GWSIPRPRCPHPHPPPLRGPS HPPSPPWACPPRTGVQSATCPF A*RPTWSFTCDPTTKRSMRGLT HILRSGEKRPLPALCARSTSGSA TTSPGT
26479	56847	A	26628	1	223	MGAVQKAYNLQKKRRRRRRGR RGRIRGRGRGRRRRRRRRRR KKKKKKKKKKKKKKKKKKKK EEEEEEEE*EEEEEEEEEEEE EEEEEEEE*EEEEEEEEEEEE FEFRRRRRRKKKKKKKKKKK KKKKKKKKKKKKKKKKKE
26480	56848	A	26629	1	341	
26481	56849	A	26630	78	354	ENDSFYNDL*ATQRRRRRRRKK KKKGEERRRKEKKGEERRRR RRRRRRRRRRRRRRRRRRGRG RGRGRGRRRRRRRRRRRRR RRRRRRRRRR
26482	56850	A	26631	1	327	
26483	56851	A	26632	41	246	
26484	56852	A	26633	1	170	RKKRKRKKKKKKKKKKKKKE KEKEKE\RRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRR RRRRRRRRRTNNETGE
26485	56853	A	26634	1	282	MCIESEREEEEEEEEEEEEEE EEEERRRGRRRRKKKKKKKK KKEEEEEERRRKKKKKKKEEE EEEEER\MRKKKKKKKKKKK KKKKRQSL
26486	56854	A	26635	1	396	
26487	56855	A	26636	1	255	MLWLPQPALGTRAAETLACSR RRRRQLYNCLYLRRKKKEEE KEKEEEKKEKEKEKEKEKRR RRRRRRRRRRRRRRRRRRRR RRRRN

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26488	56856	A	26637	1	290	MKKKKKEGRRRRKKEEGEEEEE E/DRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRTTT TTTTTT
26489	56857	A	26638	2	423	
26490	56858	A	26639	3	167	QKKEDEEKEKEEKEEEDDEEEE /ERRRRRRRRRRRRRRRRRRRR RRRRRETQEAETI
26491	56859	A	26640	1	325	MEKNEKEQEEEEKKEKNSKKK EEEEEEGGGEE/ERRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR
26492	56860	A	26641	1	618	
26493	56861	A	26642	1	291	
26494	56862	A	26643	3	155	YRHLPKKKEEKEEKEEKEE EEEEEEE/ERRRRRRRRRRRR KYEKKCL
26495	56863	A	26644	1	1410	
26496	56864	A	26645	578	842	TQEAELAVSRDHATALQPGQQ SKTPSEEEERRKKEKEEERRRR KKKKKEEG/MKKEEGRRRRRR RRRRRRRRRRRRRRRRRRRRRR KKKEEEEE
26497	56865	A	26646	215	471	
26498	56866	A	26647	432	761	
26499	56867	A	26648	1	357	
26500	56868	A	26649	2	281	
26501	56869	A	26650	533	758	EQKKKKKKEKKKKEKEKEEEE EEEEVERRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRNTEK
26502	56870	A	26651	264	429	HRAAPATSDTQE*HRNNAFGEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEETLFSNM
26503	56871	A	26652	1	279	
26504	56872	A	26653	1	795	
26505	56873	A	26654	1	642	MKKCKTSVIGIATFYLSIPHIYT PPNQTSFMAICAIEVQLTSAE PASIGFPVQKSPGHLQLNGYK SSSKQGFPPLKQESWNSSVKI TTCNVGDKKNINDRRSANMMH VNNFPFRRHSWICLDRVQSETL PQEKKEEEEEERRRRRRKKKEE ERRRRRRKKKKKEEEEEEEEE RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRKKERISL

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26509	56877	A	26658	1	2267	MKVELMGFAEGLAVRVREQEE VRLNWKVVELLWTLRDVVKPG ANSFRVSSGSGVEVFMVYNRT RVKEPIGKARWPLDADDMVV SVGTASKELKDFKVRVSYFGEQ EDQALGRSVLYLTGVDISLEVD TGRTGKVKRSQGDKKTWVWG PEGYGAILLVNCDRDNHRSAP DLTHSWMLSLADLQDMSPMLL SCNGPDKLFDHKLVLNVFSD SKRVRVFCARGPEDVCEAYRH VLGQNKVSYEVPRLHGDEERFF VEGLSFPDAGFTGLISFHVTLDD DSNEDFSASPIFTDTVVFVAP WIMTPSTLPPLEVYVCRVRNNT CFVDAVAELARKAGCKLTICPQ AENRNRDWQDEMEGLGYVQAP HKTLPVVFDSPRNGELQDFPYK RILGPDGFGYVTRPRDRSVSGL DSFGNLEVSPPVVANGKEYPLG RILIGGNLPGSSGRRVTQVVRD FLHAQKVQPPVELFVDWLAVG HVDEFLSFVPAPDGKGFMRLLA SPGACFKLFQEKQKCGHGRAL LFQGVVDDEQVKVTISINQVLSN KDLINYNKFVQSCIDWNREVVK RELGLAECIDIIPQLFKTERKK ATAFFPDVLNMLVLGKHLGIPK PFGPIJNGCCCLEEKVRSLLLEPL GLIHCTFIDDFTPYHMLHGAEYS LECRQHWGKNLYFRVGLKKK KKKKKKKEEGQEEEEEEEEEE
26510	56878	A	26659	1	990	
26511	56879	A	26660	1	235	MTAKCVCGWGVGEREREKER EEEEEEEEEEEE/ERRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR
26512	56880	A	26661	1	1101	
26513	56881	A	26662	348	806	
26514	56882	A	26663	39	684	LRCENPISSHVGHVGVSLAHTR GLFSRLILADREDISENWCSLVC CVCVCVCVCVWWLCISLPGD MMTLLMKKDTLTFEETQFYIS ETVLAIDSIHQLGFHRIKPDN LLLDKSGHVKLSDFGLCTGLKK AHRTEFYRNLNHSLPSDFTFQN MNSKRKAETWKRNRRLAFST VGTPDYIAPEVFMQTGYNKLK DWWSLGVIMYEMLIGKLHG

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26515	56883	A	26664	3	276	IKSIDDTSNFDEFPESDILKPTVLSSA*AVHWRQSESTLTSISFVATSNHPETDYKNKDWFVINYTYKRFEGLTARGAIPSYMKAAK
26516	56884	A	26665	95	405	
26517	56885	A	26666	3	349	GPGGWLSLSPLVL*ALES*KEEE EEEEEEEEEEEEEEEEEEEE/ ERRRRRRRRRRRRRRRRRRRR KREKKKSVDCTEEVAKYVGL ASLRJSRVPPDTSTKEKTIEKVN RRK
26518	56886	A	26667	1	370	MHVAVWSCPTAQSSQATVDSGK TLAETESPIGLSSKVGKNIRAG EWDELKYDRFPGQKPKKKRRK RKEEEEEEEEEEEEEKKKKKK KKKKKKKKRRRRRRRRRRMQ QSHPNPTSAILAPWA
26519	56887	A	26668	1	430	MTFFPFDKRETDILLILNFSMEH CTRGGQDPLGYQTTKKGFKDTE TPEKESLESKAELGRRRKKKN KEEKEEKEKEKEKEKEKEKEK KRKKRRKKKKKKKKKKKKKK KKKKKKKKEEEEEEEGMRKR RRRRRRRRRRRRRR*RRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRMRKRRRRRRRRRRRRR
26520	56888	A	26669	1	708	
26521	56889	A	26670	1	1233	
26522	56890	A	26671	1	366	MSYVAAYVMFFCSVLGKFMNL EEVEKRRRRKKDKKKEKEEE EEK/DERRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR EEEEEEEEKKKRRRTLYCM*IA CKLKYLWTVSGHILCPNTN
26523	56891	A	26672	1	667	MSKEGNNRHWDRLGGGWRR VRVEKRLFRDYPSSHPRGAFAF TSPDSIGRCTLRFPGQMGLHQ PALIAILRSGADLSHLEGPMLA GASACAPAVSPGDQALQQHPG EGRKVPGKRRRRKEEEEEEEE KRKKKKKKEEEEEEEEEEEE KKKRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRNKQTKGP PCKNMLVFPCQNKAPSPCLQI AAEFSAWAR
26524	56892	A	26673	365	670	
26525	56893	A	26674	29	370	

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26526	56894	A	26675	1	1364	MEMIWPSKGMPTSTSYSNKES SLLSVVQTSSYSHTHRGSSSE VESLNRPTGSEIVAINSLPTKK SPGPDGFTAIFYQRYKEELRIK YLGQLTRDVKDLFKENYKPP NEIKEDTKKWKNI PCSWVGRIN IVKMAILPKIIVEDALQIYYDMV LVCVGVGVGSCRIVISSLEVLES RGQRIFFLVQAEQVLWAFKEVS SNCNDKSTLRGSVVKLQCTSGT SAFDIFQVGSRLVGEHRLPSVH SATYMSLT YFELAGLLEKSSQL VGSTGVEDIVAIMIPEPKGKEIV SLLERNITVTMYITIGTRNLQKY ERWKKKRTKGLEYQEFGDDV KFRSLDIEAEMPDHLRLPRNM HASSPSKRTARGRNKNKSSRLT MFGVEIQEEEEEEEEEEKKKR RKEEEEEEEEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRGGRRRRRKH
26527	56895	B	26676	1	499	
26528	56896	A	26677	1	1684	
26529	56897	A	26678	2	297	
26530	56898	A	26679	68	319	IQHITS*TKKKRKRKKEEEEEEE EEERRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRSHTSIPKESTLLQSQSVGLG
26531	56899	A	26680	1	1617	
26532	56900	A	26681	92	338	LEKEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEN*VERY KKEGW*KQRRQEKGLIPDG
26533	56901	A	26682	1	548	MVDQRHLVLTSTKKNQNNNF QVFVNIENVGREPQDKIASPA GQCTASVTADLLSRDLHFTKV PSWSSDGPYPYPACHLMSEPY FWGSCCYDTPIKTKTNEEEEG EGEEEEEEEEEEDEEEEEKEE EEEEEEEGEGEE/ERRRRRRRR RRRRRRRRRRRRRRGRGRRR RKPRGGR
26534	56902	A	26683	1	1215	
26535	56903	A	26684	1	571	
26536	56904	A	26685	1022	1365	TSLLPSSSIPSRLPVVLVSRILS LWILACLAPWRWDLIRKASCL PAFSLLLSGANGSFLSGFALL GRKEEEKEEE*EKEKEKEKKK KKKKKKKKKKKKKKKKKKKK KKKKKKKNF
26537	56905	A	26686	24	355	

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26538	56906	A	26687	120	594	
26539	56907	A	26688	117	487	
26540	56908	A	26689	2	2482	
26541	56909	A	26690	2	654	KGDVGEWLSAGKGESSAMFAS EQEISKDEQGTPLVGSFYWEVD SPRKESQA WAPGQEWIKLERD TTECKMFEQLKPIEPVQKTLPW VGEVAATLQEAMKRCWREA RVKKKPVTFEDVAVNFTQEEW DCLDASQRLVYQDVMSETFKN LTSVAWVRKKEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEERKKRKRREK KKKKKKKERTTWLWGNPLT
26542	56910	A	26691	789	1072	
26543	56911	A	26692	1246	2367	
26544	56912	A	26693	579	1214	
26545	56913	A	26694	119	1870	SCSRNRLPPVSESLTRPLSLA RWLPPGLRQPSSRDYWPKGRL RLSAVPSASPWALVSCLLPPSS SQEKAGKILKKRVEKQQPEEKV GKGLEESLCPSSMSNHTKERV TMTKVTLNFYSLNIAQHEERE MR*RILFEKIEEGLKDEEVING NVFLRKETEFRLKRLRLGLE FESLKVIGRGAFGEVKITATCQ VGHVYAMKILRKADMLEKEQ VKHSCSSAFILVEADSLWVVK MFYSFQDKLNLYLIMEFLPGGN YLTMKGHKDTLTEEETQFYIAE TVLAIDSIHQLGFIHRDIKPDNL LLDSKVLGHHWHELFPQEPRLR GFLSQCCDTPFRALRFLASPSFQ VPLHSRPDLCTGLKKAHRTEF YRNLNHSLSDFS*W*QLR*PK AETWKRNRRLVSNICGF*KN AENVSLGQVRWLTVPVPIAPE VFMQTGYNKLCDWWSLGVIM YEMLGKLGHGRGLPQETYKK VMNWKETLTFPEVPISSEKAD LILRY*RTSLHLQIKSIDTSNFD EFPESDILKPTGNITTSIVSCDYK NKDWVFINYTYKRFEGLTARG
26546	56914	A	26695	271	446	YLVHILDALPRDPTALRRRQRC LGS*RKHQTRLRSGRPSSGPGG TDSVTAVSAPAK
26547	56915	A	26696	1	171	WGVIWRENGRCFSGLLRAGLG AAWEPRVGEIKILVS*LGTC*IK LICQSWVGANPRA

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26548	56916	A	26697	1	179	MWKGPKGLDMYKGSSVSPKTS DILGRD/NSPAGLEGANSGVAN CLWRGPCGRKLWEASRN
26549	56917	A	26698	2	140	DN*KGVHKRILSKLAPELGSFK GFRSLAVNTHNSYGGKGNRPL KIR
26550	56918	A	26699	3	601	
26551	56919	A	26700	232	1809	
26552	56920	A	26701	1	851	MQQEDPEESTKSPNPTNNKKQE KKLSLFGGLFTWTRVKFGAVT QIGGPPLGDQSPVLLLQRLFSK GYRVSPSKAQISSPSVTYLSNSV LIKTLTKTLLPKEAGVIHCKG HQKASDPALGNTSADKGLFRP PPFSPHQARGFAPAQDWQIDFT QH/RP/GVRKQKYLLV*VDTFT G*VKAFPTRSEKATAVISSLLSD IIPRFGLPTSIQNSRLAFISQISQ AFFQALSIQ*NLIPYSPQSSGK VEQTNGLLKTHLTKLSLQLKK DWTVLLPLALLRIRACP
26553	56921	A	26702	434	867	RLILPNRLGSPLLVWVDTFTG* VEVFPTGSEKVTAVISSLLSDIIL RFGLPTSI*SDSRPATKSSFSLSIP TLGSHDAPNPTRSSPEKHRPLSL HTIPQNFRCPTDPLFRFIFFAFF SNTLHIMGMAAEGPKSTLYC QFTEK
26554	56922	A	26703	96	415	
26555	56923	B	26704	1	933	
26556	56924	A	26705	1422	1774	DCPPSPIAFPQCTHQHHHHQYH YHHRHHRRHHHYQR*K*NPLG PLFVYCYFQNH*ACHCSWGSN EHMTIASESAQVLPQPQDSQG FFEDLELHYFFGDPSETRPQKQP KVSVQQIL
26557	56925	A	26706	355	1014	RHLRPOERAPAPSGSVSPRPGCS QAPGGLLRVGRGGMLLPGCAA VADLQEEVPGFSWDAWAVKG EQRQGGGGVVKH*DAIPQQRV SDPGPPEPLASAPGQLSPSTPEY RRPPEGESRRHRRPDLAQDQRGA AVLLLAGARGLSPLPRIPALGA ASFPPPTLQFFLQLPSSGASTTSA GFFLLVLHQPLWLLLLDFLFDN LLLLRHSLFIPHGFLKCVSIPAF
26558	56926	A	26708	95	298	GSTQVLWAAWGGAGWTPRWLP VFATWPWWQDMWPQQA WPLP QGVDIP*ACPPPLRT*WL*ENR KAGS
26559	56927	A	26709	110	195	

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26560	56928	A	26710	241	957	KSPQIGLQGSWGAVGVGMRDP KERATEASKPDLLAQRQEGGHI FILFFSDYIPIFSSYLSLQRSSRGP SFFGPFSSPHNIPCEGRONSETPP WPSLGKRSKKSSLYPLPKAPQP KSRAPSPISNNLKNFPQPSSEKDD GPQPLWPQKWPLAPLFSRSPS* DDSGPCTEYCRARRRFSFEDM AHIGPPKKVLYKIALGKFWELA DAKKRRKGTSETETCLLSRAT ELLPGKGRHCRGIL
26561	56929	A	26711	496	708	GMLFRGSGACRRGGRTGGSGH A*PEPPVLPLLLHAPEPLNSMPH GLPAPPASPCHFPNLDSCVHSHS DTPLSVLPLPHLKSPLSSDFCS YEVKKDAILSPMLSWWAGHRS AAGED
26562	56930	A	26712	302	561	TFLLQLAAVWSADRVREALRP ALWDWRSVAVPHSPSQPQTG*R GVGVHPAAASRGGESSHPTAF DRSPPPPKPLRI*PEPSARSGPL
26563	56931	A	26713	1	411	LLVFQVHQCLHCKLL*PSYVPL GYTEAFLATQNGRVSLSLWAKH GHDPDFPLARADFRAQESPSPN DPSWLL*YFER*WSQATTKG*N RCC*RC* ¹ LQAPSRRPEAVHTN DPR*REVREEHMLVLQVLTR
26564	56932	C	26714	361	642	
26565	56933	A	26715	1805	2260	
26566	56934	A	26716	472	1667	AIHLLSLQTEFLVAERSSAAGRT TPATRAAFLAASCGPLHSCPTL LCSQLCCFSRSTRVSGPKASLG IKEIASVDRVNTRRPACSTSSWL HNSGFTLSLANRDGGKRIRSET AKKGMSGDRSMKSWEVRRGY RWSSRAVRRPRACSSDGGTHF ALPMAARGSSGSPSGSPANSVR QSLKSESSISAIWVAEQAGNV PRTSAQFGTGSESANTAARLIE KLLRAELDKPEIRDERIVGWWT TFGRPQLGSRVGFACCSLAARM SSTSQNLEAFAFGGKFCFLWALL LGLDDTFESRISDTGSAGMLV EFFAPW*VHSESANTAARLIEK LLTAELDKPEIRDERIVGWWT FGRPQLGSRVGFACCSLAARMS STSQNLEAFAFGGKFCFLWALL GL

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26567	56935	A	26717	2	237	SVRQTATSPAHHKNSKRLIRSC QGF/HPEPPPTGACYKCPQPRIP HEPCPI/SQDPTENWTVQLTW QPLPELELWPKAV
26568	56936	A	26718	1	313	MESAQKEAVEIFGQPHAASSSG DVKPLLFIDFYKCSGEKVVCME HALRACYMCRKSGHWAKECP QPGIPPKLCPIC/GDPTGNQTVQ LTWQPLPELELWPKAL
26569	56937	A	26719	377	583	
26570	56938	A	26720	1221	1394	VASFYSLQQPPYPSTSFQSWR HTSISPF*FQLFSFGIFWQPLP EPLLELWPKAL
26571	56939	A	26721	160	234	
26572	56940	A	26722	163	414	
26573	56941	A	26723	212	399	YSLKDCWPLSLSLNHLILAS PFNLISLILISVPLFW*RTETRFI WQPLSEPLELWPKAL
26574	56942	A	26724	809	874	
26575	56943	A	26725	49	220	
26576	56944	A	26726	71	375	LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQT/TSRNISPILNPEL ATSARNLATRPRNACSPGFLS RVPSVRDPTGNRTFQLTWQPL PELELWPKAL
26577	56945	A	26727	1	1011	CSEYEDSSAPVPATDLSLTLSS SVPQPDGTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAH EHAGLGVQGGNGALAFNSNGH RHA VPTISSGTGRRRTPSSAFA LLNLHQWVWFGQAFSDRLKA ALSASALLRFGSDWLPSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTREL QKRKKGMPHPAYEDLNIAIT LPANVVLHQPSGFRSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLEKDPPTT SGPQT/TSRNISPISNPRQRQV LSMDPKLRHRSRTGKAAFPWC LIAGTPL
26578	56946	A	26728	150	211	
26579	56947	A	26729	445	549	
26580	56948	A	26730	193	249	
26581	56949	A	26731	372	564	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT/TSRNISPILN/PEK KETRFIRGPKTPAPVMD
26582	56950	C	26732	185	640	
26583	56951	A	26733	1662	1774	
26584	56952	A	26734	233	527	

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26585	56953	A	26735	380	731	LGSGDLPEINPLSSCSLLCEKH PPTTSGQVTSPRNISPILNQEL ATSTRNLATRPACSPGFLLS CVPSVRDPTGNQTVQLTWQPL PEPLELWPKALCLTDSFPDLLG LTAED
26586	56954	A	26736	2	182	
26587	56955	A	26737	2	89	
26588	56956	A	26738	2	89	
26589	56957	A	26739	161	460	KMKFEFMKSSRTKDRQQEQV LEPLFTIAKTWNQPKCPSTID*1 KKMWIYTYMEYYAAIKRNKIV FFAGTWMQLEAIIILSKLIQEQKT KIHMFSLIRGR
26590	56958	A	26740	2	418	WYQHLMLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDFVPHFIRKN*SLF TIKAWNHPKCTSVTDWIKKM WYIYTYMEYYAVTRRNKIVSFA ET*MELEVIIIVSKLTQEQKTKHC MFSLTSGS
26591	56959	A	26741	902	1065	
26592	56960	A	26742	326	484	WYSWDCQLVTPWRPRIIPGLG TWMELEAIIILSKLTQEQKTKHH MFSL*SGS
26593	56961	A	26743	527	825	QPLWQQLH*EVPSCWRFS*IC YSSGLTVMLSSWLDLIRPPWTL R*PREWRQCMGENHIGRGLGF* RPWTWMELEAIIILSKPTREQKT KHYMFSLISGS
26594	56962	A	26744	398	557	HYWLGTVVHTCNPSLTGS*GR QIT*AQELETSLGNKNVGCSELI LLSTLGNRV
26595	56963	A	26745	3	359	HRPIPIGTTISSWMDAWGRLEA RYMSYLHSRRGDHA*DKLQRD NRFASQTHSIHWAKSSCHCRFES RPFFLPSPSWYNRSWGGESAE RTWMKQRGTCLSHSPDLLHP GLCQHKVGAR
26596	56964	C	26746	127	216	
26597	56965	A	26747	135	197	
26598	56966	A	26748	84	202	VLIIHRRDIMIPETVD*WEY**P* RLVPGQVQVWKPAIP
26599	56967	A	26749	483	669	
26600	56968	A	26750	1	274	EIRNKIHVSENSQIKTVKEKPSIS SSVRLKGVNKRASFPEDRKD YTGSKAPKGS*GYTIN*LK*NN KRKKKQNKLLMPKTEQGQKN SIR

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26601	56969	A	26751	63	398	TPLRQPCSI RN VQ QEPVGRFSGI GLPLSVARSSPWEAWPQCKWR FQ NAGD*DIRQPD RGQGRPAE PEKREPYLR SQGA FLGSHSSGI QSQLLGLGESCSYGATGKPVHP
26602	56970	A	26752	3	231	SVHEEEKMALPLGQSHCGLLY LYY**RCFKCSFYCILFIKNAFI Y*NI*YINTHTHTHTHTHTIYIYI YNCLYI
26603	56971	A	26753	4266	4944	TDEIGASRLSRVESLAPEVKQN TTASGCELMHTEMQALRADW KQWEDSVFQTQSCLENLVSQM ALSEQEFGSQVAQLEQALEQFS ALLKTTWAQQLTLLEGKNTDDEI VECW HKGQVSWLPV*KAEPR EDLKSQNLNLCRFSRDLSTYSG KVSGLIKEYNW*A*TLKGCQN KEQILQQRFRKAFRDFQWL NAKITTA KCFDIPQNISEVSTSL QKIQVRVLSI
26604	56972	A	26754	3	556	
26605	56973	A	26755	143	724	GWIPSDNSICVQEDCRIPQIEDA EIHNKTYRHGEKLITCHEGFKI RYPDLHNMYSLCRDDGTWNN LPICQGCCLRPASSNGYVNIYEL QTSFPVGTVISYRCFPGFKLDGS AYLECLQNLWAPHPGALLW KEEDLNIFLSFSISHTSGWQLLC FIFALC*SPLPPQHLPVQ LAPP LCSKCCSPA IKDV
26606	56974	A	26756	3	1393	CLRPASSNGYVNISELQTSFPV GTVISYRCFPGFKLDGSAYLEC LQNLWSSPPRCLALEVKIPVS GAVRVTTLPVTLGHPNVVTQR WKAGASDKGELVVLKLLFSPT AQVCLPPMVSHGDFVCHPRPC ERYNHGT VVEFYCDPGYSLTSD YKYITCQYGEWFPSYQVYCIKS EQTWPSTHETLLTTWKIVAF TSVLLVLLLVILARMFQTKFKA HFPPRGPPRSSSDP D FVVVDG VPVMLPSYDEAVSGGILSALGP GYMASVGQGCPLPVDHSPPA YPGSGDTDTGPGES*TCDSVSG SSELLQRLYSPRCQESTHPASD NPDIIASTAEVASTNPGIDIAD VDSNKLDPDWTQKYRVASPAR STCEDRSGAPVGTHELFFSIPS SARQDWAPLDSQLESPQCR LPT LQRDFLVDPPAERPVLDP ELT ETWCNPNKRIERHMEHSGIEA

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26607	56975	A	26758	1	500	
26608	56976	B	26759	19	148	
26609	56977	A	26760	184	539	LPAKEEEGHKSKSGPLLGPARRA LPGTALGARGAEQGDPEADH* GADTTKRCPLGPAPVPRKGIP AEGPRRGRAGLGMWGPGLGA HRTAAPSPAEAPSPCQHPSSHSC PVACFEPVF
26610	56978	A	26761	1	441	DENRELLGVELDGIDVLIQLSV FKRHNPFSTAEQEMMENLFDLS CSCLMLSSNRERFLKGEGQLM NLMLREKKISRSSAL/KVL/DHA MIGPEGTDNCH*VCLTFLALR/T IFPLFMKSPRIKKVGTTEKEHE EQCCSILASLLRN
26611	56979	A	26762	1	2403	
26612	56980	A	26763	17	751	AKMPFDANKLYCSEVLAIFFS PLENRELLGELDGIDVLVFA*Q VFKRHNPFSTAEQEMMENLFD SLCSCLMLSSNRERFLKGEGLO LTLL*LSHSSDCEMPTWRGGS MEQGGRMGLGLVSVGLEHALL LTYGLYQRLPPQPQNAQPSFVH REKKISRSSAL/KVL/DHAMIGPE GTDNCHKFVDILGLRTIFPLFM KSPRIKKVGTTLPLPAAATPT NRPSAMNGRVRMEAEQSSAHC

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26613	56981	A	26764	1	1914	MAEGERGADVPH/GPRGLAGR RGVGGAAARGRAG/PGGT/EGGG GPESLGGSGVGDSSGGCAGPP SAPPARRRVPLAMGPRNLLIDW IWIMDTTLGLGTEGGHSPVVL PLCASVSLGGLTFGYELAVISG ALLPLQLDFGLSCLEQEFVLGS LLLALLASLVGGFLIDCYGRK QAILGSNLVLLAGSLTLGLAGS LAWLVLGRAVVGFALSSMA CCIVVSELVGPORGVLVSLYE AGITVGILLSYALNYALAGTPW GWRHMFGWATAPAVLQSLSL FLPAGTDEATHKDLIPLQGG APKLGPRPRYSFLDLFRARDN MRGRTTVGLGLVLFQQLTGQP NVLCYASTIFSSVGFHGSSAV LASVGLGAVKVAATLTAMGLV DRAGRALLLAGCALMALSVS GIGLVSFVPMDSGPSCLAVPN ATGQTGLPGDSGLLDSSLPPIP RTNEDQREPILSTAKTKPHPRS GDPSAPPRLALSSALPGPPLPAR GHALLRWTALLCLMVFSAFS FGFGPVTWLVSEIYPVEIRGRA FAFCNSFNWAANLFISLSFLDLI GTIGLSWTFLLYGLTAVLGLGFI YLFVPETKQGS LAEIDQFQKR RFTLSFGHRQNSTGIPYSRIEISA
26614	56982	A	26765	201	632	NLLLCPLSAESRPEEGVRLFCSQ FRSRQRPQAHKSAWGTTALSES MNCFAFSGASISSADQEQHLHL PGA VSGRPGEC LGPSGRCSK* GATFPGQKGRWKEARPSVPAP AAGLQSRAGHPRGIRPGRPHG ERDSAACWGR
26615	56983	A	26766	197	777	LPSRGAGLRTCSPCLSLPPTPW TPVRPEPPQARAPPTPRRPVPS TQGLRNASARRGTGR/PAPP/VS PGAGSTRIEASWAPESAARAGL WGPSNSVQRAAESASRPHFG QPPKAPARPGWLTKGFASVPS ASRRAPPAAVTSARHYLVRQPP PRPSSCPECNKIRLWPAFQLTPL CQGPAASEDRRKQKRR

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26616	56984	A	26767	178	697	ATLFIQKHQSGVKSTNP*IGRRS LTPEITAELGLERLNPRRCSSCL LGLKFEYHNSNLPLQLHGGQAC GDPTNSVQRAAESASRPHGFGQ PPKAPARPGWLTGKFPASVPSA SRRAPPAAVTSARHYLRLQPPPP RPSSCPECNTIRLWPAFQLTPLC QGPAASERDRRKPOKRR
26617	56985	A	26768	1	858	
26618	56986	A	26769	10	1332	
26619	56987	A	26770	1	1086	
26620	56988	A	26771	1	1392	
26621	56989	A	26772	1	987	
26622	56990	A	26773	1	336	
26623	56991	A	26774	46	302	APGAVKKTWFGKKGREKQGE RR*RQLGKENENIVALQLIRTD QEYWRHHSWHFFLSAAACQPE LFLKKHTAKNNRRJRVSQKWK
26624	56992	A	26775	1	1839	
26625	56993	A	26776	284	816	APGAVKKTWFGKKGREGETR EKNQPTVRTNSQTRDTFFKT* DLF*RMPSWELSPASS*ASKTI KYLGIQLTRDVKDLFEKYEKTL LNKIKEDTNKWNIPCSRIGIINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPPEAAEQQLPN SQSCYLIPLLEASSQSGSWLY

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26626	56994	A	26777	1	2547	MVKGSIQQEELTILNIYAPNTG APRFKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSKEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSOLKELEKQEQTHSKASRRQE ITKIREELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDIITDPTIEQT TIREYYKHLYANKLENLEEMD TFLDYTYLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGLT AEFYQRYKEELVPFLKLFQSIIE KEGILPNSFYEASIIIPKGRDT TKKENFRPISLMNIDTKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWENIRKSINVIQHINRAKD KNHMIISIDA EKA FDNIIQQPFML KTLNKLIGDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTTRQ GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLIISNFSK VSGYKINVOKSQAFLYTNNRQ TESQIMSELPFTIASKRKYLG QLTRDVKDLFKENYKPLLKEIK EDTNKWKNPCSWVGRINIMK
26627	56995	A	26778	1	489	SISWKLWFTEFTLFRFFQPSVSA VPVSTLAVVLGLKTL SLLFSHSF PGRHSWALRAISLLPSFLYTSSL MNSFSYTVHLYLGGLLRLCGSR DPHACGFPEGSPLPSCSAA*PFI WGMKRPSCVLAPSCSRDSFG CLFSFGHQCLHKSHVGSPPSGPQ ERLYNG
26628	56996	A	26779	354	685	YRGYLRGECFP*KALCCEPAAY LQTCNPSPSGPACSGHALHSLN VGDCVYLICPRYPPLRRAGKPR DTGIEGRTLSSGGPSVHSSFHSA VLPFPYTSKLLWIERRRPAGQS
26629	56997	C	26780	1	867	
26630	56998	A	26781	139	513	
26631	56999	C	26782	1	948	
26632	57000	A	26783	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCR*PYSRGT

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26633	57001	A	26784	1	224	SRAGYDHHVVEPVERGTSGVVRW YACCGLMVCPANPQHFAHGY/ VGKIPGYPARAGTLTGLHPMQ VCRRCRCVYEI
26634	57002	A	26785	112	254	
26635	57003	C	26786	1	567	
26636	57004	C	26787	1	543	
26637	57005	A	26788	165	633	RIPGLLLCPAYPQHFAHGYVDK IPGYPGRI GTLTGLHPMQVCR RRQAPCMKSNALIVILGTVTL DAVGGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDFRGRRPVLLASLLG ATIDYAIMATTPLWYPLVNS
26638	57006	A	26789	264	800	ISNFELCSRSIIHLCSSGYPR AGTLTGLHPMQVCRRCR*PAV
26639	57007	A	26790	1	738	
26640	57008	A	26791	84	162	AVLDLGPPTGRDPPQGSPPDYS GAFLASCAGAPLQQRQRKEQ AAIFAVLQLLVIPPGVGGTQT NRVWSGFANHGPNPGYPGRAG TLTGLHPMQVCRRCR*PPYRVI PQCGTLPQQGQPEVFVKQFWIL GLRLGETPHRGHQLIQGHSC
26641	57009	C	26792	1	531	
26642	57010	A	26793	216	519	QRESTIPSRPVERSNLGVRLYAC CGLLLCPAYRQHFAHGYVDKIP GYPGRAGTLTGLHPMQVCRRCR R*PDRRGTERVSARKHVCVFFV SLFVAACRPPLRA
26643	57011	C	26794	1	606	
26644	57012	C	26795	1	1059	
26645	57013	A	26796	1	3285	
26646	57014	C	26797	1	1390	
26647	57015	A	26798	211	679	RIFKCKADLLYDMLVYVTLWI HRAVTYTHRVNHSYRRSNIKS ETTVPTIRIVGPVERSNLGVRLY ACCGLLCPAYPQHFAHGYVD KIPGYPGRAGTLTGLHPMQVCR RCR*PKPAPLPGSPQHLCSHQPH LAQRKTGQCFLQGHCFPEKNW GTIV
26648	57016	C	26799	1	774	

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26649	57017	A	26800	542	1269	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQRKYP GCRLYASCELLLCPVNPQHFAH GYVDKIIPGYPAGAGTTLGLHP MQVCRRCRRQAPCMKSNNALIV ILGTVTLDAVGIGLVMPVLPGL LRDIVHSDSIASHYGVLLALYA LMQFLCAPVLGALSDRFGRRPV LLASLLGATIDYAIMATTPVLW
26650	57018	B	26801	1	1531	
26651	57019	A	26802	1889	2154	
26652	57020	A	26803	147	162	APSLHLKDTVDRSNLGVRLYA CCGLLLCPAYPQHFAHGYYVDKI PGYPGRAGTLTGLHPMQVCRC RR*PGAHTVVDIRPREDHLGSA GQPNCPENGCLQGFTHTGLAYPE HHPCI
26653	57021	A	26804	2381	3641	
26654	57022	A	26805	1	2367	
26655	57023	A	26806	1	488	MDLLYMAAAYMMGLAAIGAA IGIGILGGKFLEGAARQPDLIPL RTQFFIVMGLVDAIPMIAAIAFV LFVLFCMKYVWPPLMAAIEKR QKEIADGLSSAERAHKDLVLAK ASATDQLKKAKAEAQVIEQAN KRRSQILDEAKA*GRQEPLVQV FLESARKR

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26656	57024	A	26807	2125	2435	VSPRQKSARPDLT*IRTLCKVL GVLFVAVGGKGPTCILQILKG QRRQEA*GISVMAERVWASGQ A*WEVWLHWAKSIDWFLFWK QHVHALRVRLDTCLFSLEEGSS FWNQGLTWKVVRRTFSESINH TPRITLGVPPYSVHGQLPLGLNF GEFKVCFVLSPRIFNLTHENFLS SEGPERRGLLGATFNCLNKRRLA KYRMNRNVHPKPLVRYLHSRL PPEPAAAP*A WCGPRHLSRRQM SSSSQIGNDSFQLQVTPVHLLPL SHTTRKNPEMYDLPLLIINPQES AILQLFHQDGECLHCSPIVGDW CHLGHSQACPSFHVPSGLFVPS LLCGAAFGRLVANVLKRY SVC VRVCAHVHVCAVRVYACVC VRMTISLTVILIESTNEITYGLPI MVTLMVSTLPPGPCQAQGHVR PTGPFRSLLEWETEVEMDK*G HDFAHVLVSECISSSEA*GMLLL GGGPDRLSLESTFRAVWSLSRL DSVIAAGKQ*A*RT*SVGYSL CPDLKGDPSAVFILRTTVHHAF PVVTENRNGNEKFMKGNQJLISN NIKFKVKKTA*EERQVRDKRSR LTRLALPIRNMCDEDIASEPA EKEDLLQQMLERR*EPGGAPTA RRATQRWGEPLAQML*LTFFHG LILRSQVLVTLVRGVCSSESQS VSLSEAEISQARPDEARGVGRC RRADLTLLNPRMIVVRAAPAC
26657	57025	A	26808	24	369	
26658	57026	A	26809	4	371	
26659	57027	A	26810	82	703	
26660	57028	A	26812	1	1692	
26661	57029	A	26813	293	563	NVWPSSSVRGRNE*GREGRR RTQQAAGLGPAPSDLWWLWLS WCLQKNMSQGGENLPAGPGSC CGREAQEGAGTSLEDAFFFEAQ LLQLH
26662	57030	A	26814	1	488	VARLYWKRP SLHACHFRDPRA GLSENPRLLQCS PSSSSGNVWG PHLYAVPCL*NGRIIPSPWNYRS LNSITTSSTCSSFAVSSSPCPVW QLPGSCLLSRSLLRVAWSQAP VPMRSEQDQLQKPPPSAGLPA SVHANL*PGDRKGSVWTPAGV AQIPSPWP
26663	57031	B	26815	51	90	

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26664	57032	A	26816	299	707	RPPCRISCHPHTRCEGGRLRSRS PLLS*MPLSHPGPSPPAGSMS SSPPATTSTCSCSPPAAGCTRGR TTGRPFWTASGPAELDWASGSS VGL*SQGSQGLGACGASYAGLG VPPRLLGPMTSCCMSLPFPSPAR P
26665	57033	A	26817	146	330	TVARRMELTPALLRALLNGILPI SEPPSNRIFACWGKPAWTACCN SLRARR*RAISCCPSH
26666	57034	A	26818	1326	1694	IFGWFGACCSLGSCCVFTAST CTTVCGGCAIKVGSCLSLATMG CCVCTSGLGCACSCWGVVF* CLMESWGICSLCWSWSACRW MVCFLVWKHCRVFTCS*VCS SGGWLSFCCLADCD
26667	57035	A	26819	1	1407	
26668	57036	A	26820	75	1397	SRGSGREKFPAQLSYQTLTGKG PIEGTSLSNLAQQRCKEHHCHF LREQGPNCLIIERFMDRYTGKVI HMASHTTTRCPHVSRRPKARLL APATRSRSARARLRETRVRRGS PSCLLWNRRSRLPAEHSVRSPP RDMVFESLGLPSTKSSEFRSAA PEAAERAQPGDPCGLQTPAPLR PGFRRNQDPASAAAAAEVRS GGGRGRILATTLWGCNTLCITQ YTRIRKLTLYVCGVESKQEWG EYHEGVQAGLTRPGRSPKLISK FLEKELTDNRWDQDEAEAEVK SSFPKND*VLKNRAIKKAKRRN VGFEVSAPLQLLLFKGLVVPFG GGRFSGFGSGAGGKPLEGLSNG NNITSAPPFASAKAADPKVAF GK*LPSPSRLVDKVSNNKTNG DSQQPSSSGLASSKACVGNAYH KQLAALNCVSRDVIWKHVNTN
26669	57037	A	26821	3	89	AASGRSFRGYSRRHCYHRR*QL HACHCP
26670	57038	A	26822	150	383	LCLGEVWKGFFLTGTGRPGVF LSLHKKACYHHNHRYHHHH HHQTKP*QQELNSLLHFPPHQI QGDQFHHLYYL
26671	57039	A	26823	105	417	LCLGEVWKGFFLTGTGRPGVF LSLHKKACYHHNHRYHHHH HHQTKP*QQELNCENMPQYNF QNGSQSYQTLTLL/SLSTKFM*YS KFFVVISVMFIASSPETDF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
26672	57040	A	26824	89	554	AMNSCVTGDYRSPCGGFGFAF LYSSVSVSSSEYQLSPLPPAKR PLAAQQSCSIPIASVFFQTIHSLF AKDKKEFSSNLLDSKVNMCHE AHQLISHS*ANFRSICHIPQRW* NLIFEKFSVDVSMGSGITG**AEN WS*TLISIAASLVYSLLHKKIQ
26673	57041	A	26825	84	239	ACTKKACYHHNHRYHHHHHH HQTKP*QQELNSFRFSLSPQLL AVFLFLRP
26674	57042	A	26826	2	245	
26675	57043	A	26827	154	546	LIVTVHVNHLGVLINHRFRISGC GVCGTDCISHKFPGAADATGPS WTHCAVITFSLTTGSATKKTE DNNTFVFNVDVKAN*HQITRA VKKLCDIDVPEVNTLPNVISIFR FLCSTVFCTLTVFFLRENG
26676	57044	A	26828	331	612	NHRGLFPDPYIPGTYFLFFFLF FSFSSSSSSSFPASGNNHNTLY FYGINFFSFHIGMRMGIFLCLT CFT*HDVLQAHPHREGRQDLLF HD
26677	57045	B	26829	928	1617	
26678	57046	A	26830	95	929	
26679	57047	A	26831	3	1128	LYNRRRRRRCSCHRCRRLSS GLRKEEVISLGASLGRVFPVPCSP PTVSAARGPTGAPGGPNKPLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNLVEILP AIFSSFLNLQHVNLWFLAAM KAVTEQGHLSNEERNLLSVA YKNVVGARRSSWRVSSIEQKT ERNEKKQQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKRLSNYFRLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFLTILIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTLCL DI*P*QNSACVINFLNLNLDN LTVSTTSTGFVSLFTYLIHICY LQEVCSVSLCTLNIYPLCDKCK
26680	57048	A	26832	139	601	EGRGHLAQELLSERVFPVPCSP TGMTMDKSELVQKAKLAEQAE RYDDMACSSERHVTQGHLS NEEKKSCSLVAYKECW*APRR SSWRVSSIEQKTERNVEGSSR WGKEYREKIEAELQDICNDVL ELLDKYLIPNATQPSKVFYLYK MK
26681	57049	A	26833	70	122	

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26682	57050	A	26834	179	876	CIVILFFFSQFNFVGRILGPRGLT ANVNRYLELHLYGYMNLFI SIMKDVLSL*RE*F*SCTL*IF*E EQNRGKPNWEHLNEDLHVLIT VEGV*I*LLYLWTVSNAFISCVF HV*AEGEDRYCCLYTFS*ISLLT VAALAFSLAATAQAAPRIITGP APVLPPAALRTPTPAGPTIMPLI RQIQTAVMPPNGTPHPTAAIVPP GPEAGLIYTPYIYIISKYLWLLSS CSPEP
26683	57051	A	26835	3	915	AEAHPRLPDAAADERQEAHDSLP NFCGIFNHLERLLDEEISRVKRD MYNDTLNGSTEKRSaelPDAV GPVQLQEKLYVPVKEYPDFNF VGRILGPRGLTAKQLEAETGCK IMVRGKGSMDKKKEEQNRG/ KPNWEHLNEDLHVLITV/EKV LQEQGQEIKKRAVEEVKKLLV PAAEGEDSLKKMHLMEAILN GTYRDANIKSPSLAFLAGTAQ AAPRIITGPAAGLPALGTPPT AGPTIMALIRQIQGTGGMNGTP HPTAAIVPAGPEAGLRYTPYEY PYTLAIPATSILEYPIEPSGCI
26684	57052	A	26836	1182	1360	KLSCVYIYICMFHYTHVSV*FYI YIYTHRHTENHYFCNSVQFVLY LFTFFCYFIWPA
26685	57053	A	26837	3	348	RNSKHVCRAEP*GHFCYK*HF WNHTEHTAVLEI/EQINARDET DFYLGNRCTYVCKEQHSGPGS KSNTTIVIWGVKVTCAQGNKV VCAKFSQHPKAKIGHRIHVML YHWRIQH
26686	57054	A	26838	264	527	NSKHVCRAVP*GHFC*K*HFV NQREHTTVLEIEGVYARDET YLGNRCTYVCKEQHSGPGSKS NKTRVWIKERGSGWCRLSGR
26687	57055	B	26839	26	515	
26688	57056	A	26840	92	341	
26689	57057	A	26841	224	1111	
26690	57058	A	26842	2	592	HSLTGRCIFFLITGTSPGPEMST TLKIMSSKEPSISPEIRSTVRNSP WKTPTETTVPMETTVEPVTFSPQ LVFARLMTGVGLGAALPNLIAL TSEAAGPRFRGTAVSLMYCGV PIGAALAATLGFAGANLAWQT VFVWGGVVPLILVPLLMRWLP ESAVFAWRSISNKA*FRDCRC CSAAIHW*RRFPFKSKPVM
26691	57059	A	26843	2	141	

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26692	57060	A	26844	1	978	
26693	57061	A	26845	144	647	
26694	57062	A	26846	1642	2652	FGILVLLALIVIWYNNFFGAETE AILPYDQVMHRFAAYFQQGNM ESNGKYVDRNGNVVDYQTGP WGEPGTNGQHAFYQLIHGQTK MVPCDFIAPATHNPLSDHHQK LLSNFFAQTEALAFGKSREVVE QEYRDQGGKDPATLDYVVPFKV FEGNRPTK*ILLREITPFSKLE KAISDTICVIRDGQHGTRD HLTAWHPVNRHIKRVNDVSFS LKRGEILGIAGLVGAGRTETI LFGVWPGQWEGKIYIDGKQVD IRNCQQAIAQGIAMVPEDRKR GIVPVMAVGKNITLAALNKFTG GISQLDDAAEQKCILSHPRCSW QGRHLLH
26695	57063	A	26847	52	137	
26696	57064	A	26848	1	1858	MGLKVDDKVLFAVVSRLTSQ KGLDLVLEALPGLLEQGGQLA LLGAGDPVLQEGFLAAAAYP GQGVGQIGYHEAFSHRIMGGA DVILVPSRFPCGLTQLYGLKY GTLPLVRRTGGLADTVSDCSLE NLADGVASGFVFEDSNAWSLL RAIRRAFVLCQGQFHHRTT YKGDPAVKIEESEINYLNVY NTHFFKKQLSRDDIVWYSGVR PLCDDDESQPAITRDYTLDIHD ENGKAPLLSVFGGKLTTRYKLA EHALEKLTPYYQGIGPAWTKES VLPGGAIEGDRDDYAARLRRR YPFLTESLARHYARTYGSNQRA ACSAMREREARTLPQKLAGTL GMLSKVMRIPRQEVTA LQIRIGLHAAFNACEEMCQ LERQLDSEERALLIERSQTVIRQ GRDLLHAWDATWNSAQLDN ALQPDRAQGFADALEKYAADE SFFAQLDKYDIPVVVIGKVEGQ YAHVYSVDTDNFGDSIALTDAL IESGHQNIACLHAPLDVHVSVD RVNGYKQSLAAHNIAVRDEWI VDGGYTHETALKAAARQLLSQS PLPEAVFATDSLKLMSIYRAAA EKNIAIPQQLAVRILFGLHL*IV LSTRAGFNGLAHY

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26697	57065	A	26849	136	3261	PMSPTIYDIARVAGVSKSTVSR VLNKQTNISPEAREKVLRAIEEL QYQPNKLARALTSSGFDAIMVI STRSTKTTAGNPFLLEVAQAFP AKAE*KGQVLVRTSHNPAEDL KKCESKIKQKMIKGIIMLSSPAD ESFFAQLDKYDIPVVVIGKVEG QYAHVYSVDTDNFGDSIALTD ALIESGHQNIACLHAPLDVHVS VDRVNGYKQSLGAHNIARDE WIVDGGYTHETALKAAARQLLS QSVLSLVAVWSWAC
26698	57066	A	26850	73	174	
26699	57067	A	26851	252	575	PGFPRGPPPPGFAFFHVSIDWT DLSDDPAARAGLGVWRWTPDPPR RAARSPVLPRLSAGQRPAAARL LGGMEEGFRQVAVFSES*SAV CPPSPPPPLSPLAPWTETA
26700	57068	A	26852	1	462	AQSVNSQTFSELRAQTQIFVKTT SHNSPGVFHTSTKR/FIDGNPPGI FSAITA*RLMMP*RSSIFSASASI LSVSFSGSTCNNDQRPARFGVL *DTRGETGCA*TGRPRAR*LR RVEVRV*LLRVRRARNAQMA LVKTPCQTSAHNAPCRGRE
26701	57069	A	26853	692	918	
26702	57070	A	26854	1	2427	
26703	57071	A	26855	1347	1978	LPHCVANHGICALR*QKWVHD KEQTTQTLKMAENGRWVIDD IVSNHGSVLQAVNSEKTLAA LASLQKEQPEAFVAELFEHIAD YSWPWTWVSDSYRQAVNAF YKTTFTKANNPDEDMQIERQFI YDNPICFGEESLSRVDEIRVLE KTADSARIHVRFRTLNGNNEEQ ELVLQRREGKWEIADFIIRPNSG SLLKQIEAKTAARLKQ
26704	57072	A	26856	1	733	LSEVDVDVRQSIHSAHAKTLD QGLRNEFLVEKVFADEYTMV YSHIDRIHVGIMPTIKTVSVGG EVGKQLGVSYFLTNSRRITNKY LVPDVLCTQSSMGLTELAPGN *WNTMPCHTHERMEVYFYFN MDDDACVFHMMGQPQETRIH VMHNEQAVISPSWSIHSGVGTK AYTFIWGMVGENQVFDMDMDH VAVKDLRANHQRFIHSQRSDI HLTTQWIKRAAQTIHPPVSIIQQ IVAFFE
26705	57073	A	26857	2	255	
26706	57074	A	26858	1	597	

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26707	57075	A	26859	2	640	EARGRQPLHHLPHPPRASP LALQPLGRSRRCPPPGAAAPD PRPDMGDLPLGLVRLSIALRIQPN DGPVFYKVDGQRFQGNRTIKLL TGSSYKVEVKIPSTLQVENISI GGVLGPLLEKSKPEPDGDRAVY TGTYDTEGVATPTKSGER/QPIQI TMPFTDIGTFETVWQVKFYNY HKRDHCQWGSPFSVIEYECKPN ETRSLMWVNKESFL
26708	57076	A	26860	218	426	TQPRVWSQAQ/RALQPDTELQ PPQTPKSDTDQMLSVKKKKKK KKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKLYFQT
26709	57077	A	26861	1	423	
26710	57078	B	26862	1	252	
26711	57079	A	26863	1	171	
26712	57080	A	26864	5	254	
26713	57081	A	26865	16	220	ILDTPMRWTQKNFSMILAQPE QQCKTSLSQNKNDRIKKKEE KKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKEKE EEKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK KKK
26714	57082	A	26866	32	286	
26715	57083	A	26867	1	847	EVKDLYDKTFKSLKKEIKEDLR RWKDLPCSWGRINIVKMAILP KAIYRFNAIPIKIPTQFFNELEGA ICKFIWNKKPRIAKTLTKDKR TSGGITMPDLKLYRAIVIKTA WYWYRDRQVDQWNRIEDPEM NPHTYGHILFDKGAKTIQWKK DSIFNNWCWHNWLSCRRMRI DPYLSPTKVSKWIKELHIKP ETLKLIEKVGSLEDMTGGER FLNRTAMACSKKKEKEKEEED EEEKEKEKEKEKEKEEWEKK KKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKK
26716	57084	A	26868	1	376	MLMKDPQWNSSIFSTHLALQ KRRQAIEYGAQEPSRRIVGGKGS GAQVDEEEEEEEEEKEEWEKK KKKEKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKMML LSLPMIRPLPHPRWASSPSSMV AKP
26717	57085	A	26869	1	2031	
26718	57086	A	26870	1	957	

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26719	57087	A	26871	171	495	SQLLDMRKPFQKPGRLQLKTL P QYLNTR/CILDYLDNI/SPQQIRK LFYVLSTLAFSKQNEASSHIQD DMHLVIRKQLSSTVFKYKLIGII GAVTMAGIMAADRSSEPSL
26720	57088	A	26872	1	3114	
26721	57089	A	26873	173	397	
26722	57090	A	26875	823	1194	
26723	57091	A	26876	1	1263	MESNAVQLTRMEYAMKSLSL YPKSLSRHVSVRTSVVTQQLLS EPSPKAPRARPCRVSTADRSVR KGIMAYSLEDLLKVRDTLML ADKPPFLVLEEDGTTVETEEYF QALAGDVTVMVLQKGQKWQP PSEQGT*WRRTRQKDSVPSRPC STHGLQEIQ
26724	57092	A	26877	128	317	
26725	57093	A	26878	431	574	
26726	57094	A	26879	112	482	EGPEAKPKRSNCAPEKRSSPIPD WEPAFSEDGRARTVARLQHPPL GGPTHRYHHFLRRHDPLRVHP AAERQEAHPGTST*QSSPNSKQS PQGWKWTFFNSSLSTRKYVYFQ QPRGWDFFKKT
26727	57095	A	26880	3	179	
26728	57096	A	26881	977	1127	
26729	57097	A	26882	121	708	
26730	57098	A	26883	38	828	GSRLRRLQAAAAFPALPLPLPP WEWKHLPHVPEAKWWLTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESLDLAEFAK KQPWWRLFGQESGPSAEKYS VATQLFIGGVTGWCTGFIFQKV GKLAATACGEVDF/LLQLANH TWVHQSLTGNEWKDIEESPKS SLKIRKSQSDYLLRSGAKAAGC WCHFVKKNVLVTWGIFPEAFC LAWHPKEDDLHVPLFPGFFPSQ QPFTLHHRDIESLLFFWPWPSFP GHWEN
26731	57099	A	26884	1	642	
26732	57100	A	26885	1183	1349	

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26733	57101	A	26886	1	1371	MSFLIDSSIMITSQILFFGFGWLF FMRQLFKDYEIRQYVVQVFSV TFAFSCTMFELIIFELGLNSSS RYFHWKMNLCVILLIL/VFPMV PFLQLAYFIVSNIRLLAHKQRLLF SCLLWLTFFMYFFWKLGDPPIL SPKHGILSIEQLISRVGIVGVTL MALLSGFGAVNCPYTYMSYFL RNVTDTDILALERLLQTMDMI ISKKKRMA MARRTMFQKGEVH NKPSGFWGMKSVTTSASGSEN LTLIQEVDAALEELSRLFLETA DLAYATKERIEYSKTFKGYFNF LGYFFSIYCVWKIFMATINIVFD RVGKTDPTVTRGIEITVNYLGIQF DVKFWSQHISFILVGHIVTSIRG LLITLTKFFYAISSSKSSNVIVLL LAQIMGMYFVSSVLLIRMSMPL EYRTIITEVLGELQFNFYHRWF DVIFLVSALESSILFLYLAHKQAP
26734	57102	A	26887	1738	2140	
26735	57103	A	26888	81	733	
26736	57104	A	26889	1061	1154	
26737	57105	A	26890	1	3207	
26738	57106	A	26891	113	367	
26739	57107	A	26892	2	1391	
26740	57108	A	26893	154	647	
26741	57109	A	26894	40	747	
26742	57110	A	26895	1	3186	
26743	57111	A	26896	271	491	
26744	57112	A	26897	304	1836	
26745	57113	A	26898	1	2343	
26746	57114	A	26899	1	765	
26747	57115	A	26900	318	473	
26748	57116	A	26901	2	426	
26749	57117	A	26902	1	433	
26750	57118	A	26903	2	1004	
26751	57119	A	26904	125	199	
26752	57120	A	26905	3	156	
26753	57121	A	26906	2	397	VDGMGWSQDLFRALGRSLRE GKEHVGTQDFGNKYY*SRSTK TGEVRWRRGQRLRGQ*LRGQT IREKRIVEAANKKEVDYEAGDI PTEWEAWIKRTRKTPPFMEIIL KNEKHREEIKIKSQDFYEKEKL
26754	57122	A	26907	1	1350	
26755	57123	A	26908	1	582	

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26756	57124	A	26909	2	687	GARQVLPGESPCFSSVAKIVKP NGEKPDEFESG/LSPQALLEAE MNSDLKAQLREPELLRPA*GK LKVGCSSENLS/ILLFPVPSN*K SFPENPVQRA*YRELEKKFQW GSHVGLYRPQRRILP*AQLRKK PVQKNKQKASPRARLTAVHD AILEDLGLPQAKIVGARESRVK LDGSRVAIKVHLDKAQQNNVE HKVETFSGVYK/KLTGKDVNF EFPRSFNCKQK
26757	57125	C	26910	164	208	
26758	57126	A	26911	2288	2625	GSEGLHPITKRWSSLWEWRKG LSEVGSCKRNLRCLRTAI/LM GGEAGVIHCKGHQKASDPIALG NAYADKVARQAASSPTSVPHG QFFSFTLVTPITYSPAETSTYQSL PTQ GK
26759	57127	A	26912	1	400	
26760	57128	A	26913	3	277	
26761	57129	A	26914	1	630	CEIKNRKAAEKVNKTGKGFEEI NTYPGPIKTGEGSGQTKWLDI VRNLTVEEDTSSWSVRAHQPK STLTGTGRPSTNGTMSSSLARTV REEPGNQPNYRGKPSFWFPHL VRAASTQPVITRLQHGRKLP NSPYNFPLPVLKPKDKPYKLVLQ DLHLINQIVLIHPVVPNPYTLL SSIPASTTHYSVLDLKHAFFTIPL HP*FQPLFTF
26762	57130	A	26915	1	384	
26763	57131	A	26916	1113	1319	GRDPVSFAFYIWLASFNTIY*IG NPFPIACFSQVCQSRSDSCRYAA LFLRALFCSIDLFLCFTSTMLF
26764	57132	A	26917	2	2144	
26765	57133	A	26918	99	470	
26766	57134	A	26919	636	1220	GPGFQAQNCAAIWADTKLAAG IFSHTPVAPGTPVRQNHLLPWD APAWSGEECLPLRLVYVVPFS QCKQSCQEV*TGQSPPLGKAF VARLPL*IPSLWAGHLFLEHPV YCCGCVTAGRQGSWKQRRH GHFPPLPLLLQMVCCSISYQY DYPESSFLLLFLSSLCSAGKSTG SHAILLSAFVLPHLVALRS
26767	57135	A	26920	10	161	RLRMVRDIKVLNTRSLRNCIG DLTNKGRSIIIGPPL*ELSKASVM VPVGF
26768	57136	A	26921	1	855	
26769	57137	A	26922	5	1442	
26770	57138	A	26923	1061	2332	

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26771	57139	A	26924	804	1100	SPKGGPPDPSPHGTGFHSRPEET TKQAFCEQHGCLFHLGTLGALL G*QRWLHLQSRPSLGCNESHSL FQ*PPLP*E*KEIQCKVPPNLGL GVRSGKGF
26772	57140	A	26925	3	1186	
26773	57141	A	26926	126	363	SRSKQDGLDPSGTWCKRAFSPG PWPIIPVAAGGGHSGGGKSET PAHLQKGLHKVKNC*PSTYSVC QTPDAEHPVSNK
26774	57142	A	26927	1	1125	
26775	57143	A	26928	401	446	
26776	57144	A	26929	332	499	
26777	57145	A	26930	74	200	
26778	57146	A	26931	300	416	
26779	57147	A	26932	324	430	
26780	57148	A	26933	60	381	
26781	57149	A	26934	2344	2453	
26782	57150	A	26935	131	274	
26783	57151	A	26936	144	444	GGGENFSYPWYLLVCGWFFSS SPIVPDVPFSLLLPAQKKKPAP PKPEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK
26784	57152	A	26937	540	811	
26785	57153	A	26938	69	375	QHLPAAVAAATMPKKAEGD AKGDKAKVKDEPQRRSARLSA KPAAPPKPEPKKAPAKKGEKV PKGKKGKADAGKEGNNPAEN GDAKTDQAQKAEGAGDAK
26786	57154	A	26939	9294	9486	SLLYQPRCMAFRIKASS*RGMP GGSASAARKPTG/SPGREGAGR RGQWGPNNCCAGRLPGGESTV
26787	57155	A	26940	248	613	
26788	57156	C	26941	94	234	
26789	57157	A	26942	2157	2408	
26790	57158	A	26943	547	815	
26791	57159	A	26944	254	467	VFLISVYNGLAISLYLGIHQRK PVMRPNPLNCFGLV*G*AGIG *IRSSLRTLVLDFNSPKYLTF EQS
26792	57160	A	26945	238	391	
26793	57161	A	26946	232	1659	
26794	57162	A	26947	1	951	
26795	57163	A	26948	1	2046	
26796	57164	A	26949	3	97	SVR/SKFYVREPPNAKPDWLKV GFTLSVEL*M
26797	57165	A	26950	1	828	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
26798	57166	A	26951	224	475	AGPRKMAPSALLRPLSRLLAPAR/LPSGSPVR/STKFFVREPPNAK/PDWLKVGFVLGTT/VFLWIY/LIKQHNEDILEYKRRNGLE
26799	57167	A	26952	1	411	
26800	57168	A	26953	442	2490	
26801	57169	A	26954	3	1592	
26802	57170	A	26955	9	308	
26803	57171	A	26956	153	227	
26804	57172	A	26957	1	411	
26805	57173	A	26958	517	825	
26806	57174	A	26959	6	646	
26807	57175	A	26960	1	275	
26808	57176	A	26961	3	272	
26809	57177	A	26962	1	1002	
26810	57178	A	26963	1	1791	
26811	57179	A	26964	2	160	HMTTSLLAQSGFQKTSALNKIT/KGSH*VQFTSLPPPERVLVS/MAERPWGG
26812	57180	A	26965	1	892	
26813	57181	A	26966	1	549	
26814	57182	A	26967	234	387	SCLEVCEQDGPEK/ITRQALRG/VSSVTEDTLNICRLCWQPLPEPELWPKAL
26815	57183	A	26968	269	501	RARSEGAGLWSVVPASVSVFF/VSDPRCAPFHRSPSCCSP/RRPC/LSLSA*SRPRASGVGACLLWQPLPEPELWPKAV
26816	57184	A	26969	210	296	
26817	57185	A	26970	71	283	LRLGDLPSEINPLSSCSLLREKDPPTTSGPQTTSRNPISNPDS/IGNRTVQLTWQPLPEPELWPKAL
26818	57186	A	26971	1112	1180	
26819	57187	A	26972	71	284	LILGDLPSEIKPLPSCSLLREKEPPTTSGPQTTSRNPISNPDS/IGNRTVQLTWQPLPEPELWPKAL
26820	57188	B	26973	1	663	
26821	57189	A	26974	1	502	MLLTQSLFGGLFTRTHMKFGA/VTQIRGPPLGDKSPVLLLFALER/QRHVLMSMDPKLRCWSRTGKA/AFWPCLIIAEMPDISYPT/QRCQ/TTQGRLPWSFTLSSKSRFSGEG/ARACYKCQKSDHQACECPQPG/IPPKPCICAGPTGNRTVQLTWQPLPEPELWPKAL
26822	57190	A	26975	233	496	
26823	57191	A	26976	226	543	
26824	57192	A	26977	1478	1744	

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26825	57193	A	26978	3	450	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHNLI LRPNPLCPHPDLVSLCPDPFPAF LEAHKNFQTTEPQQPGVPEPP PTGACYTCRKSGHWAKECPQP GIPPNNHVPVWDPTENLTVQLT WQPLPEPELWPKAL
26826	57194	A	26979	615	724	
26827	57195	A	26980	1	1968	
26828	57196	A	26981	227	556	
26829	57197	A	26982	400	548	
26830	57198	A	26983	1	1968	
26831	57199	A	26984	65	741	
26832	57200	A	26985	1	658	
26833	57201	A	26986	1	666	
26834	57202	A	26987	67	608	NPGKGGCFVL/VLDGLLRDRKA VIREETFDGWHFPQDRPLPAHA\ LVAGIDRPTPPQK*TA/AMGKK KDRPKRSKIKSFCGKCYNY/NH\ LMPHKGTLWDIPLGQNLVQVL RDVFRDPSGLNRKA/RREGPRF KFE/EREYETGQETKVV/LPRKL AGFKNAFGFDSLKIHKKKKKK KKTTKKGRP
26835	57203	A	26988	1	352	
26836	57204	A	26989	1	1419	
26837	57205	A	26990	2	878	
26838	57206	B	26991	75	2931	
26839	57207	A	26992	229	724	IIFIVYSSQLTYVKISDSFQTFKF CLDFCLFFSEMS/FLSLNISSCS* YSAKVNNSCGKFLTKGSFSAPL TPLFFLCFSGSELVEGV*ELLAVG GLHLARIFLCLSISSLC*FTHSCS FTRVTPINLASNNSCLLGFRLQS SSIAPSLGLLDGGVCFIRDLAAA
26840	57208	A	26993	737	1048	KKYNIQLEKPYFKHLYKNKLL KLNS*NMITSVQQTIELEGNLS LSCIELVC/ILVTHCHL/CMNK AW*QKKN/WSILTC*KHWQ YYNLVNSTDFNTSSSFLSKV
26841	57209	A	26994	1	1209	
26842	57210	A	26995	2	1683	
26843	57211	A	26996	1	1386	
26844	57212	A	26997	1	471	

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26845	57213	A	26998	2	514	VTARRRGTRWLRFRASRVQK WLVLDYFYLRYYVGHKGKFG HEFLEFEFRPDGKLRVANNH YKNDVMIRKEAYVHKSVMEE KRIIDDSEITKVEDDALWPPDR VGRQELIVIGDEHISFTISKIG SLIDVNQSKDPEGLRVFYVLVQ DLKCLVFSLIGLHFKIKPI
26846	57214	A	26999	1	570	
26847	57215	A	27000	1	980	
26848	57216	A	27001	270	356	
26849	57217	A	27002	1	1032	
26850	57218	A	27003	1	1017	
26851	57219	A	27004	1	450	
26852	57220	A	27005	1	637	APIECGGIPSLPVLQCSRANDQE GVRLLPESEAMPKSKELVSSSS GSDSDSEVDKLLKRRKQVVAS ENPVKKQKTGETS/RALSS/SKQ SQPAARDNNMFQIGKMRYVS VRDFKRRQCLNDIREYWMDPE GEMKPGRRKGSINP/QQWEPL KEQISGLPIDASKTKKISEPLI KPCTVPVVLWLFSGFCFLNVL RSYCMFGLQKNL
26853	57221	A	27006	20	412	RFSPLSFLLAGDSCTCAGSKCK KECKCTSCCKSKWDPLPLPLP CPPACPLSTILRGIAVWGCPA RKLLPPQ*SLSGRAGILPGVAS THLCRLLSAPRCCSCCPVGCAC CAQGCICKGASDKCSCCA
26854	57222	C	27007	32	505	
26855	57223	A	27008	854	1021	ALGGVAEYDLKEGLLLKH*AL VQSLVATEVRLVLCITSHTDML QICFFVYATVQ
26856	57224	A	27009	1	726	
26857	57225	A	27010	99	537	
26858	57226	A	27011	1	963	
26859	57227	A	27012	146	609	VYLRCTGGEVGATSALAPKIGP LGLSPKKVGGDIKATGDWKG LRITVKLTQNRQAQIEVVPSAS ALIIKALKIEPPDRKKQKNIKH SGNITFDEIVNIARQMRHSLAR ELSGTIKEILGTAQSVGCNVDG RHPHDIIDDINSGAVECPAS
26860	57228	A	27013	3	501	
26861	57229	A	27014	1	1623	

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26862	57230	A	27015	53	1227	QPPVHTTPASSPCDDIDIAALIV VDNIGSGMCKIAGFAGDDAPRA VFPSIVGRPRHQGVMMVGMGQK DSYVGDEAQSKRGILTLKYPIE HGIVTNWDDMEKIWHHTFYNE LRVAPEEHPVLLTEAPLDPRA T REKMTQIMFETFNTPAMYVAIQ AVLSLYASG/RVTTGIVMDSG DGVHTVPIYEGYALPHAILR LDLAGRDLTDYLMKILTERGYS FTTTAEREIVRDIKEKLCYVAL DFEQEMATAASSSSLEKSYQLP DGQVITIGNERFRCPALFQPSF LGMESCGIHETTFNSIMKCDVD IRKDLYANTVLSGGTNMYPGI ADRMQKEITALAPSTMKIKIAP PERKYSVWIGGSILASLSTFQQ MWISKQEYDESGPSIVHRKCF
26863	57231	A	27016	2	438	ADLLQVSNVCVSSCPPAFLVL FSSRLPAGEGRGRPGQTQRPS LEGAWHSVTLERRCLVSHLINL REAGMYPSPRCHHLPDQLV*T EGGF*RPRLGWQRCHGTQQQA PSQPAFRSKHPRKGMPALQQQP GSGLCRPLPCRCR
26864	57232	A	27017	112	493	AHSRTPARPENRAAASAPRKPR RAMSSPPEGKLETKAGHPPAVK AGGMRIYQKHPTGDTKEEKD KDDQEWESPPKPTVFISGV I ARGDKDFRPADAQVAHQKPHA SMDKHPSPRTQHIHQPRK
26865	57233	A	27018	1	1176	
26866	57234	A	27019	3	307	
26867	57235	A	27020	86	179	SVKRRK*SLTWIGMRLQRQHR ECLAQVGS
26868	57236	A	27021	1	948	
26869	57237	A	27022	3	534	EGAHFRAAHHPRSTGSRCPGSL QPSRPLVANWLQSLPEMPVDFT GYWKMLVNENFEYLRALDV NVALRKI/APTLCLKPDKEIVQDG DHMIIRLTSTFRKLTWNFIQVG KEFEEDLTGIDDRKVHDKQ*A WDGDKL/QCVQKGEKEGRGW TQWIEGDELHLEMRVEGLVC KQVFVKVQ
26870	57238	A	27026	1	2400	
26871	57239	A	27027	294	425	
26872	57240	A	27028	1	797	
26873	57241	A	27029	1	173	
26874	57242	A	27030	1	1047	

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26875	57243	A	27031	2	1019	PTSAPIHLSLSPRAVIERRSRALDW NASPSLSDPQGLDASLPFPPSHKR SRTASPEPAEHPVMDKNE/LVH KAKLAE/QAERYDDMAACMK VTEQGAELSNERNLLSVAYK N/VVGARRSSWVVS/SIEQK/T EGA/EKKQQMAR/EYREEIETEL R/D/CNDVLSLVGKSSLIPNAFT SRRSKVF/YILENGKGDYLPFTL GWRVAAGWMDQERGLDFPVH NKAYPRKAFWKSAAKNGNPT HPURLGLVALNFSVFYYEILNSP EKACSLAKTAFDEAIAELDTLS EESYKSTLIMQLLRDNFDIVG HRDTQGRKKLEGREGGENL TGPFPTFCSWPHS
26876	57244	A	27032	177	477	
26877	57245	A	27033	1	1290	
26878	57246	B	27034	49	1112	
26879	57247	A	27035	98	245	
26880	57248	A	27036	1	351	
26881	57249	A	27037	3	471	
26882	57250	A	27038	1	440	MKMRVGCMLTAESLSDGGNS HQRTL.SLFESKESQCEARGEV SKAGVWLVPLEPSDALPKITS LVRPAVWPSPSEAGLCEVRGG VLGKASKAPIKEPQLDRGMGL GAQRRGSSGTEVQSGETLGASG SPRGLLEPRPDWVSNNGAGSLG FQQLPIVDKIRTIAQAVCGAKDI ELCPEAQVKIDRYTQQYYSC*N PKLPAPLFETQSLGSKSPLGLP LAPRVSPDCTSVP/GAP/SAAGP RAPCPDPAVAPLWGLCWFPPEL
26883	57251	A	27039	1	1113	MHQEDLRAWYLDLGLPSHQ AQPTAWKCQRAPSPYTHQDMA LIPSPARWLSPEKEPKQGEVG EKSLPDPDTLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRLLADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIIJLCTLVNKLQPGSV KINASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANNLFESG NNMQVRVSLALAGAKTKGL RSGVDIRDYSEKQNFDDTTM KASQCVIRLQITNKASQSGMT AYGTRRHLYPDKNRILPPMDNS TISLQMGNTKASQVGMTAPG TQRHIYDTKLGDCKENSSMSL

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26884	57252	A	27040	347	1061	
26885	57253	A	27041	212	386	LQGSWVTSGLERICGSILGTIPL AHEVTDTDQHGRMVYQVATAG F*SSLGAASIGTQGL
26886	57254	A	27042	1	1017	MHSRRERARGRLGAHHPLVDN GPPQSLRAPPLSPLKTAGAKSI WEPLASARRPETPERTLQKTP EQVPTNFMGALHMKTSAPLSS RNGEGRRGTSVASCSPVWVGA VCSAERQPTQRVREALMGGW RAGAQNRAEDQVDEFTEVGF RRWVIKNYDELKEHVLTCCKE VKNLDKSIHPEISRLHEFITTTHT LPVIGGKVSLLSKCQDNAEQKQ SQGCSQEGHEVYDPRLNSSSS SSSGGGQSPGLRRCSTSAAAAA ALEGAALKPMPVHAGLVGSGE GGGAGAVAGPCSRWGATTA ASSAQAQPVRRGSSGAQGH GRRRRQAGKGGPAG*TA AP*GRGAEPGAAALLNLGGGSG GAG*SAALKPMPVHAGLVGSG EGGGAGAVAGPCSRWGATTA AASSAQAQPVRRGSSGAQGH RGGRRRQAGKGGPAGSS
26887	57255	A	27043	644	949	
26888	57256	A	27044	811	1886	
26889	57257	A	27045	1	410	HAHSLNSILPTLEIHKV*IQIY A*GCKRISNNCWCHQHLLSIS PDLRINGEKECGSPWIGVEAR/ MGGELSSAVGLTSLLLYQQVPF HPHFQSPFTIPRESILLQHASCW RQHHLHTGIYSSYLPGWKQFES
26890	57258	A	27047	1	2445	
26891	57259	A	27048	1	457	
26892	57260	A	27049	1	873	
26893	57261	A	27050	2549	2728	ATSRSSALITSSKYPGKF*LILI* RSTLETANSISARLNNPFLRKYP SYFSLFMGTTRI
26894	57262	A	27051	277	394	
26895	57263	A	27052	2	1394	
26896	57264	A	27053	1	1091	
26897	57265	A	27054	1	1404	
26898	57266	A	27055	2457	2674	ANHCYLLSELQHWSDCPVVLQ SAG*RH*DRN*DGNY*SR/SL *SR*STTK*RNTPCSQVSSLSRLS TRSA

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26899	57267	A	27056	716	1455	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGNYS TGDNHTLR/DPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQS AKKRDAELANGA LGHIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG YVNSLSTGPYKPLNKTGLVLQ MVLIPNDVTFYSHFAVPQAK GNNVGIHQATLTNRGFFEIKKA TFAPSL
26900	57268	A	27057	66	197	
26901	57269	A	27058	379	905	AGNFVHITVRKMLWIRRDQQQ S/DKQDIQTAHRSYSVLKGYND MYYGWPCKKVNEISGQLASEP A*SLVLPAAQ*QAPASGSPWLS GGPQQVEDAGAGYGFAPGQPP PPPTQPRSACSRRAAGSQFHG RPLLPRQA AKARAPRLGCGSL GRFSTGVRPDKCIPFPETENAA
26902	57270	A	27059	1	1608	
26903	57271	B	27060	1	1974	
26904	57272	A	27061	2712	3216	KTGRGPTDKFGVANDPILKDQT QEWSSGAPFISDGKFRIFYTD YSGKHYGKQSLTTAQNQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENG YQGE ESLFNKAYYGGGTPFFRKESQK LQQS AKKRDAELANGALGHIEL NNDYTLKKVMKPLITSNT
26905	57273	A	27062	1	3066	
26906	57274	A	27063	1	972	
26907	57275	A	27064	14	273	
26908	57276	A	27065	42	302	
26909	57277	A	27066	1	487	MGLSLKGPESAPIKTPQFNKIL FKPIAVYNRFTQRLSETEKTN PYAMRLYESLCQYQRYQLPQS YQRLSLTSA AASCRSVLMRSTA ELQCASHTLRKRKAARRLSLS EMPRKQGDYRTRIWKFEDGLS NVLVIQLNKLII CMVLVRDCD VLKTYFHR
26910	57278	B	27067	1	1035	
26911	57279	A	27068	132	230	CHYFACMWSGCEVYS*SAPG** C*EDLSGMVR
26912	57280	A	27069	1	2784	
26913	57281	A	27070	855	980	LSCSGWRAG**ADGCIHQIG*RL SPNKCL*TWSALCKPIAE
26914	57282	B	27071	85	863	
26915	57283	A	27072	345	500	

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26916	57284	B	27073	1	1116	
26917	57285	A	27074	1	1173	
26918	57286	A	27075	1	999	
26919	57287	A	27076	771	908	
26920	57288	A	27077	104	547	LFPRLLSCLTTPHCSFSICFVIC SRTLILKGSSLMYVFCPLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLKFLKNGLNFLHSHVGTTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDDADDVLSTEVKRVITS SASNITPAFFCS
26921	57289	A	27078	34	1353	
26922	57290	A	27079	213	338	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWSALCKPIAE
26923	57291	A	27080	1	1246	MVKVGTSTYVPINVSFSKVGPG LPGINRDRITRIYLFCEVIFRHRKD RESADLGSDGQNGPRPWIGE VAAAAADGVTFSVPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRNRFTQFRLSETKEITNPYAM RLYESLCQYRKPDGSCIVSLKID WIHERYQLPQSYQLYFYELAIPV GYFYPGSFSTASRILLHPRGLR AITIAVFGKQNTYIRLEPKINV LEQITKHIEKLQCGGVVKLSR RGNNQHISSTYDINRADYPG*A RDPHMLRLRLAIETVAHDYDVIV IDSAPNLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVLDLKGFEPPDRILLTKYSN SNGSQSPWMEEQNSGCRGKTS RVEVPHRDSQFKVIKLVTLRQL VTLYDPVDFQRDDA
26924	57292	B	27081	1	1041	
26925	57293	A	27082	1	1011	
26926	57294	A	27083	2	1007	
26927	57295	A	27084	1	738	

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26928	57296	A	27085	1	1439	MAETA VINHKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYL FV DQIRKSDGTLQEHGDCIHHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPRGLYSVHIN PYLIPFFIGLQNRFTQRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIER YQLPQSYQRV WTPGINCEPCGVWTPGINCP GAWGIHGPHGSAENTGPHLPG QTSAQLETSLPSLRSAELELA QLSPRRKQNRSLQNIQVTPSLR VPWPKASNVQQFIDEQNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENG YQGEESLFNKAY YGGGTNFFRKESQKLQQSAKK RDAELANGALGHELNNDYTLK KVMKPLITSNTVTDEIERANVF KMNGKWYLFDTDSRGSKMTIDV PQAKSNVGTISYMTNRSFFED/ KKATFAPGLWNIAIKTS
26929	57297	A	27086	345	563	
26930	57298	A	27087	1	1188	
26931	57299	B	27088	1	1186	
26932	57300	B	27089	1	1090	
26933	57301	A	27090	183	410	
26934	57302	A	27091	1	1557	
26935	57303	A	27092	888	1165	CTRERRIKARGPPAGKRWLLLS GSSGRKHHL*QDPRPGSQTAGD LPEPAR/PIIVIGESQMGLEDCQ FQFRNGRWNCALGERTVFGK ELKV
26936	57304	B	27093	1	1027	
26937	57305	B	27094	1	1117	
26938	57306	B	27095	1	1377	
26939	57307	B	27096	1	1014	
26940	57308	A	27097	1040	1285	
26941	57309	A	27098	901	2277	
26942	57310	A	27099	1	1122	
26943	57311	A	27100	1	1137	
26944	57312	A	27101	1	1881	
26945	57313	B	27102	1	1211	
26946	57314	A	27103	294	506	NRRPGSAATVWAAAAEPSE NNPALENR*SSGFSWGFFSGYQ RCRESRATTAPGYGNSRTG*AT CWLYN
26947	57315	B	27104	1	1073	
26948	57316	A	27105	1	1809	

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26949	57317	A	27106	1688	2187	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVA\RKDRES ADLGSDGQNGQDLDWGGVAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS INSTEYTKVFALDVAARHRV QFAMPESDAVAMLSF
26950	57318	A	27107	782	1402	LFPRLLSCLTTPPHCSFSCFVIC SRTLILKGSSLIKLLFYKIPSMVL SSVLLLEVKSHIVGPGLPGINRD TRIYLFCEVIFRHRYLFAISSWS GVTVA\RKDRESADLGSDGQN GQDLDWGGGAAAAADGVTF VPVTPHTFRHSYAMHMLYAGI PLKVLQSLMGHKSISSTEYVTK VFALDVAARHRVQFAMPESDA VAMLKQLS
26951	57319	A	27108	197	421	LAMPGAGFSSSLRMASIFSIHVS GTRDLSRVSTILSPLYNTVAPG AN*CRELKLVLDDADDVLSTEVI RVITSSA
26952	57320	B	27109	1	934	

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26953	57321	A	27110	1	2047	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQVRVGTIEQI NHMRDVFGRRLRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWVVDLHHIAEDTLLPF YLGEKDDVYAIKPTCWPGLDI IPSCALHRIETELMGKFDGKGL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKTVDLKGFPDVRILLTKYS NSNGSQSPWMEEQIRDAWGS VLKNVVRETDEVGKGQIRMRT VFEQAIDQRSSTDTSSTPAAP MVDLSLIARVGVGMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQTPAFGRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSPGELSARSGDALQ KAFTDKEELLKQASNLHEQK KAGVIFEAEVITLLTSVLKTS ASRTSLSSRHQFAPGATVLYKG DKMALNLDERSVPAYIIRS CGRKGFASAGVGGCROWLNY AASEQVLRVHHMRCEIPIRCV
26954	57322	A	27111	1175	1298	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWASALCKPIAE
26955	57323	B	27112	1	1056	
26956	57324	A	27113	1979	2217	WLSVRVDGGANSGLKGHGSK KCCT*NG*SW*RSDFENCF*T EQ*STLFNGAWRNALSIWEPV CN/GNFRSSD*TTLGD
26957	57325	B	27114	320	1633	
26958	57326	A	27115	606	705	
26959	57327	B	27116	1	4118	
26960	57328	A	27117	4048	4051	
26961	57329	A	27118	1791	1884	ADGCIQIG*RLSPNKCL*TWAS LCKPIAE
26962	57330	B	27119	1	2436	
26963	57331	A	27120	1	2449	
26964	57332	B	27121	173	4112	

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26965	57333	A	27122	916	1568	HHSHEQQFQWPVGASGVDRW AGYLHQFRSLTQFQYGAEPDR KE* CQIFIMQKTL SCL SILGR TMSLMQ
26966	57334	A	27123	1268	1773	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVAIRKDRES ADLGSDGQNGQDLWDGGGIAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYVTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
26967	57335	A	27124	606	852	HQILFDRTPVSDQSVKEKKG*D HSVRPQ*AAPGHVHYLTIPEKS SQHYHPRTTSE*TSGRYESSGG LSFSQCMRGALEFCC
26968	57336	A	27125	1	2680	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGLTRRAEDVPPVI GVAAIKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWWPDLIHIAEDTLPLF YLGKDDVTYAIKPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPAETSQGA GTLANVVTSLANLSESLNNGDT SEIQPEDQSASEITRAFDTLAKA LNTTSSSSPSLADGIDTSGGGS IHVISRDQSTPIEVEGPLLSDTH VTFKSIREDRNGRSQKTVHTEG DMNMNIKKIVKQATVLTFTTA LLAGGATQAFAKENNQKAYKE TYGVSHITRHDMLQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTVAEYNGY HVVFALAGSPKDADDTSIYMF YQKVGDNISIDSWKNAGR VFKD SDKFDANDPILKDQQTQEWGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQNVNSKSDDTL KINGV EDHKTFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYL VFEANTGTENGYQGEE
26969	57337	A	27126	2014	2138	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWSALCNPTAE
26970	57338	B	27127	1	7616	

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26971	57339	A	27128	240	719	HSKKLVTLSHGSVMAETAVIN HKRRKNSPRIVQSNLDEAAAYS LSRDQKRMVLYLFDQIRKSDGT LPEHDGFCYIHVAQSAEITGLTS VGNPVRIYGRH*RVSRGRKVV YRPEEDAGDEKGYESFPVVIKR AHRPSRGLFSGHIPPIHSLLYR
26972	57340	A	27129	1505	3812	
26973	57341	A	27130	471	566	
26974	57342	A	27131	1	229	
26975	57343	A	27132	121	303	
26976	57344	A	27133	183	524	MSTPRPFVPAFVGRPPSLLFVP AARLTDVRGRKVRACGLSPR LRSPSSSSATRVARHSIGRPRVA RLSTVFVAVCVESPSRQRWCL FALAATPRAPGTLA*SCLTDSFS A
26977	57345	A	27134	1	1025	MIFVLQIRVRGHDDSLKNHLV FLVIYGTNGTFNQTLVTDNGL APFTLETSGWNGTDVLEKGFQ MEDLVYNPEQVPRYYQNAYLH LRPFYSTRSFLGIHRLNGLPKC GQPQEVLDVYIDPADASPDQE ISFSYYLIGKSLVMEGQKHLN SKKKGLKASFSLSLTFTSRLAPD PSLVIYAIFFSGGVVADKIQFSV EMCFDNGQDLDLTSTVRVTRSSA SVMVYGASEAIGQRQSSAAKP RRSQSDSLGPEFQGLWERLPGL RINGELITAYPQVVVVRVPTPW VQSDSDITVLRHLEKMGCLM NRPQAILNCVNKFVTFQELAG HGVPLPDTFSYGGHENFAKMD EAEVLEFPMVVKNTGRHGRMY ELLVSTMGCNSGMVTTPIKWL SMISVQCLANGTFLSPSLTKCPK GIRASVPLSGGPRSLKARTFSAF SGPVRSDQEALPEAYEPIEV NEFGEDLLAMVEDEILALPVV PVHDSEHCEVSEADMVFGELPE EAQKPNPFAVLASLKRVRMSA VQKNKPTRSKRGMRSHDALT AVTSLSDKTSGEKHLRHH*SA DLAAAPRAPGTLAQGLTDSFS
26978	57346	A	27135	79	306	SGDLPEWINPLSSCSLLREKDP MTSGPQTNPQKHLINFKSGPH WKSDCSTHLAATPKAPGTLAQ GSLTDSFSA
26979	57347	A	27136	159	254	
26980	57348	C	27137	63	370	
26981	57349	C	27138	107	408	

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26982	57350	A	27139	210	291	
26983	57351	A	27140	395	680	
26984	57352	A	27141	157	485	
26985	57353	A	27142	1	507	
26986	57354	A	27143	1	1041	
26987	57355	A	27144	1	671	GASGAAAYGADMAKSKNHTT HNQSRKWHNRNGIKKPRSQRYE SLKGVDPKFLRNMRFACKHNK KGLKKMQANNAKMSARAEA IKALVKPEVKPKIPKGVSRKL DRLAYIAHPKLGKRARARIAKG LRLCRPKAKAKDQTKAQAAAP PSVPAQAPKDDTSNIFISNRKR GCDFTKKETNIPKVLITISMAPSL MSLYSVTRNQTTKPPSRHKNL KQGLEPLY
26988	57356	A	27145	6	448	
26989	57357	A	27146	930	1307	
26990	57358	A	27147	1	675	
26991	57359	A	27148	142	456	
26992	57360	A	27149	3	175	
26993	57361	C	27150	378	434	
26994	57362	A	27151	1	792	
26995	57363	A	27152	1	578	MVRCVRLVEAGSVVRYLSTSI RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAVVRARELHTLEVTLGET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRILGASL/HTSASKHTM VRALTYCSSREFTTAI
26996	57364	A	27153	1239	1905	SAAAPATGVPACRAGAWVSA APPAEGRPARARRHPGRCLEAA GPRGQRGAHGH*ARAGSPQP GAPPCPLGIPARQPLGLPRRTR CFGIAQRGRAARHCLLSRPSA KAKRNSSYREPGMGWSPQA LGEYKGQSQAQSARLSGAASQ GRRARHLRGKAPAWNPPPPSP PPPALGLPLRTQREATRPPRE EARRPRPRPLRPGGANGSPGPP RAARA
26997	57365	A	27154	1	1275	
26998	57366	A	27155	3	92	EAVDPHSECYSS*RWCVRSFFIL VGLWSH
26999	57367	A	27156	2	367	
27000	57368	A	27157	98	293	GQTFATASISLLRYATGCGVFP RV*IRSPRAIPALSGDWAPFVS LSEPRFVCLRAMTKAAAF
27001	57369	A	27158	3	211	

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27002	57370	A	27159	1	519	GQLI/LKDTFITQSAADIRKQFQ KQALGPEHNLEALLNLAILVFY NRDQEEQAQKEKRDQRKAAPL IMALRQTLVQVRGQKMEQANH LIPGYSEIARPLYTLIKEIQRANT HQVEWEPEAETAFAKPLKQALV QAPALSLPTGQNFSLYITERAGI ALGVLQTHTGTTPLQVAYL
27003	57371	A	27160	72	381	DSHTRSGITRWGIRCSRSGSSPSR RARWGRWGGLAAVALRRPAP AAGGTAPRGCLPAA*GSPAPP SGS*SGSSDRPARMPLVVGLSH EFE*GLAGVDGEVLPPSRCVAL LLLRVERLHVAVYLPREALHQL IPLALDLDLLIARLVCHWLWG CPTLSKDKSYSCSLCDV
27004	57372	A	27161	515	747	SHGNSGNFQGTDRDTISLS*AQLT TSTKDPWTDPPALWPRVFPSSGG HYNCRAPSSPTIQQEVARAVIT QFPTAAGVSCL
27005	57373	A	27162	1	663	
27006	57374	A	27163	1	1980	
27007	57375	A	27164	1	672	
27008	57376	A	27165	1	691	
27009	57377	C	27166	1	1491	
27010	57378	A	27167	830	2592	
27011	57379	A	27168	1	3744	
27012	57380	A	27175	2	365	QWDWAPWSRGWCSSGRLGPH RSPRSGGSGGRRAAGPKPCPSP RSDAPAQPRGRSRRVLPPLQVQ AEPPEPWVPLPAAPKPLARPEA GMAGPGGRRTTSLPRRRGCCG CCPASSCFSSLSC
27013	57381	B	27176	1	1392	
27014	57382	A	27177	79	1241	
27015	57383	A	27178	3	299	

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27016	57384	A	27179	1	812	MPTVLACPAFDSRGSPICRFDPPELTSQVRALEESPNAILPVCGRDVKFTLEVLRGDSVEKTSRVVSGNERDQELLTEDALDDLPSFLLTGQQTAPAFGRRVSGVIEIADGSRRRKAAALTESDYRVLVGELDDEQMAALSRLGNDYRPTSAYERGQRYASRLQNEFAGNISALADAENISRKIITRCINTAKLPKSVVALFSPHGGELARSQGDALQKAFDTKEELLKQASNLHEQKKAGKRSRRLHHTLLRVVAEIDKPDPRDELAGLLQFAGGPLQTLFAWVSPVEAAEQQRLLAPSSGSFIP EG*DHPVRPQ*AAPGHVHYLTI PERSSQHYHPGALQE
27017	57385	A	27180	306	701	
27018	57386	A	27181	1	396	
27019	57387	A	27182	1	1263	
27020	57388	A	27183	1	873	
27021	57389	A	27184	149	421	
27022	57390	B	27185	23	268	
27023	57391	A	27186	1	363	
27024	57392	A	27187	2	398	TKFAARRPALAACAAISKIKARDLRGKKKEELKQLDDLKVELSGLRVAKV/TQGGGAASKLSKIRVVRKSIARVLTVINQTSKKKT FREILTRGKKYKPLGPCGP*GRT RAMRRRRFKPSTEGEP*RTQGSR
27025	57393	A	27188	224	547	
27026	57394	A	27189	1	888	
27027	57395	A	27190	280	1170	
27028	57396	A	27191	1	191	
27029	57397	A	27192	438	1240	
27030	57398	A	27193	168	378	
27031	57399	A	27194	1	1362	
27032	57400	A	27195	2	918	
27033	57401	A	27196	38	397	RRCRPTMPRPWCTCRGYQGPRKAQGG*AQDPKGCQPQARSTCLHCPQAW/RVLPVPLPRGSGCAGQ/MAKAKAKAKDQTKAQAAAPASVPAQAPKRTQAPTKASE*ISLPT*GQKDWDGP
27034	57402	A	27197	1	1206	
27035	57403	A	27198	734	913	
27036	57404	A	27199	3	778	
27037	57405	C	27200	164	274	
27038	57406	A	27201	1	2700	
27039	57407	A	27202	1	747	
27040	57408	A	27203	164	409	
27041	57409	A	27204	152	380	

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27042	57410	A	27205	230	2579	
27043	57411	A	27206	1	2433	
27044	57412	A	27207	1	528	NHQRNDFTISPGVKADSRTSPI PQQPASSFDITEAASFAKDSLA GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP/ TQALNFTFKDKYKQIFLDGVDK RSQFWRVYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVKG AGAERELRGFGDCLVKIKSDG IK
27045	57413	A	27208	1	292	MTSKDKTSRGTIRQQHSRFFKI RCSAATTAGTQANRVWSGPLA NSNRPAAEAGVSTAAAPDGGPPP PSVPTVDSDSLESAQFKCDNLK TCHTSHGSVMAETAVINHKKR KNSPRIVQSNDLTEAAYSLSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDEKGYESFPWFIKRAHSP SRGLYSVHINPYLIPFFIGL*PDK EGNEIWVDMYTVKPSGWTVRT FDKPRKRFIAFFIAGILFRAIKNH FLPRETLQCLPYILTGFRRGQSE YFSIFSNMDLADTVMFL
27046	57414	A	27209	1	1452	
27047	57415	B	27210	53	844	
27048	57416	A	27211	281	624	ACSDVWSKFRLRWSNPNCQE RPSAEKMSPHPPSAARHQASWS ARRLTQWPRPCHTQ*GQSEEH GHRSGLMPAGVTHQLPDEHAIT PHLQSTAPIPEPKTLSHKDSSLQ GTGK
27049	57417	A	27212	3	411	
27050	57418	A	27213	265	480	LDLTILTASDGRPTYTP*FLLS/ CFCYGFFCYIFGCSCLARAR AGGGGVPAAHRAAGGRSRAPE RIPPH
27051	57419	A	27214	294	620	
27052	57420	A	27215	1	420	
27053	57421	A	27216	1	342	
27054	57422	A	27217	175	244	DLLEMGSSFFVQCRTAIL*RKQN
27055	57423	A	27218	11	951	

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27056	57424	A	27219	20	1654	ELRFPAACSQLQFSDGLHRVDQ PPSSMCVSAADLWLCEAGKLL VVPMDGSHWFTMRSVVEKLIL RGHEVVVMPEVSWQLGRSLN CTVKTYSTSYLTEDLDREFKAF AHAQWKAQVRSLSFLSSSNG FFNLFFSHCRSLFNDRKLVEYL KESSFDAVFLDPFDACALIVAK YFSLPSVVFARGIGCHYLEEGA QCPAPLSYVPRILLGFSAMTF KERVRNHIMHLEELFCQYFSK NALEIASEILQTPVAYDLYSHT SIWLLRTDFVLDYKPKVMPNMI FIGGINCHQGKPLPMEFEAYINA SGEHGIVVFLGSMVSEIPEKKA MAIADALGKIPQTVLWRYTGT RPSNLANNLTILVKWLQNDLLG HPMTRAFITHAGSHGVYESICN GVPMMVMPLFGDQMDNAKR METKGAGVTNLNLEMTSEDLE NALKAVINDKSYKENIMRLSSL HKDRPVEPLDLAVFVVEFVMR HKGAPHLRPAADHDLTWYQYHS LDVIGFLAVVLTVAFITFKCCA YGYRCKLGKGRVKKAHKSK
27057	57425	A	27220	1	2022	
27058	57426	A	27221	124	205	
27059	57427	A	27222	248	443	
27060	57428	A	27223	263	415	
27061	57429	C	27224	1	717	
27062	57430	A	27225	349	1125	
27063	57431	A	27226	629	796	
27064	57432	B	27227	1	388	
27065	57433	A	27228	2	346	
27066	57434	A	27229	448	555	
27067	57435	A	27230	2	423	CEPIKVVYVGN\GAVGKTCLLI SYTTNAFGEYIPTFVDNYSAN VMVDGKPVNLGLWDTAGQED YDRLRPLSYPTDVFLICFSLVS PASFENV/LCKGAVKYLECSAL TQRGLKTVFDEAIRAVLCPPPV KKRRKRCLLL
27068	57436	A	27231	1	1503	
27069	57437	A	27232	1	635	

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27070	57438	A	27233	3	1107	AVFLSFGWWPLPGIGFQSAEGE AAWTAAPAPSPPPSKPRARPP RPEPAASYLSALPPPPRPSERPS MQAIKCVVVGDAVGKTCLL ISYTTQCHFLGEYIPTVFDNIYS A\NVVMVDGKTGEIWGLWDTAG QEDYDRLRLPLSYPANRMC*S I CFSLVSPA/SFENV/LVQKWYPE VRHHCPNTPNPVGTKLDLRD DKRHDSRNLEKKLT/PITYPA GS*AMAK/ERLGA VKYL/CAP AAHTSEGLKTVFDEAIRA/VLCP PPVKERGRENCLPVVNVSA PSF LGSCPLGTFCLCSKKNKKKKQ KKKNNGGAFALNANFLLQINFS IKPFFEPISNFKVL FVLNVRVQT HILLKFSPKMTSLKALFFK
27071	57439	A	27234	3	203	
27072	57440	A	27235	1	112	LGNTWG*QPCKRLKIWLSLEFT KINVIRHMKFKRL
27073	57441	A	27236	1	513	QHWGRYLKRAFEQWQVPRFG HMPDPGPVKPLQPVETVRGN DYKFLLFHFWDEWLYKFSADE FFIPGKLCAIVF*KRL*RP GAVA YACNPSTLGSGRGWIT*GQ EFE TSLTNKEVKVLSIDQRNFKLRSI GWGEEFSLSKHPQGTEVKAITY SAMQVYNEENPEVFIIDI
27074	57442	B	27237	125	302	
27075	57443	A	27238	93	432	
27076	57444	A	27239	3	279	
27077	57445	A	27240	263	446	
27078	57446	A	27241	237	369	
27079	57447	A	27242	389	836	
27080	57448	A	27243	1422	1580	
27081	57449	A	27244	103	444	RSLTCPGDMFPVVLVINIQLLT YANFCSWLES LPRKWDFLFYCI VRLQIFQTFMLCFLNLPLRNF FYQIP*HSLKFKVPQISKAEAKC HQS LCIGRVTFIPVPNKFFISI
27082	57450	A	27245	3	242	MHRNAQH HVKTAKPWGLHPL KPQPK*YSGPF*PPELQRCKAT GP*GCTQQGGPGPGQNNFSL LGLQACDGRDCHEGL
27083	57451	A	27246	506	664	
27084	57452	A	27247	1	1515	
27085	57453	A	27248	269	541	RFPNLNS*LLYTRGLTPHESCQ GLGLAPSEAMAQTI PWLLATA RLAVTGNQILMQISAAGLNFS S ENGAFISIALSGCKFFKLLCSAS
27086	57454	A	27249	1	564	

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27087	57455	A	27250	2	235	
27088	57456	A	27251	3	1393	
27089	57457	A	27252	28	271	
27090	57458	A	27253	12	485	RMAFCRASQADQDRFCIYPAY LNNKKTIAEGRRIPIKSAVENPT ATEIQDVCSAVGLNVILRKIKM YF*EWNRDVQYR/GRVRVQLK QEDGSLCLVQFPS/RLYTKPNF WFLGKSVMLYAAEMIPKLKTR TQKTGGADQVFQQGECS*GKG GKQKEVT
27091	57459	A	27254	1689	2176	APPGMGAASLCAFGLLVTFAT ASPRYAMVQPSFRLGTLGQA EADPEFVSSGVSPPSFLSPLPA APGARRG*LQRGDLGRQAPPPA PGCAPGLA*GRPPAPHL*RLCSR PTFFPPPPANSSRLALADSPPRQ LQGARPP*PVPGRLLTSTGTPRPL PRPLGP
27092	57460	A	27255	263	439	
27093	57461	A	27256	1	499	MSELPTIATKRIKHLGIQLTRD VKDLFKKNYKPLFNEIKDDTNK WKNIPCLWIGRINILKMAILPKV IYRFNAIPIKLLMTFFTEMENTT FKFMWNQKR/CPHCQDNPKPK EQSWRHAT*LQTILQGYSNQN SMG/TWMKLETILSKLSQGQK TKHRMFLIGGN
27094	57462	A	27257	1940	2062	
27095	57463	A	27258	1232	1432	
27096	57464	A	27259	168	1189	
27097	57465	A	27260	1	1760	
27098	57466	A	27261	453	543	
27099	57467	A	27262	873	962	
27100	57468	A	27263	8	411	FSRCRCSGR/YLCMASCL/CFHH CWWMAASHHWPI*RTQV*CAC WEGRHLG/CAPKCLSLGFTRL LACVLLWPLQSVIPIHIQVSITV RVLFAAAHDEARASEATFQESG GPYPLLSTPLILLKAVVVLMLD AHAS
27101	57469	A	27264	1	552	
27102	57470	A	27265	828	1211	
27103	57471	A	27266	428	655	DQKVPPLEMYFGIEVKSLLQLR SISA*SLFSSRLKEDSGLLKLK QPRSSGVIPRRFIVSWPWKMVR QPVLFSVG
27104	57472	A	27267	1	855	
27105	57473	A	27268	1	1261	
27106	57474	A	27269	164	260	

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27107	57475	A	27270	147	224	RLTLDPHLGSLLDHHRVALGNS YSGG
27108	57476	A	27271	1	837	
27109	57477	B	27272	184	288	
27110	57478	A	27273	1	286	
27111	57479	A	27274	1	699	
27112	57480	A	27275	1	3660	MTGICYTEDERSYKKNQAPTA ASKKQKETQKFCRLVDDGQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAAQRAQSLEPYGTG LRALAMPGRPESPVPFRSQEVV ETMCPVPAATSNVHMKKISI TERSCDGAEMKWEDQNIQD
27113	57481	A	27276	1059	1229	
27114	57482	A	27277	2	4735	
27115	57483	A	27278	415	825	SCADFQDYWDQREYTYNRPH ASRRIVLDFLLFPEW/PTFVAFW APLFNPSKRASLYRFLSCISSLSF GSHWGSVPGNWVLTYSWG/SL VISRCMFL*PLSCCLEHSPPFICV KEEHEQLVAISPSGVMLDNLSEQIN
27116	57484	A	27279	1	1326	
27117	57485	A	27280	2976	3068	VWTLALNRLGQQVSIQCG*PGTE DSKGDWLL
27118	57486	A	27281	78	220	APTSLHS*SYFKNCGHRLRWV ITHIRLVISWATYLVQNNIQLR LF
27119	57487	A	27282	1	1077	
27120	57488	A	27283	307	922	QVVPSSLSAISQSPAPCG/CSP*G PSPGAT
27121	57489	A	27284	1	4560	
27122	57490	A	27285	87	237	LLFFQLGGDAFSKFKSSGVNFR NSLICQAWGKRVFSALLCHLSE YTSPL
27123	57491	A	27286	1	246	
27124	57492	A	27287	46	396	
27125	57493	A	27288	1	552	
27126	57494	A	27289	3	418	AEKCPCLGAFGFGWDHPRRPG SWGAWSEGGSPPARIVKMMLR KQTPSDFLKQIIGRPVVVKLNS GVDYARGVLACLADGMNIALE QTEEYVNGQLKNKYGDADFIR GNNVLVYSTQKRPDVRTPKRA TLFIVGYIFL
27127	57495	A	27290	202	450	

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27128	57496	A	27291	304	642	
27129	57497	A	27292	75	393	
27130	57498	A	27293	1	678	VFGLGSAHMLLNKTFGSYLGVNLGFGFGVTMGVHMAGRSGAHMNAAVSLTNCALGRVPWRKFPVYVLGQFLGSFLAAATYSLFYTAILHFGSGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEAWLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWGKQVFRVHHLPLGLHWHHPITGAPEIGGFCGV
27131	57499	A	27294	2	1694	
27132	57500	A	27295	1	356	GIFVTYLPDHMTLWRGFLNEAWLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWGKQVFRYFPCGPIPLSFSVGPLCVEGWGM
27133	57501	A	27296	1	544	
27134	57502	A	27297	320	610	LREYTIINHTAHMPMEWASKKRAPRALKEIRKFAMKEMGTPDVRI DTRLNKA V WAKGIRNVPIRIRVRLSRKRNEDEDSPNKLYTLV TYVPVYHFQK
27135	57503	A	27298	1	303	
27136	57504	A	27299	1	1311	
27137	57505	A	27300	1	3126	
27138	57506	A	27301	2	779	NRVLLAMVNPTVFDDIAVDGEP LGRVSEFVRGLDTKK*LLI*SIK LC*QIG/LFADKGPRGTA*FSL* ATGEKGFL*GVPCFHRJPGFM ICQG/GDFTRHNGTGKSHLW GRNLKDENFILKHTGPGILSHG KMLDPNTNGSQFFICTA/KTEW LDGKHVVFGKVKERHEILWEA MGALLGPRNGKTQEESEPIVPG GQLRIKFDLVFYSLTTHIFPFCF KESTPPPHLLASILESLCSRLQFP FGFHVFLVPCHA
27139	57507	A	27302	143	390	
27140	57508	A	27303	249	1516	

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27141	57509	A	27304	2	645	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDITKK*LLI*SIK LC*QIGLFAADKGRGTA*FSCGL SIEEKGFGL*GVPCFHRIPGFM CQG\GDFTRHNGT\GGKSHPM GKKFE\DENFILKHTG\PGVLSH GKCLDPNTNGSQFFICTA\KTEV VGMAKHVVFVQK*KKGMKYC GRPWFRFG\SR\NGKTQQRKITI C*LVGQLRNKVLTWVF
27142	57510	A	27305	72	387	VCLQHGPWSSLKHVQGWRRD CHGLSLGPRTHVQAGTLPKPTL WAEPGSVITQGS\VTLCQGI LQTQEYRLYREKKTAPWITRIP QEIVKKGHDPISITWEHTG
27143	57511	A	27306	1	322	
27144	57512	A	27307	1	1125	
27145	57513	A	27308	1	1419	
27146	57514	A	27309	198	1634	
27147	57515	A	27310	78	216	
27148	57516	A	27311	1	489	
27149	57517	A	27312	18	463	AEGVEPGSPRVVLESEQFLTE LTRLFQKCRSTSGSVYITLKKYD GRTKPIPKKGTVEGFEP\DNKC LLRATDGGKKISTVSSKEVN* VFRWLISNPLGANMDGLKKR DKKNKTKKTKAAAAAAGP AAAAATAATTAATAAAQ
27150	57518	A	27313	1	1242	
27151	57519	A	27314	147	965	DPPSPVPAPPSPRDGHFLVPDA TMAEEQPQVELFVKAGSDGAK IGNCPFSQRLFMVLWLKGVTFN VTTVDTKRRTETVQKLCPPGEL PFLLYGTEVHTDNTKIEEFLEA VLCPPRYPKLAALNPESNTAGL DIFAKFSA\YIKNSNP\AL\NDNLE EGTPGK*\RFLDNYLTSPLPEEV DETSAEDERCLSDGTFLDGNEL TLADCNLLPKLHIVQV\CKKY RGFHHPPRPFRGVAFGYL\SNA\ YARENFRFPVPDDEEIELAYE QVAKALK
27152	57520	A	27315	1	933	

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27153	57521	A	27316	63	641	FAKMTDHHKGERGEATRYMFSR PFKKTMGVVPVCGHNN*RFYK/K GDIVD\IKMGVYCVQNGMPHK CYHGK/TKGRSLTIVTPACLLPLL *TNQF*GKVF/SKRVNRIEHIKH ISKSRDSFLKRVKENDQKKKEA QEEGT\WVQLKRPAPPREAHF VRTNGKEPELLEPIPYEFHGIN RCPKKKIKDLWATKKKKK
27154	57522	A	27317	1	390	
27155	57523	A	27318	75	394	IWGDVEKGKK\IFIMECSQCHT VEKGGKHKTPNHLGLFRKTI GQAPWDTPYTAANKNGIHWG EDTLMEYLENPKK\YIPGTKMI FAGIKKKEERADLIAYLKSSY
27156	57524	A	27319	2	529	FRQTRHAGGVRRGPRPKLQRD KAAAAAVLGAVRRKPSVVP AGQDPALSTSHPFYDVARHGIL QVAGDDRFGRRVVTFSRCRMP PSHLDHQRLLEYLKYTLQDY VENDYTIVYFHYGLNSRNKPS LGWLQSAYPEFDRKYKKNLKA LYVVHPTSFIKVLWNILKPLISH KFGKK
27157	57525	A	27320	287	445	
27158	57526	A	27321	2	362	
27159	57527	A	27322	30	365	EEAETVLVGQLKLSSCLA/VH KYRPETKQEKQRLRLARAEEK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLVCRKMGVP YCIKGGKARLGRLVHRKTCTTV AFTQVN
27160	57528	A	27323	3	432	NSRVDDFVAQAQDAKGGKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ/RLRLARAEEKAAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVIAHDVDPIELV VFLPALCRKMGVPYCIKGGKAR LGRLVHRKTCTTVAF
27161	57529	C	27324	62	217	
27162	57530	A	27325	1	1545	

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27163	57531	A	27326	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRILYKRLKVPAINQFTQAL DRQTATQLLKLAKHYRPTKQ EKKQRLLAAREKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIADVDPIELVVFLPA LCRKMGVPYCIIGKARLGR VHRKTCTTVAFTQVNSDKGA LAKLVEAIRTNYNDRYDEIRRH WGGNVLPKSPVARIAKLEKAK AKELATKLG
27164	57532	A	27327	550	827	DVSWAGRSEDIHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLQL PQEHTRKTLPLQQTSAWTYRLF HTSCEI
27165	57533	A	27328	908	1331	GDMRGREGGFGLRRTAMRC GCSPGVIREADNLVKLSRPSTV RVTRSSASVMVLTMLAPATFL RVNCWAG/RGR/C*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPKRDPL RVKDQGRHPCVV
27166	57534	A	27329	1	1134	
27167	57535	A	27330	62	310	
27168	57536	A	27331	243	578	
27169	57537	A	27332	324	995	NLVPRPGTWIRGLPLGDHSPVL LLFAP*ERSTYDLRSSDRPAQET SHQFQIRERQRRHVLSVDPKLR RRSRTGKAAPFWCLIIAGTPL*L YTHVSRVSDHAGMPALVLHP* R/LSPTFLGKGQHALKGLKPVIT RLQLQHGLLKPINSPFPSPILPVLK PDKAYKLVQNLRLINQIVLPIHP VVPNPYTLSSIPPSTTHYSVLD LKHAFITPLHPSSQPLFAFT
27170	57538	A	27333	1	1860	
27171	57539	A	27334	1	957	
27172	57540	A	27335	97	826	
27173	57541	A	27336	245	392	
27174	57542	A	27337	736	1300	
27175	57543	A	27338	590	891	
27176	57544	A	27339	1256	1654	VQPVRLVSGMQHPGSGWRRL WQGHSTSLTSKEHLHISKRGNI DNLVQRNMPASNEKPKCPFLPP FPSCLSTVHFIIIVVVQTVLFIGY IMYRSQQEAAAKKILLTIFLCT SSICVQNDVVLRFEKYLNCFIV
27177	57545	A	27340	295	852	

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27178	57546	A	27341	3	446	ILAWFGSIAEAPSAAWLCGSSQ GRYCSSFNVRVVRQNSSDAKV NVPKTRITFCCKVCGKHQPHKV TQYKKGKDSLYAQGRRRYDRK QSGYGGQTKPIFRKKAATTKKI VLRLCEVEPNCRSKRMLAIKRC KHFELEGDKKRRKQVQIF
27179	57547	A	27342	1	565	
27180	57548	A	27343	1	1050	
27181	57549	B	27344	1	2109	
27182	57550	A	27345	2916	3229	
27183	57551	A	27346	3	671	AGILAAIREANMGAYKYIQEL W/RKKPSDVHAFLLRVRCGQT RSFFVFTGVPRPTRDPKARRLG YKAKQGYVYIRVRRGGRKRP VPKGATYGKPVHHGV\NPA*KF ASKALQVPLPEGTAGRHCGG S*ESLSYVWGDS\TYKFFEVI LIDP/YSHKAIRNPDTQ\WITK PVHKKHREMRGLTSAGRSRGL GKGHKFHHTIGGSRRAA WRRR NTLQLHRYR
27184	57552	A	27347	1	1646	
27185	57553	A	27348	2	2600	
27186	57554	A	27349	1	2403	
27187	57555	A	27350	100	520	
27188	57556	A	27351	1	570	
27189	57557	B	27352	1	837	
27190	57558	B	27353	1	1434	
27191	57559	A	27354	1	2379	
27192	57560	A	27355	3	952	IDWAPKSDRIVTCGADRNAVY WSQKDGWVKPTLVILRINRAA TFVKWSPLENKFVVGSGARLIS VCYFESENDWWVSKHIKPIRS TVLSLDWHFPNNVLLAAGSCDF KCRVFSAYIKEVDEKPASTPWG SKMPFGQLMSEFGSGTGGWV HGVFSASGSRLLAVVSHDSTVS VA\DAKSVQVSTLTKTEFLPLL SVSFVSENSVVAAGHDCCPMLF NYDDRGCLTFVSKLDIPKQSIQ RNMSA/LWERFR\NMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRFCTTGIDGAMTIW DFKTF\ESSIQGLRIM
27193	57561	A	27356	3	134	
27194	57562	A	27357	1	478	
27195	57563	A	27358	1	623	
27196	57564	A	27359	425	667	
27197	57565	A	27360	121	401	
27198	57566	A	27361	1	1818	

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27199	57567	A	27362	552	2325	
27200	57568	A	27363	693	1270	
27201	57569	A	27364	18	146	
27202	57570	A	27365	270	683	
27203	57571	A	27366	1	1398	
27204	57572	B	27367	1	1152	
27205	57573	A	27368	40	538	SPSPKDSPGVRVIGISCYIGGPCQ QRLLSPVVRASKMTKKRRNNGR A\KKGPRHVRGSPSLKFLPPSSC HLTVPRCRAQGTTRPIKKFVISK P*VEAAAVVRDISEASVFDAYL\ LPKLYVKLHYCVSCAIHKQK*S GNRS\RE\ARKTRTPPPRFR\PGG *LPHGPPTKSP
27206	57574	A	27369	204	401	
27207	57575	A	27370	3	980	
27208	57576	A	27371	2124	2836	
27209	57577	A	27372	139	8892	
27210	57578	A	27373	1	2592	MAGLGASLHVWGWMLGSL LAKAQVRASAPRHLFSRLRRG LSFSDTEARCARELIHVHTSTN APARTEAYPAGSAEPPRRRPRAG REHSFFSQRYVPLPPLGGALGS GPAKLPPPRAPCPVRFCADLET LCGALDCYKVRGGAAPARPAP RPAGGIQVSSLSGFGTESLPGON PPPHRDHRESGTMDSPLTVAT PLSLTPPIPRELACGDWRRVGG GAGGGGLRRRLGGLGDKAGKR KSSDLPCGPGFLQSLQKRRHW ESGLGLPGCGCELSVSGCGAP TLRQHIIIPAEGRNGVKEKSADL GCGGSQGLRAKKGTNPGIENG KRKGKGEMLDAWICRRSAFGP GREKLGGEVGCNDKGKIRFIE VKMSKKISGGSVEMQGDEMT RIIWELIKEKLIFPYVELDLHSY DLGIENRD/ATNDQVTKDAAEA DKKHNVGVKCATITPDEKRV EFKLKQMWSKSPNGTIRNLGGT VFREAIJCKNIPRLVSGWVKPIII GRHAYGDQDQGSNMQNAIMK KLKWLHLARVKGFSANAKFY CRLYYAGEFHKMREIVILDSSEE DFIRSLSHSSPWQARGGKSGAA FYATEDDRFILKQMPRLEVQSF LDFAPHYFNITNAVQKRP LAKILGVYRIGYKNSQNNTTEKK LDLLVMENLFYGRKMAQVFDL KGLSRNRNVKDTGKESCDVV
27211	57579	A	27374	2	2138	

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27212	57580	A	27375	1	2355	
27213	57581	A	27376	249	1544	EIYSLSRFIEVKMSKKISGGSVV EMQGDEMTRIHWELIKEKLIFFY VELDLHSYDLGIENRDATNDQ VTKDAAEAIAKKHNHVGKCATI TPDEKRVEEFKLKQMWKSPNG TIRNILGGTVFREAIICKNIPRLV SGWVKPIIIGRAHYGDQYRATD FVVPGPVKVEITYTPSDGTQKV TYLVHNFEEGGVAMGMYNQ DKSIEDFAHSSQMAKSGWPL YLSTKNITLKKYDGRFKDIFQE MYDKQYKQFEAQKIWYEHR LNDMDMVAQAMKSEGGFIWAC KNYDGDVQSDSVAQGYGSLG MMTSVLVCPDGKTVEAIEAAH GTVTRHYRMYQKGQGDVHIP LASIFAWGPEGLVAHRAKLDNN KELAFFANALEESFYETHEVAGF MTKDLAACIKGLPNVQRSDYL NTEFEMDKLGENLKIKLAQAK
27214	57582	A	27377	1	692	
27215	57583	A	27378	251	2150	
27216	57584	C	27379	93	293	
27217	57585	A	27380	308	534	
27218	57586	A	27381	2	856	
27219	57587	A	27382	3	327	AQELHIFTEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCQGEALTTLEVAGRM LGGIAKQEKKKKKTGRAKRRM QYNRRFVNVPFTGKKKGPNA
27220	57588	A	27383	150	456	
27221	57589	A	27384	651	835	
27222	57590	B	27385	1	2193	
27223	57591	B	27386	109	714	
27224	57592	A	27387	150	458	
27225	57593	A	27388	1	2055	
27226	57594	A	27389	1	804	
27227	57595	A	27390	645	1828	
27228	57596	A	27391	899	1216	
27229	57597	A	27392	79	156	
27230	57598	A	27393	1796	2215	
27231	57599	A	27394	107	724	
27232	57600	A	27395	854	926	PLEIPHEPPPRG*HAPQLPRGQ
27233	57601	A	27396	2	413	
27234	57602	A	27397	54	442	FAKMTNTNLNRRGTRYMFSSRP FRKHGVVPLATYMRIVYKGGDI VHIKMGTVQKGMPHKCYHG KTRGVYVNTQHAVGIVVKNQKQ KGGILAKRINVRIEHITHSKSRH SFLKRAKENDPEYEALENGT

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27243	57611	A	27406	142	1285	SRMSKAFGLLRQICQSILAESSQ SPADLEEKKEEDSNMKREQPR ERPRAWDYPHGLVGLHNIWT DLACLNSLIQVFMNVDFTRIL KRITVPRGADEQRRSVPFQML LLEKMQDSRQKAVRPLELAY CLQKCNVPLFVQHDAALQYLK LWNLIKDQITDVHLVERLQALY TIRVKDSLICVDCAMESSRNSS MLTLPLSLFDVDSKPLKTLAEDG LHCFQPRELSSKSKFCFCENG KKTRGQKVLKLTHTLPTLTIHL MRFSIRNSQTEKDLATPLYFPQS LDFKPRSFQKRESCDAEEQS GGQYELFAVIAHVGMADESGHY ICVYIRNAVVGKWFVCFNDSNIC LVSWEIQCTYGNPNYHWQET AYLLVYMKMEC
27244	57612	A	27407	1	1077	
27245	57613	A	27408	3	242	
27246	57614	A	27409	213	928	EGPARQLLSPVRASKMTKKR RNNGRAQKRAAAHVVRGSP/LK/ CFPSGPLPPNCAR/CVPGQTRPI KKFVIRINIVGGRSRQGHISEAS RLRMPISLPLKLYVKLHYCVSC AIHKQK*FR/NRS/RESPAKTRTP PPRF*DLAGGCPTVPPKAHDL GPEYCRHQTCVNVWCCRQATI LGKELCGQIRKLPSQQMSPGWL PSGYSCWLKYKTEATTALQS RGEVYHPLQALWSRPPGRDPL
27247	57615	A	27410	1	267	
27248	57616	A	27411	257	322	
27249	57617	A	27412	2	176	
27250	57618	A	27413	218	923	
27251	57619	A	27414	2	429	TKFAARRPALAACAAISKIKAR DLRGKKKEELLKQLDDLK/VE LSQLRVA*VTGGAASKLSKIRV VRKSIARVLTIDNTSGKKTFR EILTRGKKYKPLGPCGP*GRTR AMRRRLNKHEENLKTKKQQRK ERLYPLRKYAVKA
27252	57620	A	27415	1	1146	

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27253	57621	A	27416	2	670	IAGEITRRGSRARPRPGPQCPCPPG PPGTAMIKAILIFNNHNGKPRLSK FYQPYSEDQTQQIIRETFHLVSK RDENVNCFLEGGLIGSDNK/ LIYRHYATLYFVFCVDSSESEL GILDLIQVFVETLDKCFENVCEL DLIFHVDKVNILAEVMVMGGM VLETNMNEIVTQIDAQNKLEKS EAGLAGAPA/RAVSAVKNMNL PEIPRNINIGDISIK/VPNLPSFK
27254	57622	A	27417	5	379	
27255	57623	A	27418	536	675	LEWSSAKFPTAVGVSLLSVVC RSQ*FLMDAMSRMDLVRYTSA RVS
27256	57624	A	27419	2	1220	
27257	57625	A	27420	435	552	
27258	57626	A	27421	5	379	
27259	57627	A	27422	1	1062	
27260	57628	A	27423	17	467	
27261	57629	A	27424	105	355	
27262	57630	A	27425	283	466	APRSARPIVHGKATRPKPRNL LDKDMFSKSDPLCMYTOGME NKQWR/EFGRTVIDNTLN
27263	57631	C	27426	167	379	
27264	57632	A	27427	164	1185	
27265	57633	A	27428	1	873	
27266	57634	B	27429	20	523	
27267	57635	A	27430	3	1225	
27268	57636	A	27431	1	884	GTRDATAEENRVLLAMVNPTV FFDIADVGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGSSIFITS D*KNSCLPLIVQQCLFLRLPL FADKVPKTAENFRALSTGEKGF GL*GVPCFHRHIFGM/CQG/GDF TRHNGTGGKSIYGEK/FEDENF ILKHTGPGILS/MANAGPNTNG SQFFICTAKTEWLDGKPA/VVF KVKE/GMNIVEAMERF/GS/RNG KTSKKITADCGQLRIKFDLVF YSLTTKIIPSGSPRESTPPTHLLA SILESLCSRLQFPFGFHVFLVPS
27269	57637	A	27432	27	410	LQDEATGCKLIEVDDERKLRT FYEKRMATEVAADALGEEWK GYVVRISGNDKQGFPMKQGV LTHGRVRLLSKGHSCYRPRRT GERKRKSVRGCIVDANL/SVLN LVIVKKGKEDIPGLTDTTVPR

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27270	57638	A	27433	93	866	TVSFPATGCGQLIEVDDEKRL RTFYEKRMATEVAADALGEE WKGYYVVRISGGNDKQGFPMK QGVLTGHRVRLLLSKGHSCY RPRRTIGERKVRKSSSVGCIIVDS KSWSVLQLGLLLKKKKK*RRIF PGLTDTTVPRLGPOK/RASRIR KLFNL SKIEDDVRQYVVRKPLN KEGKKPRTKAPKIQRLVTPRVL QHKRRRIALKKQRTKKNKEEA AEYAKLLAKRMKEAKEKRQE QIAKRRRLSSLRASTSKSESSQ
27271	57639	A	27434	2	401	
27272	57640	A	27435	1373	1838	
27273	57641	A	27436	1	257	MNRQLSDSYTEDTKEPSDVTT ERTRSPPGSAKTTMIDTLKKLQ DVQKLRTPKIPQSQQICWNN MSRLRDQS*RSSKKRQLWK
27274	57642	A	27437	247	831	
27275	57643	A	27438	1	993	
27276	57644	A	27439	267	281	CNCPNIFEARWVNLKSLSKIHE* RPFQP
27277	57645	A	27440	274	482	
27278	57646	A	27441	1	219	
27279	57647	A	27442	1	681	
27280	57648	A	27443	11	1094	
27281	57649	A	27444	51	65	NNTFLKYC*IDFND*DCGGEDIS PN*LGLPIPLSMVLCEIHF
27282	57650	A	27445	1	1563	
27283	57651	A	27446	3	318	
27284	57652	A	27447	1	294	
27285	57653	A	27448	7	259	
27286	57654	A	27449	29	191	
27287	57655	A	27450	2	519	KSQDYKSLNATCAGTGSFGC ARRLLSTCSSGWSRGGSLRG GKMELEA/MSRYTQPSEPQLSS PHLTVVLLAIGMFFTAWFFVY EVTSTKYTRDIYKEAPHPP*VA LTPSMGGVLFLL/VWGYIRV SHPRVTTQNGFHWKPAFCKINF FFYLF AWEVFPPAAHNKVQML
27288	57656	A	27451	144	386	VCECKMPKVQPNFTHWSRS*N DDLNRSSLWQA*PQAASVEIHL RS
27289	57657	A	27452	462	672	
27290	57658	A	27453	1	475	
27291	57659	A	27454	1	741	
27292	57660	A	27455	62	390	
27293	57661	A	27456	549	641	
27294	57662	A	27457	456	774	
27295	57663	A	27458	2852	2935	

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27296	57664	A	27459	699	761	
27297	57665	A	27460	399	434	
27298	57666	A	27461	683	1661	
27299	57667	A	27462	1	95	
27300	57668	A	27463	3	517	
27301	57669	A	27464	6	401	RGLTEVPETSGGRVSVGAMAK HHDPILFCRKQAGVAIGRLCEK CEGKCVICDSYERPTLVRICDE RNYGSYQGRVCVCGPGVSDA YYCKEVHHPGERTRDGCSKIV NLGSSKTDLFL* TAKNTGFQER
27302	57670	A	27465	1	321	
27303	57671	A	27466	67	348	
27304	57672	A	27467	1	642	
27305	57673	B	27468	193	445	
27306	57674	A	27469	32	216	AGPSQPTNQTTGKSPQLQQDYF PRRSYRCSHRLIICLVNIGDAV* STVQLKALMLRGRNYK
27307	57675	A	27470	214	440	QDRWGLAPHPPAPGLPLPGPTN QTTGKSPQLQQDYFPRRSYRCS HRLIICLVNIGAL*STVQLKAL MLRGRNYK
27308	57676	A	27471	35	3801	
27309	57677	A	27472	1	2901	
27310	57678	A	27473	1	1317	
27311	57679	A	27474	1698	3255	RVACPCVVWLCWAHWELWRT EEVEGGIAGTDVAR/EASDFILT DAIFSSIVKAVMASLQRRGSRE L*LPAAGVWKLQTD* AQS/ AE EGIECKSIKPVLA KYLVWTRLF VGLLAELRDESAPETTPAGRRR QPQVWSGARQTCGQRTERLAG GLGEMQACSGNLGAEKEKQSK KLAGGWPMSPSTLHALGPKLV PAKSQRRHRAEHMSTWQVGVVS SSYFTGNLVGTLTGYVVIKRGF NRSYYLASFIFAAGCAGLGLMI GFWSWLA WRFVAGVGCAMIW VVVESALMCSGTSRNRGRLLA AYMMVYYYVGTFLGQLLVSKVS TELMSVLPWVTGLTAGILPLL FTRVLNQAEHNDSTSTSMKL LRQARLGVNGCIISGIVLGSLYG LMPYLNYKGGKSSPTAVRPA RHNSLPGPEAKKYRPGFIGLTS CIAFSVQAANVDEYITQLPAGA NLALMVQKVGASAPAYDHSQ QMALPASTQKVITALAALQLG PDFRFTTTLETGKNVENGVLKG

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27312	57680	A	27475	152	468	GLGIQ*LLCCSSFCQLLPEKKE GRLAGDAGAARPAKSGRFLGL TSGLPSEWSARTGPEPPKSLSG GGELNGSSLGFGTQDGRGTRE GRDRGLHPARPPQYQHSP
27313	57681	A	27476	541	4172	
27314	57682	A	27477	3	1110	
27315	57683	A	27478	340	1032	
27316	57684	A	27479	2	779	
27317	57685	A	27480	3	281	
27318	57686	A	27481	519	737	VPDLLQLPNAGLCGHFCDPGD SLQCCLCHQGPFGQAQNWAAV WADTKPAAGAEAREPGDLA*L VPPTWSPTR
27319	57687	B	27482	1	915	
27320	57688	A	27483	68	145	
27321	57689	A	27484	1281	1433	
27322	57690	A	27485	171	708	
27323	57691	A	27486	1	270	
27324	57692	A	27487	278	588	VYIKRMPKKKV/SEGTIKEPKR RLAQLSAKPAPAKVEAKLKKK AAKDKSSGKNVQTKGKRRK GKQAKVANQETKEDLPAENGE MKTEESPASDEAGEKETKSD
27325	57693	A	27488	304	513	PVRHGAFFQDKSSDKKVVQTKG KRGAKGKQAEVANQETKEDL PVDISGETKTNEESPSSLIEAGEK EAKS
27326	57694	A	27489	1	435	
27327	57695	A	27490	3	273	
27328	57696	A	27491	9	293	
27329	57697	A	27492	1	504	
27330	57698	A	27493	1	529	IPPPRLFLPVATEVARVRLPPP PPQNAARDALTSPSYLAWASPR KQTPSPPAAKDIKILEQRGYP KADDDR/LNKVISEAEWKYTL KDVIAPGVLASLPSVPAAGGAV AVSACPQALAAPCCLGSAPA/A AEGEEKMKKKEEVLKES/DDD/ MGFGPFELKSLPPLQIKGLFYTS R
27331	57699	A	27494	1	396	
27332	57700	A	27495	2	398	
27333	57701	A	27496	1	702	
27334	57702	A	27497	1060	1446	
27335	57703	A	27498	46	216	HPLQLSVIPFLPVK*HVDQMFG AD/CVLSN*VNCLASRLFAVS ALRSSRFITMVP
27336	57704	A	27499	1	1152	
27337	57705	A	27500	126	184	
27338	57706	A	27501	238	498	

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27339	57707	A	27502	1	852	
27340	57708	A	27503	3	171	
27341	57709	A	27504	1064	1302	
27342	57710	A	27505	449	668	SPGDYFISLMAAMGRPVGVYW APELLQKMMRKRMR/VKKLI QNYKQLK/CSLT.LNNHVKLVRT NLRFHLAGLLG
27343	57711	A	27506	1	2454	
27344	57712	A	27507	2	408	
27345	57713	A	27508	205	715	
27346	57714	A	27509	1	813	
27347	57715	A	27510	1	864	
27348	57716	A	27511	17	396	
27349	57717	A	27512	3	428	LTNYAAAYCTGLLLARRLLNR LGMDKIYEGQVEVPNGEYNVE SIDGQPGAFTCYLVADLARTTT GNKVFGAPEGAVDGGLSNPHS SKRFLGLSIPHSTK*ILGYDSEN KEFNAEVRKRHIMGQKFADDL HCLIEEDENASKK
27350	57718	A	27513	164	431	EFFFTSNIGVYLQIIHIVGKPI*H /YLV*ILSY*HLAARTISSKIKSN SLVPCASNRGDVGSTRPRVTR RSVRYSAAPLRSPFLAR
27351	57719	A	27514	1307	1947	TNEGSGNSAPLFGARNQTRMI VRGTNR/DIICQIAYARTEGDMI VCTAYVHELPHYGVKVDLTNY AAAYCTGLLDRLRLNRFDM KIYEGQVEATGDDYNVVSIDG QPEVHRKHIMGHNVADYMCY LMEEDEDGYKKQFSQYMKNSV TPDMMEEMCKKAHAAIRES CEKKPKKEVKKKWNRPKMS LAQKDWVAQKKASFLRAQE RAAES
27352	57720	A	27515	1	987	
27353	57721	A	27516	1521	1641	
27354	57722	A	27517	2	614	ILSRVVEFPLTAEVPPPELLAAAG FFHTGHQDKVRCFFCYGGLQS WKRGGDDPWTEHAKWFPSCQFL LRSKGRDFVHSVQETHSOLLGS WDPWEEPEDEPLWPPPSLPLG TLSCPHGERSSLKVPVRSQEGSV QPRPRGRGGFLSPQ/DARDVEA QLRRLQEERTCKVCLDRAVSIV FVPCGHLVCAEACPLQLCPI WQKPPSRSR
27355	57723	A	27518	3	89	

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27356	57724	A	27519	1	1618	ASSHVETRAHAERLLKKLFSG YNKWSRPVANISDVVLVRFGLS IAQLIDVDEKNQMMTTNVVVK QEWHDYKLRWDPADYENVTSI RIPSELIWRPDIIVLYNNADGDFA VTHLTKAHLFHDGRVQWTPPA IYKSSCSIDVTFFPFDQONCTMK FGSWTYDKAKIDLVMHRSVD QLDFWESGEWVIVDAVGTYNT RKYECCAIEIPDITYAFVIRRLP LFYTINLIIPCLISCLTVLVFYLP SECGEKITLCISVLLSLTVFLLLI TEIIPSTSLVIPLIGEYLLFTMIFV TLSIVITVFVLNVHHRSPRTHTM FTWVRRVFLDIVPRLLLMKRPS VVKDNCRRLLIESMHKMASAPR FWPEPEGEPPATSGTQSLHPPSP SFCVPLDVPAEPGPSCKSPSDQL PPQQPLEAEKASPHSPGPCRPP HGTQAPGLAKARSLSVQHMS PGEAVEGGVRCRSRSIQYCVPR DDAAPEQMARLPAPWPLATPT RLSSHPQTSPLRANAHARRSPL RCPRVPRSRPAAPKHRPRTCCP
27357	57725	A	27520	1	3158	
27358	57726	A	27521	2	237	
27359	57727	A	27522	76	254	PLHITFFSRACFPSLHNCCHEY*Q PGF*TSKTPQLWCQLRQYSFK HSFLVVP TPCVPLLG
27360	57728	A	27523	86	376	SLEGRLSDYTPTFQGCQTQGR LPWSFTLSGKSRFSGEGARACY KCQKSDHQARNACSPGFLLSRI PSVRDPTGNRTVQLTWQPLPEP LELWPKAL
27361	57729	A	27524	1	167	MPEPQRPGVPEPPPPGACYAC RKSGHWAARNARSPGFLLSRVP SPPGPSRTPSFG
27362	57730	C	27525	1	381	
27363	57731	A	27526	243	437	VTSTVRQTPATSPAHNKFMPE PQRPGVTPEPSPGACYKCQKS DYQARNACSPGFLLSRVPVS
27364	57732	B	27527	88	1485	
27365	57733	A	27528	1	3759	
27366	57734	A	27529	36	438	RNDRVRPHRDVYSLQGRSDH SPTTFQGCQTQGRLPWSFTLSG KFRFSGEGATTSPAHNKFTPE PQWPGIPPEPPPTGACYTCRKSG HWAARNARRPGFLLSRIPSVWD PTENRTVQLTWQPLPELELWPKAL

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27367	57735	A	27530	314	691	SLQGHLSDYTLTFQGCQTQGH LPWSFTLSGKSRFSEEGTKGDV SGSQDNCGERVSRQTRQRLSH HRQGACYTCRKSGHWAIRNAR CPGFLLSVCPSVWDPTENRTVR LTWQPLPEPLELWPKAL
27368	57736	A	27531	383	2907	RSPTSKTKDICHRSWRRGL/WV NKASEGDELDLRDVSVASNIEP WTGWCRAPLQADLGNSSSA SAPPPYNPFITSPPHWGLQFR SVTSPPPAQQFTLKKVAGAKG IVKHALKRLKPVITRLLQHGLL KPINSYPNSPLPVLKPKPYKL VQDLRLINQIVLPIHPVLGIIGLT SSVRRDAGQDLKRDRAEFLIG DEVHHPHRRRIAEARRLLLGQH FDPLHRLIGQVLEGEARYAPP VEQHRLAPARRTGQRLHPL QFQAGRAQRNRNLGIEHRDR LDRPDDGAGNALAGDGFRRG CLFAGIGIRPRYCRYRQSQDDR RPSHAAPRPRALPIHPATPIA DVMVMFSAVMSQLRLVLRHI DGISRWPPAVVFITDKIWL VY PSDDCRKRSNDRDDMQGEAPA MSMNAAARVGDPIGHSFSQGL FGEALDGLFFARRSEVDMRAG NLGRILARLSSGGRWTPADGQ LTLGSRDVFINGPPATMTIRSTG QCRQHSGLRTVTRTETDSIGPIE VPADAYWGAQTERSENFPFG AREQMPIGIVHALAIVKKAAR INRGHGLAGEKADAIESAAHDV IEGRHDDQFPLVIWQTGSGTQS NMNANESSNDTFPTALHYAAA LAVTKQLFSALDRHLAALDAK AKEWDSIVKIGRTHLQDATPLT LGQEFSGYVQQLANARDRIEGL
27369	57737	A	27532	929	1227	PENGTTFESILQVLDNSCHKMG KWS/RGA*RPGILLHIGPSLVSA PNVTHPKSFFFLSFLFRSPQV PSPLNPSFLWTHLTSPL.LPRL.LL ARLSQVPILT
27370	57738	A	27533	98	412	LGSGDLPEWINPLSSCSLLCEKH PPITSGPQTDQPKKHLTNFKSG ACYMCRKSGHWA/RANARSPG FLLSRIPSVWDPT*KFGLVQLTL GKPLPEPLELRPLRLSD
27371	57739	A	27534	14	249	
27372	57740	A	27535	49	341	
27373	57741	A	27536	392	371	

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27374	57742	A	27537	1	1590	MPNGTNEISHRYNASERSQTKQ DEQTKGKTVGPPEWTPLVRRNG GDSGLDFHFFAEKLIKIIIVDSAG RAGTGHMRPPAVHFGHRGQA MITLSPLRAKQKAVLQKPPPLT STYSLMLPLFLPDKRPPTTEWF LPVMEADAHELTLAWLMLALYR KPNASVQGSQAETLCVFRVKE PLEWQALFADVHSGVNDKGP INCSLYEHKINVSEIVLNLAQTQ KNPAHSDPSSTPAGCMVGTTA GGSVMSACCPSPAAPGPLPGP ATGSC/SPSAAPRPDPPPP GIMAIRAAPSCLGACITLQDEET CEQTHTHSRIMYILFARCLLH AIARGRSRKCAASAGGTCPIHVR VPGGGSYFRVSLQGGQTHWMR PENGFTCVRTKSRRCPIIREQH PTKIPKALTANANQAFFLLVNG HSMVASPHQSQRADLGGFWR DASSLLANSQVQVCGSLRKR HGWWVPFSLRCAVPLTADDSR LRTASLEMSTPPMIHVQDDWQL RRGLPAGTAVTVSELIYLNAN GRLQVEKFLF
27375	57743	A	27538	279	759	
27376	57744	A	27539	443	696	
27377	57745	A	27540	1	179	
27378	57746	A	27541	3	1237	
27379	57747	A	27542	4	152	
27380	57748	A	27543	760	908	
27381	57749	A	27544	203	570	
27382	57750	A	27545	312	500	
27383	57751	A	27546	1	441	
27384	57752	A	27547	1	630	
27385	57753	A	27548	1	1254	
27386	57754	C	27549	236	408	
27387	57755	C	27550	220	398	
27388	57756	C	27551	254	445	
27389	57757	A	27552	1	2742	
27390	57758	A	27553	1	744	
27391	57759	A	27554	1135	1751	RPGSTLQVRQNYHQGLRRPPIN RQINLELYASIVVYLSMSYVF DRDIDVALKNFAKYFLHQSHE EREHAET**KLQNRRLAEF FLQDYQRNQD/CDDWGRAGLN VAMECALAFWKKNVESHYV NLHKLAT/DKN*PPIWCDFHV RHIYLE*AG*KAIRIWGDHVN QTFA/RKMGSAPNLGFGYLF* QSTPWGSDNESSPWG

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27392	57760	A	27555	224	547	
27393	57761	B	27556	22	130	
27394	57762	A	27557	1	408	
27395	57763	A	27558	1	1011	
27396	57764	A	27559	56	822	
27397	57765	A	27560	146	411	
27398	57766	A	27561	1	885	
27399	57767	A	27562	115	1200	
27400	57768	A	27563	791	1114	
27401	57769	A	27564	67	401	RLGSSGREVIHPGERGLENNVC/ H*SSGNQENELEMNKTANGDC RRDPRESRSPIERAVAPTMSLH GSHLYTSLPSLGLLEQPLATKN SLDASRPAGLSPTLTPGERQQN
27402	57770	A	27565	109	345	HPLFIFFDPLPPTFFHPLIGPRMC FSPGLALCPHPNLILNCSSHNSY VLWEGPGGK*FESWGRFPDHT VLVIVNKS HKI
27403	57771	C	27566	63	167	
27404	57772	A	27567	231	314	
27405	57773	C	27568	99	323	
27406	57774	A	27569	1	1347	
27407	57775	A	27570	192	269	WFYKGEFLCTHS/HCLLPKRTC LLPAAM*YCDQFSMAGETSQS WQKAKEEQRHILHGGQRKARL TWQQAGECVHRNSPL
27408	57776	A	27571	107	797	AQWRRAAPPAAGVTCFRLQP GMETPLDVLRAASLVHADDE KREAAALRGEPRMQTLPVASAL SSHRTGPPPIPSKRKF*SMEP*G DEDLDCDNDHVSKMS*RIQPPI LNKTANGLRLARRDPRESRSP ERAVAPTMSLHGSHLYTSLPSL GLLEQPLATKNLSDASRPAGLS PILTPGERQQNRPSVITCASAG ARNCNLSHCPIAHSGCAAPGPA SYRRPPSATCV
27409	57777	A	27572	1	1686	
27410	57778	A	27573	1	1614	
27411	57779	B	27574	208	366	
27412	57780	A	27575	15	1729	
27413	57781	A	27578	1	1614	
27414	57782	A	27579	308	464	KAHHHWLEKCKSEPQ*DTISW TWMKLETHILSKLPQEQKTRNC MFSLSIGS
27415	57783	A	27580	291	378	
27416	57784	A	27581	2	91	
27417	57785	A	27582	439	519	
27418	57786	A	27583	2	91	
27419	57787	A	27584	2	91	
27420	57788	A	27585	2	91	

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27421	57789	A	27586	50	394	
27422	57790	A	27587	1	666	
27423	57791	A	27588	2	91	
27424	57792	A	27589	5	91	
27425	57793	A	27590	884	991	
27426	57794	A	27591	290	460	
27427	57795	A	27592	86	349	
27428	57796	A	27593	2	89	
27429	57797	A	27594	723	882	
27430	57798	A	27595	255	352	TGTWMKLETLISKLTEQEQKTK HCMFSLISGS
27431	57799	A	27596	1	1685	
27432	57800	B	27597	82	263	
27433	57801	A	27598	491	816	RHRGAQRKAFLQRVNCGLCCT WNLCPQKLRGRKWPVQVSPA AGRDPGGPLL*PEGTWLGAPFC LGAPPPLLTAAAPAGRAGGT RGAAPACPEDRTNAHSQHHP HV
27434	57802	A	27599	645	1142	
27435	57803	A	27600	218	326	
27436	57804	A	27601	181	2316	
27437	57805	A	27602	2	238	
27438	57806	A	27603	709	1416	
27439	57807	A	27604	3	501	SSRALRLLGVVVRIRQAGTMA VTKELLQMDLYALLGIEEKA DKEVKKAYRQKALSCHPDKNP DNPRAELFHQLSQALEVLTDA AARAAYDKVRKAKKQAAERT QKLDEKRRKKVKLDLEARERQA QQQGE*GGRRESRSTRLEQEIE RLREKGSRLQEEQRLI
27440	57808	A	27605	1	963	
27441	57809	A	27606	135	384	
27442	57810	A	27607	349	679	SETYWFPPRESQHLDLDVWPPR SEHHSQSTGTHSGVSESLSPRYF QRCNAHSPSQGHIEEQYLAPWK HRLYQRMSDLPLNDR*FQYSK GHHRCSQNEAVQNPQQLQSL
27443	57811	A	27608	1590	2758	
27444	57812	A	27609	123	2312	
27445	57813	A	27610	1	1809	
27446	57814	C	27611	79	309	
27447	57815	C	27612	77	325	
27448	57816	A	27613	1	606	

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27449	57817	A	27614	2	686	SQCAELASPLSPAPGLPRHSRL HALLGLAMPVDLSKWSGPLSL QEVDEQPQHPLHVITYAGAAVD ELGKVLTPQVKNRPTSSISWDG LDSGKLYTLVLTDPDAPSRKDP KYREWHHFLVVMNMGNDISS GTVLSGIVGSGPKGTGLHRY VWLVEQGRPLKCDEPILASNA RSGDHRGKIQRWASLPVKKIYE APGPPVAGHRVTPSPKWDEPM CPQTVTKQLSWGK
27450	57818	A	27615	446	1300	
27451	57819	A	27616	2	346	
27452	57820	A	27617	1	305	MAISTGSSVPWPSPA/PSGPHGR GSWPWGFLATCWQSIHQGGD PWSAGSGHPGKASAPGPGE GQSGGDSGSA/GR*GSHHLP ASFRAGSGQAWDGKKG
27453	57821	A	27618	287	475	
27454	57822	A	27619	37	314	
27455	57823	A	27620	1	367	
27456	57824	C	27621	360	610	
27457	57825	A	27622	604	980	
27458	57826	B	27623	8	442	
27459	57827	A	27624	1	2268	
27460	57828	A	27625	296	398	APPGPTLPWASTPSRGCT*APPG PTLPWASTPSRGCTSSWFMLPA MRRCGAPC
27461	57829	A	27626	1	3633	
27462	57830	A	27627	1853	3809	
27463	57831	A	27628	1	656	MTNHQEKNKSTNTEMTMMMK LADKDDKTAMINMLQVVKV EEAMSMRRNKDVKNHGRA RWVKPMIPALWEAKEVEGKYS AHNFWGSWKFSSSSSSSGPE SPARTHASFQPDGPTNKLGT KAFRVSPASSLLVDLNTQVEII NVRKATPTCSLELGRKRRDGA AERAALDVVVVIYQLAPAAAP NCLNPVTSRR/PPQTPAPEGQGR RQSFE
27464	57832	A	27629	127	273	
27465	57833	A	27630	3	405	AAFHARGHRAGLSASSCSWRC CPSSAPCAPYAAPAARMLQTC LKQSPAGMPPASPSPAASHWG STSFKYSYPRSTSTSCCPICSSW ESWPCPTPSSPL*NKFFPASFPN RQYQLLFTQSGSNGEKDHL
27466	57834	A	27631	689	987	
27467	57835	A	27632	228	527	

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27468	57836	A	27633	108	441	
27469	57837	C	27634	156	287	
27470	57838	A	27635	2	363	RFTKVEKMK/MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPFIENILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKALNMERNNW YQPLQKHAKL
27471	57839	A	27636	2	367	
27472	57840	A	27637	1	936	
27473	57841	A	27638	1	865	
27474	57842	A	27639	1	1287	
27475	57843	A	27640	1	2565	MGPGRALALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLRRYLRGEEARLRL TRCNDETITYLLDKRLTVLTA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLSRWAVGGATG SWVLSKGDRAASGERVVTGWA TLNVGRSFAYCLTTCVQPLDV GPRKEHAPRPPSLPTSTRQGRQ SERSQDANGRRKQKTKSEPERF EDAVLLAGFKVEEPPVQPRRK EWFQGPSPGHCCPAQPDASAPC ILATHAPARAQNA PGTA WAAA LEGTS TVSLDHFHVVG VVVVS GGEIILL SFRFYDKVLSLHEDS TTPVANPLLAFTLIKRLQSDWR NVVHSL EASENIRALKDGYEKV EQDLPAFEDLEGAARALMLRQ DVYMLNVKGLARGVFQRTGS AITDLYSPKRLFSLTGDDCFQV GKVAYDMGDYYHAI PWLEEA VSLFRGSYGEWKTEDEASLED ALDHLAFAFYREQSSPATEQS WMENDFDELREEGFRRSNYSE LQEEIRNTNGEVKSFEEKLDEW ITRITNAEKS LKDL MELKTKAR ELRDECRSLSSRCNQL EERVSV MEDEMNETKRGKFR EKRRIKR NEQSIQEIW DYVKRPNLRLIGV LESRENGTKLENTLQDIQENF
27476	57844	A	27641	219	451	APAAEGAGRIS/PCSRHSPAGLE/ WLCPLCALF*QCPP/PTCHQSA SPR/WP*G/RPAAGPHPPAATVA PKRKGKTKSSSTRE
27477	57845	A	27642	237	561	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
27478	57846	A	27643	3	461	TRTRRGSRTAEAR*CTPGWRPA GRRSALCSRGLGP*RPPTRS GAAPGPHSPCGRPDGPACSRLP PHRSRSPPHGSHVPAAGWLSAG PHQRWPAAGPGTDQCRVVG PERASPHIWKGSTVPFLPSWIFL RVLSVPGCSLPRCCWLGHQC
27479	57847	A	27644	2	159	
27480	57848	A	27645	1	243	
27481	57849	A	27646	219	462	
27482	57850	A	27647	256	427	
27483	57851	A	27648	1	954	
27484	57852	A	27649	2	4690	
27485	57853	A	27650	1	1275	
27486	57854	A	27651	1	867	
27487	57855	A	27652	1	472	
27488	57856	A	27653	2	1215	
27489	57857	A	27654	3	401	
27490	57858	A	27655	712	1245	
27491	57859	A	27656	2	1178	
27492	57860	A	27657	278	339	
27493	57861	A	27658	1	1407	
27494	57862	A	27659	1	687	
27495	57863	A	27660	484	776	
27496	57864	A	27661	299	1318	
27497	57865	A	27662	1	960	
27498	57866	A	27663	122	282	
27499	57867	A	27664	1	600	
27500	57868	B	27665	1	375	
27501	57869	A	27667	356	439	
27502	57870	A	27668	49	360	
27503	57871	A	27669	2	580	GRVCGGPWAARVGERIPNMA GRKLAS*KPTD*VAFARD/IIPQ NPKAPLPSFLKS/WNGDPSPSRL AALP*ESHPAIDWA*LPRPNVA QGLAWVDDFE/KKFNAERFPC PEDK/YTAQVDA/EEK/EDVKS C/AEWVLSKA/RIVEYEKEME KMKNLIPFDQMT/IEDLNEAFP ETKLDKCKKYPYWAHQPIENL
27504	57872	A	27670	1	675	
27505	57873	C	27671	137	1357	
27506	57874	A	27672	1	1032	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
27507	57875	A	27673	3	938	MANNPGANGQ\PGGPGGPGMG KPRCF/RGEVFGI VIRGRGSR/R GRGRGR\GRGARGSKGRG*RD WVPVHVQVGAALVKDH*RSKF PWKEIYLFSLPH/IKESIIDF\FL GGLLSKDEGFE*LCPVQEQ\TRA GPAATR\FAFCCYPGTNGJIV G\LGVKCSQE\VAHRPFRGAML AKLSIVPVVR\RGY WGNKIRKP\ HTVPICKVT\GRCGSVL VRLIP/S QPRGTGIVSAPVVPNKLLMMAG IDDCYTSARGICTATLG\NFAK ATVFD\AISKTYSYLTPDLWKET VFTKSPYQEFDTQLVKDHTRVS VQRTQAPAVATT
27508	57876	A	27674	1	864	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLL PAMVNPMTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFH\ALSTGEKFGFYKGSCFH RIIPFGMCQGGDCE/RHHNGTG GKSIYTEKFEDENFILKHTGPGI LSMANAGPNTNGSQFFICTAKT EWLDGKHVLF\GKVKEGTNIVE AMERFGSRNGKTSKKITIADCG QLLISLTCVLS
27509	57877	A	27675	2	752	
27510	57878	A	27676	3	327	AQELHTFEVTGQETVAQIKAHV ASLEGIAPEQVVLLAGAPLED EATLGQCGVEALTTLEVAGRM LGG\AKQEKKKKKTGRAKRRM QYNRRFVNVPVTFGKKKGPN
27511	57879	A	27677	567	838	

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27512	57880	A	27678	3	1923	ATMAQGLEVALTDLQSSRNNV RHHTTEITVDHLLVRRGQAFNL TLYFRNRSFQPLDNIHFVETE DAVYLDSEPRQOEYVMNDYGF IYQGSKNWIRPCPWNYGQFED KIIDICLKLDDKSLHFQTDPATD CALRGSPVYVSRVVCAMINSN DDNGVLNGNWSENYTDGANP AEWTGSAVILKQWNATGCQPV RYGQCWVFAAVMCTVMRCLG IPTRVITNFDSGHDTDGNLIIDE YYDNTGRILGNKKKDTIWNFH VWNECW MARKDLPAYGGWQ VLDA TPQEMSNGVYCCGPASV RAIKEGEVDLNYDTPFFVSMVN ADCMSWL VQGGKEQKLHQDT SSVGNFISTKSIQSDERDDITEN YKYEEGSLQERQVFLKALQKL KARSFHGSQRGAELQPSRPTSL SQDSPRSLHTPSLRPSDVVQVSL KFKLLDPNMGQDICFVLLALN MSSQFKDLKVNLSAQSLLDHG SPLSPFWQDTAFITLSPKEAKTY PCKISYSQYSQYLSTDKLIRISA LGEEKSSPEKILVNKIITLSYPSI TINV LGAAVVNQP LSIQVIFSNP LSEQVEDCVLTVEGSLFKKQKQ KVFLGV LK PQHQASIIETVPFK SGQRQIQANMRSNKFCDIKGY
27513	57881	A	27679	1	756	
27514	57882	A	27680	1	2601	

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27515	57883	A	27681	1	1677	MARKDLPPAYGGWQVLDATP QEMSNQVYCCGPASVRAIKEG EVDLNYDTPFVFSMVNADCMCS WLVQGGKEQKLHQDTSSVGNF ISTKSIQSDERDDITENYKYEEE HFEAFQSVAQ/LPITRPFSWILRP F*RP*RKISTSFIRPLFTFL/LRLM NAHPEFRMAMKDAKTYPGKIS YSQDSQDLSTDKLIRISALGEEK SSPEKILVNKIITLSYPSITINLLA RVLSPSLPGPAGLASRSEYGPA KPTPTGNSSWPASAAARSPGSRP CLSLHTSPQAEAGAGSLDQPRE RLPQCSGELKGSSSAARMGAE NEEAPRASEGCGGCQQA VTSQ QDGGPLLQNRFFWDCGDENGA DAVYLDSEPPRQEYVMNDYGF IYQGSKNWIRPCPNWYGQAASP WRYGQWWVFVA VMCTALGIK SCDFQAARNNEEHHTKALSSRR LFVRRGQPFTHLYFRAPVRAFL PALKKANKGKLESFSYICFFSIV FGSKNSYAKVAYLEVAYPATL QNGALRKYLVLGA AVVNQPLS IQVIFSNPLSEQVEDCVLTVEGS GLFKKQKQVLIP
27516	57884	A	27682	1	1653	
27517	57885	A	27683	3	2170	
27518	57886	A	27684	2	244	ACPSTSTSHCRGATCSCSRTS/C SGVLQHSRLRHCA SGRGFSSRCP ACCGSPGLGLPAALPPAAWGL QIAPSPQGTGPNQSQS
27519	57887	A	27685	618	851	
27520	57888	A	27686	78	240	
27521	57889	A	27687	860	1246	
27522	57890	B	27688	1	2301	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
27523	57891	A	27689	1	1719	MHINTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNRREHGKKERSSPAME QSWMENDFDELREEGFRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRLSRCDQLEERR KQERSKIDTLTSQLEKELEKQEQ THSKAGRRQETKIRAEKLEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTIEIQTIREYYKHLA NKLLENLEMDTFLDTYTLPRLN QEEVESLNRPTTGSEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL HINRAKDKNIHIIISIDAEKAFD KIQQPFMLKTLNKLVLLEVLA IRQKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKVIYRFNAVPIKLP TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP

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27524	57892	A	27690	1	1902	MNAKALPTLSPLPQATTESVSL TQERSSSPATEQSWTENDFDEL REEGFRRSNYSSELREDIRTKGK EVENFEKNLEECITRIINTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSADEEMNEMK REGKFREKRIRKNEQSLQEIWD YVKRPNVRLIGVPESHGNGTK LENTLQDIIQENFPNLRQANIQ IQEIQRTPQRYSSRRATPRHIIVR FTKVEMKERMLRAAREKEIQ TIREYYKHLYANKLENLEEMD KFLDTYTLRRNLQEEVESLNRPI TGAGIEAIINSLPTKKIPGPDGFT AEFYQRYKEELRIKYLGIQFTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCS WVGRINIVKMAILP KVIVRFNAIPIKLPMTFFTELEK TTLKFIWNQKRARIKSLSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTEPSEI MPHIYNYLIDFKPEKNKQRGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITQIDIDMGKDFMS KTPKAMATKAKIDKWDLIK ELLTAKETTIRVNRQPTKWEKI FTTYSDDGLISRIYNEL/KQIYK KKTNNPIKKWAKDM
27525	57893	A	27691	1	2781	MGKKQNRKTGNSKKQASAPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSSELREDIQTGK EVENFEKNLEECITRIINTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMNEMN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTQORYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTLKIYAPNTGAP RFTKQVLSDLQRDL
27526	57894	B	27692	1	756	
27527	57895	B	27693	1	1743	
27528	57896	A	27694	1	1407	
27529	57897	A	27695	3	391	
27530	57898	A	27696	604	955	SSVFLGDDPILIGNKEMCLSSVL LINGSINFLHPFREDKGAVDVP GVATQQLILLNDPVLTAISELGL LVSSLSK*TSPIPGPGGNA*AR QPSCP*KGELSWRSAPSLVQFSS

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27531	57899	A	27697	1	1783	MGARAGGSCSCLMWLLASG HFMGCVAAAGDTVGPEKFRSCY TITLLQSKLSYSFGKNNKNFQL RKCLQTVDNLFVPNQNGYYCH SQTSLDRAQIDLNGRIRNGSVY SAHSTNSLNNPQPYLQSPMSS NPSTIGSDVMRPDYLPSHRISA VIPPSYRPTPDYETVMKQLNRG LVHAERQSHSLRNLNIGSSYAY SRPAALVYSQPEIREHAQLPSA AAHCPFSLSYSFHSPPYPYPAE RRPVVGA VSPVELTNAQLQAQ DYPSPNIMRTQVYRPPPPYPPR PANSTPDLRHL YISSNPD LITR RVHHSVQTFQEDSLPVAHSLQE ERSSSPATEQSWTENDFDELRE EGFRRSNYSELREDIQTKGKEV ENFEKSLEECITRITNTEKYLKE LMELKTKARELCCECRSLRSQC DQLEERVSA MEDEMNMKRE GKFKREKRKRNEQSLQEIWDYV KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLAKQANVQI QEIQRTPQRYSSRRATPRHIVR FTKVMKEKMLRAAREKGRVT LKG/THQT/RORISRQKLYKPEE SGGQYSTFLKKRIFNPEFHQPN
27532	57900	A	27698	3	1046	
27533	57901	A	27699	1	3585	
27534	57902	A	27700	937	1119	

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27535	57903	A	27701	1	2231	MGKKQSRKTGNSKKQASPPP KERSSPTATEQSWSENDPDEL EEGFRRSNYSKLQEEIQTGKE VKHFEKNLDECITRITNREKCL KELMELKAKARELREECRLRS QCDQVEERTLARLIKKKREKN QIDAIKIDKGDITTNPTETQTIR EYYKHLTYTNKLENLEEMDKFL DTYTLPRLNQDDVESLNRPTG SEIEAINHSLPTKKSPGDRFTA KFYQSLPSSCDYGHAPHPDVF RVSSFVWVRGLAGSGVKLQTF AVSVTALKAAARLELFPDGA QLASPSGSLTRTGGGAACQSHA VCPHSSAFGWSMGLGAMEQG AALIGEARASREPMEVGGSG MAACRSQALPRQLRPSEKSR APEHSSPAMEQSWMENDFDE LREEGFRRSNYSELREDIQTG KEVENFEKNLEECITRITNTEK LKELMELKTKARELREECRLR SRCDQLEERSVAMEDEMNEMK QEGKFREKRIKRNEQSLQEIWD YVKRPNLHLIGVPESDGENGT LENTLQDIQENFPNLRQANIQ IQEIQRTPTQYSSRRATPRHIVR FTKVMKEKMLRAAREKGDSV ERSFSNKAELLFQLHGHQRESL SKKEAQVWRDKGLYFRKGLLD QAQSWSRQVASILGAQIQVEGS PEQRLNVELAGGHLNLTAKAIP MVAVAGGISFKCGAVLLLGAA
27536	57904	A	27702	596	1593	KPRENLYVKNAEASGANAINW KKGY/LVMEDEMNMKQEGKF REKRLKRNEQSLQEIWDYVKR PNLRLIGVPESDGENGTLENT LQDIQENFPNLRQATVHIREI QRTPTQRFSLRRSTPRHIVRFSKV ETKEKMLRAAREKEIQTIREY YKHLTYTNKLENLEMEKFLDT YTLPRLNQKEVESMKRPITSSEI EAVINILPIKRSPGPDGLTATFY QRYKEELERSSPATEQSWMEN DFDELREEGFRRSNYSELREDIQ TKVKEVENFEKNLEECITRITNT EKCLKELMELKTKARELREECR SLRSRCDQLEERSVAMEDEM

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27537	57905	A	27703	717	1803	STGRKAPHHTYSKIDHILGSKALPSKCKRT/EIITNCLSDHSAIKLELRKKPTQNPSTTWKLNLLLN DYWVNKEMKSEIKMFFETNE NKNTTYQNLWDAFKAVCRGKFIALNAHKGKQERSKIDLTQSLRELEKQEQTHSKVSRQEITKIRAEPKETQKTLQKINESRSWFERINKIDRRLARLIKKKREKNQRDAIKNDEGDITDPTETIQTIR EYYKHL YANKLENLKEMDKFLNTYTLPRLNQEEAESLNRIAGSEIVAIHNSLPTKKSPGPDGFTA EYQRYKEKLVFGAGYFGMWAL AALPSNLLKLSQLCQEAEEVNV LVQFVCICPAQEPTIDVLFVSL PPLSLILN
27538	57906	A	27704	407	1696	NILRNAVPHQQONKA*RRMTL TS*EKKASDDQTPSYRRKFKA KAKKLNT/YEKNLDECITRITNR EKCLKELMELKAKARELREEC RSLRSQCDRL EERVSVMEDEM NEMKREGKPREKGIKRNEQSL QEIW DYVKRPNLHLIGVPESDR ENGTKLENTLQDIQENFPNLAR QANIQIQEIQRMPQRYSSRRATP RHIIVRYTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLLAET LQARREWGPFI NIKELKNFQPRI SYPDKLRFISEGEIKYFTDKQML R D F V T T R P A L I E A L K E V L N M E R N N R S P S S S P A T E Q S W M E N D F D E L R E E G F R R S N Y S E L R E D I Q T K G K E V E N F E K N L E E C I T R I N T E K C L K E L M E L K T K A R E L R E E C R S L R S R C D Q L E E R V S A M E D E M N E M K R E G K F R E K N N K K K
27539	57907	A	27705	2597	5904	
27540	57908	A	27706	1	675	
27541	57909	C	27707	137	1357	
27542	57910	A	27708	1	1032	

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27543	57911	A	27709	3	959	MANNPGANGQIPGGPGGPGMG KPRCF/RGEVFGIVIRGRGSRP/R GRGRGR/GRGARGSKGRG*RE WNAVHVGVGAALVKDH*RSKFP WKEIYLFSLPH*RNQRIIDFVFLG GLLSKDEGFE*LCPVQKQTRA\ GQPHPGFKAIFVAIGDYNGHV GLGVKCSKEIVATGHPVPGAINL AKLSIRPRCAEGYLGKVLAKP VHTVPLQGDGKRGCGSVLVRLH PLHPRGTGIVSAPVA\KKLLM MAIGIDDCYTLS/ARGCTATLG QIWPRATFDAISKTYKLP*PPD LWKETVFTKVPYQIEFTDHLV KDPHPRESSVQQDSELQLVATT
27544	57912	B	27710	50	1598	
27545	57913	A	27711	1	3916	
27546	57914	A	27712	334	462	PAFITVNKCSSARKLIQV*GPVA CRVHILPLVVRCPKPGTTG
27547	57915	A	27713	256	654	
27548	57916	A	27714	1	855	
27549	57917	A	27715	211	436	
27550	57918	A	27716	19	319	
27551	57919	A	27717	987	1392	RHCLCSPSRSSSELQPTASSSSA RSSPSPASQVPPGPAGAAAAAP HPPCCPPESTCWTWPC*SPLCH WAVA*ARSGPGLGECFETHGP HGCPGQSPRPQ*APSAWWTE VQPR*PRPAEGSSRRPPPGAP
27552	57920	A	27718	285	1266	RSQIQRGTDRAKCTSGPPHVRV AQODDAPREPPYLPNGMPFG RDAPHLDPWAASQRGSSHPRR WPPSQRRSLLPRRVADRPEAAI SALWEAKAGGWETLPEMEITH NKTRQSKRITHQTNRPNTSSKTI RITKTDLTSWETQSPGSPDRHR KPSTATKHNRFSKIYSRFSIFQC DQGLNGRCGQKGAGKEQRM QEQQENFQAPPFQSHPALRSLQ MQQVQTEEHFGTLECGKLAQC SFHPTREEDRNQDGKTDMLHF KLELPLQSTEHVLGVQLITFSY RLHSCGIPSVLSRYPYFMSLAFG ILSRTLRRFVTVSSLLITGI
27553	57921	A	27719	1518	1779	ARSGPGLGECFETHGPHGCPP GQSPRPQ*APSAWWTEVQPR* PRPAEGSSRRPPPGAPCPAQ PTRRCFGRHQTPAAGAAVP
27554	57922	A	27720	507	1114	
27555	57923	C	27721	80	223	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
27556	57924	A	27722	1	2373	
27557	57925	A	27723	2	272	RARTPLWPRARGPGSRVSGAP WFLLDLAGGGLPPAVLCDLSA ASSTVSGRSNPHC*AWGGLLEFF GEVERAESGFPVPEPSLISEMPH
27558	57926	A	27724	195	489	
27559	57927	A	27725	210	1308	
27560	57928	A	27726	203	474	
27561	57929	A	27727	224	892	
27562	57930	A	27728	1	457	
27563	57931	A	27729	3	1325	
27564	57932	A	27730	322	512	
27565	57933	A	27731	621	737	
27566	57934	A	27732	441	588	
27567	57935	A	27733	1	792	
27568	57936	A	27734	8	488	SGCRNSARADADPSLHASPPAP TMA TVQLLEGRWRLVDSKGF DEYMKELVGVGIALRKMGAAMP KPDCHITCDGKNLTAKTESTLK TTQFSCITLGEKFEETADGRKT QTVCNFTD GALVQH QEWGDK ESTITRKLKDGKL VVECVMN VTCTRIYEKVE
27569	57937	A	27735	861	2161	
27570	57938	A	27736	349	625	
27571	57939	A	27737	1	630	MAQETNHSQVPMCLSTGCGFY GNPRTNGMCSVCYKEHLQRQN SSNGRISPPATSVSSLSLPVQC TDGSPVEAQSALDSTSSMQPS PCIKQSLLESVASSQLDSTSV KAVPETEDVQASVSDTAQQPSE EQSKSLEKPKQKNRCFCMRK KVGLTGFECCGNGVSCSHRY SDVHNCSSYKADAAEEN/LE KENPVVVGKIQKI
27572	57940	A	27738	1	1089	
27573	57941	A	27739	41	334	AGKMTKLEEHLLEGIVNISPO*S VRKGHFDTLKGLKQLLTKE LANTIKNIKDKAVIDEIF/QGLD ANQDEQVDFQEFIS/LVAIALK AAHYHTHKE
27574	57942	A	27740	1	519	
27575	57943	A	27741	28	314	
27576	57944	A	27742	208	421	
27577	57945	A	27743	619	890	
27578	57946	A	27744	113	328	LGSGAWGGDLPEWENPLSSCS LLREKDLLTSGPQVTSPPNISP ILNRDPTVQLTWQPLPEPELW PKAL
27579	57947	A	27745	501	680	

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27580	57948	A	27746	166	405	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQPRNISPISNRD PTGKWTVQLTRQPLPEPELWLP KALRLTPSQIFSA
27581	57949	A	27747	425	484	
27582	57950	A	27748	448	520	
27583	57951	A	27749	3	679	GGGFSRDRDTRIALQPQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGKFFYPKAMG AMEGSGQRRTLPDPAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFCAVT RIGGLPWVFNPLSSCLLREKD PPTTSGPQTVTSRNISPILNPELA TLAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP EPELWPKAL
27584	57952	A	27750	3618	3848	NLCCKEPSSRRSIHKESLLNFPLM GLDPRPQEGFPRDSPR*REESTS LHDPMASSSTVFWGLKRQKY FLWPFRAST
27585	57953	A	27751	1	297	
27586	57954	A	27752	244	420	RKETKERSRTPP*SPRTGQMTP CKLQPGVLSFPRTAQSWEPAPV PQSPLKNELRRKYLT
27587	57955	A	27753	1993	2205	
27588	57956	A	27754	138	833	
27589	57957	A	27755	1	875	
27590	57958	A	27756	1	1041	
27591	57959	A	27757	3	1447	
27592	57960	A	27758	23	3257	
27593	57961	A	27759	2	168	GKAGCWPRSRARKCRTSSPSIW AAWRPPT*LTVTSRPGTSGSE PWMAAASRWQ
27594	57962	A	27760	85	1271	
27595	57963	A	27761	5871	6056	TSSAASTAPRWRRKPHGHQKSL PASLRFPGR*TPQDLPGPAPQ PAQPGPPQAATVPGRW
27596	57964	A	27762	1	280	
27597	57965	A	27763	1	714	
27598	57966	A	27764	2	558	RRAHACARRRRKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLLAMVNPMTFFH IADVGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFGYKGSFCH RIIPGFTCSQSGDFTRHT/GIGGKS ICREKFDCKNFILKHTGPGLISM ANAGPSVNV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
27599	57967	A	27765	1	927	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSVFVRGLD TKK*LLI*SIKLC*QIGSSSIFTS D*KNSCLPLIVQQCLFLRLPL FADKVPKTAENFRALSTGEKGF GL*GVPCFHR/IIPGFM/CQG/GD FTPP*MAPGGKSIYGK/FEDEN FINLKHGTGPGILS/IMANAGPNTN GSQFFICTAKTEWLDGKPVVF GK/VKKGLNIVEAMERFGSRNG KTSKKITADCGQLISFDLCFIL NHQDHSFCALLSGEHPSTPFAR RILRILWLSQLFLWGSMSFLFPP MPSWIAAVKFMIIKTK
27600	57968	A	27766	1	798	
27601	57969	A	27767	1	575	PTRPPTRPPTRPIMAQDQGEKE NPMRELRIKRLCLNICVGESGD RLTRAAKVLEQLTGQTPVFSKA IRYTVRSFGIRRNEKIAVHCTVR GAKAEIELEKGLKVREYELRKN NFSDTGNFGFMQDHIDLGIY DPSIGIYGLDFYVVLGRPGFSIA DKKRRGTGCGIAKHRSKEEAMR WFQKQYDGILPGK
27602	57970	A	27768	1	1695	
27603	57971	A	27769	1	228	
27604	57972	A	27770	1098	1938	IWPRPRDC/RVSYTTVFPPATVT APV/VSGGSHDHIQQYSDIEDFR QATAASSVMVARAAMWNPSIF LKEGLRPLEEVMQKYIRYGGM GAALLSDPDIEKAPSMGTLT GVYLPCLQNIQFVILFLRLTWM VGTAGVLQALLIVLICCCCTLL TAISMSAIATNGVVPGYLHTLV QNLVNNGYVRDETVRAPYD WRLEPGQQEEYRKLGLVVEE MHAAYGKPVFLIGHSLGCLHLL YFLLRQPAWKDRFIDGFISLG APWGGSIKPMLVLASGSGTRA
27605	57973	A	27771	1	1710	
27606	57974	A	27772	163	1659	
27607	57975	A	27773	3	297	
27608	57976	A	27774	3	447	SSPHSSRSLSAPPLPGLPLWRHL RSPSAHRCTVGAPFWAGEGRSP LPQLAGRCGGRASGNRGARG ACGPAGVPGGRGLGGPALGAA GRPGP*LPSRGAAGLTA/GPPCL SLPPPPWVPVQPEPPRRAPPAP RRPVPSAQGLRSASA

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27609	57977	A	27775	3	197	RPDVAPARSLEMKRFMPMPPPP G*FSPGASLDVNP GCYKQAPSC SLAQILSNLSNLWSSAVSNF
27610	57978	A	27776	77	379	GRLLDKAGIPH/PPFPSSGLGCQ H*RRSPLHEHPSSGP/PAGLKPS LSCLPAGQGSGPAARY/GLSLPP TPWAPVQPEPPRRAPPPAPGRS VPSTTQGLRSASA
27611	57979	A	27777	177	444	RGGQSGSPAACYA*/RLPTPW APVRPEPPQRAPPPAPRRPVVST TQGLRSASTRRVTGRQLHLQP WCGIHWVKPAGLLSLVGRWRV LMS
27612	57980	A	27778	165	591	QRAGSPHSPRSLSAPPLPGLFLW RHLRSPSAHRCTVRAPFWAGQ GRSRLPQLAGRCGGRGASGNP GSHGACGPAGVPGGRGLGGPR TGSSQLALPAGNEGLSTPAG RRKKLRTHPSIRRNKLQTRYLK SCNTHREGPRLH
27613	57981	A	27779	1	1605	
27614	57982	A	27780	2	1970	
27615	57983	A	27781	1	3522	
27616	57984	C	27782	183	254	
27617	57985	A	27783	39	346	QYISELQFLASTVVRQTPATSPA KNFQTPEPQQGIPPEPPPGAC YKCKWSGHQAKECLQFGIPRK/ HASHLWQPLPEPPGTLAGQSLT DSFPDLLGLAAED
27618	57986	A	27784	1	354	
27619	57987	A	27785	72	299	
27620	57988	A	27786	273	530	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQKEHLTNFKSG PH*KSDCSTAPGATPRAGPTLA QGALTDSFPDLLSLAAED
27621	57989	A	27790	1	1068	
27622	57990	A	27791	148	527	
27623	57991	A	27792	2	1910	
27624	57992	A	27793	1	1047	
27625	57993	A	27794	96	488	WDRMAGSSNTFGFPPLPYR SCER*QRDGGPRSPGSLVPPW PR/PPILAALEEPSPLHRRGRPS LGWPRPELAPSAQRSAS/RPEA SKDHEPTRKKE/TPDTQP*EL* HSLPRSSASLALGPHYLYEL
27626	57994	A	27795	3	2086	
27627	57995	A	27796	3	412	
27628	57996	A	27797	2	390	

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27629	57997	A	27798	1	629	MKVGLDQHIEVVPVSHSVTSGLAA AGECGGVHCDSDVCAEGRWGP CSLPCYCKNGASCSPDDGICEC APGFRGTTCQRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNE/RLFTVCPSPGR FGKNCAGICTCTNNGTCNPIDR SCQCYPGWIGSDCSQPHCADKC VHGRCIAPNTQCCEPGWGGTN CSSVKKQSTVCES
27630	57998	A	27799	108	1071	YPLFLSSISACDGDHWGPCHTS RCQCKNGALCNPIGTACHCAA GFRGWRCEDRCEQGTGNDCH QRCQCNQATCDHVTGECRCP PGYTGAFCEDLCPGKHGPQCE QRCPCQNGGVCHHVTGECSCP SGWMLSPFGWRPI*FSKSL*MQ GTVCGQPCPEGRFGKNCSEQC CHNGGTCDAAATGQCHCSPGYT GERAAVPDVRKCCQDECPVGYT GVLCAETCQCVNNGKCYHVS ACLCEAGFAGERCEARLCPPEL YGIKCDKRCPCHELENTHSILIA AKKSNSLHAIALDFRAQCQSVK DRCHASDLPIDIVSTETLR
27631	57999	A	27800	243	1296	ETQEESSFEPLCPGSHQPNQ*LLF CSTYKRCLCNWGPC*AY*RACP CPALQCCPD/CPQAQLAIPCAP QQQQLSRCLSPFSSLLQDPNTP G/EYRKDEGRAGSRGAGEKQC THNSPRWLQNTVSNQGSSMPG FQSHVPSLLGAFVQCTNCTRV SSPANKIFTTFLRGDPLVSPCHQ GFGSNTHCCVESWQSSCSGMH KDLGALHTPAPGSPTNVAATQ ARREPRCLAVLSTLDRSTRQK VNKDIOELNSALHQADLTDIYR TLHPKSTEYTFSEPHRTYSKTD HLVGSKGLLSKCKRTEHTNCLS DHSAILKLELRKKLTQNCSTTW KLNNLLNDYWVHNEMKAEID
27632	58000	A	27801	552	827	
27633	58001	A	27802	70	200	
27634	58002	A	27803	18	1057	
27635	58003	A	27804	652	960	
27636	58004	A	27805	1	474	
27637	58005	A	27806	1	140	
27638	58006	A	27807	1	1260	

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27639	58007	A	27808	126	893	EDGSGGGKFPEGARQGGTGQR RRRKAMRRGTGAPAQADSRGRG RARGGCPGGEATLSQPPRGGT RGQEPQMKETIMNQEKTTHTC RHKVRIGGKGTARKKKKVHH TATA/DDKKLQFLKGS*GVN NISGIE/VNMFNTNPRNKLHIF*Q PLKVQGISWAANTFHHLQGH *DKSSWTEMLPSIFKPSLGAG*V *LVLRRLA/EALPQTNLWDGKS TTLLEDGDDGDDDESSQLWEY FGWRVPRNEANLNLSSTF
27640	58008	A	27809	180	589	KELPLLIFCRWQFESLHNLNVPF FKVSGDGTNNFPYLEKTAKKG SPNGDLPGCKSNHGP*SKFIRS VKPLNPQLLASLQCTSAAYPLQP EDVNLRVISVSRREGVFPFLGHL LWGRRLSFYNQNSNKHGILYN
27641	58009	A	27810	623	1082	
27642	58010	A	27811	548	645	
27643	58011	A	27812	329	510	
27644	58012	A	27813	3254	3628	
27645	58013	A	27814	1	960	
27646	58014	A	27815	349	681	PMASNRAITLTAWPKIPFLGICE AKNPRSENML/AHHFGSLPP SWELWEQPPGNSSRYIEFLNK HTYIKGTLRVYTKKFCMLVIKS FESKSCVWRYDFDSKSSVNVTV
27647	58015	A	27816	240	473	
27648	58016	A	27817	825	1043	
27649	58017	A	27818	2	418	GKVVCFEAFLOQLGKHQFYW CLEGLGHCHHHIGAKYPEDIVD EESAQQDAASADIVEVQELYSI KGEQAKKVVGNPVLPPQQVPD ANDAAQAQAHQVLGVKFHDD L*AERP GKSTP*GRATPPTFLVF PRTLCEGI
27650	58018	A	27819	2	427	
27651	58019	B	27820	51	672	
27652	58020	A	27821	43	667	
27653	58021	A	27822	516	1056	WSRAPAPQQCQHWLHPAGRTL HLRCLLGIWHQCDGDSGQVLR GTNENLVFPQDLLEKGLEANNF AMLGTWEMSSFPGIFIALLLRF DISLKKNTHTYFYTSFAAYIFGL GLTIFIMHIFKHAQL*GVKS*GS SGSDRIQRGNRGISIEGA GEERE MMQLVPEPLRARPDWGLGPH RRA
27654	58022	A	27823	1	1019	
27655	58023	A	27824	1061	1258	

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27656	58024	A	27825	44	621	
27657	58025	A	27826	406	727	
27658	58026	A	27827	2	1337	
27659	58027	A	27828	1236	1391	
27660	58028	A	27829	228	502	
27661	58029	A	27830	1	1035	
27662	58030	A	27831	146	392	GHRSHQSP EETPNLIPRTPIPLPG TGTSIRSTRIPRTEASGPNGLN WYLTPTPPGGQRPSSAASPRGF PPTNNSRLPAEPE
27663	58031	A	27832	15	300	
27664	58032	C	27833	289	414	
27665	58033	A	27834	3	576	AALAERWLGEVLVRVGVVRVPG GSGGLRHWCPGGLLRGLGQA PEHKVRLSMEFCSTCTADHISLS SFWRSSFQQPLVPAVSLQSPDR RLSHDPAASSWSGFCGISPAFSA FSECPSSSLRSHPPALLQAAES* FAASSPSPPTWSLGSSTRKPW S/VACNWLLSDSSSHRSPFWS GHITMVLALTEELV
27666	58034	A	27835	1	231	DELLVGGNPRGDAEEGRCP GGVGVRVYQIQIWPRLCSRNP GAAD*GPGS*RWDRCPRDEIWR FLGALVGSVSSG
27667	58035	A	27836	18	398	KVRWERSWSESESESEQGRRR AQALVPSVAS*/SSRPWDRPPST K*GCLWSSAARAQQTIYHSVPS GGHPSSSHWLPAVSLQSPDRRL SHDPAASSWSGFCGISPAFSAFS ECPSSSLRSHPPALGSF
27668	58036	A	27837	1059	1446	AVWSLPAPPAPCLLAGLLTCC RTP*TASLCARGVPVRPRA*EAT RGTS*A*ALHSPPGTLPTVTRTS PSHLSARAAAAPSHPARPTASRSS RLPAWLAVRLSIPPRRGLGGA GAQAAAASTRFTCCS
27669	58037	A	27838	1	211	ATAAERWLGEVLVRVGVVRVP CGEWRAQALVPIVAS*ATRPSG RGPTTQQT*RTSRIGRS*QTMR HART
27670	58038	A	27839	316	537	
27671	58039	A	27840	255	475	RPWVRAPYKLLPALLHAPLCAP PSSPWRPV/PASAPSKLLKS*IF CKQLSLPTWSLGSSTRKPWS GPVTGS
27672	58040	A	27841	622	1127	
27673	58041	A	27842	364	666	

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27674	58042	A	27843	37	299	ILLCSVQTLPLLRREFYGHIPKC QQSLNIICSPSLRIPGFLHRNRL STPFHVQQPQREHF*YCRSQIH GENSAWHIRSHHAKEKAHF
27675	58043	A	27844	84	428	PAEIERSTAKTPGPPGSLEMGLL TFRDVAIEFSLSEEWQCLDTAQR NLYKNVILENYRNLVFLGIAVS KQDLITCLEQEKEPLTVKRHEM VNEPTGPRQKRRVTSSR**MKR YVII
27676	58044	A	27845	1	719	
27677	58045	A	27846	669	830	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLHLPLNDQAPVWT ENQPGGHW
27678	58046	A	27847	223	382	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLHLPLNDQAPVWT ENQPGGHW
27679	58047	B	27848	1	491	
27680	58048	A	27849	1	1113	
27681	58049	A	27850	505	1105	ITCTLYPSLRIVYEAFPATGDNM FRRIJKDALFRTIQFCQIMNRSQ YMFTCRCRTEMQVPQHRKKKT FKFTVLLNHFMVIEIIVLTAGRID AAFDQDEVAASEGFLKQPVGKD YKFGGSPVKDEKLFVGVTGMG HHN*LSV*TSIQHLLSNTQG/CL RVCAPALRL/HSRNLAMVISFSF SCGARSAISPINARKRWASPVC
27682	58050	A	27851	1	2697	
27683	58051	A	27852	1	1998	
27684	58052	A	27853	864	1025	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLHLPLNDQAPVWT ENQPGGHW
27685	58053	A	27854	1605	1766	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLHLPLNDQAPVWT ENQPGGHW
27686	58054	A	27855	677	735	
27687	58055	A	27856	1126	1568	SSSSTGRSRHKEVSPGCQDGL RCQEWWSVRPGYEATGGVWG KQLGIPASGLPGRSSSPRKSC TPVTSRTGLPVCWAALESER SFSLSVRPVVCVCGTKMSCA PECCFFLYLSLLSLFLRLLLGL AAHCQFFPAVPLCIL
27688	58056	A	27857	1142	2450	
27689	58057	A	27858	1	1131	
27690	58058	A	27859	229	402	
27691	58059	A	27860	505	597	
27692	58060	A	27861	1	657	
27693	58061	A	27862	248	382	QPPKITLLYQQWIQTKKSLKS FLP*QEFRMKQKHKSTKSSITL

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27694	58062	A	27863	1	1341	
27695	58063	A	27864	1	739	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRKIKLTQNHSTTQQLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWYVKDTRI SGMLWYVKA VCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKTSRRQEITKIRAELEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKREKNQIDAIAK DKGDIITDPTEIQTITREYYKHL YGNKLENL*H*MPTRESRKDLK LTP*HHN*KN*RSKSKHIQKLAE GKK*LRSEQN*RK*RHKKPFKK SMNAGAGFLKRSTKLIDR
27696	58064	A	27865	1	1920	
27697	58065	A	27866	444	763	
27698	58066	A	27867	1	651	
27699	58067	A	27868	94	964	VNADWVLQRELEQTSWSSKQ RACCLSHVVGLRMISSCTTRKM AEEQQRKIPLVENLLKKRKA Y QALKATQAKQALFGKEGAEER KRAQ/WFKRLESFLHDSLAAET *QG/RISRQLEVQPHALELPDKC SLAFVVRIRKIDGSGLLVQRTIA RLCLKKIFSGVFVKAPPRIQKW LRIVEPYVTWGFNPKSVRELIL KRGQAKVKNKTIPLTDITVME EHLGKFGVICLEDLIHEIAFPKG HFQEISWVLRPFHLSVAHHATK NRVGFLEKMGTLGYRGERINQ LIRQLN
27700	58068	A	27869	176	334	
27701	58069	A	27870	3	452	AASTGGGSHLLSIMALRPLV KPKIVKKRTKKFIRHQSDRYVK IKRNWRKPRGIDNRVRRRFKQ ILMPNIGYGSNKKTKHMLPSGF RKFLVHNVKELEVLLMCNKS YCAEIAHNVSNNRKAIVERA VLAIRVTNPNARLRSEENE
27702	58070	A	27871	2	423	
27703	58071	B	27872	193	1698	

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27704	58072	A	27873	263	714	KLNVPPIKATNTIMNMTMNLK MSLTAPPSDICRGPKLSFAGKIQ AIEPKLKTATAQRPLDTIGLEV PVPAAWLLSAVRNCSKLRATS GPNLDTMNGSRRTGSGWTEGS RSSMKPHLLSDITGALR/SPKVS *AFCRLATWPFNLFQSGILS
27705	58073	A	27874	347	902	
27706	58074	A	27875	17	1178	
27707	58075	A	27876	1	1155	
27708	58076	A	27877	3	1109	EKETMQSLNDRLASVLDVRVS LETENRRLESKIREHLEKKGPQ VRDWSHYFKIIEDLRAQIFANT VDNARIVLQIDNARLAADDFRV KYETELAMRQSVENDIHGLRK VIDDTNITRLQLETEIEA/LKEEL LFMKKNHEE/EVKGKLTPTYA ALG*TVVEVDAPKQDLAKI/M ADIRVAQ/YDELGSERTEKLDK YWSQIEESTTVFTTQSA/EVGA AETNLHRSCLKRTV/QSLEDPRW TSMRNLKAQLGEQP*GEVEAPL RPTRWSQLNGILLHLES/ELAQT /RAEGQRQA/QEYEALLNIKVKL /EAELATYRRLLEDGEDFN/LGD ALDSSNSMQTQKTTTTRIVDG KVVSETNDTKVLEALSQQKAG
27709	58077	A	27878	1	1305	
27710	58078	A	27879	209	560	
27711	58079	A	27880	219	512	
27712	58080	A	27881	528	803	
27713	58081	A	27882	3	432	SSPCVEFSTSMGACLRPATARSP SATCTAWTCTGWRGRPWWR WTPENSGVAGGDGTSEEDSEE VEGAEWGRRRRQRRGERCG GLRRAPCQGAPGKCLCPRP/PGP SPC*/CEALGAQRAS*PHRELK VGGPGPGCELSPMV
27714	58082	A	27883	117	483	
27715	58083	A	27884	1	1497	
27716	58084	A	27885	228	776	
27717	58085	A	27886	1012	1677	
27718	58086	A	27887	194	562	
27719	58087	A	27888	1	423	
27720	58088	A	27889	232	308	
27721	58089	A	27890	1	1692	
27722	58090	A	27891	186	2191	
27723	58091	A	27892	2	141	
27724	58092	A	27893	1	1692	

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27725	58093	A	27894	186	2192	QRRPRPFPSQGISMTECFLPPTSS PSEHRRVEHGSGLTRTPSSEIS PTKFPGLVYRTGEPSPPHDLHEP PDVVSDDEKDHGKKKGKFKKK EKRTGYAAAFQEDSSGDEAESP SKMKRSKGHVFKKPSFKKKKE KDFKIKEKPKEKHKEEKHKEE KHKEKSKDLTAADVVKQWK EKKKKKKPIQEPVPQIDVPNL KPIFGIPLADAVERTMMYDGIR LPAVFRECIDYVEKYGKMKCEGI YRVSGIKSKVDELKAAAYDREES TNLEDYEPNTVASLLKQYLRLD PENLLTKELMPRFEEACGRTE TEKVQEFQRLKELPECNLLIS WLIVHMDHVIKLETKMNIQ NISIVLSPVTQISNRVLYVFFTH VQELFGNVVLKQVMKPLRWSN MATMPTLPETQAGIKEIRKQE FLNLCLHRDLQGGIKDLSKEER LWEVQRILTALKRKLREAKRQ ECETKIAQEIASLSKEDVSKHEE NENEEVINILLAQENELTQEE LLAMEQFLRRQIASEKKEIERLR AEIAEIQRQHQHGRSEETEEYSSE SESESEDEELQIILEDLQRQNE ELEIKNNHLNQAIHEEREAIIE RVQLRLLMQRAKAEQQAQE DEEPEWRGGAVQPPRDGVLEP KAAKEQPKAGKEPAKPSPSRDR
27726	58094	A	27895	12	413	PSRAPGLQKACTGHGEMAVHP PRIPVQSDHLISIEGLLCKLP GQVTKESGLVSFSLRPVLPQNT LSNSFYLFPGYASPYVETFLPG AHSGPAPPLPVRTPTAKRL/G VAVAPSPTF*ISPRALRSTFVSN
27727	58095	A	27896	1	361	
27728	58096	A	27897	2	162	
27729	58097	A	27898	248	381	
27730	58098	A	27899	73	254	
27731	58099	A	27900	1	729	
27732	58100	A	27901	1	762	
27733	58101	A	27902	2	334	
27734	58102	A	27903	3	369	
27735	58103	A	27904	669	1006	
27736	58104	A	27905	3	250	
27737	58105	A	27906	721	876	
27738	58106	A	27907	3887	4013	
27739	58107	A	27908	3423	3627	

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27740	58108	A	27909	3	226	HETGCCGQAAERDSCWERPPIP LLLPSLSGDYETVRNGGLIFAG LAFIVGLVILLSRRFRFCGGTKKR RRINEDEP
27741	58109	A	27910	67	264	
27742	58110	A	27911	161	851	
27743	58111	A	27912	139	351	GGRRIETGGWERPPILLPSLS GDYETVRINGGLIFAGLAFIVG LLILL\SRRFRCGGNKKRRQINE
27744	58112	A	27913	2	431	
27745	58113	A	27914	217	289	
27746	58114	A	27915	255	389	KPNACSHS*VGTEQ*EHMDTG RGTSHTGACREALDRGPAWEK L
27747	58115	A	27916	14	460	NCLTRRRRRRRRTFLEERLKP SRKKITKKHTKKRTASLILHAM ICCRSLNSSKTKNTKCLNSINQR LKILSLQKDL\CGTAGRCKTLT EQ*LNNTAII\CLLLREARKTL MTHQSTWTWMKLETIILSKLTQ EQKTKQRMFSLISGS
27748	58116	A	27917	503	1046	
27749	58117	A	27918	3	198	
27750	58118	A	27919	54	320	
27751	58119	A	27920	443	477	
27752	58120	A	27921	1	963	
27753	58121	A	27922	1	2292	
27754	58122	A	27923	3	736	SCCLHSRLVRARRLRRAVAVM AAQCVR\ARRSLPALASVRPI FPGL\CTATK\QRTSAKNLKG MGQSEQRADPPATEKTL\EEK VK\LEEQ\KETV\EKYKRALAID TEELTGRGSQNLLREAKLLRHF KPFCKDLLEVADVLEKATQCV PK\EEIKDDNPHLKNPLWRGLV MTEVQIQKVFTKHGLLKNPV GAKFDPYEHEALFHTPVGEKEP GTVALVSKVG\YKLHGRTLRP ALVGVVKEA
27755	58123	A	27924	253	363	
27756	58124	A	27925	235	318	
27757	58125	A	27926	1	426	
27758	58126	A	27927	146	254	
27759	58127	A	27928	1	1401	
27760	58128	A	27929	61	457	LESTLATAERFLIPSPSTGN*L VCFCTT*GQECYSVTRFSLGYG SPGCLYA*SSLIPCWRWGTPLRL CCEKPFTHFCLRFVSPSKLAVS RWHIPLGSEKRRSMSAGTISL HFIWMKSPTRTSFQHFCT
27761	58129	A	27930	1	567	

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27762	58130	A	27931	128	586	
27763	58131	A	27932	271	465	HLTRPGTLLRQNFQRNDQAAT LAVHQYPLLCNSRC/CIPRQT/W VWSGPPANSNRPAEAGPDC*KE N
27764	58132	A	27933	1	375	MQKSPFCVAHAGSCLLEFLF GHLGGHHDPDKPRDTRKDN FRPISLMNIDAKILNKILANRIQ QHIKKLIHRDQVGFISGVQGW NIRKSINVIQHINRTKDNHMI SIDAEKAFDKIQGFMLKILNK LGIDGMYLKIIARIYDKPTAKIIL NGQKLEVFPLKTGTQRCPCLSP LLFNIELEVLARAIQKEIKGI QLGKEEVKLSLFAHDMIVYLEN PIVSPQNLLKLISNFSKVSQYKI NVQNSQAFLYSNRQT*AIAGA PPASLPPCSLISDCCASNE*GSV GIGPSKPGAGYNLLCHLISPSIS PTSSPKSDTCPIADFSNKSPPDRSS AGDILLAMQSLGSMIAFTLILP THEHGMFFHLFVSSFISLSSGL
27765	58133	A	27934	1	1059	
27766	58134	A	27935	1	533	LSKQGHNLQRFLLPFGIC*CLP LRGGVYVRGRQASLSCGGLHP V*ASIRQLCLPTQALAMAGTPP PASLPPCSLISDCCASNERGSVG MGPSEPRCGNNNLVVC/RFLSL SEKRSSIRVGVTRFS/RCHLSQL CLATKGNLTPCTSQVRRCLTL LQLTLGAMQPLSCGLPTLSDKP
27767	58135	A	27936	140	426	
27768	58136	A	27937	1	918	
27769	58137	A	27938	54	102	
27770	58138	C	27939	244	462	
27771	58139	A	27940	234	282	
27772	58140	A	27941	328	1212	
27773	58141	B	27942	245	338	
27774	58142	A	27943	483	635	
27775	58143	A	27944	9882	10134	
27776	58144	A	27945	2	370	
27777	58145	A	27946	1682	1945	
27778	58146	A	27947	1172	1732	ESTAAEADTRFGCSWAVWAVE AEGEDCCCCCCCCCCCCCCCC CCCCCCCCCCCCCLPPSAGGRGP SGSARYFALIDAAQREDGGDA YRVGLAAALEVNAAETVACGG LEGGEAPTDAGTRYVYLEPAAPQ LSVLWKRVEVQRLVPVRVVVA AWHAARKARWLRRRAARPGP PASCALRRPSGYAARN

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27779	58147	A	27948	272	393	
27780	58148	A	27949	333	622	
27781	58149	A	27950	11	1850	
27782	58150	A	27951	1	1107	
27783	58151	A	27952	1	1348	
27784	58152	A	27953	3	431	KLQNEILLHLVSHPGHADAKG GFPWP*AAPPLWLCRVQPSFWL LSWAGIEGLWLFHTHDTSCQWI YHSGVALADVI.HESPAIQOTS VWTSRSFHTSSEIQAEVPPKQLL TSVHAQAQYSMEAPKAWGLYP LKPWPELYLGP
27785	58153	A	27954	364	1117	EGHRAEGQCTGSVVLLTSSIGR SGKQSSGCHFWLLQHICITCPS RVMGPRKKHRTARGSRPPQPL PSGFPSAGAMGQVHCLAAPHS LERVRNPRQTQ/PPG WEG/PPTR ANLALLPTPAATATNSSIPDSP PGSDGSVPAGLTTWLAVLTLD CPKAFGKVASQACLLWKGEQP PKTPPVTPSRVSLLAEPNTIRL KNVFPFRVPACTWKSHRHSTPA HESSQKGLYPAPKPGWSCPRL WEPTSCISVTWM
27786	58154	A	27955	1	224	QWRHCNRSLLPVQKSGALEG IGPPRVFPPE*RAFGGQRAAPPDI PPPSPRHPTKDRRTAARSGPRR KRGQTNE
27787	58155	A	27956	681	879	LQISHPGHADASGGFPWPWAA PPLWLCRVQSPS*LLSQPGVECP QLFQAHSASRHLNMRPMQMS S
27788	58156	A	27957	835	1482	
27789	58157	A	27959	1	522	
27790	58158	A	27960	2	396	
27791	58159	A	27961	1	1501	
27792	58160	A	27962	473	860	
27793	58161	A	27963	370	3675	
27794	58162	A	27964	52	117	
27795	58163	A	27965	3	290	PRKTQVFGGTVEVLLKYKTG ETNDFELKNQLLDDPAIRDD/QII NWLEFRSSVMYLTK/DFE/QII SIILRLPWLNRSQ/TVVEEYLAF LGNLVA
27796	58164	A	27966	1	2988	
27797	58165	A	27967	1	666	
27798	58166	A	27968	274	930	
27799	58167	C	27969	13	231	
27800	58168	A	27970	46	386	
27801	58169	A	27971	3	451	
27802	58170	A	27972	160	494	

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27803	58171	A	27973	1	2406	
27804	58172	A	27974	201	1069	
27805	58173	A	27975	450	647	
27806	58174	A	27976	329	697	
27807	58175	A	27977	141	1506	
27808	58176	A	27978	1	1773	
27809	58177	A	27979	3	460	PHRVMGVPISRGTL*SVFP*PS* CTTWPGSLGSCCTTACQVRCQPQ APHQP*APPERTTSAPAAQSPSR SSLWVTAPLVASCTCSPATHP TRSQMPSTHTPCCRGSPPRGRS PSWTRTWITCPKASKADPKAP WPCSLMPFYAQQTGLGET
27810	58178	A	27980	1	1803	MGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRYNRE PTKWEKIFTTYSDDKGLISRIYN VLKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKKHMKKCS SLAIGEMQIKTTKKMLLYYDVI RICHDSHKELEQKLAFLGMED AILYSSCFDANGGLFETLLGAE DAIISDALNHSIIDGVRCLKAK RYYRYANNMDELEAAYRRSTR PLSTRLFSFRSRVLTFRVCPCL VHTTWGGNLMRLSARSLWQR AAVNIPKLEGIIEEY/ALLV/WR AML/TEVNLSPNGLVDRINFG AHKDMALEDFHRSAIAIQGWL PRFIEFGACSAEMAPEAVLHGL RPIGMACEGDMFRATAGVNTH KGSIFSGLLCAAIGRLLQLNQ VTPTTVCSTAASFRCGLTDREL RTNNSQLTAGRLYQQLGLTG ARGEAEAGYPLVINHALPHYL LLDQGLDPELALLDTLLLMAL NGDTNVASRGEGGLRWLQRE AQTLKQGGIRTPADLDYLRQF DRDTSQGSRRVDCSVWELCRA GRTAGVMAVAATKNAGKWH NHIIRFDINPGDRLYDQGGRA HHPFAGTHHQYYRHRSRR
27811	58179	A	27981	1	1974	
27812	58180	A	27982	344	508	
27813	58181	A	27983	3	492	
27814	58182	A	27984	65	261	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
27815	58183	A	27985	3	529	DAWAFHKMAPKAKNEAPAPP KA/EAKAKGF*RAKKGFSF*KVS HSHKKKKIPHVHPTFRAGRPL R/LRRQPMKYPSGRALPWRNKL DHLCLSIKFLTH*VLPKKIE DNNTLVFIVDVKANKHQIKQA VKKL\YD\DVAKVNT/LWIRPD GEKNGICSLAPIDYDA\LDVA NKIGII
27816	58184	A	27986	105	241	PFFFFEMESPSVAQAVFSLVFRS PHCGGIQAHLFNL*RDLFKIWT
27817	58185	C	27987	175	363	
27818	58186	A	27988	724	958	
27819	58187	A	27989	3	823	
27820	58188	A	27990	1	877	
27821	58189	A	27991	487	786	
27822	58190	A	27992	147	623	RSVAVANGLTKRRMGLKLNTRY ISLILAVQIAYLVQAVRAAGKC DAVFKGFSGLFCSSLGDTMAQ LPAGPGDDKTNIKTVCTYWG ISHSCTVITALIDCQEGAKNMW DKLRKESKLNLIQGSFLFCGN GNGAAGSLKLPFPVLLVSLAA LTTWLSF
27823	58191	A	27993	213	579	ASLLLLAFLAELASLKAGLQKS REYSCSSFISLSSTDAHCVLSE YARPLS/QRPAPNGSSPRCQASE AQSPGHRPPPLFSSPLAALQLD SHRFPSPDPNGKDESRPRLCTKL GRGCAGCGK
27824	58192	A	27994	1	800	
27825	58193	B	27995	54	165	
27826	58194	A	27996	46	313	
27827	58195	C	27997	30	151	
27828	58196	A	27998	169	1173	
27829	58197	A	27999	456	651	
27830	58198	A	28000	487	833	RNKFCDQDTEGNKIKNRREEK HRCRGQSKLNIIDNVVKA VNGKKSQREAEFADCIITGIRHNTS PKMSRVVRGGG/TPWAVLGMA EASSLSQSSQNPGQAGWQTGP WVVS LGC
27831	58199	B	28001	1	2268	
27832	58200	A	28002	1	639	

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27833	58201	A	28003	1913	2388	PIIHNTTAMKKAAKAEPPTTIV CTE*AILSQRTCSL*FTVINDICP GPAH/VVQDIHGKLTGSAIA NRFQDAMAIPFLGTQGRVPR NGMAIPFGNRRNVIAGAFIPHR QHLGQIQLNPVRQCSNLFALL AQRSEAFHMRRIHHRDVTVKK TILF
27834	58202	A	28004	1	1566	
27835	58203	A	28005	951	1217	
27836	58204	A	28006	1294	3108	
27837	58205	A	28007	1	1896	LFDWLVSQNELKANPAKGVSA PKAPRHLPKNIDVDDMNRLDI DINDPLAVRDRAMLEVMYGAG LRLSELVGLDIKHLDESSEVW VMGKSGKERRLPGRNAVAVI EHWLDRDLFGSEDDALFLSKL GKRJSARNVQKRFAEWGIKQG LNNHVHPHKLHHSFATHMLES SGDLRARGAYLCAKLLSGAAQ VPEWRSFAFAWFCARCAEQARQN QYLQVSSC/PALEGCDVNGAS FTLEQMLAWRDHPQVTGLAEM MDYPGVISQNALDKLDAFR HLTLDGHCPLGGGKELNAYITA GIENCHESYQLEEGRRKLQGM SLMIREGSAARNLNALAPLINEF NSPQCMCTDDRNPPWEIGHEG HIDALIRRLIEQHNVPVHVAYR VASWSTARHFGNLHGLLAPG KQADIVLLSDARKVTVQVQLV KGEPIDAQTLPAEEIGRLAQFA PAYGNTIGRQPLSASDFALQFTP GKRYRVIDVIHNELITHSHSSVY SENGFDRDDVSFIAVLERVYGR LAPACGLLGSGLNEGALAAT VSHDSHNVVIGRSAEEMALAV NQVIQDGGGLCVVRNGQVTSE GAKERMGMKRYKETSGSIGLK VPAPLNLNLSLQPREQLGQST
27838	58206	A	28008	1	3257	
27839	58207	A	28009	1	2145	
27840	58208	C	28010	193	363	
27841	58209	A	28011	1	397	
27842	58210	A	28012	2	405	FVSAQPGGKRGFTAPATPGCL VHDL*APCLRWYQHPTEELR ILAGKQQKGKTKKDRKYNGHI ESKPLTIPKDIDLHLETKSYTEV DTLALHYFPEYQWLVDFTVAA TVVYLVTEVYYNFMKPTQEMN ISLV

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27843	58211	A	28013	3	353	GYIEKRISCIALLE/SF*IPVNFLR FHDTFI*FCYSS*SIQLSLWQSQI LLCV*LLRSIDFLYLW*PLTYN EHASILSLRAPHYQLFDL*NDRS HIRYSATLVNNPAVCFVAVGHD
27844	58212	A	28014	106	1814	
27845	58213	A	28015	37	2847	
27846	58214	A	28016	1	2430	
27847	58215	A	28017	1	2660	
27848	58216	C	28018	80	328	
27849	58217	B	28019	1	1074	
27850	58218	A	28020	602	853	
27851	58219	A	28021	505	649	
27852	58220	A	28022	672	1903	
27853	58221	A	28023	3	319	
27854	58222	A	28024	1	219	
27855	58223	A	28025	2	508	
27856	58224	A	28026	1	1011	
27857	58225	A	28027	1	699	
27858	58226	A	28028	175	351	
27859	58227	A	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	C	28031	115	231	
27862	58230	A	28032	2	139	
27863	58231	A	28033	1	788	
27864	58232	A	28034	115	358	LIVVRSRRGTSRSGSPRATAMA FKDTGKTPVEPEVAIHRIRITLT SRNVKSLEKVCADLIRGAKEKN LKVKGPVRMPKVK*IVVRSRR GTSRSGSPRATAMAFKDTGKTP VEPEVAIHRIRITLTSRNVKSLE KVCADLIRGAKEKNLKVKGPV RMPTKVK
27865	58233	C	28035	179	283	
27866	58234	A	28036	57	431	
27867	58235	A	28037	54	440	RVPELVWGTEVKERKNARSGV PSTQRLECGSAESAAGAPASVS VQVTAVPAFLPFGWTGGGRAV NLTEAERMVVINSVCHWRLY E*TANRFS*KQDVGKLTNCVCH PEGMLKAVTTQAQVFLVIRHN
27868	58236	A	28038	1	2693	
27869	58237	B	28039	131	350	

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27870	58238	A	28040	1	594	MLDITNDQGNASQNIINAIPPYS CKNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTP LHPPALLAVDRGSRSSVPATDS LPSAHDRQQQFHTWVCSRLLA TVRADPADGQQPARADVCGCR RGTGFNLVMIHLMGFVEGRIQ QLEQVAPRPQGVSWVEVDSSDH LQGSPRVEPPGTWDLRVLCSSQG Q*EAVNCGPQTPLD/SFDYGH SCRKVVSHCGFDLHFPDH**C KNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTPL HPPALLAVDRGSRSSVPATDSL PSAHDRQQQFHTWVCSRLLAT VRADPADGQQPARADVCGCR GTGFNLVMIHLMGFVEGRIQQ LEQVAPRPQGVSWVEVDSSDHL QGSPRVEPPGTWDLRVLCSSQG
27871	58239	A	28041	1	285	
27872	58240	A	28042	1	1059	HNLSSNSFPKMSFPNNSPAANT FLVDLSISACRSDSFYSSASMY MPPPSADMGTYGMQTCGLLPS LAKREVNHNQMGMNHPYIPQ VDSWTDPNRSRIEQPVTTQVP TCSFTTNKEESNCCMYSDKRN KLISAEVPSYQRLVPESCPVENP EVPVPRYFRLSQTATGKTQEQY NNSPEGSSTVMLQLNPRGAAP QLSAAQLQMEKKMNEPVSQGE PTKVSQVESPEAKGGLPEERSC LAEVSVSSPEVQEKESKEIKSD TPTSNNLTAKSGRKKRCPTYK HQTLELEKEFLNMYLTRER/R ALEISKSVNLTD/RQVKIWFQN RRMKLKKMSRENRIELTANL
27873	58241	A	28043	358	2292	
27874	58242	A	28044	2	300	HSL/SFFFFFFFFFFFFFFFFFFFF FFFLFFFFFFLLLVFSFSFSFS SFSFSFSFSFSFSFSFFLLPSSSS SSSFFFFFFLLLPFFFFFFFEME
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	
27878	58246	A	28048	3	212	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27879	58247	A	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP NNNNNFFFFFFFFFFFFFFFFF FLLLPLLLPLLLLPLLLPLLLP SSSFFLLLSSSHSPSPSPSPSPS SPSPSPSPSSSSSSSSSSSSSS SSSSSSSSSSSFSFSFSFSFSFSF SFFFFFFFFLLFED
27880	58248	A	28050	544	729	
27881	58249	A	28051	1667	1896	
27882	58250	A	28052	1	477	
27883	58251	A	28053	25	448	RSQFFFFFFFFFFFFFFFFFFFF/ ILLVLLVLLVLLLLLLLLLLLLL LLLL/ASSSSSPSPSPSPSSSSSS FSSSSSSSSSLGAYVLYFMVT HSSPVLCCLCNLIINI*EE*FFR FRHNCDFLAASIT.GVDWLL
27884	58252	A	28054	47	376	
27885	58253	A	28055	1	1740	
27886	58254	A	28056	3	1464	
27887	58255	A	28057	1	394	
27888	58256	A	28058	143	429	STLQKKEARARHLVTPLDILQL FNGFPLLVDCYKLLRYSRVHSF PRFWIFFSIKDHIGFPKENTQRK MRLHPPQS*TPPRE*VPSFSSG VGKSS
27889	58257	A	28059	165	408	
27890	58258	B	28060	21	253	
27891	58259	A	28061	1	150	
27892	58260	A	28062	1081	1303	
27893	58261	A	28063	147	437	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
27894	58262	A	28064	107	2499	PIEDPEGRRRMREFILRSIQGVL RMAPQIQPKLLTKSSTSVSQA RL/TSKQKALLPRQCSGSAKAQ AEREKIEETCQVGMKPPVPGGY TLQGKWITTCNQVQLDTIKIN GCLKGKLIYLLGDSLRLQWIYY FPKVVKTLKFFDLHETGIFKKH LLLDAERHTQIQWKHSYPFVT FQLYSLIDHDYIPREIDRLSGDK NTAIVITFGQHFRFPIDIFIRRAI GVQKAIERLFLRSPATKASVSK LKCFWEPTRGTKYEQSVTG AFPLRPKGAATPSQLVIVNSS DAHNCDEESEVRKSTLGLKL DCKKGTAITKGTKEDEEDGAM SGVDQLCLLSSVDSSGRPQLMT DWHVGKGQFSCFCGEEKELQ QKRKLTGKGWNVFFMVLEV KTKIKALEVLASGKG TASWFIQ DFLAVNSSHGRWGKKEEFLQ KWKVDPWLPVRWELVQTGTL THLVPEGRSDSVTCAWMLGS KQVYKEPAGFPDMLRLRGRV RMAVVTVHSQRLNLSLGDQHF NYPLPLKKKKKKKKDLIYPA DWLESCQSDNLSAERDLVLV LRLALCALYGLLAPGNGNTESA ELHPGDKTEAQRPMALFKVTR PLNERPGDLASHVSRFAKSLK PAMESLECPQSRVLVGEARKGHS ELVEKIERGCESTVGEGTTRKG SKRDHLDSQCKLGQRSPWQG
27895	58263	A	28065	1	1770	
27896	58264	A	28066	85	204	SPCSTSPFRQLA**RRGPHRSPFP TVAHLIGEWRLMRNAG
27897	58265	A	28067	1280	1531	
27898	58266	A	28068	1	882	
27899	58267	B	28069	77	1188	
27900	58268	A	28070	1016	1400	
27901	58269	A	28071	1091	1770	CRGGSGCAVCAELAPGAVHTV AAERAGAQEAAAGAGPPQLGG LIAWATHLQHSAAVPLLSQRM CHTCLSPRKLVIQCRAAKSLSS SPCGKWLCAALIRQPSVKGLPS CGVPLPLSLRIQMCSSSEATSSW ELNPDFGEAAATSP**ESGF/LQS VVSTALLPDNTTGTFHHDGRA DIGSQFIHRLVCCHLLVLRWLI TLDTKADVVVDIGHRLRCFDCRC VDSTICD
27902	58270	A	28072	1568	1819	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
27903	58271	A	28073	778	879	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27904	58272	A	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT LKVLIIIGKLSGGRKLSRILPLLRS SSM*PTRAPN*SSASFTTTSVSG
27905	58273	A	28075	355	614	CMRRPSCSCPASTRDNTAPHSR TLKVLIIIGKRSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTTTSVSP L*NFIRLHPVY
27906	58274	A	28076	1	2226	
27907	58275	A	28077	31	117	
27908	58276	A	28078	1	547	
27909	58277	A	28079	290	730	
27910	58278	A	28080	3	267	TLVKVKDAEDQLGARVGYIEL DLNSGKILESFRPEERFPMSTF KVLICGAVLSRIDAGQEQLGRR ITILRMTWLSLTHQSQKSILRMA
27911	58279	A	28081	1	1785	
27912	58280	A	28082	551	685	
27913	58281	A	28083	2	211	
27914	58282	A	28084	1407	1874	PRAAAAPTNLSPELSASPRPV ACASAWGAGTDVTGWAEAMP RVGRCLPRTGLGSARRLRPEL GGGAGPAPEAMRGFGADAGST EQPRLPARS*PRLPQPRRRPKS ERPAGLAPRLRPPQPAEPPGLGS QERGRGTDRAAADPGLPTSPE SS
27915	58283	A	28085	1284	1786	
27916	58284	A	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR CL
27917	58285	A	28087	423	676	
27918	58286	A	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27919	58287	B	28089	743	852	
27920	58288	A	28090	1	1100	
27921	58289	A	28091	548	652	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY

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27922	58290	A	28092	1	2438	MRLFGYARVSTSQQSLDIQVRA LKDAGVKANRIFTDKASGSSSD RKGLDLRMKVEEGDVLVKK LDRLGRDTADMIQLIKEFDAQG VSIRFIDDGISTDGEMGKMVVTI LSA VAQAERQRILER INEGRQE AMAKGVVFAENDKKMLSNFI ETADFRTLIETDRTIVVGRRGRT GSFNLAARAATRLWRYAMLME IASYISSHYKLSSQISSETLLNEH LKKWNSAQGDILRKRLVAKE YLDENNPEESIGDLQFNLNISEI ENNVLSLLERSDRKVILMDKL DEAYEPDNIGIGIAGLAYASIE LNQKAKCIRPIIFLRDNIFRSLSK EDPDYSRNIEGQVIRLHWDWA QLLMLSAKRMKVAFKLDIEKD QRVWDRCTADDP*KGNGFKR CLQFTLYRPRDLLSLNEAFFSA FRENRETIINTDLEYAAKSISMA RLEDLWKEYQKIFPSIQVITSF RSIEPELTVYTCLKKIEASFELIE ENGDPKTISEIQLLKASGILQSL YSVGFVGRDKNTSSYSFCHDG RTPDKGFESNEKLHPCYWL LNLNRNALAPEEAEEINDEYDI NIISDNSAIRNKTIGQITTHLDQI PIGNEGATEFEQWCLDALRIVF ASHLTDIKSHPNGNNAVQRDII GTNGGKSDFWKRVLEDYKTRQ VVFDAKNFEELGPSEYRQLQSY LTGPYKGLGFIINRDESEVVRSK
27923	58291	A	28093	673	916	
27924	58292	B	28094	1	4725	
27925	58293	A	28095	959	1387	CMRRPSCSPASIRDNTAPHSR LKVLIJGKRSSGRKLSRLPLLR SSM*PTRAPN*SSASFTFTSVCS RCMSAVMVMAVLTACRFLKM TVSVGHICSLNFALQTSTTAMA VPAAATRASRAQPNRHPWRI CWKTQKA
27926	58294	C	28096	997	1302	
27927	58295	A	28097	659	2534	
27928	58296	A	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	
27932	58300	A	28102	40	198	QAARTTGFIYHLLRHYKTPVG HS*Y*WKLHGENKSSAFVC*P TCRNPFDICW
27933	58301	A	28103	390	1186	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
27934	58302	A	28104	2	1287	GRVGFASDAQSPRILRSEPVRTP PIPAFSPKLTLRIMSLHQFLLEPI TCHAWNRRDTRPVCLDYYSLV VSFEIKK*IALSPNNHEVHIYKK NGSQWVKAHELKEHNGHITGI DWAPKSDRIVTCGADRNAVYVW SQKDGWVKPTLVILRINRAATF VKWSPLENKFAVGSGARLISVC YFSENDWWYSKHKKPIRSTV LSLDWHPNNVLLAAGSCDFKC RVFSAYIKEVDEKKAATPWGSK MPFGQLMSEFGISGTGGVWVH GVSFASAGSRLGWGSAATDSTV SVCWMPKSLQVSTLKTFLPL LSVSFVSENSVVAAGHDCCPM LFNYYDRGCLTFVSKLDIPKQSI QRNMSAMERFRNMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRKCTTGIDGAMTIWD FKTLESSIQGLRIM
27935	58303	C	28105	198	362	
27936	58304	A	28106	1	915	
27937	58305	A	28107	403	519	
27938	58306	A	28108	88	237	
27939	58307	A	28109	527	1205	
27940	58308	A	28110	2	272	
27941	58309	A	28111	39	543	
27942	58310	A	28112	1	789	
27943	58311	A	28113	401	912	
27944	58312	B	28114	147	653	
27945	58313	A	28115	586	650	KIQCLCLWLLFLIIFLHAFQETIL ALRVLVNFNKRINSLGKNLAFN LFVYNKANSMP*RLWLKAPRS DK*IQ*SLRIQNQCQISSTAVH STVTKLRKSRTOPLLQQL
27946	58314	A	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL KSGSGKVYQGPAGKAADTTIIL SDEFHGRWSGASLTLLRRHSLV AG
27948	58316	C	28118	183	254	
27949	58317	A	28119	98	445	LGSGLPWENPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ACYMCRKSGHWAECECPQGIPP KPRPICVGP*KSDCSTHLAATP RAPGTPAQGSLTDSFPDGLGLA AED
27950	58318	A	28120	32	143	

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27951	58319	A	28121	39	346	QYISELQLFASTVVRQTPATSPA KNFQTPEPQQGIPPEPPPGAC YKCWKSQGHQAECQLQGIPIRK/ HASHLWQPLPEPPGTLAQGSLT DSFPDLLGLAAED
27952	58320	A	28122	159	306	LGSNLP*EINPLSSCSLFREEDP PTTSGPQTNQKEHLTNFKSAA ED
27953	58321	C	28123	80	106	
27954	58322	A	28124	166	423	RPRSERLLWGTSPSL/CALTL*G DPPITSGPQTNQLKEHLTNFKS GPHWKMDCPHTPAATPRAPGT LAQGSALTDSFPDLLGSAED
27955	58323	A	28125	1	354	
27956	58324	A	28126	1	702	
27957	58325	A	28127	317	427	
27958	58326	A	28128	467	640	SARKRFQLSP**NKITLLKPASS AISALAAATPRAPGTLAQGSALT SFPDFLSLAAED
27959	58327	B	28129	1	320	
27960	58328	A	28130	1	605	
27961	58329	A	28131	273	529	LGSGLDPWGINPLSSCSLLREK DPLTISGPQTHQPKHLTNFKSG PH*KSDCSTAPGATPRAPGT LAQGSALTDSFPDLLSLAAED
27962	58330	A	28132	459	601	DVDRHVRGNSFHHNEIRSLAAT PRAPGTLAQ/GLTDSFPDLLGLA AED
27963	58331	A	28133	112	331	LGLGLDPWEINPLSSCSLLHEK DPPITSGPQTDQPKRLTNFKS ATPRAPGTLAQGSALTDSFPDLL GLAAED
27964	58332	A	28134	1	579	
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	A	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	B	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	A	28146	1	573	

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27977	58345	A	28147	163	593	GFLEVQTPHPNLDGPRRANRN TFLWTCVGVGIDLPALPAPASFL GTQLTLKKASDGPRTKEKVTQD LAQPFWTTGRQLRFVLHLSLQQ KDLSKCWRGAEVVLGPTRLFL* GYSEGKENGTTGGVVK*AFSM CDSKWFNPCLTF
27978	58346	A	28148	159	405	PRLRVKYTQCLIL*/S/CWRERKK FHLGKRVELRQGITLGRVGVW KRRLSQGSAGCFPAGLAHSPPH LAEPGSGFCTALFLWL
27979	58347	B	28149	123	1561	
27980	58348	A	28150	1	1771	
27981	58349	A	28151	68	698	
27982	58350	A	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	A	28154	1	245	
27985	58353	A	28155	5	422	
27986	58354	A	28156	3	1372	
27987	58355	A	28157	1	1653	
27988	58356	A	28158	586	867	
27989	58357	A	28159	1	1410	
27990	58358	A	28160	1	1441	MDIKKGITDISASLRVESGWEA RTRKEKTHINTVIGHVDSGKST TTGHLIYKCGGVDKRTIEKFEK EAAEMGKCSFKYAWVLDKLL AEREHGITIDISLWKFETSKYY VTIIGAPGHRDFIKNMITG/TSQ A/DCAVLIVAAGVGEFESWYSP RNGQTREHALLAYTLCG* NKL IVGVNKMDSLEPPYSQKRYE EIVKEGSTYIKKIGYNPSTVAF VPMISGWNG*QHCLEAKWLTCP WFQGDGKVTP*GLAIASWEPRL LWRALALQSPPTPTDQAPLR PASPRMSYQKLGGINVATEV KSVEMIHEALSEVLPGDN/VGA FNVKNVSVDVRRGNVAGDSK NDPPMEAAGFTAQVILNHPGQ ISAGYAPVLDCHTAHACKFAE LKEKIDRRSGKKLEDGPKFLKS GDAIIVDMVPGKPMCVESFSD YPPLGRFAVRDMRQTVAVGVI KAVDKKAAAGAKVTK/SAQK
27991	58359	A	28161	125	370	
27992	58360	A	28162	156	547	
27993	58361	A	28163	108	919	

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27994	58362	A	28164	1	712	LNSEGNSSGSDSISYDAPAGNS FLEDCELSRQIGAQLKLLPMND QIRELQTIIRDKTASRGDFMFA DRLITLVVEEGLNQLPYKECMV TTPTYGKYEGVKFEKGNCVSI MRSGEAMEQGLRDCCRSIRIGK ILIQSGGETHRAQVYYAQFPDI YRRKVLLMYPILQTG\NTEFEA VKVL*DHGVHPSVILQLSPFLIP HGGQ\SHQRFPFPI*PTEVHPV APTHFGQKYFGTD
27995	58363	A	28165	1	606	GIRSAMQNTQNLQMPYGCGE QNMVLFAPNIYGLDELNETQQ LTPEIKSKAIGYLTNGYQRLN YKHYDGSYSTFGERYGRNOGN TWLTAFLVLTFAQARAYIFIDE AHITQALIWLSQLKNDNGCFRS SGSLNNAIKVNHSYGASFDLSI MISARMRIGSDNVKNSKGPQ RKIKPGWHQKRGDRTKVDCDT LSYRDGYG
27996	58364	A	28166	1	4626	
27997	58365	A	28167	15	4479	
27998	58366	A	28168	256	852	
27999	58367	A	28169	319	405	
28000	58368	A	28170	606	896	
28001	58369	A	28171	1	372	FRRVACVGSAGDITAGAEPR/G ACATAWVCEMAADISESSGAD CKGDPNRNSAKLDADYPLRVLY CGEYCEYMPDVAKCRQWLEK NFPNEFAKLTVENSPPQKEAGISE GGQTAGEEEEEKKQKRGT
28002	58370	A	28172	1	731	LSRGSAAAGGRALGRPWGARRV ACVGSAGDITAGAEPRGACAT AWVCEMAADISESSGADCKGD PRNSAKLDADYPLRVLYCGVC SLPTEYCEYMPDVAKCRQWLE KNFPNEFAKLTVENSPPQKEAGI SEQGQTAGEEEEEKKQKRGR GQIKQKKKTVPQKVIAKIPRA KKKYVTRVCGLATFEIDLKEAQ RFFAQKFCSCGASVTGEDEIIQG DFTDAIINDVIQEKWPEVG**QPL EDLGRK
28003	58371	A	28173	335	2297	
28004	58372	A	28174	23	416	
28005	58373	A	28175	1	681	
28006	58374	A	28176	1	1668	
28007	58375	A	28177	1	1587	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
28008	58376	A	28178	250	687	AATSLPFRASTIASANSILRVGV MTSIHHFVFSKRVCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQTQIKSVRPDYLLVE PPHHMGPSPFASSGLHYDQ*PH HRLHLYWVFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	C	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	C	28181	151	351	
28012	58380	A	28182	2	355	
28013	58381	A	28183	19	428	
28014	58382	B	28184	61	2118	
28015	58383	A	28185	1	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEFG KRPAEDMEEQAFKRSRNTDE MVELRLILQSKNAGAVIGKGG KNIKALRTDYNASVSPDSSGP ERILSISADIEITGEILKKIIPTEE GLQLPSPATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIIGVKGAKIKELRENTQTTI KLFECCPHSTDRVVIGGKPD RFVIECIKILDLISESPIKGR/AQP YDPNFYGWKPM DYG/GFTMMF DDRRGRPVGFPMRGRGGFDRM PPGRGRPMPPSRRDYDDMSPR RGPPPPPPRGRGSGSRANLPL PPPPPPRGGDL MAYDRRGRPGD RYDGMVGFSADETWD SAIDTW SPSEWQMA YEPQGGSGYDYSY AGGRGSYGD LGGPITTTQVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGSEDRIITTTGTQDQI QNAQYLLQNSVKQYSGKFF

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28017	58385	A	28187	221	1634	KNMETEQPEETFPNTEINGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSVDPSSGP ERILSISADIETIGEILKKIIPTEE GLQLPSPATSQLPLESDAVECL NYQHVKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECPPHSTDRVVLIGGKPD RVVECIKILDLISESPIKGRAQP YDPNFYDETYDYGFTMMFDD RRGRPVGFPMRGRGGFDRMP GRGGRPMPPSRDYDDMSPRR GPPPPPPRGGGRGGSRAARNLPL PPPPPPRGGDLMA YDRRGRPGD RYDGMVGFSADETWD SAIDTW SPSEWQMA YEPQGG/SGYDYS Y/AQGGRGSGYDGLGGPIITTQVT IPKDLAG/SLFIGKGGQR/IKQIR HESGS/SSIKIDEPL/EGSEDRIIT TGTQDQIQNAQYLLQNSVKQ
28018	58386	A	28188	218	497	
28019	58387	C	28189	183	254	
28020	58388	A	28190	1	1056	
28021	58389	A	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYA EIG NR*GRNLGLTEVTGAVCEALR QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	
28024	58392	A	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN FSSFPFLVENGDAFYLAATLRA PGTVAQGSLLTPSQIFSA*WRHPS ISFPS
28025	58393	A	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ SPWNSGPRLSL*LLPKSSGLSG
28026	58394	A	28196	372	782	LRSA DL PWEINPLSSCSLLHEKD PPTSSGPQTDPQKEHLTNFKSE KKETR FIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWSFTLSKSHFSGG RGKSLQLVPEIWPPGQMPAA QDSS
28027	58395	A	28197	189	380	SLCIFSSASALQQQWQHEGWC GQLLPRGHGPNRKLQQQRQWI LL*VPEILPGQGM PAAQDSS
28028	58396	A	28198	33	302	FRICALSTKLFCLSTPWCQTHIL SY PQYLPLLPIYSVLDLRHAFFT IALHPSSQPLFAFT*TDPDTH*A QQITWAALPQGFTDSPHYVQ

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28029	58397	A	28199	1	532	MRVRNREEGNVGVKVGGERQVD QRDAVMRVRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTEGA GGAESISVRLPRRSGSVSLQLLS REDLGRSQSESLGPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA*QLKTD AARSPRKPDYTFCSPGSFSCTH S/SVESHNYHCSRPLQSGLPHY SRYHT*PS*LHSLIHLTFTFPFHI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRVPLVENQILT ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFLSPCLHCQGGKRLCG HHEEARRRKNVSIIPKEAGIIHC KGHQK\ASDP\AQDNAYADKL AKKAASVPTSVPHGISQAPPLP THQARYWQIDFTHMPRVKLLK YLLVWVDFTGWVEAFPTGSK KATAVISLSDIIPQFSLPTSIS DSRLAFISQITQAVSQALGIK
28032	58400	A	28202	3	518	KRPHPYLPLTLFSDSAHLHPG EINNHHVATRPVWWSLHTDVH EIWCRDSDRGTSLGRSIPCPVL CSVRKIHLQPQVLRPTSPRNISPI LNQVSGLLSPTSLSLTVQPLS PFNLGATLQS/APFS*FQFLSFG RDKGDTFYPWSQNSGACHRLG KAAFPWCLIIAGTPL

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28033	58401	A	28203	3	1626	SEGEAKGSITLTCTALYKLKT LFHKTGTVFGPLRFPVNTLNPS PFHDGTRELGAESAIGQCQSSA AKLRRSGKESESLGPEFQGLWK WLPGSSQCFARESLLEKLSLCF RPSDPGAEPPTAVRPITERSL QGDEYCCALGGVNPWPSTDR YWNWATLQEI GPSSCRKTSSGL PLILRYGHVVDLHGSSSHHRPG GPKRNKWFRELGLGSACCMRP RDLVPCVPAAPVAERGESTA QAVASEGASPKPWQLPGGVGP VGAQKSRIEVWEPLIFRRMYG KACMSRQKFAAGAGFSWYVPV AVVGAKVHDVNLHMLSFPSK WKLHTCMKFGAVTQIVTSLGR SSCSLLEKDPMLVLRPTSPRNI SPISNLTKETRFIRGPKTPAVT DWEGLPLVFNHCRDASLIHP GFRGVRPRRDACLSPSPLANLIN LTFKVYNNRKKLQFLAFTVRQ TSAMSPAHNKQ/SLNLSGQAF LQNLPLQELATSARNPATRPRN ACSPGFLLSHVPSVRDPTGNWT VQLTWHPLPELELWPKAL
28034	58402	A	28204	921	1009	
28035	58403	A	28205	1	1005	
28036	58404	A	28206	1	2706	
28037	58405	A	28207	1336	1490	
28038	58406	A	28208	466	560	
28039	58407	A	28209	863	1672	
28040	58408	A	28210	1	876	
28041	58409	A	28211	133	746	SVKMVRYSLDPENPMKSK/S QRGSNLRVPFKDHS*KLQPAHQ RVCHIRKSPTKYLKDVHLTRN QCVPIPDYNG*QLGGVCRRPK QMGPGTTKGR/WPQKGVLFKL PAHALKTAEM*C*TLRVLDVDS LVIEHIQVNAKPKMRRRTYR AHGRINPYMSSPCHNEM/LTEK EQIVPKPEEEVAQKKKIS/QKKL KETPLTWHGE
28042	58410	A	28212	3	466	
28043	58411	A	28213	1	2772	
28044	58412	A	28214	1	1353	
28045	58413	A	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR S*DY*CWR

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28046	58414	A	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEKASSQATLPNQPVKEAI IMQLGTLTLTFLHELVPPTALPSGS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQKIWNSW*SC LVLI*PPCVILSFLYVQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
28047	58415	A	28217	2383	2651	
28048	58416	A	28218	125	1396	
28049	58417	A	28219	466	643	
28050	58418	A	28220	73	150	
28051	58419	C	28221	1	240	
28052	58420	A	28222	2	499	
28053	58421	A	28223	192	351	
28054	58422	B	28224	1	2103	
28055	58423	A	28225	247	400	
28056	58424	A	28226	288	589	WCSRRRGWYLLLGPHNYWRSS TFLVRCPTSPCGGCCPRYGIYPV RSCPRLPGGVSRYGSIHSG/RWC SWSPSWPWLTSVTPRLYVAL M*AVVCPVVGKQF
28057	58425	A	28227	319	398	
28058	58426	A	28228	1299	1506	
28059	58427	A	28229	1250	1907	
28060	58428	A	28230	547	638	EKRKSNCPCLQMT*LYI*KTPSS QPKISLS

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28061	58429	A	28231	488	2358	RLSLGHWAAAGKQGASDSCCKP TQPPSGVLESTTP/CAAPSPPNR DSGPCPASSPLSRLLSGTAW APPPAPPWARVRPPREVRAD LLTPQGGGPATGVSGGECDSP VGGNPGIWKAWGHRRTVRAGI GRRGGPGGADKQPLLVLRLQTG SGVDLQQTPTDLQLRVLTVRR NTNKRKGHPHQNPICSTPSSKT EGRSMRQKVNKDIQELNSALH QVDLIDYRTLHPKSTEYTFSSA PHHTYSNIDHIVGSKALLNCKK RTEIVANCLSDHSAIKPELRIKK LTQNCSTTWKLNLLNDYWR SKRKTHSKASRRQEITKIRAEK ELETQNTLQKINESRSWFFENIN KIDRLRLERLIKEREKNQIDA NDKGDITTDPTKIQTITREYYKH LYKNKLLNLEEMDKFLDTYTL PRLNQEEIESLNRPIGTYEIAII NSLPTTKSPGSDGFTAIFYQRY KQELVTLFLKLQSTEKELPN SFHEASIIILPKGRDRTTKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHDQLGFIPGMQGLFSTC KSNVIHHINKTKDKNHMIIISID AEMASDKIQPFMLKTLNKLGI DGMYLKIIIRAIYDKPTANIILNG
28062	58430	B	28232	1	2664	
28063	58431	A	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPACPKRAPE GSTKHGKEQPVPAATAKTQIV
28064	58432	A	28234	804	920	RDIYSNKCQPEKPEKI*NGHPNI TIKRIREARAKTFKS
28065	58433	A	28235	786	935	
28066	58434	B	28236	3	1555	
28067	58435	A	28237	895	1389	GELLEVMTLAWSWGLFLARII QTQVFKAFNLVILIRSSWAF WTHGDELWALVSRKPK*HPGF CDHAPSTFPPGLCP/EPTPPGA VSQYPCPPSPCWPRWLVLPLP VLAGTSSPWKGFSYPPCCFSPF HLPARFLHRGNCLSTFDLVVLP PLEMPVLALS
28068	58436	A	28238	704	799	EKRKSNCLCLQMT*LCI*KTPTS QPKISLGW
28069	58437	C	28239	178	1287	
28070	58438	B	28240	1	1028	
28071	58439	A	28241	476	678	
28072	58440	B	28242	1	1059	
28073	58441	B	28243	1	924	

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28074	58442	A	28244	39	200	LPLFLIECLFPSPA*LPWPGLPTLC*IGVVREGIPVLCPFSGMLPVFAHSV
28075	58443	A	28245	225	314	
28076	58444	A	28246	243	311	
28077	58445	A	28247	21	1593	KKRTAPAGPRRHPKHCEPCNCGSGKGRPS/CSQTHPPGKLKSSP*SRKAENSKNQSAFSPPKDHSSPVMEQSWMENDFDELTEVGFRSLAETQQQKQKFRPISLMNIDVKILNKILANRIQQHIKKLIHHDQVGFISGMQGWFNICKSINVIHHINRTNDKNHMIISIDAEEKAFDKIQQPFMLKTLKLGIDGTLYLKIIIRAIYDKSTASHLNGQKLEAFP LKDRTRQGCP LSP LFNIALEVLARAI RQEKDIKICLGKEKVRLLSFAEDMIVYLENPVSA PNLFKLISNFSKVSGYKINVQKSQVFLYINNRRQESQIMNEFPFTIARRR IKYLGQLTRDVKDLFKENYKPLLKEIKEDTNKWKMPCSWIGRINIMKMAILAKVIYRFNAIPKLPMTFFTELEKTTLKFIWNQK
28078	58446	A	28248	129	239	FFLTMSMECSSICLCPPLFR*AVVCRSP*RGPSHPL
28079	58447	A	28249	3	254	GTAWAPPPAPPWAVRVRPEKCGAPTC SHPREAPRLASPA GKNVTPVPWGETQSGRLGVTGEPELLGLGGAGALARLISSLCW
28080	58448	A	28250	80	517	GHFLGQQPRPQLHSPAPDPPAPTPTDAEGLPQQQLPQLEPQPECQGPVEAEARQLKSCMKPVRRRPAEEELKTKNMDDNTFAMAEHPDVQESVGLVAITPLRPWPQMTLQVCWSLLEFHSRPLPGYHQQLQNSKDCCLFLP
28081	58449	A	28251	1	670	
28082	58450	A	28252	1450	1650	QWISRQKLYKPEESGGQYSTFLKKRIFNPEFHIQPN*AS*VKEK*NPLQTSKC*EILSPGPLPYKSS
28083	58451	A	28253	1010	1294	QRF SWQKLYKPEESGGQYSTFLKKRIFNPEFHIQPN*AS*VKEK*NPLQTSKC*EILSPGPLPYKSPESAKHGKEQPIPTAKTCQIVKTIQA
28084	58452	A	28254	41	812	
28085	58453	B	28255	1	2957	
28086	58454	B	28256	650	3212	
28087	58455	A	28257	1	556	

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28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA SRDSS*AVSHLCGTPLEIGWSNL PGSHSQSPWNSGPRLS
28089	58457	A	28259	1	253	
28090	58458	A	28260	409	884	
28091	58459	A	28261	1	2256	
28092	58460	A	28262	118	302	
28093	58461	A	28263	558	659	
28094	58462	A	28264	1	400	
28095	58463	A	28265	308	433	
28096	58464	A	28266	1	711	
28097	58465	A	28267	559	657	
28098	58466	A	28268	1	400	
28099	58467	B	28269	232	498	
28100	58468	A	28270	1	2978	
28101	58469	B	28271	128	290	
28102	58470	A	28272	3	193	DVNIFIRYGLWCFLSPFGL*QF WRLEVQYQDAADSMSSGGDPLS HS
28103	58471	B	28273	125	197	
28104	58472	A	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGKNNGGEASM VRGCLERAET*GCPNGMPQGE RLSRFGLRTETGTVTFLHCL QQSR
28106	58474	A	28276	3	334	
28107	58475	A	28277	2	1698	
28108	58476	B	28278	1	1281	
28109	58477	A	28279	198	532	NSLFLLLCLQALVSG*CWPHK MS*GGFPLFLLTGIVS/GRNGTS SSLYLW*NSA/VNPSGGPGLFLVS RLLTIASISEPVIGLFRDSTSSWF SLGRVYVSRNLSISSRFSLLFA
28110	58478	A	28280	3	610	TDFCFFWLPGLSVLFLSFFLSF FLSFFLSFFLSLFSFSLFLFLS VLSFLPSFLFLSLSLFLSLFS LL/YCLSLFLSFFLFLSFLSLS SLLFSLLFSSLLFSSLLFLLLLL LSLSLLFSLFSLFSESVLWEGSV AGLQTPALSSALNRAVLPVSCS MIDQLCDPGKYFISLCLFLHLR VRTCGVWFVSVLVIVC
28111	58479	A	28281	203	470	QAKSVVWKILSFRI*LHRMSDG IFWLCFYISMHLCLWLVLYWAV WFKLQTTIRSLRWLTDSPVSVY GYCQGMNEGCSQFKTVPTLFS SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK EISKGLTKTPRLVMSPPSSCSR RGIWPNPDTCLLLLL
28113	58481	C	28283	1	603	

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28114	58482	A	28284	179	445	QLSGLASGMRESRDVGLRFTPLLLWIVHSRAWLVESAVMSTWECWVGDERTGTGVLGAHTELP TGPGV*YSPPCVHVFLSFLNSHL
28115	58483	A	28285	128	381	
28116	58484	A	28286	1	1392	
28117	58485	C	28287	1	3169	
28118	58486	A	28288	1905	2449	AQLPTAPLPFLGRRWGTWGFPGHAFHSWFWYSTGEGAMGSFLALLSFPLGMKLAILEDFFGISGTAAPLGGSSFGSSLSVTEALLARSL/HFLILLPLFLLLFLIAFQRTLLVGQCPAKSPLGNALECNLGAAGSRAHGGEHATGGLQLLALFEAGQSLQPLTACVPGPRPLTCL
28119	58487	A	28289	693	905	EESIS*KWPYCPSFHNLPQAYKAIPHPASLGK*YNDQNNNAGKLFKANRNPALGCQPVCSKT DGRF
28120	58488	A	28290	3	427	
28121	58489	A	28291	1	1195	
28122	58490	A	28292	158	779	
28123	58491	A	28293	227	378	
28124	58492	A	28294	1	621	
28125	58493	A	28295	1	351	
28126	58494	A	28296	1	507	
28127	58495	A	28297	1	543	
28128	58496	A	28298	343	428	
28129	58497	A	28299	785	1178	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
28130	58498	A	28300	842	2592	IREEVESLKRPTSSDIEAVINSL SIKKKVQYQTDSPQNSTRGENL GNTIQDGTGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TIIRVNRQPTWEKIFEIYPSNK GLISRIYKELKQIYKKKTNDPIK KWAKDMNRHFSKEDIYAAKK H/DEKMLIITGTWMKLETILSK LTQEQTCKHRMFSLLIPDDGNS LTRRMLLIGISVKTPVGTGAIPG PVGGTAAAGAYGRKEKALSNC DSILALALAKMSENQMSMESFF EKGKDPMRQKQKTLTLTKKKN AFKRKYQESYLNFGIATVRAS FLVANCIVKAKKPFITGEELILP AAKDICYELLGEAAVQKVPHV PLPVSTITRPIDEIAEDIAQFLE RINESLWYTIQIDKSTIADNKAT MLVFVQYIFQEDVHEDVFFQES LRATSQPLKTPQTGKEWVHDPF VDKPSSESTLSMLEEDQLEIAN DGLSKSMFEKTSNLHIVCIKVK AEYPEIATKALRRLLAFPVWAA VDRECQWGSRDVEMRRLDPK AGFSLGVGNCCHCLRTLEFVGL SMSSLCGAMLLCGLRAAPYISL RDHKGQGTLL
28131	58499	A	28301	1	1662	
28132	58500	A	28302	2	406	CWWDCKLVQPLWKSVMRFLR DLELEIPFDPAILLGIYPKDYKS CCYKDICT/RVCVPAALFTIANT WNQPKCTSMIDWVKKMWHIY TMEYYAAIKKDEFMSFAGT*M KLETILSKLTQEQTCKHRMFSL YWKs
28133	58501	A	28303	1	1404	
28134	58502	A	28304	68	2269	

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28135	58503	A	28305	189	1890	MKMASSLAFLLLNFHVSLLLV QLLTPCSAQFSVLGSPGPILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDRQSAPYRGRTSILRDGITAG KAALRIHNVTASDSGKYLCYFQ DGDIFYEKALVELKVAALGSNL HVEVKGVEDGGIHL ECRSTGW YPQPQIQWSNAKGENIPAVEAP VVADGVGLYEVAA SVIMRGG GEGVSCIIRNSLLGLEKTASISIA DPFFRSAPWIAALAGTLPILL LLAGASYFLWRQQEITALSSEI ESEQEMKEMGYAATEREISLRE RKKIQYLTDPVILYPDMANAIL LVSEDQRSVQRAEPPHLDLPNP ERFEWRYCVLGCEFSMERHY WEVEVGDRKEWHIGVCSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTEPRTNLKLPEPPR KVGVIDLYETGHISFYNDGDS HIYTFHASSSEPLYPVFRILTLE PTALTVCPIPK/GREFRPFPTLVP DHSLEIPLTPGLANESGEPQAEV TSLLPAQPGAKGLTLHNSQSE PYSYRHTLKHFTDIHSIIP

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28136	58504	A	28306	172	1905	MKMASSLAFLLLNFHVSFLVQ LLTPCSAQFSVLGPSGPILAMV GEDADLPCHLFPTMSAETMELR WVSSSLRQVVNVYADGKEVED RQSAPYRGRTSILRDGITAGKA ALRHHNVTASDSGKYLCTYFQDG DFYEKALVELKVAALGSDLHIE VKGYEDGGIHLCECRSTGWYPQ PQIKWSDTKGENIPAVEAPVVA DGVGLYAVAASVIMRGSSGGG VSCIIRNSLLGLEKTASISADPF FRSAQPWIAALAGTLPISLLLLA GASYFLWRQQEKIALSRETER EREMKEMGYAATEQEISLREKL QEELKWRKIQYMARGEKSLAY HEWKMALFKPADVILDPDTAN AILLVSEDQRSVQRAEPRDL DNPERFEWRYCVLGCENFTSGR HYWEVEVGDRKEWHIGVCSK NVERKKGWVKMTPENGYWTM GLTDGNKYRALTEPRTNLKLPE PPRKVGIFLDYETGEISFYNATD GSHIYTFPHASFSELYPVFRILT LEPTALTICPIKEVRRVPPI/AD LVPDHSLLEPLDPA*LMKVGE PQAGK*HLCFSLPTLGAELPLF
28137	58505	A	28307	1	2220	
28138	58506	A	28308	134	509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAQRSP AEKMGETPGAASVSRILGGRV ALRRHVGRGELRAPDCLGPD WVPTRGSHFPGFFPREQSL/W GATPPSYRSSEVRSGAESGRAP DSVSGSGVQAH
28140	58508	A	28310	1	1066	
28141	58509	A	28311	77	273	
28142	58510	A	28312	1	415	
28143	58511	A	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	A	28315	2	671	PGEFTRAPRVRRRAMGISRDN WHKRRKTGGIRKPYHKRRKYE LGRPAANTKIGPRIHTVVRG GNKKYRALRLDVGNFWSGSQ CCTRKTRIIDVVYNASNNELVR TKTLVKNCIVLIDSTPYRQWYE SHYALPLGRKKGAKLTPEEEI LNKKRSKKIQKKYDERKKNAK ISSLLEEQFQQKLLACIASRPG QCGRADGYVLEKLEFLYLRKI
28146	58514	A	28316	3	1259	
28147	58515	A	28317	1745	2681	

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28148	58516	A	28318	1	2502	
28149	58517	A	28319	1097	1417	
28150	58518	A	28320	1	398	MTAEERDKFPTDQQAIPSMDPH WDPSDSHDGDSHKKHLLTCVLE GLRRIRKKPMNYSMMSTITQG KEENPSAFKWLREALRKYTPL SPNSLRGQLIKDTFITQSAADI RRKLQKQALGPEQNL EALLNQ ATSVFYNRDQEEAQKKEKRLSS RSVTIRGILGQSVTRPEAHKGL QDIVKHLKAQGLVRKCSSDCN TPILGVQKLNQWRLVQDLGLI NKAIIPLYPVVNPYTLLSQISEE AEWFTVLDLKD AFFCIPLHSDS QFLFACEDPTDHTS QLTQTILPH GFRDSPYLFQGQALAQDLGHFSS SGTLALQYVDDLPLATSEASC QQATLDLNLNLANQGYKASRS KAQCLQQRDGGQTTLYSNQGA PEGKYSSSRMRPVRNSLQNLK AGPSTTPALSLPTGQNL SLYVT ETAGIALGVLTQA HGMNPQPV AYLSKKIDVVAKGWPHCLRVV VAVAILVSEAIIQGGDLTVWT THDVNGILGAKGSLWLSDNCL LRYQALLLEGPVLQIPMCAALN PATFLPEDGEPIS**PLTLRWPLP QLPLNSEASLLH QFSYLGMF LVGSSSHEPA
28151	58519	A	28321	318	363	
28152	58520	A	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP PLPARWPIH
28153	58521	A	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD TSEHLKEQTADTSSSLRTVTLTA RVCGFILEVSETKNSPEGTNSG HILTSQMGLSPIAKRRETSASAA ALVSATIPICRVQGPLRVLGQE VFLLLLRLPTA PLPINDKPP/PN/ TPLPRRQAKKSPKDHKNPWAI GYVPFKQ*GEGNLA*PGYMSPS

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28154	58522	A	28324	350	1563	FLYIQLYPTPITCSLKYQRKQNG SLFWTSRMPSSVFPCTLTPSFSL PLRIP/PDHTSQLTWTVLPPGFR DSPPLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSSEASCQQA TLDLLNFLANQGYKVSRSKAQ LCLQQVKYLGILAKGTRALIK ERIQPILAYPCPKTLKQLRGFLG ITGFCQLWIPGYSEIARPLYTLIK DTQRANTHLVWESEAEAFK TLKQALVQAPGLSLPTGQNFSL YVTERAGIALGVLTQTRGTTTPQ PVAHLSKETDVVAKGWPHCLR VVAAVA VLVSEAIKIIQGGDLIV WTTHEVNGILGEKEVYGYQTN AYLDTRRSALRDWCFKYARPV AAIILLALAFGPCINLPVKFVSS RIEAIKLMVLQMDPQISSTNN FYRGLD
28155	58523	A	28325	830	1143	
28156	58524	A	28326	234	510	PWQSLP*VAQKVPKDHRSLPLE P*TRSLNNS*QHWLCPPARAP STCSTSCPARDGPPPPSPAPHGP RNTSVPGVHSRGPSPPPRTPPP VS
28157	58525	A	28327	2	816	
28158	58526	A	28328	1	1311	
28159	58527	A	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	1	484	
28162	58530	A	28332	72	299	
28163	58531	A	28333	737	847	
28164	58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	A	28339	65	244	
28170	58538	A	28340	2	584	GKSRMFPAQEEADRTVFVGN LEARVREILYELFLQFLIAGPL TKVTICKDREGKPKSFGFVCFK HPESVSYAIALNNGIRLYGRPIN VQYRFGSSRSSEPANQSFESCV KINSHNYRNEEMVVGSSFFPM QYFPINNTSLPQEYFLQKMQR HVYNPVLQLPYEYMTAPLPNS ASVSSSLNHVPDLEAGPSS

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28171	58539	A	28341	2	367	MTMHYEIPVTRRSKGT*LPQ NA/SVNNMPH*TGAI*ADISM YARIERNHLGRGNSNSKDPKLR ESSEHLRKLKTRVVNEQTRLGL IMETVVGGRGEAPFYFQCDKHL SRSPQGLGLICL
28172	58540	A	28342	98	387	RKQPPKVLQWLLAF*SHRSW LSSPWPDLWRPWAGGACARL LLQPPRDSASLKERQQPSGAY R*NSHLPGEHLGEGVAVCAAS ADLNVTAACWL
28173	58541	A	28344	1	269	
28174	58542	A	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	A	28347	59	310	
28177	58545	A	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQ LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSFLSVSKNIFI SAFISLCTQ*SFRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQCGQFW NRCGVVLKKMYILLIWGGFC RCLLGLLGAELSSIPGYSC
28178	58546	A	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQ LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC VSILDLSCFPLWAFSAINFPLHT ALSASQRFWYVVSFLSVSKNI FISAFISLCTQ*SFRLFSFHV ERL*VRF/CNPEF*FDCTVV/WR *FVIVSVLLHLRRLPTMWSI LE*VWCGAEKNVYSVDLGRW VL*MSIRSAWCRAEFNSWVSL TFCLVDLSFSLAALNIFSFISTLV NLTIMCLGVALL EYLCGLVCI
28179	58547	B	28350	1	3135	
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNQ LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSFLSVSKNIFI SAFISLCTQ*SFRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQCGQFW NRCGVVLKKMYILLIWGGFC RCLLGLLGAELSSIPGYPC

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28181	58549	A	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSFSSSFNC DVR VSILDLSCFL*AFSAINFPLHTA LNASQRFWYVVSLSLFSKNIFI SAFISLCTQ*SFRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFPVCGQFW NRCGVVLKKMYILLIWGGEFC RCLLGLLGAELSSIPGYPC
28182	58550	A	28353	1	3531	
28183	58551	A	28354	1	3126	
28184	58552	A	28355	2357	3083	FFSLFFFILASGLSILLIPSKNQL LDSLI*RVFCVSISFSSALILVIS CLLLAFECVCSFSSSFNC DVR VSILDLSCFLWAFSAINFPLHT ALNASQRFWYVVSLSLFSKNIFI ISAFISLCTQ*SFRLFSFHVVE RF*VRF/CNPEF*FDCTVV/WRD SLL*FLFFYIC*GELYFQVCGQF WNRCGVVLKKMYILLIWGGEF CRCLLGLLGAELSSIPGYPC*FF VLLICMLTVGC
28185	58553	A	28356	6412	7092	FFSLFFFISLASGLSILLILSKNQL LDSLSF*RVFCVSISFSSALILVIS CLLLAFECVCSFSSSFNC DVR VSILDLSCFLWAFSAINFPLHT ALNVSRFWYVVSLSLFSKNIFI FISAFISLCTQ*TFRLFSFHVV ERL*VRF/CNPEF*FDCTVV/WR DSLL*FVFFYIC*GELYFQLCGQ FWNRCGVVLKKMYILLIWGGE FCRCLLGLLGAELSSIPGYPC
28186	58554	A	28357	1	2019	
28187	58555	A	28358	1	1263	
28188	58556	A	28359	77	304	
28189	58557	A	28360	1	756	
28190	58558	A	28361	1	369	QQRLLASNEAFKSAKASQSP ASKYMKENDQLKKGAADVGG KLDVGNAEVKLEENRSLKAD LQKLKDELASTKQKLEAENQ VLAMRKQ/SPEGLTKEYDRLL EHAQLQAADVGDPMDDKEE
28191	58559	A	28362	879	1156	
28192	58560	A	28363	54	407	

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28193	58561	A	28364	620	1246	GSTWHGWDGSRCSQRNWS MTKRSSQPSSL*SRRRRWS SSPNW*KTGPSSMSRMSSAG* SAASSRSCATRWTRRRPAAWR G*GVTPVAWWPPWTCWSRPR EPGSGWPKPSVCWNSSEMRTT MSSGSGSTPWPPVSRRPWTER RLGSRGDRRLERSRPAVNRT RMSRVPSGAPRGTPSRWW MKCWDHQMRGLVEEVG
28194	58562	A	28365	86	402	KGWCCRKGWNWKRSWFLT FLQGLLEGPHPSPTAPRRTT* SLYSAPSRMVQLDDLLHKWF LYSCLVSAISIGIKFPLKIHISPG GVLEARETMSHFKEAAL
28195	58563	A	28366	54	353	
28196	58564	A	28367	66	352	
28197	58565	A	28368	442	700	HWNKVPAENPHLPWVRCSPT PLGKPKPCSSWNRSGTDVSGT GLSESGSWPSGSCNGVTGTDA YGP/GYVKSGSFPGRVRGT
28198	58566	A	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR SKDATPDPPRLGKGFPPRLPQA PRLLGSQRLSTLCSTLSGRGG KNTSRLSFSPSGSVKGRVRDVK EPGPIRAHRTAFFPNASS/GSEG R*SPSVVAVRGRF/CVGVWRFP TVGVVWHAPRCTR*SPITGSAP LSVWSPACTGSPCTAGA
28199	58567	B	28370	163	387	
28200	58568	B	28371	112	419	
28201	58569	A	28372	1	1902	MSRIA WKLWKLIQGYLGQPA GTARRHPGIGFKSPPGDFTCNG LIAVIKQSDNQRMSPGWSW GRENNPTLVEVLGVRLPETV HTAVRYTSIELVGEMSEVVDNR PQFLDPVLGYLMKGLCEKPLAS AAAKAIHNCSVCRDHMAQHF NGLLEIARSLDSFLSPAAVGL LKGTALVLRPLDKITECLSEL CSVQVMALKKVFVGATSRRA KLFRGLKAHGNSFETSGEAE CCTWRPKEMTCVE
28202	58570	A	28373	1	2019	

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28203	58571	A	28374	2	1455	SAAVAARSPPQRPSPATLGGPG QRRPPSAAPTAWAAAAAPGS RRRRPLPARPLWAPARGAAAA GPAEAPMLARRKPVRAALTINP VITAEGSPVITSEGALEANLGIDL QKKLEELELDEQ/QKKRLEAFL TQKA/RRVGELKDDDFERISEL GAGNGVGVVTKSPAQDPSPGLIM IARKLIHLLEIQAGASGNQIIPR/D LQVLHDGTWPTMGGVFGAFY SDGEISICIEHMDGGSLDQVLK EAKRIPEENLGKVSHSRFSGGL AYLREKHQIMH/RDVKPSNIV VNSRGEIKLCDFGVSGQLDSM/ ANSFVG/TRYCMAPERLQG/TH YSVQSDIWSMGLSLVELAVGR VPIPPRDAEELEAIFGRPVVDG EEGEPHSISPRPPGRPVSGHG MDSRPAMAIFFELLDYIVNEPP KL/PNGVFTPDFQEFVNKCLIKN PLAERADLKMLTNHTFIKRSEG/ EEVDFAGWLCKTPAG*TKPGTP VTRTAV
28204	58572	A	28375	229	257	VSLSASPLVSLAGRSPRLGRG CQSLDGYGVGWQAQSPGADE GNRSFT*PELADKNVPNLHVM KAMQSLKSRGYVKERLPSSAP GDCACHPT
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP KQKQ*PGGTEDS/YDASGPPPKF LIKEIKLGVPFRFFPIRGV*NPGG KNFGGPFKKT*FCWARVPKM* FFKGGPSSSSPAVSLFNAKESPI LLRWMTSTTSKAYKLEFGC
28206	58574	A	28377	1	367	
28207	58575	A	28378	1	1001	MSWEMEQQDEVYKEMSINHKN EGTRVEKPNRYRIIHQPDAINH VSRKKDVPSASGAGHSRSTGS RPGVRRLWPLLLRSAPSGPLNN AVPAPGKGPRWGGSPSLSRSG GKASTRVAPGLSAHSQAASGV PEPAEPQHRTKASGSRRLSLR VVPEAPKPRTRTAREGKGAGA GHTGGAQEQRRRRRWACRGLR GRPGAVSPGGAEAINQLASEHC GNPAAALHRCIASLPRNLLVW AGRMLMPKKNRIAIYELLFKEE VTVVKKDPVHMPKHLEADKNS RGYYVKEQFAWRHVYWYLTN ED/MPVSP*LPSAPGDCACHPT PQPSRDWQASV

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28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG ADEGNHGDGTGYPHW*GTSRNV SRQTVQTRSLGT
28210	58578	A	28381	168	378	
28211	58579	A	28382	1	900	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPGRVSVFVRGLD TKK*LI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILPL FADKVPKTAENFRALSTGEKG FGL*GVPCFHRUIPGFMCQGGDF TRHNGVGGKSIYGEKFEDENFI LKHTGPGNLSMAKCDPTQN GSQFFNLALAKTEWLGWASHV GVLA*KKGMNIVEAMERFGS RNGKTSKMITTADCGQLRIKFD LVFYLNHQDHSFWKPQGEHPS NPFARRILRLWLSLAVPFWVPC FPCSLPCLAGLQS
28212	58580	A	28383	393	683	HAKDGMEOGRNNECPKVGGKQ VTLQHSDEDRKTSRGENLY MSSDPTSWSIAQSWYDEILD VYGVGPKSPNIVLLVII*HIERIPR TNKEHLVPV
28213	58581	A	28384	119	193	
28214	58582	A	28385	1	567	
28215	58583	A	28386	957	1145	EQNLLIYLVSIQDCMDKGCII* LRHTSGNCMYVSDKDFDKEQCI FSRSSHQSLSGNDLQK
28216	58584	A	28387	153	2257	
28217	58585	A	28388	369	539	KKPARRRHFLTLLCCVFSPKLC TAGGPMRRTFKSYDEAGTGLL SVADFRTVLRQYSINLSEEFFH ILEYDKTLSSKISYNDFLRAFL Q*TPKL
28218	58586	A	28389	3	1364	
28219	58587	A	28390	1	996	
28220	58588	A	28391	296	549	ETSSSVTVSDPEMENKGGQTLA NNSSLMAEAPGTMCRFTLAPH VLAQVGTITDLPDHLLSYDGSE NLSRFWYDFTLENSVLCDS
28221	58589	A	28392	1	1065	
28222	58590	A	28393	412	428	WILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPLPARWPDLSL MQLARQVSRLESGQ
28223	58591	A	28394	3	505	
28224	58592	A	28395	1	1201	
28225	58593	B	28396	518	1606	
28226	58594	A	28397	1	798	
28227	58595	A	28398	737	3067	

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28228	58596	B	28399	133	239	
28229	58597	A	28400	3	376	
28230	58598	A	28401	1	1194	
28231	58599	A	28402	405	611	
28232	58600	A	28403	204	4198	
28233	58601	A	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMTFTITQLLVVEV KDSLERLAVEVVFILQKAMY KQAHYIMKSLCPQMVLMLRFI QWVQIMPMLKLENLQHLMAR WNETVKEKK*D'LLFSMHERN
28235	58603	A	28406	359	517	
28236	58604	A	28407	68	487	
28237	58605	A	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQQTQEPSWLHPVDP APGLQVELPASHAPCARTPQPL GGRWDWAPWSRGWCSLGRLG PHRSPWSGWAEQA*QWIPHQ CRWSCLPVTTRVLALLSPWV DGTGRRGAGGARWGGSGRT GAHGVGGRLRHSRLQVPSPAL LFKYYVCDFK
28239	58607	A	28410	1	609	MVFSNLKGHWLQPIRLDSGSR NTAIGCDNQYKPTGVKLQTF VSVTALKAAARLGLFVPPGGLV VSLGSGVKLQIFASQVVCDFRA LIGAFTIPELDTKVLHVPIRLVR YRVVWTRFSKAPPDSSGAQLASP SESHTRAAGGAACQSQCRAPA LLSPWVVDGTGRRGAGGGAHR GGSGCTGTHGVGGRLRHSGLQ VPSSA*VSHPLRGFL/LQPEPR* APPPAPRRPVPSTTQGLRSAGA RHWWDQAAPPAALVWDSLGE ASWAPESGGALENLCVHTLYL TNLMGTWRTFVSSGIVNAPIS ALSKQTTWLAKICSFTPEPRETT SPPGGTNNPRAALRAVTLTAK VCSFTPVGLYWLSQLPMAVLE PESNLIGWSQWPFRLKT
28240	58608	A	28411	548	753	TLLWE*SRLRKKSHLMMTLNH STHSITFGLDKHCASYLMGFLYI VELLIAQCGSPGATLIQWRMAS MD

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28241	58609	A	28412	1	903	MAKKIQLTYKCVQNWVVLGLTDFKNEAADPRRVKLQTFVVS VTALKAAARLELFIPPGGVVSL ASGVKLQTFAVSVTAHKGVSVD PKTRHKGSPSPHQIQEPSWLHP VDPAPGLQVELPASPAPCARTP QPLGGQWDWVPWSRGRCSSG RLGRSSPRWGAGSGMAGCRS RALPHGEAAKARQKVTAAGP GAKHLTA WGWQGQLATPSVG PAEPTHTQNSHWPA S V C S P S S R L R L S L H T Y P Q A E G A G S G L G Q P R K G L P Q C S S R L K G S S A A K V G A Q A E E V P R A S E A C E G * R A P Q V L P K W E P R Q R C R E R A R P A R A A S T L S P L I S I
28242	58610	A	28413	1178	1480	CRHLIQSHSICLHQWDCHTQHL YHPQ**WNQQQLHHRCLLQG SIHLVFGPQWDPRRRRPLRGTR SAMARMDILRISREYITQEITEA ATKRKVLSVPKE
28243	58611	A	28414	126	407	WIPHRGCRWSCLPVPCRALALL SPWVVDGTGRRGAGGGARQG GWGSTGAHGVGRRLRHGGGLQ VPSPAPRESS*GPARNRSQRRRS DSSLRERK
28244	58612	A	28415	27	363	
28245	58613	A	28416	1	576	
28246	58614	A	28417	813	923	YSLIHAAPQQR*SLSGPHQTY DISSYTQCCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVP TRLRSPASFTQWIPHWGCRWSC LPVPRRPALLSPWVVDGTGG CGAGGGAHRRGGWGCTGAHGG GGRLRHGGGLQVASPAPREGS*G PARN*AQSRWAGTAGGSPSTPSA AAGPGA KPLIAPGRQGNPECH WCGARQAHAPQLATASASW TRAFRECVPSPWPSCLGAACFV CLLIGPFPFSFSSQHLSTSLGHLV LLSWHLTSLSVSFRILTRLRLRVF TGSWGGGAA
28248	58616	A	28419	1	616	
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28253	58621	A	28424	1300	1648	
28254	58622	A	28425	1	599	

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28255	58623	A	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK YVGLWDFKSRDDELSFRAGD VFHVARKEEQWWATLLDEA GGAVAQGYVPHNYLAERETVE SEPRDQTQAVRHYKIWRAGGR LHLNEAVSFLSLPELVNYHRAQ SLSHGLR
28256	58624	A	28427	3	438	
28257	58625	A	28428	37	403	
28258	58626	B	28429	1	1176	
28259	58627	A	28430	2	2150	
28260	58628	A	28431	1593	3025	
28261	58629	A	28432	322	2168	
28262	58630	A	28433	183	591	
28263	58631	A	28434	2	258	
28264	58632	C	28435	52	363	
28265	58633	A	28436	1	3363	
28266	58634	A	28437	1	918	
28267	58635	A	28438	1	1422	
28268	58636	A	28439	3	10899	
28269	58637	A	28440	277	586	
28270	58638	A	28441	3	3364	
28271	58639	A	28442	1	1851	
28272	58640	A	28444	3	253	CGIEDNNFSLALNPDTILLS/HS GGRGAEAPTMCCLKTVSKRAC FEGLEWQFNLWRNKK**C*DK KHKTAGCSIS*VMRSVYR
28273	58641	A	28445	1	950	MGSSAVQSQAALAPRVLTTG LADVTALLRAPATPGRVLVAGA RGGWGYVQSCRGAGAAVKP LGS AETA VPIARLGCRRFSRSC CRRRGRGSLLSFSAAKPIVFKEK LTMKTDSLMEEKLECSLWCCL SDPSTPGRCVLERRJPVWMOQ LLANIKQAEKHEKNHPEVTVA MALTDIDLQLQFSMSQPE/GPPS PGSRPS*PPAAALLWTPAGQA CPGPGGAEADPSRSTEWLRP PHHSSDCLRGLAHIVSQWVSEC LLCSPGSPPRSPLWALCWEHWE TWPALPEGNQSPPEGLPPCSRS QWPQTTPASDPQ
28274	58642	A	28446	3	213	LTQHCWTHLVRSSHSRTGSSRL HNHQLHQPAC*SLCQKEHASR GWSEGFNLWRNKK**C*DKKH KTAG

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28275	58643	A	28447	142	772	LVNVVDVADLVGLCVSHRHVT EEQYSTLALLNHGPQVALKYV HMDEVMPACCLEGGCLPAL CGECKLQGSFILSAPGRQGSQR VGPREAQGHVIGRKLFFSTALM LIGGQRLEESAAIESGCMETP QGMAGSPQVGQAQKSPSPVNPKE PIGDF*GGSQDYRGGIQKPID*Q CGPVI/SRQSELWCGGRSHSVE FLLGSAASAPPGPQA
28276	58644	A	28448	1	1935	
28277	58645	A	28449	2	1571	
28278	58646	A	28450	2	301	PRPFYSKNFYKILSYSSSEFNNS FVDA/LGSD/QDSGNEVDVDM YTEAAEELKRNAEVIVFIPEYS WSNSVSLFPLCPGAKGPTFSVH CRVHFGPFSSH
28279	58647	A	28451	1	1329	
28280	58648	A	28452	240	503	
28281	58649	A	28453	1039	1896	
28282	58650	A	28454	1	2397	
28283	58651	A	28455	1	4011	
28284	58652	A	28456	3	1088	
28285	58653	A	28457	1	4878	
28286	58654	A	28458	1	174	
28287	58655	A	28459	3	161	
28288	58656	A	28460	992	1102	
28289	58657	A	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV GFPOGQCLVHIW*/M/PLDAGPE HNSLKGFLVPLFPLAATPRAPG TPAQGSLTDSFPDLLGLAAED
28290	58658	A	28462	3	278	HEAAMSMRLRQKRLASSVLRC GKKKVWVRPL*/TNEIANANSR QKIRKLKLDGLNRTFVTAHSWP SCRNTLSRRMGHS*/SLRTLDD PVNM*GLLNASWITKC*LLDPV NM
28291	58659	A	28463	1	1043	
28292	58660	A	28464	185	804	VTSGCGKKKVWLDPNETNEI ANANSRQQIPEASSKMGLIRK PVTVHHSRA/RCPVKTP/LARRG RGRATWGIR*/GGKGYKPNARN AQRKFTWMRENGGL*/TRGCL RKIPVNPCKDRIANMYHSLPLE G*RGNVFKNKADFSWEHIHKL EGRQRPRKKAPWLTAQ*GPAG S*/DPRKPKRR*/RAPRPPKKEI HQRLFSKE/EETKK
28293	58661	A	28465	221	350	GPSSFRLPTLSSLVHSHGREET* HSLET*/RDAVSLRIFKSLSV

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28294	58662	A	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQGNKRGYKQME EHSMLMGRKNQYRENGHTAQ GNLQVHAIPIKLPMTFFTELEKT TSKFIWNQKRARITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKLK SFCTAKETTIRVNRQPKKWEKI FATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAHQKSG NNRCWRGCGEIGTLLHCWWD CKLVPHILTHRWELNNEITWTQ EGEYHTLGTTVVGWGGGGIAL GDIPNAR
28295	58663	A	28467	1	1863	
28296	58664	A	28468	2	1308	

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28297	58665	A	28469	1	1901	MPESPTLLGRDILAKAGAIHL NIGEGTPVCCPL.LKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFYQQRQYPLRPEAQQLGQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNQWRLVQDLRIIDE AIVPLYPAPNPYTLSSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPPQ FRDSPHLFHHTLAQDL.SQFSYL DTLV.LCLPLRNQCECHQATQV LLNVLATCGYKYSKQAKLCS QQVKYLGVKLSKGRALNNEE QIEHNCQQVIAQTYATRGLLE VPLTDPNLSLYTDGSSFVEKGL QKGGYAVVSDNGILERNLTPG TSAQLVELIALPRALELGEGKR GSSESICFLSFLVPPMTIYTEQDL YNHVVPKPRNKRVPILTFVVGA GGLGGLGTGIGGITTSTQFYFK LSQELNGDMEWVADSLVTLQD QLNSLVAVVLQNRALDLLTA KRGGTCLFLGEECCYYVNSQGI VTEKVKEIRDQIQRRAEEI.QNT GPWGLVSQWMPWILPFLGPLA AIIILLFLFGPCIFNLLVKFVSKI EAVKLQIILQMPEQMMSMT/KI YHGPLDQPASPCSDVNDIKGTP PEEISTAQHLLCPNSAGSS
28298	58666	A	28470	1	432	
28299	58667	A	28471	1	4314	
28300	58668	A	28472	1	330	
28301	58669	A	28473	1	1425	
28302	58670	A	28474	3	1110	NEEQIEHNCQQVIAQTYATRGD LLEVLPTDPNLSLYTDGSSFVE KGLQKGGYAVVSDNGILERNP LTPGTSAQLVELIALPRALELGE GKRGSSESICFLSFLVPPMTIYT EQDLYNHVVPKPRNKRVPILTF VVGAGGLGGLGTGIGGITTSTQ FYYKLSQELNGDMEWVADSLV TLQDQLNSLVAVVLQNRALD LLTAKRGGTCLFLGEECCYYV NQSIVTEKVKEIRDQIQRRAEE LQNTGPWGLVSQWMPWILPFL GPLAAIILLFLFGPCIFNLLVKFV SSKIEAVKLQIILQMPEQMMSMT TKIYRGSLDQPASPCSDVNDIEG TPPEEISNAQPLLCPN*AGSSWS SRRPTSPALGFSC
28303	58671	B	28475	1	1989	

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28304	58672	A	28476	1	1280	MGNITADNSSMSCTIDHTIHQT LAPVVYVTVLVVGFPPANCLSL YFGYLQIKARNELGVYLCNLT ADLFYICSLPFWLQYVLQHDN WSHGDLSQVCGILLYENIYIS VGFLCCISVDRLAVAHPPFRFH QFRTLKAAVGVSVVIWAKELL TSIYFLMHVEEVIDENQHRVCF EHYPIQAWQRINYYRFLVGFL FPICLLASYQGILRAVRRSHGT QKSRKDQIQRLVLTVVIFLACF LPYHVLLLVRRYWEASCDFAK GVFNAYHFSLLTTSFNCVADPV LYCFVSETTHRDRLARLRGACLA FLTCSRTGRAREAYPLGAPEAS GKSGAQEEVTKFEGGRNGHT AKKSPCNSVQDFTGIKAVKLQI VLQMEPQMOS/KLKIYSRPLDR PASPCSDVNDIEGTPPEEISTAQ
28305	58673	A	28477	1	717	
28306	58674	A	28478	2	409	
28307	58675	A	28479	1	675	
28308	58676	A	28480	227	399	
28309	58677	A	28481	332	436	
28310	58678	A	28482	980	1399	
28311	58679	A	28483	132	218	RINLMHFRN*TSQQALSLSYNL FLMQRH
28312	58680	A	28484	1	34	
28313	58681	A	28485	985	1170	
28314	58682	A	28486	1	1203	
28315	58683	A	28487	505	716	REPCVPSQREVWRPGCLD/HCP RQSGSLGETLRGTAEQPWPHS QVLSNLRVLQLPLISPLSRRA LFPA
28316	58684	A	28488	1	998	
28317	58685	A	28489	477	955	TPIHNGFKENKIPRNPYKGC EGLQGEQTAEAGNKRGYKQM EEHSMMLGRKNQYRENGHTA QGNLQVQCHPHQATNDFLHRI GKNYFKVHMEPKKSPHRQVNP KPKEQSWRHHIT* ¹ LQYYTTRL Q*PK*HGTGKTKEI*INGTEQSP QK*CRISTTI
28318	58686	A	28490	37	430	
28319	58687	A	28491	507	829	
28320	58688	A	28492	643	945	CALLHSLPQHCVQHPYRSYTHR MASCRWKWGHCHSGIKMYSIP WYSTPMEGKALGDAHPQIAHS H*GAFL*ALY*EKS*SMANRL WYSRL*PLAGDGRRE
28321	58689	A	28493	1092	1346	

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28322	58690	A	28494	173	527	
28323	58691	A	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSVSPALPCSLKYPFYD HRTKFTLTTPQFSHTLAQKENQ SPLKHMGGKKRLQNIFLPIRP*DQ TPWLEERS
28325	58693	A	28498	921	1008	
28326	58694	B	28499	1	2169	
28327	58695	A	28500	455	523	YPLYHFLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVYSEIQLLPGLVL GGCMCRGIYPFLDFLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLLRVFSMKSC *ILSKAFASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFASILLRIFTS MFIRDIGLKFSFFVVS L PGFGIK MMLAS
28330	58698	A	28503	1	957	
28331	58699	A	28504	41	412	IALIILRYIPSILLRVFSMKGC* ILSEAIASIEIIMWFLSLVLF I *W ITFIDLHVLNKPICPGMKPS*SW WISFLMCCWIWFASILLRIFASM FIRDIGLKFSFFVVS L PGFGIRM MLAS

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28332	58700	A	28505	1	1699	MDEFLDITYTLPRLNQEEIESLN RPITSSEIEAVINSLPTKKCPGPD GFTAEFYQRYKEELVPILLKLIQ TIEKEGLLPNSFYEATNIIIPKPG RDTTKKENFRPISLMNINAKILN EILATESSIKKLIHHDDQDSFPGM QGWFNICKSINVIHHINRNNKN HMIISVNAEKAFAKDRIHFLMLK TLIKLGIDETSLKTVRAIYDKPT ANIHLNGQKLEAFPLKTGIRQGC LLSSLLFNIVLEVLAIRAIQEKEI KDIQIGREEVKLSLFADDMIVY FKNPIVSAQNLLKIGNFSKVSG YKINVQKLQAFLYTNNRQTESQ IVSELPTIAAKRIKYLGIQLTRD VKYLFKENYKPLHKEIIEDTNK WKNIPCSWIGRINIMKMAILPK VIYRFNASPIKLLNFFTELEKN CLNFIWNQKRAHIAKTILSKKN KAGGITLPDFKLYYKSTVTKTT WYWYQNRVIDQWNRTEASEIT PHIYNHILFDESDDKNQWGKDS LHNKWWYENWLAICRKLKLD SFLTHYTKINSRWIKDLNAGSKI QYHADRTKSRERRAIASSYVSS
28333	58701	A	28506	2	1689	WRAWGRGATRRESSCHRQSAPS LSRVGRSSQIRALSAAASGLWR RKPAKAFGRPRTGSLHLVPK* KAFVSLQESSA*MNLRO*PE*D WISWIN*QNFGN/CQGSTLKIPV VERKILDLIALSKEHSFSPATEQ SWTENDFDELREEGFRSDSE LKEEVTRTHRKEAKNLVVKRLDK WLNRTSVEKSLNDLMELKTM AREQLRDECTSFSSQFDHLEER KYKLPSENKHLIYANKLENLEE MDKFLETYTLPRLNQEEVESLN RPITGSEIEAIINSLPTKNSPGPD RFTAKFYQMYKEELVPFFLKLF QSIEQEGILPNSFYEASIIIPKPG RDPITKKENFRPISLMNIDAKIFN KILANQIQHKKLIHHDDQMGFI PGMQDWFNIRKSINVIQHINRT KDKNHTIISIDA EKAFAFDKIQQCF MLKTLNKLIGDGTYYVHIRAIY DKPTANIILDGQKLEAFPLKTST IQGCPLSPLFNIVLEVLAIRAVR QEKEIKGIQSGKEEVKLSLFAD DMTVYLENPIISAQNLLKLSN FSKVSQYKINVQKSQAFLYTNN
28334	58702	A	28507	1	1428	

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28335	58703	A	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC WIMFIDLRMLNQPCTPGMKPT* SWWISFLMCCWIRFASILLRIFA SMFIRDIGLKFSFFVVSPLPGFGIR MMLTS
28336	58704	A	28509	765	950	LLPQFQNLILLVYSEIQLPLGLVL GGCMCPGIYPFLLDLFLVYLHRG VYSIL*W*FVFLWDQW
28337	58705	A	28510	778	981	SQKEWYQLLFVPLVEFGCESIW SWAFFGWQAINYCLNFRITCHW SIQRFNFFLV*SWEGVCVQEFIH FF
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI* TLK
28339	58707	A	28512	1	1641	
28340	58708	A	28513	1	2307	
28341	58709	A	28514	1	3793	
28342	58710	A	28515	178	674	ERPRIMDLAAGLLKSQFLCHLVF CYVFIASGLIINTIQLFTLLWPI NKQLFRKINCLSYCISSQLVM LLEWWSGTECTIFTDPRAYSS MGKENAIVLNHKFGN/DFLC GWSLSERFGLLVGSQKCIPLCL THFFGSAPPLVFLLLVIQNLQKN QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCGLFFGSI* TLKYFFPIL
28344	58712	A	28517	1	2167	
28345	58713	B	28518	65	2652	
28346	58714	A	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	A	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	1	669	
28351	58719	A	28524	1	1089	
28352	58720	A	28525	91	507	AGTASASPAPNRSLSGSEPTSS VTQENGADVQGHervVPWKKAR SRRFCPMEGTRKVPVSHGSHVP EVSMLWKACSGSFRPVEGHV RCALTASGCS*AGTASASPAP NRSLSGSEPTSSVTQENGADV QGHervVPWKKARSRRFCPMEGT FRKVPVSHGSHVPEVSMLWKAC SGSFRPVEGHSVRCALTASGCS SPSKSKATVGCRCSDFTVEEF LQKIFLQVESLDRRRPCLPLT
28353	58721	A	28526	1	1213	
28354	58722	A	28527	130	211	KPHYAAHGQPFAT*RPGETDNR ADNRQ

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28355	58723	A	28528	793	1382	NTTAAGRIVRLTSENGSHTTFR YDVLDRLIQETGDFDGRTRQRYH HDLTGKLRSEDEGLVTHWHY DEADRLTHTRVKGETAERWQY DERGWLTDISHISEGHRVAVHY RYDEKGRLTGERQTVVHPQTE ALLWQHETRHAYNAQGLANR CIPDSLPAVEWLTYGSGYLAG MKLGDTPLV**ERPADR*ASDG ASPADGSTALAA*DQTCVQRA GAGEPLYTGQPARRGMADLRQ RLPGRHETRRHTAGGVHPRPPA PGNAAQLRPL
28356	58724	A	28529	1039	1689	
28357	58725	A	28530	1	2406	
28358	58726	A	28531	1	2928	
28359	58727	A	28532	2	1271	
28360	58728	A	28533	250	929	
28361	58729	A	28534	3	273	GKLIIVIGDEDVTGFLGIG ELNKNRHPNPLVVEKDDTTINEIE DTFRQFLNRDDIGAFLRLGLCW LRNRKPDHLPPLPCA VTQCH
28362	58730	A	28535	2	415	
28363	58731	A	28536	1	690	
28364	58732	A	28537	2551	2651	
28365	58733	A	28538	2	295	
28366	58734	A	28539	1	316	CGHGGRQSWVSLR* CQEAAG MADSCPRSGGAILAFKSAPEVI RRALSAQSLRATSSSSASGAGA FCLSPSKYFPETSASSSATARYV LGWAASSGLLTSSQKMG
28367	58735	A	28540	1	400	
28368	58736	A	28541	257	516	
28369	58737	A	28542	1	590	EQIASDTHLQRVVFKNISPAD AHRNLCLALRGHKT VTYLT LQ GNDQDDMPALCEVLRHPECN LRYLGLVSCSATTQQWADLSL ALEVNQSLTCVNLSDNELLG*G C*YAVHN/S*DTPSAFLQRVVV GKTGHLTEANLQGTLLLCWVF SRELTHLCLAKNPVNTGVKYL CEGLRYPECKLQTLVLWNCDDT
28370	58738	A	28543	1	2633	
28371	58739	A	28545	127	2030	
28372	58740	A	28546	1	3066	
28373	58741	A	28547	259	3222	
28374	58742	B	28548	1	2640	

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28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADQRLIF AKSWPRASRYQQGHQDLFILRS DLPSQVVQTQNISSCRNRC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QK\SDGTLQEHDGICEIHVAKY AEIFGLTSAEPNRFQTQRLSETK EITNPYAMRLYESLCQYRKPDG SGIVSLKIDWIIERYQLPQSYQR TSPCCCHMKKDVFASTMISS SRVSNNTSKTTIKNQCQKDDS RRSLLVKNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGVVR RCLQQQCEQTVRILHAKVAQK SYGNEKRLIIRPTIRVGPWSQTN NQTDSTSGTVVQSDYQTDSTS GTVVRTNNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	B	28551	1	1954	

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28378	58746	A	28552	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAFA KENNQKAYKETYGVSHTHRD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGPS KDADDTSIYMFYQKVGDNIDS WKNAGRNVFKDSKDFDANDPIL KDQTQEWGSAFTTSDGKIRLF YTDYSGKHGKQSLTTAQVNV SKSDDTLKINGVEDHKTFIDGD GKTYQNVQFIDEQNYTGDPL EAETA VINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAESKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPMYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRT PDFRRRFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIIKAWIERY QPPQSYQRMPPDFRRRFLQSRPA CMHDWLCAEALWSIQTASYL VTMQVNLTSLSSDTRDLSSVS NSGWVSSGSLVRFNTIKTSSEGEI KRTVPRLPDPDDPRSAIAEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLI.PKAVHLA
28379	58747	A	28553	2372	3570	EALLPGDQDSQSGKGVAAAREV WFLPSSFAPVLLRLVGNHHVG DNSIDSWKNAGR/VFKDSKDFD ANDPILKDQTQEWGSAFTTSD GKIRLFYTDYSGKHGKQSLTT AQVNVSKSDDTLKINGVEDHK TIFDGDGKTYQNVQFIDEQNY TSGDNHTRLRPHYVEDKGHKY LVFEANTGTENG YQGEESLFNK AYYGGGTNFRKESQKLQSSA KKRDAELANGALGIELNNDYT LKKVMKPLITSNTVTDEI
28380	58748	B	28554	1	2232	
28381	58749	B	28555	200	2602	
28382	58750	B	28556	1	3198	
28383	58751	A	28557	1	2169	
28384	58752	A	28558	1	2259	
28385	58753	A	28559	1	2418	
28386	58754	B	28560	1	1974	

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28387	58755	A	28561	3	2077	
28388	58756	A	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETVGS HITRHDMLQIPKQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDSIYMFYQKVGD NSIDSWKNAGR VFKDS DKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKT FDGDGKTYQNVQQFIDEGNEGI LPISPEPIKQDFRLLG
28389	58757	A	28563	610	2303	SLPNLDNA AICSSSSPTRTR*SL SEGATQAFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDSIYMFY QKVGDNISIDSWKNAGR VFKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTA QVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHLLRDPHYVEDK GHKYRGPLESPSTHQEFNPTS CVSSLGTLQGFPAWLAALAH VHPLKHKSGGSNRLSAAIWGIK RKPARVCPGTGIHASSQIQGEW RTECAVGP KAKAKATAGWRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQTY ESIVDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEVDVRI LLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVKGQIR MRTVFEQAIDQRSSTGAWRNA LSIWEPCNEIFDRILKIPRWEIR
28390	58758	A	28564	1	2079	
28391	58759	A	28565	1	774	

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28392	58760	A	28566	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDDTSIYMFFRK GAIFRVHKHAVNPMSPKCRPPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKETYPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKADDDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYSNDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFDTSRGSKMTIDGINSNDI YMLGYVNSLTGPYKPLNTTG LVLQMGGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ MNNASTMSKRTSAGCHCWQG
28393	58761	A	28567	1	3987	

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28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNAAGR/VFKDSD KFDANDPILKQDTQEWGSGATF TSDGKIRLPHYTGSLSNKKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNAAGR/VFKDSD KFDANDPILKQDTQEWGSGATF TSDGKIRLPHYTDSYSGKHGKQS LTTAQVNVKSDDTLKINGVED HKTIFDGDGKTYQNVQGFIDE NYTSGDNHTLRDPHYVEDKGH KYL/VFEANTGTEHPQPQ/ERP RTQSFSAFAERECIPNVPADT KLSKIKTLRLATSIAIYLMDDL AKDDQNGEAEAFKAEIKKTDV KEEKRRKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAAPPPTHMEGFEL FHL.PDLCSPSQDAQTITGRQM PDHSPRPSHRVPQAKGNNVVIT SYMTRNGFFEDKKATFAPFLM NIKNKTSVVKNISILEQQLTV
28395	58763	A	28569	2	1778	
28396	58764	A	28570	1099	2224	DGQQLIALHRLALRELQQA VHAGLPQQA KILFDGGSE/TRQNPL QQLVHMG LPRPLDKKNFQEP
28397	58765	B	28571	1	1938	
28398	58766	A	28572	1	2367	
28399	58767	A	28573	4659	13369	TVFRPFHVGVHLLIVDSCSKL EQHSTLSRAILLIYKGC FRFRNHQTFGSPAGANQR GPLAATLSGGEGQSA VARLTGEKKNHPG AQYANRLSPRVGRF INAAGTTGFP TKRAVSATQLMD FADFGTTIKQDFR LGGTSVDRLLQL SQGQAVKGNQLLP VSVVKRKTTL APNTQTASPRAL ADSLMQLAR QVSRL ESGQGGEDSPN RFFDGG RKKQIRTVRQFID EGNNTPADT QTLRDPHYVEDKG HKY
28400	58768	A	28574	6803	8521	
28401	58769	B	28575	2010	17745	
28402	58770	A	28576	1	1060	

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28403	58771	A	28577	1	3585	
28404	58772	A	28578	44	317	LKALLLTQSLFGGLLTQTRMKF GAVTRIGDLPWEINPLSSCSLL HEKDPPTTSGPQTHQPKHELTN FKSGCSPCRAKSQFFLSLCSST
28405	58773	A	28579	98	617	KALLLTQSLFGGLFTTRTRMKFG AVTQIGDLPWEINPLSSCSLLR EKDPPTTSGPQTHQPKHELTNF KSARFKKIKACYHSPATAWPFK AYKLSLQFPHTCPKTRQALQV SSGSVPYQPNCFAYPPHGAKPI YSPILNTSLHNPLFCSGSQTCFL YYSFAPFIPASLRFHLD
28406	58774	A	28580	1	1500	
28407	58775	A	28581	42	257	
28408	58776	A	28582	3	425	KTGKYD/AVIALGTVIRGGTAH FEYVAGGAS/NTLAHVA/QDSEI PGAFGVLT/LKA*TNDRAGTKL HGGWGGKCLTACRSALWADL QIRPYDHKNRGSNVHNRVPAS GAAAMAIHCLECGWAPLAAGD NVGKVCVPDAGLLPA
28409	58777	A	28583	327	1512	SYWTIHQVSLINHSYLPGGIS SLKKMAGRNSERKTVLVKSSF QEVNRGTEALALWENGDFEAP VLTFTTALLPEGATQAFGKENT QKASKERYGSLNITRNMLQIL NKQQTEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNIDSWKNA GRVFKDSDKFDANDPILKDQQT EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHILRDP HYVEDKGHKYLVEANTGTEN GYGGGVNADVGDVVVRLPVW HRRGGEAVFMQVSRQLRLRHL HGVAVD RDHHAHDRRRHVA GDRSGSVRL
28410	58778	A	28584	845	966	
28411	58779	A	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIACTGHIDP VTRFRPRAR*GSSHRNKAVDTR RH
28412	58780	A	28586	464	847	

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28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ GIKRPDALPGPLLA*PDNLRC CPRSGTAAGSIHQDARLRYSVW RWGLLDRLAAVICRQSTHSRCR RKQRRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	A	28589	404	733	
28416	58784	A	28590	2	246	
28417	58785	A	28591	466	861	
28418	58786	A	28592	122	926	
28419	58787	A	28593	171	733	
28420	58788	A	28594	1	774	
28421	58789	A	28595	1	1575	
28422	58790	A	28596	1	105	SVKLGWNGVSTYVPFLCTICSV SFFQENLHLTTCRA*PSIPPPAA RRSPKKCS*KLRLP*LSGSSS YNL
28423	58791	A	28597	237	461	
28424	58792	A	28598	1	1341	
28425	58793	A	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGLFPRKSSSRHRGKVKSF KDDPSKPVHLTAFLGYKAGMT HIVREVDPRPGSKVNNKEVVEA VTIVETPPMVVGVIGYVETPR GLRTFKTVFAEHISDE/CRLLPL RQKKAHLMEIHVNGGTVAEKL DWARELEQQVPVNPVFGQDE
28427	58795	A	28601	1	1251	
28428	58796	A	28602	37	1307	EFGFDGVMSHRKFSAPRHGSLG FLPRKSSSRHRGKVKSPKDDP SKPVHLTAFLGYKAGMTHIVRE VDR/PGIHRCNKKERWWRAVT HCIRPPMVVGGHVLGYVETVP RGLRTFKTVFAEHISDECKRRF YKNWHKA/KKKAFTKYCKKRQ DEDGKKQLEKDFSSMKK/YCQ VNRVIAHTQ/MRLPL/RQKKA HLMETQVINGGTVA/EKLDWA REKLE/QQ/VPVNP/QVFGQDEM DVIGGDQRAKGFQGVTR/WPT N*L/PFKA/HGL/SRVACFGAW HPARVAFSVARAGQKGYHHRT EINKKIYKIGQGYLIKDGKLIK NASTDYDLSDKSINPLGGFVHY GEVTNDFVMLKGCVVGTKKR VLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	A	28603	1	2133	
28430	58798	A	28604	3	245	

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28431	58799	A	28605	1	1824	
28432	58800	A	28606	1	1035	
28433	58801	A	28607	1	496	
28434	58802	A	28608	1568	1793	
28435	58803	A	28609	1	1392	
28436	58804	A	28610	1	1389	
28437	58805	C	28611	104	253	
28438	58806	A	28612	114	469	VSRPTYAKVFVTSKTAPQKVFPTA WCSA/TGHETALSA/TQVPIQWIATAPNSPAPSPDPRRQSWVSQIPSSATSPNFTM*EPRTIQEVTEPHDSRPAIPSAVPRRESCTGRPHLPATTP
28439	58807	A	28613	3	2196	
28440	58808	A	28614	237	348	NPVN*SQTT*TSE
28441	58809	A	28615	950	1094	
28442	58810	A	28616	146	822	LGFLRLRLSEMPRKQGVYRTRIRWKFEDGLSNVLI/PIEQINHMMDVFGSGSERATCLARGGYINSLARCQNLVNRDL/DHLSLPQDSTLVHYIDIVLHGFSEEKGGQVAQSADL/DEGLLKIPGDTFGPEADKDFLHKDLSTEIVGQSYNTHHMAQDSIPWNPSPQEPQVREHEACHHLGSGSPSPWELCEQGPVTESFQVLVTSGLDKENMAYMHCGIICSNNKKG
28443	58811	A	28617	1	1791	
28444	58812	A	28618	244	416	
28445	58813	A	28619	2	1520	
28446	58814	A	28620	95	421	PVTSTSTKRTPTQKPHPKVISLKDQIHV/DKSMRMRKNQCKNV ESKSNQNSSPHDHNSP/SARAENWTEYESDKLTEVGRGWVINSSELKEHVLTHCKEAQNLHN
28447	58815	C	28621	46	174	
28448	58816	A	28622	425	1291	
28449	58817	A	28623	1	1410	
28450	58818	A	28624	14	348	GLFPNKPFSVLEIRTWAHLSGRHHSACHTSCAWPQVACLPLATHPSCCTCFCSLQAPGRPGQSPLSPRRACGPEDLPPPPYV*DLAPSLGPSLGLPLMSQSQPRRTPLRG
28451	58819	A	28625	96	295	PWKPHPAWRQRWELCHPPFP/I RPLTAALREQGLLGRSTTVFTLMAREPPQAAADSLCIVQME A

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28452	58820	A	28626	105	389	CQFAHGTASSPRVCLRHRCRS WQKAWAVVCTFCSLQAPGRP GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQPRRT PPLAWGS
28453	58821	A	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	A	28629	301	987	
28456	58824	A	28630	239	384	VLPAGAAQAARSSDTRP*PEPH FSVESVFRWIFSFAQLNNFFQARF
28457	58825	A	28631	1	1054	
28458	58826	C	28632	243	392	
28459	58827	A	28633	1	1104	
28460	58828	A	28634	194	863	YLLFVKNMSSLEISSCSFLETK LPLSPPLVEDSAFEPSPKDMDE VEEKSKDVINFIAEKLSDVEVS QLVISPLCGAIS/LNWKGLTENT FEGKKVISLIEYAYLPMANE VRKICSDIRQKWPVKHIAVFHR LGLVPVSEAKP*SFAVSSAHRA AISLKLLSYC/AEDTFKRPRVPI WKKIEIYESSTWKGKNECFW ASNTLITYVFRACNLNFVKLL
28461	58829	A	28635	3	338	SSPPTAPAKLRIVPLVGGLPAR WCLSVCAQCQPDTRVHVFHLHW WCSSLCPAPVCLSLCRGL*GHF PPDSEDQSSPNCSGYTLEEKYKL LRSQTIPSCNGKFPCCPRRAYDG
28462	58830	A	28636	405	800	
28463	58831	A	28637	265	539	
28464	58832	A	28638	3	1116	
28465	58833	A	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	A	28641	563	594	
28467	58835	A	28642	245	580	
28468	58836	B	28643	1	435	
28469	58837	A	28644	673	1012	QPQVSFSSEYAIHMRCPHSHKIS SLYYFNCFRY*DCYCHVIFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLTGA WVRAWKATSTSVVHLTKWVL
28470	58838	A	28645	1171	1328	MVIGGTKNERKHIDSEPLFPSP NSSARGRAISST*ALVPGVRGF LSSIPLSLTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGSVDLSHGLHLGLHL KNDL*FYFNSGIDKPEIAKLSG CSFGGTFLLIWG
28472	58840	C	28647	199	309	

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28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLPLKLL L*SYKSFFKWSRCS
28474	58842	B	28649	107	264	
28475	58843	A	28650	301	470	EIQVLVLSGGGYSHAVLMIVS SHKI**FYKGLFPTFALHFSLLP CEEGCICFPF
28476	58844	A	28651	2	263	WEKKDTEWRKKVILSSV*LRL VIF**PFSMLMLFSPVWR*ARSH ESHLAITHLWALYF*PPCQICFL *DRGHQATDGLTNGTPSELN
28477	58845	A	28652	63	191	DLPWTPGPAC*PMLQC**GGAN IYARRQGADAAGDQGSCL
28478	58846	A	28653	1	554	MPTYCPGASLLITYKTPKELLS IYVSTIRKSRERRRRLGAR NFRSEEQIYDQWRDLQVGKFFP FPRPRENYHFGSEHVGSFSLDK CCNEKLYEVIDLHLKKFLNTE TSLSVKCEVSRCWVTLNLLLPY H/VLFQI*LSWRERQNSCKTTN GSSNGAPDAVHN*NLLWSLGP AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWPALPEN GYMKQFCVSGLGVLFHGCVFL CWHHCCFVL*VWSLGSPPSRG LHLVKAFFLCYPRSNCFLLNWG IVGVQRLRFQEGCLWCH
28480	58848	B	28655	1	400	
28481	58849	B	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTALPVSSQPSLHTA EVQGCAGVILTQGPQCPVAF SKQLDLTVLGSPLHAVAASAA LILLEALKITNYAQLTYSSHNF QNLFSFSLTHLSAPRLQLYS LFVESPTITLPGPDFNLASHILD TTPDDDCMSLIYLTFTPFPHISF FSVPHVDHIIWFTDGSSTRPDRH SPAKAGYAESSTSIIEATLPPS TTSQQAEIALTRAFTLAKGLH VNIYTDSKYAFHILHHHVIWA ERGLT/IARVLHH*CLFNKNSS QGCFSTKGSWSHTLQGPCKGV RSHYSRKCLC
28483	58851	A	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	A	28661	1	704	
28487	58855	A	28662	41	275	
28488	58856	A	28663	159	1504	
28489	58857	A	28664	275	552	
28490	58858	A	28665	178	619	
28491	58859	A	28666	3	369	

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28492	58860	A	28667	1	340	
28493	58861	A	28668	516	734	WTGDWRRRTCDRENQHVSGAA RTAFIPTNGAISPGINYSFGH*Y* DCHLPQA*P*LCRAAGQNRCH VARTCLG
28494	58862	A	28669	1	1163	MHTHARETCLALGKPADDATL TAAIEAVGLENAARVCLKLYPFE MSGGMLQRMAMIAMVLCESPF IIADEPTTDL DVVAQARILDLLE SIMQKQAPGMLLVTHDMDKW GRIIADVESQYRYQTNPKEIFAG GDVARGADLVVTAMAEGRHA AQGIIDWGLDVKLGAELEERR KVLQVKTENLQAERNRSRKSIG QAKARGEDIEPLRLVKNLGE LDAAKAELDALQAEIRDIALTIP NLPADEVVPVGKDENDNVESVR WGTPREFDFEVRDHVTLGEMH SGLDFAAA VKLTGSRFVVMKG QIARMHRALSQFMLDLHTEQH GYSENYVPLYVNQDTLYGVGL YPLGALASGW/WALASGWLPK RRERKD/GDTGAHGVPGRSRKP RIARKVRGT
28495	58863	B	28670	1	4770	
28496	58864	A	28671	1069	1398	VIGAQPVLRIIRKQARRQINRL TLILLHYCLTTKLKNVKGPIV AAFYFLPGAG*IHPAGCHGTQL *SFGKMRVQYTRVTLSQQASG KISAYLIDLKGKLLKLIHCGVH
28497	58865	A	28672	4246	4453	
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	A	28675	1085	1246	
28501	58869	A	28676	1	1254	
28502	58870	A	28677	1	2175	
28503	58871	A	28678	340	994	
28504	58872	A	28679	37	261	TITPAGRRMHCKGACMKPLLD VLMILDAVRELE*TITPAGRRM HCKGACMKPLLDVLMILDAVR ELEKQAIKLHEGWENELVIGVD DTFPFSLAPLIEAFYQHHSVTR
28505	58873	A	28680	410	896	WAWAASAVQPRSIWQ/GAGVG NLTLDFDTVSLNLQRQTLHS DATVGGPKVESARDAPHIAITP VNALLDDAELALIAEHDVL D/WYG*RCGT*STERQR*RG* RSAPAMTAHDRDAJASSETCA RSRWSVEYASPCAPPDSRSKR RSASNSAASHVF
28506	58874	B	28681	1	2298	

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28507	58875	A	28682	1915	5313	
28508	58876	A	28683	1	4221	
28509	58877	A	28684	1	1007	MAALQMVNGQKQWVSSNQKY WLVYKTTDPRLRPFGVQPM CPFNGRPFWIHKNPMPGVHWAV ATGLALIPVIGAEFGWFVFGG ETYMMAWNVSGLGTGAIQST FNVTLWSFIGVESASVAGVVK NPKRNVPIATIGGVLIAAVCYV LSTTAIMGMPNAAALRVASPF GDAARMALGDTAGAIVSFCAA AGCLGSLGGWTLLAGQTKAAA ADDGLFPPIFARVKNKAGTPVA GLIIVGILMTIFQLSSISPATKE FGLVSSSVIFTLVPYLYTCAAL LLLGHGHFGKARPAYLAVTTIA FLYCIWAVYITHIDACVVVYIA GYRAAKLTCA
28510	58878	A	28685	867	1681	
28511	58879	A	28686	865	1290	RWWENLRFKRNPARAQKMLV PERFG*SAYPNGFAGTWRLDKL PIAQIHAHMIGYLAADVMEKQ QISPAQVVRVHRNRCPIAIVHLI GRARELSLKD.VVGKKNQPATV KAFIRPTAPDVLAKLLQAV NRHFGNVMQMVA
28512	58880	A	28687	1	709	
28513	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPQT AFIQVGPRVHAHLQPRAPL*A GEVWKPRLVGRSHWASRPSA LQKGEPGSPSWENACVPQAPH RLLHQKAF
28514	58882	A	28689	3	227	NSQDFPACGGGLCHAEELRTAA GLVHQHVRHPGHTSVAAEKLCH GDVEGDGCNGPASD/PGYI*GQ AAAPAPLPDLL
28515	58883	A	28690	1227	1719	
28516	58884	A	28691	1	1701	
28517	58885	A	28692	15	3298	
28518	58886	A	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR AVWRYQTDIAANLE*RRLPSCA GKSDWSSGDSEKAKTAAHTIY RDAGRRVRGYRQL
28519	58887	A	28694	1	370	

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28520	58888	A	28695	1	910	MDKERIIQEFVPGKQVTLAHLI AHPGEELAKKIGVPDAGAIGIM TLTPGETAMIAAGDLALKAADV HIGFLDRFSGALVIYSGNYTL ARKTQAVEFNDKGDIDTPGEYF NHPRWYHALITTLQDQDMLSP LIWGFERNYKDVQVIKATPHKIV ILMGILLSPSVFATDINVEFTAT VKATTCTNITLTGNNVTNDGNN NYTLRIPKMGDLKIANKTTESQ ADFKLV\MGAAVASVGLIPL* PEMHQAHLISLLYRSLVIHLRR QVISVWVSKNGLLMMPLSLNL TVRKRYAGAQTCSPIRVLK
28521	58889	A	28696	605	2021	
28522	58890	A	28697	2256	2336	CIKCCARRIAREPGYLF**RCK YPG
28523	58891	A	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN V*SWIKSS/MQMGQKMGVKISD EQLDQAIAIANAKQNNMTLDQM RSRLAYDGLNYNTYRNQIRKE MIIEVRNNEVRRRITILPQEVES LAQQVGNQNDASTELNLSHILI PLPENPTSDQVNEAESQARAIV DQARNGADFGKLAIAHSADQQ ALNGGQMGWGRIHASLPGIFA QALSTAKKGDIVGPISGGRFD GTVEVKDGLHIVNGKKIRVTAE RDPANLKWDEVGVDVVAEAT GLFLTDEETARKHITADTPAALR WLEENQLEDGHECLLRVVISSD GRSRGFINGTAVPLSQLRETSTT TGARRVIRAIRINSSDASTIPTL MAITISNNTVSDMHSSMTMMS TRIRTLITTYNGDLRMIRQRKL CKTAIARTYGNDDTFHPGMRH QRMHIRVFNAPILDDQPVVTLN IYPKADESSSLKASRGTRGAAY RPARQNLYSASSGKKDENPVIE FKNVSKHFGPTQVLHNIDLNIA QGEVVVHIGPSGSGKSTLLRCIN KLEEFITSGDLIVDGLKVNDPKV DERLIRQEAQMVVFQGFYLFPHL TALENVMFGPLRVRGANKEEA EKLAARELLAKVGLAERAHHP SELSGGQQQRVAIARTLAVKH KMMLFDETTDFDPVLVHEVL KVIHEFAEKGITNDSL TENPAKT QGEQGCLQSQERGPREPTPRH
28524	58892	A	28699	1	2307	
28525	58893	A	28700	3	976	

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28526	58894	A	28701	2	136	YLSAV*FCSPGQPPSALLVCGR RGYWCLWPLSSCHLLRLRLCVS
28527	58895	A	28702	1	608	
28528	58896	A	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	A	28705	1	1184	
28531	58899	A	28706	478	627	
28532	58900	A	28707	33	1072	
28533	58901	A	28708	35	516	RVVEFADEGQGPAALSLWSGS SPETLKLHWPVHQ*IRFSSWK TFRIRSRDFWADRLMRTLRLNRF LSKWDHL*QTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRDDGLAGLRGN SGAQGGDA
28534	58902	A	28709	1	777	
28535	58903	A	28710	531	704	
28536	58904	A	28711	294	617	
28537	58905	A	28712	804	1020	HFLSGGRRQRPPRWITVA*SPR* PRCRCWGS*RPGRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRQRPPRWITVA*SP R*PRCRCWGS*RPGRGALPV VRKQPGDPKTPLASCEPQLNPV PEPAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSGLRLLGR PSHEGPWLKGTSCRS GTTCRDR PWV
28539	58907	A	28714	2	1580	
28540	58908	A	28715	286	352	
28541	58909	A	28716	1	531	
28542	58910	A	28717	1	1440	
28543	58911	A	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLQLVEVLPE ANRQLRQSGADGGQQA VF*F HRFLASVHQHKAASAPPYLFR IKCPVPLRAKPAALLIDNRLYG
28544	58912	A	28719	1	3534	
28545	58913	A	28720	1846	2121	
28546	58914	A	28721	176	462	TSRHSVYISDTCLKPRKSSKPTF CGCDLSFSPICHP/HGLSDVALI VQQLRQG*PLQPARLPVHWR HQNAVVDGVLSENGGAGWG RAWLRIRRS
28547	58915	A	28722	225	3465	
28548	58916	A	28723	937	1770	
28549	58917	A	28724	142	484	

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28550	58918	A	28725	1	1521	MIPITWPKFAELHPFCPEQAEG YQQMIAQLADWLVKLTGYDA VCMQPNSGAQGEYAGLLAIRH YHESRNEGHRDCLIPASAHGT NPASAHMAGMQVVVVACDKN GNIDLTDLRAKAEQAGDNLSI MVTYPSTHGVYEETIREVEVV HQFGGQVYLDGANMNAQRDD MAGKPGPLTVRKMGRSRTVTR AL*/ASVWIGFDDHRRNLGHTT ASGAIKDQISGYEGGAKSAQPA WDAYMKAVLEGVPEQPLTPPP GIVTVNIDRSTGQLANGGNSRE EYFIEVNEIVNPNATLDWQLA LRQAAGKTDLRDMLQMLLDF LPEVRNKVEEQLVGENPEGLV DLIHLKHGSCGYSVPRMKNL CQLIEQQLRSGTKEEDLEPILLE LLEDMDNVAREASKILGGHDN GGNALLHKALPPGNVGVKAWM APIPPPPQPGKSVTICWKPASS ENRSNLLIEFLRELISNASDAAD KLRFRLSNPDLYEGDGLRVR VDEVLSPASVPYS
28551	58919	A	28726	1	1279	
28552	58920	A	28727	3	762	
28553	58921	A	28728	1	1472	MTQDELKKA V GWAALQYVQP GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFIDLNEVDLSLGIYVDGADEIW QTKCAQRCQSPCKTLGAQPEN PDLQSISRFPQDERRISNCSSGK AANPVLYWSKJEEKIASEPASIIY SPMTLKD FSKFVKDEIGFSYTG YSRSGGTASHGSPKSWAIGSL GRFGNEYSGWFDLQLKQRYVN ENGKRVDAVVMMDGNVGGQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFVVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWKVGP GKIDIALVR EDVDDYDRSLQNKQINTNTID LRYKDIPLWDKATLMPRIPTQR YGLAKA/SLEAD/VRY/MANAM GPEGVRVNAISAGQTRTLAAPG IK/DSRK/MLAHCEPVTPIRRTVT IEDVGNSSAFLCSDLSAGISGEV VHVDGGFSIAAMNERDPFTDL HRYRMNLMNMNYGAQRNM

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28554	58922	A	28729	2	419	RPRPRPHMLQGTTHQRHLHA GPGVARRRWGGMARRAAGRR PRLRLCIFSRSQLGLRLRFLSST VNEGQDVKTVA\RSGHFCGGLS SFSFSSSFSSGKKRPSNPGSMR LGSPSPGAGRAGGIVTVAC*AR LSTCNTKQ
28555	58923	A	28730	725	2804	
28556	58924	A	28731	661	1218	DVREGDRDPFMIVHSCVFVDF AKTMHDGA/SVSLRGNLISHKG EDRY/VFRDKSGEINVVIPAA/V FDGREVQPDQMINISGIADKLP VIAPTNATSKLKLASQPEDDSEI YDGCNGAQPGDYWFAAFVSG MFSRWLAKTILSRHILSVTIRSC KNGEWLAVGGAENGAYSDSR VAVMLLLSAWGLFDF
28557	58925	A	28732	1	624	
28558	58926	A	28733	1	1281	
28559	58927	A	28734	114	266	
28560	58928	A	28735	1487	1570	
28561	58929	A	28736	1	3402	
28562	58930	A	28737	1	2466	
28563	58931	A	28738	372	647	SGWSWNTKFPTGGFRWPAQPG TELESSQPR*LVMPATTSPFRAL DVCEYLPACVAVISGCHPSRFA RSYVSAPD*QNVQLTYPHIVLN RHL
28564	58932	A	28739	1	2235	
28565	58933	A	28740	3	293	
28566	58934	A	28741	737	963	
28567	58935	A	28742	3	282	RRLRASGCIDKLPSG**YARPAR *DPAPGFR*STPVRKCDQTRSPA MKVIAAADRKLCWGAICPLSA KPPAGRAPNAPAPASPNRPMPT PSL
28568	58936	A	28743	2	289	
28569	58937	A	28744	1	1662	
28570	58938	A	28745	421	2634	
28571	58939	A	28746	134	954	
28572	58940	A	28747	1036	1383	
28573	58941	A	28748	2	589	
28574	58942	A	28749	1	801	
28575	58943	B	28750	14	499	
28576	58944	A	28751	3	916	
28577	58945	A	28752	3	589	
28578	58946	A	28753	1	1675	
28579	58947	A	28754	1	522	

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28580	58948	A	28755	1229	1660	LMVSGFLTSPKDHRIIVAKPEQ FWKLQVMFMAIVISLPTIGER FSPFLLLKSLIPSRGCTDIFISG LTARPEFSQSRMVLIAASTITSL MCAGSFLPIRPLASICSLSNATTS **LPSSGRDSSRRKRRQTATCSP RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF NSIWSCASAILGNLIGITGSPPL ALCRTLCCLTYPI*CPRDAKALR RPRECVIRHD
28582	58950	A	28757	1	850	MPVMFLASLSGKHQGHFFPKG ERGFKIKERGTVATEDRRSGD STFYAIQPTRRQKRVYGLALLL QLHRRRQNLNIDSVSSVGLAAL VTAFIGVDFFFANGEQTYSQPLW TWMVSGDFNIGFNLVLDGLSLT MLSVVTEGYSR*EHRPTSPQPR YISSRLSASTRTTM/PGDEQVGV SEEARVALSDHREHGQRQAVQ HQVKTDVKVAYRHRPRPQRLAV CLLAVSEEINADKGGYQRRQA HRAV
28583	58951	A	28758	20	282	
28584	58952	A	28759	38	966	RDGLESRGVCSLRTAFQRSS EAFSTDQAELQNRASNRPAR IGHAHLVIFPVQSSWM*KLAS PRNNLVIPQEKALKEYIKGNLV MSLAAAPLNR*GLL/IWVNDND GGCKGACDRVPHQNVTAALNLR DQCINGECYDEVLFHGLEEYIN NLQGDGVIVLHTIGSHGPTYYN RYPPQFRKFTPTCDTNEIQTCTK EQLVNTYDNTLVYVDYIVDKAI NLKEHQDKFTTSLVYLSDHGE SLGENGIYHLGLPYAIAPDSQK QVPMLLWLSDEYQKRYQVDQ NCLQKQAQTKQKCVLLIFAKQ
28585	58953	A	28760	1120	1335	
28586	58954	A	28761	846	1245	TVRKRGTRHPHGSRRTLSPLR HSSDRCNRTSADRSTGPRL/A QPRYISSRLSASTRTTMPVTES MVSDRPSSTRLKPMLKSPTDIH VHSGWLVCSPVAKKSTPMKA GTTAGRPTEPTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	A	28763	188	322	

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28589	58957	A	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE TTNRPRKVKIRHPVASFFHLFFR VSAIIVCLLCELLSSSFTCMSKK WLAIVVIVGVVLQGANLYGYLR CKGQEVRETFAEPSLQATQMK LKRARLADDLNEKIAQRPGPM ELVEKNILPVDSSVKEAIIIGKTL KIYYLGAPAEAAATKEDERTTSG PGHHATNYHFLKFDLYLSWL HFVHKDAILSGHPLVRLSTRV LRGPNDVFHGVSSVDSVLAIFV LAEPMGSLASLEN
28590	58958	A	28765	1	3219	
28591	58959	A	28766	3	245	
28592	58960	A	28767	2	1193	CANQLRDCLVIPITIGLVRV AGANGDRLGQPTVGADVRLSR CRKVMPSRSVEMGLVPSSSVIV TVLPLIGFVLLAFSGRGRWSENV SAIVGVGSVGLAALVTAFIGVD FFANGEQTSQPLWTWMSVGD FNIGFNLVDGLSLTMLS VVTG VGFIIHMYASWYMRGEGYSR FFAYTNLFIASMVVLVLADNLL LMYLGWEGVGLCSYLLIGFYY TDPKNGAAAMKAFVTVRVGD VFLAFALFILYNELGTLNFRM VELAPAHFADGNMMLMWATL MLLGGAVGKSAQLPLQTLWAD AMAGPTPVSAIHAATMVTAG VYLIARTHGLFLMTPEVLHLVG IVGAVTLLLAGFAAL*Q*K*HP RHPKHRNAG**TRVLQRGAGC AGAIRVTDHFRG
28593	58961	A	28768	3	2191	
28594	58962	B	28769	1	2263	
28595	58963	A	28770	1089	4965	
28596	58964	A	28771	41	249	
28597	58965	A	28772	533	709	VSFLIVSSSLIALWSEKQFVIV LLHLLRSALLPTMWSILE*VVC GAENNVYSVDLG
28598	58966	A	28773	2714	3599	LGSQWH*IIYKLPWAVWFSQY
28599	58967	A	28774	45	188	GKVOCHRGLIHVNWLPPVKKF *LRQKGKPTSSSQETPKTEPGR LKP
28600	58968	A	28775	722	856	GNDLCPKTIRTGDAWCVPGT RKSAWK*GKISGSLFPLVRDG

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28601	58969	A	28776	474	1338	PANQKKPRTRWIHSRLPEVRR GAGTIPSETIPNNRKGNNP*LIL *GQHHPDTKTWQRJHNKK*KFQ ANIPDEH*CENPQ*NGKPNPÆ HSKKLIHHNQVGFISGMQGW NICKSINIHHNRTNDKNHMIISI DAEKAFDKIQHPFMLKALNKL GIDGTHLKIIAIFDKPTANIILN GQKLEAFLKTDTRQGCPPLSPL LFNVVLEVLARAJRQEKEITGIQ IGKEEAPQKQRLFCRYHGGK RAPQLLITHLEEDDEWDIIRYY NVMSEEEIKRMKEIVKPKII
28602	58970	A	28777	2289	3225	LTNQNKSRTRWIHSRLPEVQR GAGTVSSETIPNNRKRWTTP*L L*GQHHPDTKTWHRHNKKRK QANIPDERQCKNPQ*NTSKPNP AAHQKAYP**PSQLHPWDARL VQHMOTNKHNP SHKQNVHDKN HMIISRDAEKSFNKIQQPFMLKT LNKLGISGTYLKIVKMHTMSSS HLFYALCLLFTSSATAGPETL CGAELVDALQFVCGDRGFYFM EQCTMAVSIRGRELLGPSEQEM LHKESGKQRQKANTIPVTSKIV HLALYATLLLFVMEQFLGESHK SREIFSFEQQISELGKESMKFSEE KEKE
28603	58971	A	28778	1177	1272	
28604	58972	A	28779	480	766	SSEIQHWFGQGPWRSCRVSGR RHEASTVLPLCFLLPNSSSMQ LG*NRSMPLHVSESSRTLVL*EV TKHQVSSNFKMRDKDRSGRAS SLRKHRR
28605	58973	A	28780	1	1344	

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28606	58974	A	28781	971	2314	PTNQKKSRTRWIHSRLPEVQG GAGTIPSETIPINRKRNP.LIL* GQHHPDTKAWQRHNKKEEL* TNSPDEH*CKNPQ*NTGKPNPEH IKKLIHHDQVGFIPGMQGWENI HKSINVIQHINRTKDKNHMHSI DAEKAFDKIQPFMLKTLNKL GIDGTYLKIIIRAIYDKPTASILN GQKLEAFPLKTGTROGCSSLF LFNVVLEVLARAVRQEKEIEGI QLGKDEVKLSLFADNMIVYVE NPIISAQNLKLSNFSKVSGYKI NVQKSQAFLYTNNRQTKSQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKTLSQKNKT GGIMLPDFKLYYKPTVTKTKW YWYQNRDIDQWNRIEPPEIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHH* GSIPSRSLLVATTPTRGVTAALAE
28608	58976	A	28783	1	1938	
28609	58977	A	28784	1389	1499	
28610	58978	A	28785	1	351	
28611	58979	A	28786	1	329	KNLDEKLLPASSSSCRIWATSP VHHLWQVLKKILF/GLEPYEIST LFEQRQAM/LQSIKEGVVAVD RGEVTLINDAAQELLYNHNFI RSRLPVFVLASACGSGTRRRRA
28612	58980	A	28787	1	419	VRPGHLLDIDDTDMPSLRYSDP EAQRIGQPFKGDDILKALNGEE NVAINRGFLAQLRVFTPIYDE NHKQIGVVAIGLELSRVTTQQN DSRWSIIWSVLFGLMGLVGLIGTCI LVKVLLG/IIFG*TYKSQLEFRQ QAMGRL

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28613	58981	A	28788	1	1795	MWII SCVMKRTAMNCVLWRK RRRKVCASIFGKNRANQKRD NVELFDARCPNLNDAADTVRY LPVLTVQLLDKQPRLTVLKKIL FGLPEYEISTLFEQRQAMLQSIK EGVVAVDDRGEVTLINDAAQE LLNYRKSQDDEKLSTLSHSWSQ VVDVSEVL RDGTTPRDEEITIK\ DRLLIITVPVRSNGVIIGAISTF RDKTEVRKLMQRLDGLVNYA DALRERSHEFMNKLHVILGLLH LKS YKQLEDYILKTANNYQEEI GSLLGKIKSPVIAAGFLISKINRA TDLGHTLILNSESQLPDSGTA CGQSLNVLYQRIVGERKLHTGS LMSAAGKSNPLAISGLVVLTLI WSYSWIFMKQVTSYIGAFDFTA LRCIFGALVLFIVLLRGRGMRP TPFKYTLAIALQTCGMVGLAQ WALVSGGAGKVAILS YTMPFW VVIFAALFLGERLRRGQYFAILI AAFGICTATQRNLLPCKNQPC KANQYQGTGDVNLQHLIDFRA FSGVMVAGSRQIFANEISSGAS NVGVVIFSTQDSANTFNVLNAS GGSRSVYPVMSDDMNGSSWK FSTRMQKIDPALSVTSQQLMSHV
28614	58982	A	28789	190	2058	
28615	58983	A	28790	199	293	RYPPAETELS*RLCRLLR*STTV RL*LCRPL
28616	58984	A	28791	685	1557	
28617	58985	A	28792	1	2850	
28618	58986	A	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR TATTQRHCRRMHMMTIGYQFQ PGALVR*SRANHFPGRGDVNLS SRYSNAPGRRRHQHMRRGFVA RSQ
28619	58987	A	28794	409	1305	

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28620	58988	A	28795	379	1703	LKTVLVDGVVKAELKVEGAKA VLRQAINGDLWDKAKRQPKLE PLKLSKIEATMSFTIAKGMVAQ TAGKHYPAPITAVKTIEAARF GREEALNLENKSFVPLAHTNEA RALVGIFLNDQYVKGAKAKLT KDVETPKQAAVLGAAGIMGGGI AYQSAWKGVVPMKDINDKSL TLGMTEAAKLLNKQLERGGID GLKLAGVISTIHPTLDYAGFDR VDIVVEAVVENPKVKKYPASG VFHQLYCRDVPVPMFAIYTFGP QIVGLLGLGVGKNAALGNVVIS LFFMLGCIIPMLWLNTAGRRPL LIGSFAMMTLALALLGLIPDMG IWLVMFAFVYAFFSGGPGNG FNRVKEEFDHERFLVALTNYGT AMCAFEDAARYAN/LARAVWR GYWSFPVDSGKIRPHGDQIKLH EKHAV*SSVESRQRHHHLWRC SDVQILLRQCGI
28621	58989	A	28796	713	902	CRLARPSPKRCFCFSCSTTHSCI PPPLAATRWPVRRRWPRSPMCC WSRTYR\PG*AKRRYTSPA
28622	58990	B	28797	1	1521	
28623	58991	A	28798	348	599	RHFORSLSRSSDSNP*LDPTLFA SALASRQRVTESWSERHPDPLQ VRRKTEDVKTTPPFLQQSARHS VNIVLWIRGFSPDLLV
28624	58992	A	28799	582	732	
28625	58993	A	28800	1	1443	
28626	58994	A	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA SGG*TGETAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	A	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDH/K RPREALLDSLKKLQLDYIDLVL MHWVPVPAIDHYVEAWKGMIEL KQEGLIKISIGVCNFQIHHLQRLI DETGVTPTVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQG GKGVFQDKVIRDLADKYGKTP AQIVIRWHLDSGLVVPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDPDQFGG
28629	58997	A	28804	1040	1079	
28630	58998	A	28805	300	567	SAGFKKSGTRHCDVRPGACGT TLYQRR*VH*WSTVHKPETSS SKMHGQRGSLLAASLVANVI CSLIRNPLPIMPMLCAFVSLKM IKKRPRRH

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28631	58999	A	28806	167	327	KNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTDRRTN SPAYLSEL
28632	59000	A	28807	1	1197	
28633	59001	A	28808	1	4104	
28634	59002	A	28809	1	1368	
28635	59003	A	28810	82	1143	
28636	59004	A	28811	72	212	
28637	59005	A	28812	1	1078	MKDVTLVPRPDAGANTCAHIL SQLPHLQLPTLETGLINALGY APGDMQPSDSATWGVVLAELQHE GGDTFMGHQEILGTRPLPLRM PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQVAIGDNL EADLGQVYNITANLSVISFDDAI KIGRIVREQVQVGRVITFGGLLT DSQRILDAAESKEGRFIGINAPR SGAYDNGFQVVMHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ RVFAIFAVIDITQVINIQCRC QQAACGRRKQCRNQSKENQY GNITQTDITRTIAHGVVIAAMI DNPPIRKPTKKS*LWWPLFY LLAVSLFTLVNRYRVFVHGLSAS SSPLRPTPY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVEDHNG YSGNACTRLHHAGGIRQ**PNF GYSPASPSCGQVSQNSS
28639	59007	B	28814	1	2703	
28640	59008	A	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWTITTAVCV SSCRRWKPAALVRPLPPASAP GFITTSAPKPCASRNG*KSSFQR TLHVSRRHQSRTS*SPOVDTSN SSEIVNNQAPTARTGSGLRVAV LEQRVQEPLAANAPPQLRVSAI NAAS
28641	59009	B	28816	430	823	
28642	59010	A	28817	1	2667	
28643	59011	B	28818	204	2659	
28644	59012	A	28819	1	2817	
28645	59013	A	28820	1	1089	
28646	59014	A	28821	1	1891	
28647	59015	A	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRALPTEE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPYELPERRDPV SSAGALFVSRWIVERSCADKFR VFCGASGFR

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28648	59016	A	28823	1	1030	MMCMYRTASSLANQYHIDSE QARRGSQNAFDVNFEAWQLEI NHVLEAASQSQRNQYISALVF ISMIHVAAYISSALWWTRKMIV QPLAIIGSHFDSIAAGNLARPIA VYGRNEITAIFASLKTMMQALR GTVSDVRKGSQEMHIGIAEIVA GNNDLSSRTEQQAASLAQTAA SMEQLTATVGGQADNARQALG TGKNAATTAQAAAVQFIDRCQ ADFRGAYRYRSGTYFICQYLT VTVSGIDAHQRGQTDQTRILLQ LFLVQFDTHRQTLNDFDPVTGR ILRWKQLDRAAGDITGHRTDN TSTLQRQPGVTYFGGSLHGW *SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	
28650	59018	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLAFLWKKHFRFLDQVQN FYPSPLANSTMYTGNKPLAK IGYKSEDFVFPKGDQRRLLHK ALLRYHDPANWPLIRQALEAM GKKHLIGSRDCLVPAPTEEM REARRQNRNTRPALTKHTPMA TQRQTPATAKKAASQSRPVNA GAKKRPKAAELQCPLVMTSGN LSGKPPAISNEQALADLQGIAD GFLIHNRRDIVQRMDDSVVRESG EMLRRSRGFLPTGRGLRIDYKQ KMRGTRRAGCNFNQSGQGRPS LKRGEQTDIKKAKKQATGLAG ESMLQDDAFYAVITHAAGPQG ALPLTPQMLMESPSATCSA*RR TPGWAGTPTSSPAKRC*LALRI TSSGSTPSCSRHRWRKRARRSD ACHHSRFSPTVWPVTPKPKGR
28652	59020	A	28827	1	1392	
28653	59021	A	28828	1050	1154	
28654	59022	A	28829	1	2649	
28655	59023	A	28830	59	511	
28656	59024	A	28831	1	2421	
28657	59025	A	28832	4594	4770	PSTSTIHA YVSGKSRISPHTREA MINDHAKRAWLYALRRRAGR TRHRCPGRTGRQRL
28658	59026	A	28833	1	727	
28659	59027	A	28834	1	3069	
28660	59028	A	28835	1521	1841	FLPKSLGDSSGESRKHRRRRRA FSPDQHPAGNRYRTRLSARPFV* RCLYYSR*ARRGNYRQH*TTSP ALYQAASPFQ*SIAG*RAKGR YRSSVYLCVDHFDHSGSW

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28661	59029	A	28836	1	1644	
28662	59030	A	28837	1	1245	
28663	59031	A	28838	1	1518	
28664	59032	A	28839	3	491	
28665	59033	A	28840	1092	2827	
28666	59034	A	28841	162	1760	
28667	59035	B	28842	1	3378	
28668	59036	A	28843	434	763	
28669	59037	A	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLENLPAADADQLAGN GGCHSQVRSIWIMGLHAFKAC ETRMYPEEPVYLPPRYRGSIVIH SIAF
28671	59039	A	28846	855	1134	PGNVLRLENLPAADADQLAGN GGCHSQVRSIWIMGLHAFKAC ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCACNLCVAVWP VGCISLVS
28672	59040	A	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARHNAQQ EDALVEKAKQ/VTWRLAAGV CLLTVSS/VARADSLDEQSRSY AQ/KQAWDNQOMDV/VFIHAM PTNTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCR ELSRRLRLHAQYQNTKRVIHT QFSGYKTPEMANTAVPTISSQR RALFNPH
28674	59042	A	28849	1	1247	
28675	59043	A	28850	533	1029	SKSIMLLCRSVVSMIRRTVAA FTLAAISVARSVLNLIIIDIGM QAMPLCRSTTGRNRWTSACK TILR*QRILPLTPC*HRMFRSFL KKILSDGKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIQPAQ KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	A	28851	749	1050	SPHMPGITAGTPFSVPLAISAPSI SAKSLPGKTA*AWPNIMALTPG ISLR**TEFSAILYGSADSPACA RTT/NIGTFLAHRFHVFAHGF NIIHRHFPF
28677	59045	A	28852	260	717	RQLRTELSAGIAAFRTGNAPAIL RFMKLAPP**WRRKPLTGV*RV *RGRDSVR*VAFVPTVSAIQQL DPRSLQQDAFKAGLDPEQPP KT/WQDLA/VLCRETSLRHEV RLRQRLAGLDPTGKL*AWNGM MPYDADAKDAPQKPLSAEPAC
28678	59046	A	28853	776	2730	

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28679	59047	A	28854	383	1367	RPTCWTSEIWWRRVRTAALRSS GKTWVFCCRRRIAGELMLTNR HTGGVMVTTFRASEAFAGALE LTGKATLVALINRCIGAVIRYM LIAVIPDIFQRLQVVLNVWILAV ANETTVRQRRVRRFKVDLVVR VHLLHIEVETVGVTTFIGHAR HHAKLSIETAEAIQVTFTRA VETETITRFFFLIHCLTQTFNN GDTFRAKLLVVNMLAAEQRV NGFVDADVTRQNRRTTVFEDF RNIIVSIETHATSTRYG*CVGPP AMRACSGAVQPQVWLHPGKL RQGEPSRDLVRQRPAAALCLPRR HRLRGYNGNIQRRLYSTGNGL
28680	59048	A	28855	1	1477	
28681	59049	A	28856	1	793	
28682	59050	A	28857	1	1020	
28683	59051	A	28858	1	613	SAGDGARIEQFDRKGMVNNKF NYFIMSKLAEGIPTQMERLLS DTECLVKKLDMPVECVVRNR AAGSLVKRLGIEEGIELNPPLF DLFLKNDAMHDPMVNE/SYCE TFGWVSKENLARMKELTYKAN DVLKCLFDDAGLILVDFKLEFG PVQGEVVLGDEF/SPDGSRLWA QETLEKMDKDGFRQSLGGLIG AYEAVARRLGYT
28684	59052	A	28859	1	1002	
28685	59053	A	28860	1	422	
28686	59054	A	28861	625	750	RNVQALQGAHGTGGALTDPAA* QHILGTLCADLL*NLSPSPRD
28687	59055	A	28862	1	1449	
28688	59056	A	28863	105	297	
28689	59057	A	28864	55	423	DRPQRNRATLMQLYSRSGPGIR RLEHRFEKVQKPGFEVFIPIGF KQKGLGRPLGVKALVFIDTGL FQLQAVKNLDGF*FDEASASQP GSDNILRELVRATGRADGSGT GFTEDANSFTSYR
28690	59058	A	28865	1	2340	
28691	59059	A	28866	314	696	

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28692	59060	A	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK CHGINPLRSWVG*VE*EEKY NMQT*E/LENWKPSNLHDMSS SHSKTLGYKRLTKSNPISCQILL YKSRSGRKNQRSTRTHCHHPS PKIYSASAKEPWILATNLPVEIR TPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDI MLLIALMLQLTCWLAGVHAQK QGWDKHFQANTVRNRNVLST VRLGMEVLRHSGYTITREDSLV AATLLTQNLFTHEEAPANSVPA AAVIRRVQALIGITGRKAHAGG SWNGTASSDNFPNIFILPQDNF MALAAAVAPPELEALLAAGKV SVKIQEPCEILFSRAKVWNGE KWACVTVIVGGHTNIVHIETHDG VVFTQQAQVAEGEQESPLTVLS RTTLAEILKFVNEVPFAAIRFIL DSAKLNCALSQEGLSGKWGLH IGATLEKQCERGLLAKDLSSIV IRTSAADARMGGATLPAMSNS GSGNQIGITELNVSCRFPATNL FVHDPTQQAMQRNQRRFAVQT FPVWRVAQIICAVRPFQRIGQ LRDIFHLKGDQFTNRPKAVAF
28693	59061	A	28868	2095	2722	
28694	59062	A	28869	789	2509	
28695	59063	A	28870	57	440	CSWDPQDPHGILQGAGKEDSQ AQKTTARQKRKTRKTATROKK HEKQSEESTNEDT*ARKVEETQ HKHDAESTSGSVIQGCQVLFQ SFTATPAASATTATRPITLCSSR ARAGVPSTTGVSRRRESPL
28696	59064	A	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK KGHFVVAHPA/P/DQFLHAAM DIKQPVISIDNLLAIHKQAEVTR FIGGDMQRADRDHPRIVALID KRIRFGISRRFRAQSIHRIFAQR MHIFRPVIGQHQAATGNSRLSAS TQRLHHPNPAFFGPFH
28697	59065	A	28872	1609	2112	HQPVLTVVMVPVPSLIIRADNP FRDEVGFLCPA VTVIPVKIVR VTGDTVIRPHAEGAVRVQLRV GQAVTCRVCGIRDADIQIRCGG VNAGQPAGGAVAVTPGLARAA DADEFV VVVPGVIAVRQQA VQ VLAL*LPGRGISGGEFITAEVRS VSRCRRSRVYSTRGIL
28698	59066	A	28873	2	712	
28699	59067	A	28874	337	383	

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28700	59068	A	28875	65	436	REVWEHAKRMLGDSLLDMGM DDELTVMVAYEYIGRLGKTATI HWKVKSPPSMVWSASVWKKM ALR*LSRTLRLPNQEHSL*ASVP ELKCAASWTKRKKNSTFIASSA IRLTL.TWKPKPFLSRL
28701	59069	A	28876	206	403	
28702	59070	B	28877	1	2046	
28703	59071	A	28878	1	1335	
28704	59072	A	28879	1	974	MEAPPIDVSSRDNRNRNRYGH PADLFWFYSLRALPEVYASSD AHEKFDKDFVAAWSLNLVYQR IVGERKLHTGSLMSAAGKSNPL AISGLVVLTLIWSYSWIFMKQV TSYIGAFDFTALRCIFGALVLF1 VLLLRGRGMRPTPFKYTLAIAL LQTCGMVGLAQWALVSGGAG KVAISYTMPFWVVFALFLG ERLRRGQYFALIAAFGLFLVLQ PWQLDFSSMKSAMLAISLGSV WGASAIYAKRLYARHPRVDLLA SLTSWQMHVCRQLASQLPLSH GAMPRCRRPGHSSNPDRLANVI ARRVLRGMSNRQPVSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDNLNTQ LWISTNAFRFGN
28706	59074	A	28881	568	717	
28707	59075	A	28882	1760	3092	
28708	59076	A	28883	1	1206	
28709	59077	A	28884	1	575	MSGSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKPQLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPPSRWDDGIS GHADYSITAQTQHAKLNTEDD/ SNSTGSVWQGLWRLQDD
28710	59078	A	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YYAWRALPSLKAKLALGEDY LNSDIFDGFNYVGGSVSTDDQ MLPPNLRGYAPDISGVAHTAK VTVSQMGRVIYETQVPAGPFRI QDLGDSVSGTLHRIIEEQNGQV QEYDISTASMPYLTRPGQVRYK IMMGRPQEWGHHVEGGFFSGA EASWGIANGWSLYGGALGDEN YQSAALGVGRDLSTFEA

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28712	59080	A	28887	491	681	PTGHRAQKKWNT*TRHSNSY* KNFAKKLI*GDIREKLQKLEGF AGMNATQLIEVATEVYINCQDE AKKETEQLRKKANLLAAALT KRKINIVKGRECSHGCGHGRGQ VEQRAKRWLRLRGGWVKAF VRTEKAREVTKVLLRDIIPGFGL PLTLASDNGPAFIKIVQELTQL LKIKWKLHIAYWPQSSEKVEH MNQTLKQLLKFCQETHLRWD QVLPMLVLLRVRYTPTKQTGY PMRSCSANLK
28713	59081	A	28888	1	963	
28714	59082	A	28889	123	593	KRQVLGAGFLITPRRLPKNWT HCWVWSM/PAQVKQVLFGETG VAQHLKPGTAVMVSSTIASAD AQEIATALAGFDLEMLDAPVSG GAVKAANGEMTVMASGSDIAF ERLAPVLEAVAGKVYRIGAE PGVQVRP*KLFTSC*RAYILL PEPKRWHLPYR
28715	59083	A	28890	263	467	
28716	59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPL YTLGLPRGPHGRAAGNPVDQ QFAAGDLGLSPHADHPGGTD DVRWCLIST*KRWD SGV*AG AGQYSGWRRSLRWR
28717	59085	B	28892	1	2118	
28718	59086	A	28893	1084	8334	
28719	59087	A	28894	2029	3313	
28720	59088	A	28895	1168	1236	
28721	59089	A	28896	1	284	
28722	59090	A	28897	1	1188	
28723	59091	C	28898	20	878	
28724	59092	A	28899	1904	2281	CSAYAGLHPFWLKSTRFCTH ILAPATAISPNTTIDAPPITA AGMV*ISAPNFGKPNMAMTAA ATNTSVE*TLVTAITPISFA* VVTPLPPTESPESIVARPSPT NARPIYGILRPVIPATALR

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28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV RLCWNLLISLGLWSCFSKGVVT TPITLSCSPPPRRGRMAPWAW GRSRARMCMWSWSWTRPSRPC AVRWSSSGATGSCWRRPVST APPRPPWPAPAAPTPAPLWART RMPSHWPSTTAPAAATAY*/DPD AGYQPTPLAAPAEPGSKYSLAS LDRGQGRGGGGGGALEYVPKA VSQPRRHSPVPSCKYVVDNSR PPTDLEYDPLSNYSARHLSRAS SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSPCLMWAASCRN PASLLASE*TVSNA*IPAERAAC KMEQRANSSSVPSGERSVRRLR T*SSAPRAIPKRSEA*AISTARVI PSGDSIAASRPVLPGRSPQAFSIR RISFSISRTS
28727	59095	A	28902	1	2916	
28728	59096	A	28903	1	2001	
28729	59097	A	28904	179	324	
28730	59098	A	28905	1591	1806	
28731	59099	A	28906	531	949	
28732	59100	A	28907	44	477	
28733	59101	A	28908	161	333	
28734	59102	A	28909	1	394	MEGVAFLTFLAARAAGVGNRPA SPQIVRKQREGHGILTRDPVA FDDVAVNFQTQEEWALLDISQR KLYKEVMLETFKNLTSVGKSW KDQNIIEYEQNPRNFRSLIEK KVNEIKDDSHCGETFTQVPDDR LNFQEKKASPEVKSCDSFVCAE VGIGNSSFNMSIRGDTGHKAYE YQEYGPKPYPKQCPKNKKA FRYRPSIRTQERDHTGEKPYACKV CGKTFIFHSSIRRHMMNSHWEKP YECISKCDKAFHSSSSYH
28735	59103	B	28910	1	534	
28736	59104	A	28911	238	434	LPCKIHTPNHGPKLNIPSTKN*Q RRRNTSQR*LHRQPFSSASRPG SRLRFAIGLPAPAEAGMVT
28737	59105	A	28912	358	878	KLCHIAICHSVSFQCESFHVFTG FLSSVCPFMKSKIFDRSEGFPKL LTLIGVLSSVSPFMISKGSEGNK GFPTLLTLIGFLSSVRFFMYLK* LGRIKAPPTYLTIFIRSLYRVHYV CLCPFMNSKVLGRSEGFPFTLT CIGLLSIVCRFPPTLLTLIGFLSSV SPYMISKGTGMR
28738	59106	A	28913	1382	1416	

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28739	59107	A	28914	1	333	MFQDPVAFDDVAVNFTQEWEA LLDISQRKLYKEVMLETFRNL SVGKSWKDKQNIYEYQNP FRSLIEKKVNEIKDDSHCGE TFTQVPPDRLNFOEKKASPEIK SCDSFVCGEVLGNSSFMNIR GDI GHKAYEYQYGPCKCQ QPK KAFRYHPSFRTPQRDHTGE KPY ACKECGKTFISHSSIQ RHVVMHSGDGPYKCKFCG KAFHCLSLYL IHERIHTGE KPYECKQCGKSFSY SATL RIHERHTHTGEKPYECQ QCGKAFHSPRCYRRHERI HTGEKAYQCKECGKAFTCP QYVRIHERHSTRKKPYEC TQCGKAL*YSLKSGSLMP *ALFFWLRIVLAMWAL LWFHMNFVVFNSVKKVIG SLMGMAWNLQITLGSMAIF MILI LPIHEHGMFFHLFV SSLISLSSGL
28740	59108	A	28915	1619	2353	
28741	59109	A	28916	1	1252	MSYSVMFALLLLTPLLFS LLCFACRKRRLSATRTVT VLHSLGIT LLLILALWV VQTAADAGEIFAA GLWL HIDGLGGLFLAILGVIG FLTGIIYSIGYMRHEVAH GELSPTVLCDDYGGFFH LFLFTMLLVVTSN NLIV MWAAIEATTLSSAFLVG IYGGQRSSLEAAWKYI IICTVGVAFGLFGTVLV YANAASVCGTDH GGR MMRSWNGGQLISKLLA ITPDKLVLDGFSQAEDN IAVLKAQHISISAETQGA KVEFTVDQLQ QSEY LQLPAFTVPPPTLWFV QRRYFRISAPLHPPYFC QTKLADNSTLRFRLYD LSLGGMGALLET AKPA ELQEGMRFAQIEVNMG QWGVFHFDALQISISER KVIDGKNETIPTPRLS FRFLNVSPPTVERQLQ RIIFSLEREAREKADKVRD
28742	59110	A	28917	2	2282	
28743	59111	A	28918	518	1046	
28744	59112	A	28919	8	893	
28745	59113	B	28920	1	3129	
28746	59114	A	28921	1	1284	

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28747	59115	A	28922	3612	5412	PGLKHQNNHGRGPD AETKGV RDFGPN AKPLAG/VRLN/LERLR DTHHIDVAPLVARLDQMMEVS SQLQLARAGQSFSSGNYQHV KLLEDVILPSYDELSTMLDQRQ QTL L L PESAADITVQGDATLLR MLLRNLVENAHRYSPQGSNIMI KLQEDDGAVMAVEDEGPIDE SKCGELSKAFVRMDSRYGGIGL GLSIVSRITQLHHGQFFLQNRQE TSGTRA VVRLKKDQGA YPMSE KVVSQLSRK FIDENDATPAEA QQV V YSLAIGHHLGVIDCLEA ALTCPWDEYLAWIATLEAGSE ARRKMEGVPKYGEIVIDINHVP MLANAFDKARAAQTSQQQEW STMLLSMLHDHJQENAIYLMG VFIMLIFFPAPVASEKPLSPDCW TTTTLRLMIGENSGLVSYMREK AVSPNCWNVIHYSGLFHLLELS SYDDVDN QIINTICEWISLIKTR GVRRPEFQTLTSGSGEGERFI MNRPTLFFTDLAHFHVDRTQYV HDTAQSRFTYRDFNRVFEVFI QTATQT VGGTHCDAPGW WFP GAVQSVPAALIAVAAAPGLA SFLPFARRVPRTVVALLAQAAA YADGMPARADGSFNSP
28748	59116	A	28923	1	2910	
28749	59117	A	28924	470	723	PGFGDARKLISLNFFIWV*TA* M*/P/LAGSDFVYRNS*RNVFIAQ TLQLRSRQPV TMHHATRAFQT EHNILRFECCEYSRYLFT
28750	59118	A	28925	599	1117	
28751	59119	A	28926	279	455	SLSHSSGRCSRGGISFVWVWF GPVACLAASVV*L*VS VVWLW LSPSGQGCLGCRVWL
28752	59120	A	28927	1	2913	
28753	59121	A	28928	1	2328	
28754	59122	B	28929	55	327	
28755	59123	A	28930	9	107	
28756	59124	A	28931	1	2106	
28757	59125	A	28932	1	1123	
28758	59126	A	28933	260	709	
28759	59127	A	28934	467	631	LEVIEAPQPNWS*SVQQSACST WPGCWVDLED PQV VVWYEW TTKRASLLPIFQD*LKALRKAQ VWAFAS*STWPGCWVDLED PQ VVWVWYEWITKRASLLPIFQD
28760	59128	A	28935	989	3010	

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28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	A	28937	1	1006	
28763	59131	A	28938	185	384	
28764	59132	A	28939	2	615	WAFRVIRFIVTANWSLKAVWM RRLIVVA/ALLTLRTVPMRQLNR LLLITPSLSRHMVSTGPAATSCVN RGFLSPTVVSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGE QISLGVRNTSPDVPYLIQSWVM TPDNKKSADFIITPPFVFLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRVPSTTKRKEGNTLKIAHK RMITN
28765	59133	A	28940	1	1686	
28766	59134	A	28941	76	981	
28767	59135	A	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPHRQWSASYWRS *SSSFRNLNKKCHTQNHNSCIKM ARE

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28769	59137	A	28944	1	2539	MPIEELALRSWQRPFLK WAGG KYSLLELDRLIPAGKRLIEPFV GGGSVFLNSDKHERFLADVSA DLINLYQMLAVVPDSVIYEAM KAFRHLNDAENVTILIREAFNAQ RLDAVERAAAFYLYLNHCFNG LIRYNLDVFFNVGFGKHKQMT NNEKSGPFEGLLVIDMTHVLNG PFGTQLLCNMGARVIKVEPPGH GDDTRTFGPYVDGQSLYYSFN HGKESVVLDLKNHDHDKSFHGT GPLKDA PAYDTIQAMS GIMME TGYPDAPPVRVGTSLADLCGG VYLFSGIVSALYGREKSQRGAH VDIAMFDATLSLEHGLMAYIA TGKSPQRLGNRHPYMAPFDVF NTQDKPITICCGNDKLSALCQ ALELTEL VNDPRFSSNLRVQN QAILKQYIERTLKTAAEVWFT PFSNKYNGHRIARTDKASMPVT YSESLFVEGIIRASTSMITKQGP SLRTGRTLRKFCPLSETAATDTS SIFPSKFTPTASRLPGFSIRSPK MTQSVLLPPGPFTRRQAQFTT TYSNITLEDQGSFHLVVRDT EGRMASVQTRPPADREAFTRI LPEHTLYPHTPAIAAGVFIDGDI PMTTQTQHD LAPANQPEFELTV TPVPDEQRIDFWPQYFGAIPQW LLEPHIFAWMDRFCEGYSGGI WSFYTLNNGGAFMSPEPDNDET WRLFNCLNATMPPYRMTCGTV
28770	59138	A	28945	907	1917	
28771	59139	A	28946	1	3033	MVWGFTCSSTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQIDTLTQMMTSTLFSPPSV HNVMETVTQETAPPEDEMTTSFP SSVTNTLMMTSKTIITMTTSDS TLGNTEETSTAGTESSTPVTSAV SITAGQEGQSRRTTSWRTSIQDTS ASSQNHWTSTQTTRTSQTSTL THRITTSPTSPSPSVHNVGTIVSQ KTSPPGETATSSLCVNTNTSMM TSEKITVTTSTGSLGNPGETSS VPVGTSLMP
28772	59140	A	28947	636	725	
28773	59141	A	28948	1	1123	
28774	59142	A	28949	2345	3644	

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28775	59143	A	28950	34	437	CGRLLQKSGFVSVVGIDGIERL NTRRARGLPNGTACGQQFSSFR GAFCTQVAHIVFCTEGD TDQ/D ARKRERFPLRG*SPA EIQSP PAG RCCRVHDHRLFRYAGSFFQYPE HPERYRFSADAQRP HHRERRLP
28776	59144	A	28951	1	457	
28777	59145	A	28952	176	757	KPMKSTAAAADAALLSAERQ VIDDAAAHLSVAQGGDDVD AI EQAIKNVDKQTQDFAARRMDQ SVRRADRSDLIETFDHVCTVIFI RDGITS AEVETADTARGNV DVI RTGEVGA VCGTEETKSILQYLQ YAI TKDIFATLCVLLQDGKNNV LLTHTSQVFQPHIFAESDQLRN RRIFGDRFDSVPSIRMMFGI
28778	59146	A	28953	1	1503	
28779	59147	A	28954	425	619	AGWSFLPSPA EQNRWRPFLSRF CQIPAPLQVRS* LACRFFAA YSP PLL RKSPAASMAYTTSRLH
28780	59148	A	28955	55	476	SYHALANVFYQRRMAITQVAG RQAQVFK AHLRDDVHHHIDGQ VTATESVM EGNRHAVL*TRAT NRFFQVGAQFAIARFFSLVGLL WRVLES GKIAFSATIPGRYPFLS LRLFNFLRHFDCLILRGCRKVL HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	B	28957	12	271	
28783	59151	A	28958	309	1238	GS GSCYSALVKRKWSARSLRA DRNGARRGAYVGRKFHFGPG LAGFFSAHASNLRRSDRAPAH YHQLLNFADPVDMMQ*KRGM VFLLLM DQQRQVDDWRRLPS LLSVWQSCGDSGRRAPGGR*FH WRFQATVFQALAE DLRRNLQ! VVATVAF/GMGINKPNVRFV VH FD/PRNIESYYQETGRAGR/DGL PAEAMLFYDPADMA/WLRRCL EEKPQGLQD/IERHKLNAMGA FAEAQT/CRRLVLLNYFGEGRQ EP/CGNCDICLDPPKQYDG/STD AQIALSTIGRVNQR/FGMGYV V EVIRVA AFLEPDYSHRP
28784	59152	B	28959	1	2123	
28785	59153	A	28960	1	2834	
28786	59154	A	28961	1	2505	
28787	59155	B	28962	145	494	

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28788	59156	A	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHAF*PLLGDFGCRNGVVIQGRENAHLMNGGGRRVTALHFQQYRFHHLFNILTARHHLDNANHQAQIDR*RFAMRLAGGTATHQ
28789	59157	A	28964	1	1423	
28790	59158	A	28965	1	863	
28791	59159	A	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	A	28968	1	1215	
28794	59162	A	28969	1	1678	
28795	59163	A	28970	1	4674	
28796	59164	A	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFQHQLIAGDHFHHFQAHLVQFGGDFQLFNLGEGQLVVSIFTPVRLAVHGVKIE TVFVGFSSLIHGSQTVLVSSASG ASVASTRGKCTIVTSGISG/VIA KND/GLPRVHGATAPSCASQFL VFAAPTPRPDRHG*RTDDSTPQ RLSSPAVEKAPTASSAGNSRN DKPLREITLITSDRPVPDAAVSP TGFWPLTIPFHRCRRMSSLPGIPI RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSGRRAPGGR*FWH RFGHGHGFGAGGSPAKPVNR RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	
28800	59168	A	28975	904	1473	
28801	59169	A	28976	738	893	
28802	59170	A	28977	1	1108	MADTRYFGMHMSQETPASTTE AQIKNERRISPFWLLPFIALMIA SWLIWDSYQDRGNTVTIDFMS ADGIVPGRTPVRYQGVEVGTV QDISLSDDLRKIEVKVSIKSDMK DALREETQFWLVTPKASLAGV SGLDALVGGNYIGMMPGKGKE QDHFVALDTQPKYRLDNGDLM IHLQAPDLGSLNSGSLVYFRKIP VGKVVYDYAINPNKQGVVIDVLI ERRFTDLVKKGSRFWNVSGVD ANVSISGAKVKIESLAA
28803	59171	A	28978	1	861	
28804	59172	A	28979	5	337	
28805	59173	A	28980	1	612	
28806	59174	A	28981	128	1742	
28807	59175	A	28982	1	2688	

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28808	59176	A	28983	361	738	FLQPPFPFKREINKFIRDIANNMK TDFSAVTLFTDCVTVMLWII*F FQRKFLLKGF*PPLGSFYRE*IT SLFLYLLCNIFLATHRISCDDFSF NIQHVKKFWDSNLIIRFLIRLDL SDDQTVHC
28809	59177	B	28984	1	1263	
28810	59178	A	28985	363	569	KGYRRSGKHRQGCCNVLRRL FPDQHTAPRPMPLKQTRAPGQ SPPLPADPHPGQF*LPLLRGRF AR
28811	59179	A	28986	1	1035	
28812	59180	A	28987	275	721	LMVSGFLTSPKDERIMSGEAR AILIASNSSVLCAFRNFKSFT DLLPSELAQSASERISFNNTLKD SGMPGSI*WLPSTMFLYLVRPF TSSDLTVSISCRVYAAPYASSA HTSISPKR*PPNTQRLLTGPGVT FWGRKPPLFPTP
28813	59181	B	28988	1	2082	
28814	59182	A	28989	1	1567	
28815	59183	A	28990	1	453	
28816	59184	A	28991	1	777	
28817	59185	A	28992	1	1431	
28818	59186	A	28993	1	561	VDSRGYPYSGRGAGKCRESERL GSESRNPGSIGLENELTAEDVAS ADMVILTKDIGKFEERFAGKTI VRVNISDAEFLMTNRISRLKTA LFANTREISLERALLYTASHRQT EGEPVILRRAKATAYILEHVEISI RDEELIAGNRTV/ITARRDYVA GNGPLLAERAGSIPDASAGPL CYQRRRL
28819	59187	B	28994	1	3414	
28820	59188	A	28995	1082	1297	MIMWLAAVAIREINHDSGSATF RTPRPRTVAGKYNLGASLYK SELLA*LHSAGAGCLSCQRAKL GLGRKR
28821	59189	A	28996	1	2115	
28822	59190	A	28997	168	317	
28823	59191	A	28998	1331	1471	RWSNGTLENGTL*LLTLPASLI STNKSPLDDVE*RSLSIKAPGDT
28824	59192	A	28999	147	1456	
28825	59193	A	29000	1	439	

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28826	59194	A	29001	722	2805	TPRAERTASSVALPTSRLLRAR AETTTAPSTPMKTHRIVISMVFF TCSQTGTPSASPVKSSLKVSSLN IIIASTTNRPS/VQQF/WPVSPPG DGTRRYPISISLTVLTGNDNVNL LRAGIDLAIYFDDAPSAQLTHH FLMDEEILPVCSPEYAAQRHALT DTVINLCHCTLLHDRQAWSND SGTDEHWSWAQHYAVNLPTSS GIGFDRSDLAVIAAMNHIGVAM GRKRLVQKRLASGVYPPRCAY PRTHLETTSTSGVNGVGTYS PFWRMLLNSFVMAFSITLGKIT VMSLSAFAIVWFRFPLRNLFFW MIFITLMLPVEVRJFPTVEVIAN LQMLDSYAGLTLPMLASATAT FLFRQFFMTLPDELVEAARIDG ASPMRFFCDIVFPLSKTNLAALF VITFIYGWNQYLWPLLITDIDL GTTVAGIKGMIA TEGGTTEWNS VMVAMLLTLPPVVIVLVMQR AFVRGLVDNPAANYIHVGVRE SGMTAIAAGIAHHGGFVPTAT FLMFVEYARNAARMAALMKA RQIMVYTHDSIGLGEDGPTHQA VEQLASRLTPNFSTWRPCDQV EAAVGWKLAVRHNGPTALIL SRQNLAQVERTPDQVKEIARGG YVLKDSGGKPDIIIIATGSEMEI TLQAAEKLAGEGRNVRVVS LP STDIFDAQDEEYRESVLP SNVA ARVAEAGIADYWYKYVG
28827	59195	A	29002	2253	2546	
28828	59196	A	29003	279	629	NGAGHL*RPVPDGAATAAPAGG RYAHLRVCPESLPWLHLPWRI YRSGS*SAPCHCRNHRSGSAWQ KHYGNRFRFRTPVRYRGRALH LRGRNTAITQAADWRLATAQL LEIAGVGDE
28829	59197	A	29004	313	638	RWRQRWFVWCLHCLVLFRTPR TFALSQCRPWDDSRSDTSM SH SIQWNRMYCNCMSQDEQEADE ANGKGPAQVQDRQA WAGR/CR SHRREGTIPGNPHPRAS* RAGW QR
28830	59198	A	29005	1	1182	

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28831	59199	A	29006	1	535	RPVVLPIVAGSNALGALGYVES ALEIAQQCEGAVNISSVVVASG SAGTHAGLAVGLEHLMPESELI GVTVSRSVADQLPKVVNLQQA IAKELELTASAEILLWDDYFAP GYGVPNDEGMEA VKLLARLEG ILLDPVYT GKAMAGLIDGISQK RFKDEGPILFIHTGGAPALFAYH PHV
28832	59200	A	29007	1	1953	
28833	59201	A	29008	1	656	MKLMAIQEQARGEQCFRDSEW DLQFHIQVALATQNSALAAIVE KMWTQRSHNPYWKLLHEHIDS RTVDNWCDDHDQILKALIRKD PHAAKLAMWQHLENTKIMLFN ETSDDFEFNADRYLFAENPVAI AKELELTASAEILLWDDYFAPG YGVPNDEGMEA VKLLPRLEGIL LDPVYT GKAMRGLIDGISQKRF KDEGPILFIHTGGAPALFAYHP HV
28834	59202	A	29009	1172	1371	
28835	59203	A	29010	338	528	RHPRCDPYGFCPFTADADDA** LGACHHYWRGQRKIYAGSGDS RCQPDGRRSAPARRPLRRQR
28836	59204	A	29011	413	2798	
28837	59205	A	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P SSFKEGIDHSATFFFAARFALVA AAIFCVFADGFFAFLASFFAAG FVFFSPRKALSGSKFTFLPT

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28838	59206	A	29013	767	1428	FTPLSLRAVVIQLANRQYLDEK SDRAVHQGHIPRQFY*SLRRNL TNRHQLIAIGGAIGTGLFMGSG KTISLAGPSIIFVYMIIGFMLFFV MRAMGELLNLEYSFSDSFAS DLLGPWAGYFTGWYWF CWV VTGMADVVAITAYAQFWF PDL SDWVASLAVIVLLTLNLATVK NVGEMEFWFAMIKIVRPLSGSR TKKMSKSDNNRNVIGLLED KSVVKKIKRAVTDSEPPVVRV DVQRPKRSALLERAPERFQEVF ILKGREDKRLPLIHAIHESQGG GYPVGKPPISREKRPCRASGA YSPVLLILIMDPLGNLPIMSV LKHTEPKRRRAIMVRELLIAL VMLVFLFAGEKILAFSLRAET VSISGGIILFLIAIKMIFPSAGNS SGLPAGEEPFIVPLAIPVAGPTI LATLMLLSHQYPNQMGHLVIA LLLAWGGTFVILLQSSFLRL GEKRVNALERLMLGLVMMAP
28839	59207	A	29014	1	632	
28840	59208	A	29015	1	1215	
28841	59209	A	29016	38	457	LNRLKLVAHSQSSRAMVFSSI RSFMFFSTLFLVRRQFSR*TIML SANSDSLTSLLPIWLLFISFCLT ALARTSSTVLKRSGESGHPCLV PVFRGNTFNFSFIMLAVGGV LHCEINCRICSTGRSANPPLDSCI
28842	59210	A	29017	899	991	
28843	59211	A	29018	1740	1868	
28844	59212	A	29019	1	1084	MSAEITAPWYRLQLDLFTKLVA TCMEQFRPKTIPLAIPERLNAH CEELYELIASNNILNLYMPAG QEAHRFAMGELPDEVLEICQR LAKLTEMLRGLAELFLNDLSEK TGSHDIVRLHRLIQMNRLGM FEAQSKLWRLASLAQSSGAPVT KWATREEREGQLHLWFHCVGI RVSDQLERLLWRSIPHIIVTSAT LRSLNSFSRLQEMSGLKEKAGD RFVALDSPFNHCQGGKIVPRM RVEPSIDNEEQHIAEMAFFRK QVESKKHLGMLVLFASGRAMQ RFLDYVTDRLMLLVQGDQPR YRLVELPANASPTVSAACWW AYSHLPKGLI*KVICARCISTK SLFRPSTARW
28845	59213	A	29020	1	2022	

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28846	59214	A	29021	878	1267	LNSWLPSPVPTV*SSVFNAL*TG* ISPAFNPADDM*SASGLP*IKSPL STSTLFFTSRLASLRLA VRTSPN FSVAVSL**SKSIMLLCRSVVSM IRRSTVAAFTLAAISVARSVALN RFLIKSTGNACK
28847	59215	A	29022	294	2305	
28848	59216	A	29023	5	337	GAPQHQMMSYRINGRESPML TYPSTPNFFWLA WQARDFMSK KYGRRFPARFLWRSTPAGVVR KTIFIFISLVFVLMCANSWITI RTSAAAGCHCQVVCAGMNTW RVG
28849	59217	A	29024	1	1753	MPSTRYQKINAHHYRHIWVVG DIHGEYQLLQSLHQLSFFPKID LLISVGDNIDRGPESLDVLRLN QPWFTSVKGNHEAMALEAFET GDGNMWLASGVYRIPLA VIWII GSLTSKAYKAEVQQRREAFNR AKMDYDHLVRQIQVGGLEGF IAKRTMLEKMKDEILGLPEEEK RALAALHDTARERQKQKFLG FFIDVASIPGVGPARKAALRSFG IETAADVTRRGVKQVKGFGDH LTQAVIDWKASCERRFVFRPNE AITPADRQAVMAKMTAKRHRL ESALTVGATELQRFRLHAPART MPLMEPLQPTSVVVDKVVKEK GTKEVAEAYLKYLSPGQEI AKNYRPRDAEVAKKYENAF KLKLTIDEFFGGWTKAQKEHF ANGVIAVVAAGIGYWKLTGEE SDTLRKIVLECLTNQQQNQNP SPCAEVKPNAGYVVLKDLGSL PYLLMPTYRINGTESPLTDPST PNFFWLA WQARDFMSKKYGR RFPIARFLWRSTPAGVVRKTIF ISLVFVLMCANSWITWRTSAA AGCHCQPTGIAQALLSTRQHGG AQCPDLLPLSPLSSSF
28850	59218	A	29025	865	974	IMPRISGSQSGEHQQPLVATAR WFARA*ILIIL
28851	59219	A	29026	1936	2490	
28852	59220	A	29027	1105	1518	
28853	59221	A	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	A	29030	3338	3553	
28856	59224	A	29031	95	1289	
28857	59225	A	29032	1	732	
28858	59226	A	29033	1	672	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTTTL AEGGLEAAEEAGIPLVNVHVG MFGIFTDAESVTCYQDVMAC D/GGTL*AFLPYDAGRRLQHG RYQ
28860	59228	A	29035	852	933	PAPYALLLLPMHPHGLRRDR QGRHNLNDRRRHWHVRVCH LLRRERSRKDAPADGHPPLRA VGGRNQN*FGE LR TTTCTQT D FLT FNLT SVTSNEASFTQFR TQG LVVFHQSGAGDTVDR TSL TRDT TTFNGDVQVQFLNHVDQFRL TNYHAGSF TTEVLFQRTLV DYD FTVARFDENASCGTFAATS AVV LIFSHCLRLLCRVVVLVTR VNF QFTEHSTTQRAFWQHA FNRDF NHTLRTASNHLFKGRL FDITDV AGVVIVHFVSTLVAGYS NFVSV QNDDVITGIYVRSVFR FVLTAQ ATSQFSSQTAQSFTGR VNNIPV AFYGFWFSCAKYYRH GARWCS NGRKIDQRHTHCF FCPCIRTDFA VEIGKEEFIT
28861	59229	A	29036	1	797	MIVFIENFKTSSPKYADILL PDL MTVEQEDIIPNDYAGNMG YLIF LQPVTSSEKFERKPIY WILSEVAK RLGPDVYQKFTEGRTQEQ WLQ HLYAKMLAKDPALPSY DELKK MGIYKRKDPNGHFVAY KAFRD DPEANPLKTPSGKIEIY SSRLAEI ARTWELEKDEVISPLPV YASTF EGWNSPERRTFPLQLFG FHYKS RTHSTYGNIDLLKAA CRQEVWI NPIDAQKRGIANGDM VRVFNH RGEVRLPAKVTPHPV GTWTA E
28862	59230	A	29037	1	1019	
28863	59231	B	29038	1	2727	
28864	59232	A	29039	1	2250	
28865	59233	A	29040	1	2850	

SEQ ID NO:	SEQ ID NO; of peptide sequence	Method	SEQ ID NO; in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28866	59234	A	29041	1	1339	MTGKCGKFGNFLESWRAQKGTG ICGKVWNFLENLLNGFGQNAY SDTDNEVQAEVVSDDKDELVG NWSKGHSCYAKRLAAFCPLR DLWNFELERDDLGYLVVEISKQ QTIQEEADHKNLESQTEDAIE KKTPFSGEKFKLAAEICISNKDP NINSQDDGENVPRVAVHPNGC FAWKLPVLSRKFERKPIYWLS EVAKRLGPDVYQKFTGRTQE QWLQHL YAKMLAKDPALPSY DELKKMGIFYKRKDPNGHFVAY KAFRDDPEANPLKTPSGKIEIYS SRLAEIARTWELEKDEVISPLPV YASTFEGWNSPERRTFPLQLFG FHDKSRTSTYGNIDLLKAACR QEVWINPIDAQKRGIANGMMP YVFSSQMAKFTPRTGLSLIWK AHKCGEAETLQKQ*C*QSGAT LPAGPRARAWPPYPRLPFTGLA CVDLHGNARKAT
28867	59235	A	29042	378	530	AFLPYDAGRRCPLPGTVSV*SGL YVRGAQHGRYQ*HHRCTSDK IWRADKG
28868	59236	B	29043	1	1617	
28869	59237	A	29044	417	607	
28870	59238	A	29045	954	1163	
28871	59239	A	29046	444	3793	
28872	59240	A	29047	475	732	
28873	59241	A	29048	1	219	
28874	59242	A	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	A	29051	1	411	
28877	59245	A	29052	172	378	LSLLRELGPVVAALLFAGRAGS ALT/VRNRPDARYRATLQYGD DGGGSAASGYFSPFLGWGYFIT TVDG
28878	59246	B	29053	1	1641	
28879	59247	A	29054	1	3036	
28880	59248	A	29055	1	1419	
28881	59249	A	29056	1	1500	

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28882	59250	A	29057	2	1760	KSQQLHDPCCAPIQQEAVRAVV GQPPQQHLGFPVERGVQCQREC DFEKELEARIASLSDSVSNAREE RMALRQEQEQI.QSRIQSLMQR APVWLAQAQNSLNQLSEQCGEE FTSSQRTHHGSEGNITKRGLLG ELRFENGDPSPNDQSYGRHKDG MAEIGTFHGGDLRGLTNKLDY LQQLGVNALWISAPFEQIHGW VGGGTGKDFPHYAYHGYTQ DWTNLDANMGNADLRLTLD SAHQRGIRILFDVVMNHTGYAT LADMQEYQFGALYLSGDEVKK SLGERWSDWKPAAGQTWHSFN DYINFSDKTGWKWWGKNWI RTDIGDYDNPGFDDLTMSLAFL PDIKTESTTASGLPVFYKNKMD THAKAIDGYTPRDYLTWLNQ WVRDYGID/GFRVDTPKCLRCN PSITIGTNYAS*PQWSSIPGAL* G*/PAWAG/GLPWAPSVLLLDH LRQGTMTLEENLGNITQDIGMG KDFMSKTPKATVTKAKIEKW LIKLSFCTAKETTIRVNRQPT WEKIFAIYSSDKGLISRIYKEL QIYKEKNKQPHQQVGEHEQT LLKRRHGCSQQTHEKMLNHQ
28883	59251	A	29058	1	1119	
28884	59252	A	29059	3	2599	
28885	59253	A	29060	225	1245	RGSTGAHPRSAGKHYAKTSAG NAAGDP*YQMGPHHRGCGKP VLPDPHQSENLRWW**RAAWCG SGGYR/MAEGRHAAQGIIDWLG LDVDKLGALFERRKVLQVTE NLQAERNRSKSGQAKARGED IEPLRLVKNLGEELDAAKAE DALQAEIRDIALTIPNLPADEV VGKDENDNVEVSRWGTPREFD FEVRDHVTLGEMHSGLDFAAA VKLTGSRFVVMKGLIARMHRA LSQFMLDLHTEQHGYSENYVP YLVNQDTLYGVGLYPLGALAS GWLPRRERKDATPGTGYPG AHGNLELPERSEGPRAGGEPRR RTGHTQKGSPPDRGQTPPKGP
28886	59254	C	29061	201	1244	
28887	59255	A	29062	1	2530	
28888	59256	A	29063	675	920	RTYRLAGRKQRRGGGTDSSRS QNPWRSHRRHL*RSSGAGKR GGKRFAGGAERNRPLCRCKPEP PAGGDGRRRRRLAAAGAD

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28889	59257	A	29064	498	707	
28890	59258	A	29065	510	554	
28891	59259	A	29066	600	734	PECLSPADH*YKHCSTGTQAR QPDADCP LLPRLAAHNERQTR
28892	59260	A	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD LWPGEVLGIVGESGSKTLLK SISARLTQQGEIHYENRSLYA MSEADRRLLRTEWGVVHQHP LDGLRRQVSAGGNIGERLMA T GARHYGDIRATAQKWLEVEIP ANRIDDLPPTTFSGGMQQLQIA RNLVTHPKLVFMDEPTGGLDV SVQARLLDLRLGLVVELNLAV VIVTSSPDQDWGFTPEPRLAAR FPGSTHSSRRNRGRHRPRRS LPTPSAPHSRAPGDGVKLVPPP ARVTRNEPAPSDSVTLGVPH EP GACIGTPILTFVRPSTAINAAA EESTGTILFGAGGFKRTDLNDT ESDSTTLVASRYWDLSSGWQR AINLRWLDHFTQGEITNTTML FYPGVMISRTSRGGLMPTWG DSQRYSIDYSNTAWGSDVDFS V FQANVWIRTLYDRHRFVTRG TLGWETGDFDKVPPDL*LKSR VGQRSELGSQYTPRARVEPPKL LSRKVRAHFGSRAPAGRA*RH LRAPDCGVRVWVWAGSGAGDG GGRGCGSGTSEWILSGRRGE
28893	59261	A	29068	84	128	
28894	59262	A	29069	1547	1822	CSRCSIFAFRVKPAPLKPRVFSP AWWNPERLWHLAPSTFSGGEQ QRVNIAR/ELYRRLPHSAA*RN YRLP*RQNSAALSRLYA AFLPR PQYHH
28895	59263	A	29070	1520	1656	
28896	59264	A	29071	563	976	
28897	59265	A	29072	1	1011	
28898	59266	A	29073	1	1097	
28899	59267	A	29074	1	2490	
28900	59268	A	29075	1	879	
28901	59269	A	29076	1	1317	
28902	59270	A	29077	1428	1619	YAAARRALCGSPCFPGGCNGE NCRLPPQLHADLTARIFYETRG WWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG* HQLWARWQNNGLAHTPRADS THQQSALDGRISLIT

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28904	59272	A	29079	1886	2329	PLL V W I N T R P S L T T G R E S A S P A T L V C H A T V P S L V I A S H V L S F L * W S F T V L V I S R I G V A F A H A I F W S I T A S L A I R M A P A G K R A Q A L S L I A T G T A L A M V L G L P L G R I V G Q Y F G W R M T F F A I G I G A L I T L L C L I K L L P L L R R T V K Y T S G C
28905	59273	A	29080	1	2319	
28906	59274	A	29081	3	194	STSSLA A Q S L R F G Y E T S Q T G L A T Y C G E K I Q * F F A D L Q P V C A D S Y P L L V Q M K K L G P I V F F F D I
28907	59275	A	29082	3109	3384	
28908	59276	A	29083	703	1000	D C F L R R L I K R P F G T S M K D Q A V R F E E G F M A M G A L G L A M V G M T A L A P V L A H V L G P V I I P V Y E M L G A N P S M F A G T L L A W I W A A V F L A K E L A G G V R L L V L I F
28909	59277	A	29084	2040	4603	
28910	59278	A	29085	3	94	
28911	59279	A	29086	3	148	Y A E H M L E V M S S I G D Y T / N P R P A S R P V T K F D Q R G H R L G H G V W N L M F E R V K
28912	59280	A	29087	27	227	
28913	59281	A	29088	344	1067	
28914	59282	A	29089	798	1049	
28915	59283	A	29090	1	1473	
28916	59284	A	29091	1	720	
28917	59285	A	29092	45	208	
28918	59286	A	29093	1	2499	

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28919	59287	A	29094	1	725	MHPRFQTAFQAQLADNLQSALE PILADKYFPALLTGEQVSSLKSA TGLDEDALAFALLPLAAACART PLSNFNVGAIARGASRRSAKNIP RAVRQVFWRILLFYVFAIILSLI IPYTDPSLLRNDVKDISVSPFTL VFQHAGLLSAAVMNAVILTA VLSAGNSGMYASTRMLYTLAC DGKAPRIFAKLSRGGVPRNALY ATTVIAGLCFLTSMFGNQTVYL WLLNTSGMTGFIAWLGIAISHY RFRRGYVLQGHNDNDLPYRSGF FPLGPFAFILCLIIITLGQNYEAF LKDTIDWGGVAGTYIASGGPEPA VNSHAFGVLRNVVSIIVFFHQF GDAIKRLFPTDLLPFIRTWRTVF RKLQTAFGVDEIHQASAFRTKC TAVDRVIRIAFDMDRLDFFSWR SGYISRIPLIGLYFACALERHQN ERQPIILSDQNAIATINQLAIER DVLNCRVRIARSLSELVAIREEIE PLLIINNSHYLLDDAVNNYITVK NIITAAGIEQIKHFLATAFIROQP ERFFSAPGSFHYSNVRGESWQH ITRQICACLVAQHHTADEAQRI IAREGEGENLIVNRLAIPHWCSE QERRFR*TVAWWRAA*CAVCD DGDRCRSVLPDLHVWQPDGIPV AAEHLRDDGIFYRLAGDCH
28920	59288	A	29095	3	453	
28921	59289	B	29096	1	3684	
28922	59290	A	29097	1	231	LLVFINQEEADFHTQRGGPVFQ QATFTL*QLALFAIEPGLMTDP DIQVRGTTLPYGRGAAHGVTY SNWKLTFRRILY
28923	59291	A	29098	1	2862	

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28924	59292	A	29099	1	1567	MKLNKAGFNVPESYSLKMP VGCLISALKKAEADRQEVILRL NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLGPF RVRAGESIKFFNVLLADTPGLDI DTMDKDV AHDSSISQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLEKDLALNQAMIPGSGCT MKLNAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLD AEIARIEKMGVPJIKCTTEV GNTLTLEQVKAENRAVLVTGV LSSGSGLPFEHSDVEIAVDFLQ RARQAQGDISIPQSALIGGGDV AMDVASTLKVLCQAVTCVAR EELDEFFASEKEFTSARELGSII DGFTPVA VEGNKVTFKHGDLR TAPFLGVADKRNKSAGNHP
28925	59293	A	29100	107	892	LAICTGTYSGRQVLPFRVDRGA SLIAEERNAGRRRAGIRTTSA GGGLCA Y AIVEF* CWRNCARFE LN/AGISVPI/SEFIGATMQQTVH AEQSAISHA WLSGEKALAAITV NYTPCGHCRQFMNELNSGLDL RIHLPGREAHALRDYLPDAFGP KDLEIKTLLMDEQDHGYALTG DALSQAAIAAANRSHMPYSKSP SGVALECKDGRIFSSEYAENAA FNPTPDIQRAVLAEKADAPLIQ WDATSATLKALGCHSIDRVLL
28926	59294	A	29101	1	3100	
28927	59295	A	29102	1878	2699	GTARNLTVSLSYSSSGTPSNA PNARMEELGPHPEASSLFHPE SPLLDELFLPEYKAGRTNPDI GHYVRRADVADGKSRLRLGLDS NKDQSYFLYTLSEHQIAQSLFP VGELEKQVQRKIAEDLGLVTAK KKDSTGICFIGERKFREFLGRYL PAQPGKIITVDGDEIGEHLGLM YHTLGQRKGLIGGTKEGTEEP WYVVDKDVENNILVVAQGH HPRLMSVGLIAQQLHWVDREP FTGTMRCTVKTRYRQTISLGPL RKPPHNRCLEI
28928	59296	A	29103	358	1160	

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28929	59297	A	29104	234	930	KRAFLCSFCANRRNAANSALALPGNCPVAHAQKRHSAPGTLSPDARNEKQPLYGGAAPETPNRLLPPLDSGILGGYIAPDNLITLISVGHSLFDERFGLAPQMPKKLQKMTRFPNDSLDAAALCHGDVLLQICANTQDVTIHALRDIKHPTDLLSVRWKREGFISDHAARSKGKETPINLLGFKDGTANPDSQNDKLMQKVVVWTADQQEPAWTIGGSYQAVRLNQFRSVMN
28930	59298	B	29105	1	837	
28931	59299	A	29106	1	1701	
28932	59300	A	29107	733	1323	
28933	59301	A	29108	1	736	MKPSVILYKALPDDLQRLQEHFTVHQVANLSPTVEQNAIFAEEGLLGSNNVNAALLEKMPKLRASTISVGYDNFDVDAALRKILLMHTPTVLTETVADTLMALVLSARRVVEVAERVKAGEWTSIGPDWYGTDVHHKTLGIVGMGRIGMALAQRAHFGFNMP/R L*RAPPP*RSRRTLQRLPLRFY SVTRVRFRLLPDAVN**DASSV WRRRTIRGPSLGLSPGWNTVRSLCAFFG
28934	59302	B	29109	1	1359	
28935	59303	A	29110	874	1926	
28936	59304	A	29111	1	777	
28937	59305	A	29112	137	376	
28938	59306	A	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGNFC*RHGS*KITAGYIVPLPEESA TATGASWTHPWGRQDASW
28939	59307	A	29114	1846	2126	LMELIEKHVSFGGWQNMVRYHSQSLKCEMNNGVYLPKKAANEKLPLVYLWLSGLTCNEQNFITKSGMQRYAAEHNIIVVAPDTSPRGSHVADADRYDLGQAGACFYLANAQAPWNEHYKMYDYIRNELPLVMHHFPATAKKSISGHSMGGLGALVLA LRNPDEYVVSFAFSPIVSPSQVPWQQQAFAYLAENKDAWL DYDPVSLISQQG/LRCGNHG*SGVE**FLRRQLRLQI*KDWPO*EAHVH

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28940	59308	A	29115	184	985	LGKRLVTYHTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEGGVEIEKVAEETPLHIHKVALDPLTGMPYQGRELAFKLGLEGKLVQQTQKFMGLATIFLERDLALIEINPLVITKQGGDLICLDGKLGADGNELFRSLILREMRDQSQEDPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATKERVTEAFNPPGYIGPYQGVPPAGPGVTRMGKSVRRIVQVGCQVAAGSH
28941	59309	A	29116	1825	3186	
28942	59310	A	29117	366	1903	
28943	59311	A	29118	1	2139	
28944	59312	A	29119	345	431	AASGSADDNLHHQYN*GDIACLHALLP
28945	59313	B	29120	1	2616	
28946	59314	A	29121	1	1521	
28947	59315	A	29122	1	783	
28948	59316	A	29123	96	215	
28949	59317	A	29124	1	292	MWWGGLLYWLAALVTLLWAASQIQALKKLTCAISQTLTEEQPV LNSKSWLTSQNDYSLPDSLTERJWLTLISQRISRGELREF*TGRRKLVTQECLV
28950	59318	A	29125	3	529	
28951	59319	A	29126	1	884	MVDSLIA RVGV MARGNAITLPVCGRDVKFTLEVLRGDSVEKTSRVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI GDGSRRRKAAALTESDYRLVY GELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLRMKVEEG DVILVKKLDRLGRDTADMIQLI KEFDAQGV SIRFIDDGISTDGEM VLDKLARGYADLSKAESQWDE MMRTAGSLKGTIHASELIRSLKSSRPSGLAQAIMEVGRVNKT LYLLNYIDDEDYRRRILTQLNR GEGRHAVARAICYGQRGEIRKR YREGQEDQLGALGLVTNAVVL WNTLYMEEALSWMRRNGEEI DEDIARLSPLMHGHINMLGHYFTLPEDILKGLR*RHLPPSSSA SPALPIGIHVHKHLLGDNRYP I WIMQPSAHHPARQPEHDNHR

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28952	59320	A	29127	143	523	NQTLMIKGAAGHGFNPLCIKAT AGVAGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPLILPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	B	29128	I	4107	
28954	59322	A	29129	1892	2720	PTAWSPPRPTSMTSISWVICCM ERSNLSQPMPTATKGRQARGAG VEVDVDWLIARPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRQFGFVKARFKGLLK NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFALISTA SALAGLILLCLFGPALLAGYITE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRNGRVFLLVFILPFS LRRVGHAAH
28955	59323	A	29130	1332	1635	
28956	59324	C	29131	I	1677	

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28957	59325	A	29132	1	1114	MAEACNIGLEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFTVPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGLTRDSNLFVLEGLLEQQTG LNPVEIMTDTGCGLEKQEEPPS LLRLNNRIKQLLPPVDLTELLE IDAQTGFTEFAHVSSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFTVPVK TINSGSNRKYFGSGRGITWYNF VSDQYSGFHGIVVPGLTRDSNF VLEGLLEQQTGLNP/D*NHDRH LRLSGETGRATIASK*SDQTA TPTGRFNGTVEIDAQTGFTE FAHVSSESGARAQDLHISLRY* WLKPVIS/ALEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFTVPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGLTRDSNLFVLEGLLEQQTG LNPVEIMTDTGCGLEKQEEPPS LLRLNNRIKQLLPPVDLTELLE IDAQTGFTEFAHVSSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFTVPVK
28958	59326	A	29133	1	2908	
28959	59327	A	29134	735	932	
28960	59328	B	29135	1	1413	
28961	59329	A	29136	1	1469	
28962	59330	A	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	A	29139	1	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNL/L RRFHEATAQNAPDVVWVGSGT PMREFLHVDDMAAASIHVMEL AHEVWLENTQPMLSHINVGTG VDCTIRELAQTIKVVGYKGRV VFDASKPDGTPRKLLD/TRLHQ LGWYHEISLEAGLASTYQWFL NQDRFRG
28967	59335	A	29142	538	1116	
28968	59336	C	29143	1	2967	
28969	59337	C	29144	1	2214	

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28970	59338	A	29145	1	469	
28971	59339	A	29146	780	1052	
28972	59340	A	29147	617	2408	
28973	59341	A	29148	2	488	
28974	59342	A	29149	1	1083	
28975	59343	A	29150	527	3213	SWRSVQLLPATSIPIWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNLKEHGCGVTPIMS MRRWLAKNRPQADVRVINYVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSLGKFTKLQPAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGYAVVALIKPGAQIGR SPVNCDVASCHVISFNLRLVELAI MRRLLCRIAVLMSYRIEQRLMF LERLRHVGLIAHPAKKAIKKTR KPGMKVTFEQLKAAFNRLISR GVDSETADACAEMFARTTESG VYSIIGVNRFRFIQQLENGDIIP DAQPKRITSLGAIEQWDAQRSI GNLTAKKMMDRALIELAADHGI GLRLLAGGGKRLYWHLLDQLH RRNDNISLDLGNNAEAVILRED MLPRENFRPGDRVRGVLVSVRP EARGAQLFVTRSKPEMLIELFRI EVPEIGEEVIEIKAAARDPGSRA KIAVKTNDKRIDPPTQHEDEED EGLYDDPFPLNECSVGPGHRRR FAPPEAQFRRPETLKGAPTSRIP ETSVGVSGSDFEPHLMRELTC RLTAITWCYPGSAYAVHPQDE
28976	59344	A	29151	1	812	
28977	59345	A	29152	1	1830	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \=possible nucleotide insertion)
28978	59346	A	29153	1	1308	MMPLIDLEDPRLVLRREIGMLL HVDYLDLVHEKVICRGRNGGQ DREKTTMEKVRSSGTICPQAPE VVNHYFTDDGYRIISARFGVP RTQVRTWVALYEKHGEKGLIP KPKGVSADEPLRIKVVKAIVIEQ HMSLNQAAAHFMLAGSGSVAR WLKVVEERGEAGLRALKIGTK RNIAISVDPEKAASALELSKDRR IEDLERQVRFLERLMLYKELK ALAHPTKKVTLSHREGKQINH KAVQRLMGTLSLKAIAIKVKRY RSYRGEVGGTAPNVLQRDFKA TRPNEKVVTDVTEFAVNGRKL YLSPVIDLFNNEVISYLSERP MNMVENMLDQAFKKLNPHEH PVLHSDQGQWYRMRRYQNLK EHGKQMSMRKGNCLDNVVE CFFGTLKSECFYLDSEFSNSELK DAVTEYIEYYNSRRISLKLKGL
28979	59347	A	29154	1	836	
28980	59348	A	29155	1	1566	
28981	59349	A	29156	297	936	RTSSSLMRSSSLRLRISGVSPRS IPRWFTSVSLPSSFRIRITTFRYT PGHVAPASRRSCYKYRR*PMRL YTMQISLS/VGSRPSGLRAFSSD CSPLPRTCSLRRRVLMITTSRS *SLTYGVDPVSVPVLAASEYF SRRYAGFQNPNNLLVSG*YQG NYRHFGLRGYPG/TLKNSNFQL TRSARISLSSRSISCTSTGGNTTL PPSSPPDC
28982	59350	A	29157	5	861	SWRSVQLLPATSPVQWETNQ FMGRDRPTTAESPYAVLLRP LAKLNIQRPVNMNMVENMLDQ AFKKLNPHEHPVLHSDQGQWY RMRRYQNLKEHGCQVTPIMS MRRWLAKNRQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCCKTKVVSGEYTVSSTMTLT DAEIAEGY
28983	59351	A	29158	1818	1991	SPSHIRRTAFNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPPQGW
28984	59352	A	29159	3	601	
28985	59353	A	29160	415	549	

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28986	59354	A	29161	2	501	
28987	59355	A	29162	1	1347	
28988	59356	A	29163	3	2461	
28989	59357	A	29164	1419	1640	IFCASLSGLGYAGIEARILTKGY TRK*IQQ*APSDQKRDVLPVHG ADSAMAKHGGSHRAVLPGQC DPHMESLI
28990	59358	A	29165	1135	2067	
28991	59359	A	29166	1	1364	MAGNRRFMCTPKTHGLSISOH GTFPEHAGCKIRCAGRSGRVVRP AELLAPYTGIDIAEGISKAMRG GAKFLHHGIKQQRYVVAEAIT EWRMAPGPLEVAVFAGVIYHL YYYRARFFCAAQPLVSGFHEAE LSLDDAKWVLHPGPDAGFHV DVDGRFVLAWMLFQGSYLAG ALGDQPVHIIHGLQLALWRPL QITQLIEVMLVGRGDQAVGQ ATLGIDTNGGLYAKGPLIAFLG LMHLRIALLFLVLRGTGCAYDG GRPQLAEKLYSELRAQIEVL DDRKERPGYMFADMEIGIPHT IVLGDRNLNDNDIEYKYRNGE KQLIKTGDIYEYLNALLIAVT VLTSMESDLVDLGMTLSPAD YAERLAALTQKCGLDGVVCSA QEAVRFKQVFGQEFKLVTPGIR PQGSEAGDQRRIMTPEQALSAG VDYMVIGRPVTQSVDPQAQTLK ATNASLQRSA*CRDAGTLRLRA WLC*FLQRRYHRYKGPVFPQV ELCQICQRNEFCTQRPVGMCHV
28992	59360	A	29167	627	854	NAGDRNRNFSCTAARQYGS RFYNCRR*RHGRKNLSAERNGL PEYRNCNPDHRPSVFLAAGRCF APTMCCHDASE
28993	59361	A	29168	1	1593	
28994	59362	B	29169	1	3789	
28995	59363	A	29170	940	1326	
28996	59364	A	29171	1	1377	
28997	59365	A	29172	1	2547	
28998	59366	A	29173	561	845	AKIVQLRPRI LRPSRSARRCP PSRRQRRRSGPLPEPAPRV S*QIFPSQYWR YRQSTENQKQRL DP RGQIVNVPARRIIRQKRCK CKV AGSA
28999	59367	A	29174	1	1284	
29000	59368	A	29175	624	866	
29001	59369	A	29176	1	1384	

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29002	59370	A	29177	2268	2684	RCRRCKRLLRRFRSLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRC HCG* RQC SSDGRKITSVHRGRNADGREL T HQA VRL LAYL SDRFARHHRHL RNAHRRGPDRIKERHFPATKL RHTPAV
29003	59371	A	29178	1	2142	
29004	59372	A	29179	1	2463	
29005	59373	A	29180	3	126	
29006	59374	A	29181	1	2013	
29007	59375	A	29182	891	1000	FDSFHWHSHPMLCCDRGQHK E NPQSRGPISQC*IQQ
29008	59376	A	29183	1	846	
29009	59377	A	29184	90	411	
29010	59378	A	29185	1	1580	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPR TQVRTWV ALYEKHGEKGLIPKPGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNAISVDPE KAASALELSDKDRRIEDLERQVR FLETRLMYLLKKLALAHPTKK AAEIPRSTFYHHLKALSKPDY ADVKKRISEIYHENRGYGYRR VTLSLHREGKQINHKAVQRLM GTLSLKAAIKVKRYRSYRGEVG QTAPNVLQRDFKATRPNEKVV TDVTEFAVNGRKL YLSPVIDLF NNEVISYLSERPVMNMVENM LDQAFKCLNPHEHPVLHSDQG WQYRMRRYQNLKEHGKQSM SRKGNCLDNVVECLFGLTKS ECFYLDEFSNISELKDAVTEYIE YYNSRRISLKLKDL YASCLTVQ LFGVSTVMGLLIRILGSIFQKAL NISKIESFVAVTTIFLGQNEIPAI VKRFMIAESHEVLPHLYGMGH CGSRRWYAEWRPLHRVHEPSG
29011	59379	A	29186	1375	3174	
29012	59380	A	29187	604	1268	
29013	59381	A	29188	1	288	
29014	59382	A	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	A	29192	1	3156	
29018	59386	A	29193	1	1824	
29019	59387	A	29194	1	1922	
29020	59388	A	29195	1369	1743	

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29021	59389	A	29196	21	432	GPGCNGVHRLCTE QRDVRGTV RIVLKTFFNCRDVTVFVAFEVNN TVSLLVATTDMTSGDTAIVVTT TGFVSAANEVQILAFFQGDVSF FPVATTTDTLSVTFNFPPNYQG VNDFFDFKQFLHSSDFCFGR VFSNFE
29022	59390	C	29197	1	1743	
29023	59391	A	29198	2005	2571	
29024	59392	A	29199	170	486	LQTQKDGIPAVVERLEYDPNLP RTSRWFRNDFSVVPLQLLGSP*
29025	59393	A	29200	1	1713	
29026	59394	A	29201	1	6729	
29027	59395	A	29202	1	753	
29028	59396	A	29203	1	1470	
29029	59397	A	29204	665	1773	ASSQVKSGWLSAKIPVISSYGP LLSVRLLSHAWPNLCPQLHCF LPGAIWSASSLLKSGNRPLIRLA SIVLPVPGGPISKRLCPAAV/HF QSSLSLFLTDNITEIML*RPDTW THVMYVLHHADKPNLYHGLPE NPEISETVKFWKGIWKPLAAVG FAATFAASIFHYVGVGPNRADE EENNLHEEKDEERKCSQDIQLV KERVIFLTGQVEDHMANLIVAQ MLFLEAENPEKDIYLYINSPGG VITAGMSIYDTMQFIKPDVSTIC MGQAASMGAFLLTAGAKGKR FCLPNSRVMIHQPLGGYQGQAT DIEIHAREILVKGRMNELMAL HTGQSLEQIERDTERDRFLSAPE AVEYGLVDSILTHRN
29030	59398	A	29205	948	1620	

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29031	59399	A	29206	1782	3667	HRRRCRHGYPPVPAAYRCRIWKCGQFHPTGIAGCGRTGHRRLPW*RRLSAEQWTWRTFYGALCAERQRPGGP*RG/SRSIMIEIREGRGCDGPWGPFAKLLDHLGKEVLESRLPGILELSRTFAHVDPSRFRLSLSLHDGRYSQSYRYNDTRDMVPINGSIHRIGREPHYHYQRCGQQYIGLCRNCNVIDTHICIYLVDPQIMDDIRRLLYSEISSAIHWLLPVVQGEHYMLVDPDTNEREERGRSETRGFPRVPLGRTVSTVWYPLSNAATLAATRCRSRSPHAFAPSSNNGFITATPLGRTHFLGMAFPSPACWRLRAEPERVEAVLSASGMNKAMRCGVSLICNFRLLDYAPIEKQWDLHFADYFAEDLKLAPLAKDGLVDVDEKGIQVTAKGRIIRRLRIRHLSMMPDAALVASYQAYDFLRIRHKQASAKQPNHCGTQHGSNGSLRTLWNSIDSGSVLTWCASLIFSSRKSLSPIQLVRSVDRCGDVKKRYSMREFSLGETHSEAEFRELEQNPSFVFFKPQSFAPVKGASAVPLVGRASVASDRSHPPGTTLLAEVPLLNNKGKFNQGYELRLMVALDVGGAIKGQHFIDIYQGIGPEAGHRAGWYNHYGRVWVLKTAPGA
29032	59400	A	29207	1351	1806	VIVGITSNSVTVAAVSSWCRTWVPVSVLCLNCYPASMALVRGVI RGV*TCLSLCPNCAAIIFAFGA VIFCITSVGFLFPMPVYKSGLRF FVFT*MRDTGVPQRLRAPRRSL SAKLGPACPFAYIVPHIWCRIWGWGTCVCLAICVCVCVAD
29033	59401	A	29208	1308	1647	RSWEVSIVFYVVVRPTGHV*HASGNLSHHRKRHPLADQAARKGETVPPRGRRSWRTQAHP*HLRQHRGQHPASLPTRTGTPQGRRAIYRIPVRTAGQFQRIEVDGFQRVGHQ
29034	59402	A	29209	1	2184	
29035	59403	B	29210	81	1356	
29036	59404	A	29211	1	2349	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29037	59405	A	29212	514	1136	ILRIMQRMGMKQFAGLLRLSGIK MLPSA**LGELLHAAGSFFQRG CLLFSTGGKIGVARRNFTGTGI DGI*TFADMSDGVSQRALHM* NALRQVAHFAPVNGQGIQV TTGDFANVSNNFCQRSKQHTA NAVPRHQNNQYHHQRDNRLP LGKSVIICVVSDDIAIQFFTAEG VLSKRFAHCLMPSLGGLSKIGP SMPLFRIISQFS
29038	59406	A	29213	1	2992	
29039	59407	A	29214	1	168	
29040	59408	A	29215	1	537	
29041	59409	A	29216	1	1881	
29042	59410	A	29217	1532	2160	KHWSDSIPGTEADWSASTTSGC AGFAAFACSSS*VICLLSGAVA AYAPQLRHQAIKRVIRRTSAFP LMD*TWFLSSTNGLASCASIS SAGSGAGSASGVTKVSVSDTAS GWPIFVTDRLSSCSTRFTLPKAN RLITVEPSLKRPISWPFSA TEPS FSPAGQVQRLMIPSRGGVMVP AQTVMSLPTIVATPGPYSHLL GSFTLSPP
29043	59411	A	29218	1	1713	
29044	59412	A	29219	2159	2715	TIPAKPVPSMVASGTVRFGFLT PVLTAADSTPTKAHRQSRILLMI A*PSVVS AVFLAA*VAASNQC QPTIAVITTGIRTSTRPIVA/CITG FVTGA VEIVLVANSVIDISVGSP FSIPQMFSARLGIATMAICPIMV SFSVAAINSASHNRQGFALQFFF NDAACGSGEFRILMQEEHPDSV VFC
29045	59413	A	29220	2	102	DFADFGTTIKQDFRLLGQTSVD RLQLSQGQAVKGNQLLPVSL VKRKTTLPNTQTASPRALADS LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM SVDLCHRDFAFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLPNTQTAS PRALADSLMQLARQVSRLESGV IGGAGSLAFPLPALIWCAVRYT PQVTCLLTFVTGILPISEPPSNRI FACWGKPAWTACCNLRARR
29046	59414	A	29221	1	1464	

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29047	59415	A	29222	3	29	MQTEQQRAVTRLICQGLFLL QHGAESALVDELSRLGRALG MDSVSESSISNAIVLTITK/D/GQC L.TSTRKNHDRGINMHVVTEVQ HIVI/LAEHHLDPPEP*EQQRR
29048	59416	A	29223	5	307	
29049	59417	A	29224	5	948	
29050	59418	B	29225	1	696	
29051	59419	A	29226	1	1083	
29052	59420	A	29227	817	978	LAGCYTMLPGNGPAGMHACIS KLDK*A/VKKRISEIIHENRGY GYRRVPLSLH
29053	59421	A	29228	198	362	
29054	59422	A	29229	1	2907	
29055	59423	A	29230	1	2541	
29056	59424	A	29231	1	1566	
29057	59425	A	29232	3	601	
29058	59426	A	29233	1	1347	
29059	59427	A	29234	940	1326	
29060	59428	A	29235	1	2547	
29061	59429	A	29236	527	1383	SWRSVQLLPATSPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNLKEHGGCVTPIMS MRRWLAKNRQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFTPVAAEA TSGLKFTKLQFAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCKTKVVSGETVSSMTMLT DAEIAEGY
29062	59430	A	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	A	29239	1135	2067	
29065	59433	A	29240	1	1566	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29066	59434	A	29241	1	1605	MKVPRGDMVFMQLNRKDDGQ FEDQLLLVLLPKHRGHLLQV ADDVWFKNNRAKCRQRRQQQ KQQQPPGGQAKARPAKRKAG TSRPRSTDFRSRDGIPEKATRTS CPSDSSVSFLQRPLSSTGRGSS LSWDSSQVLVILSTLTPSGTIVT AEPKYPFKEKLEVVNHVFTTDD GYRIISARFGVPRTVRTVVAL YEKHGEKGLIPKPGVSADPEL RIKVVKAVIEQHMSLNQAAAH FMLAGSGSVARWLKVVEERGE AGLRALKIGTKRNIASVDPEKA ASALELSKDRRIEDLERQVRFL ETRLMYLKKLALAHPTKKVT LSLHREGKQJNHKAVQRLMGT LSLKAIAIKVKRYRSYRGEVGQT APNVLQDRDFKATRPNEKVVTD VTEFAVNGRKLKLYLSPVIDLFNN EVISYLSERPVMNMVENMLD QAFKKLNPHIEHPVLHSDQGWQ YRMRRYQNILKEHGKQSMRSR KGNCLDNAVVECFGTGLKSECF YLDEFNSISELKDAVTEYIEYYN SRRISLEKLKG/LTPI
29067	59435	A	29242	3	1119	
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRRIEI SIEAGRVSDDGEIAKLGDNVE AWYRRLAGAFTLQECVMAA STFFIPSVNVIGADSLTDAMNM MADYGFRTRLVSDTNMLTKLG MAGDVQKALEERNIFSVIYDGT QPNPTTENVAAGLKLKENNC DSVISLGGGSPHDCAKGIALVA ANGGDIRDYEGVDRSAKPQLP MIINTTAGTASEMTRFCITDE ARHIKMAIVDKHVTPLLSVND SLMIGMPKSLTAATGMD
29070	59438	A	29245	104	1381	
29071	59439	A	29246	1	375	
29072	59440	B	29247	1	5082	
29073	59441	A	29248	119	343	RMPKRRRWGKLSTIRCSSTTCKK RLT*IVLPVRTPGRLCSSLSKSV ASHCLASCKAYSNPWKRPQS KRHYVTMR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
29074	59442	A	29249	468	935	VPLAVPYGRLWRTIFSLPSSFR STRVR*EVSGRSSPSISLASLVR PIT/LLIVNAHPVELLQVVFP DKHIAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPTE AVDLFFHFNAVTGFGHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	A	29250	407	2145	
29076	59444	A	29251	1	177	
29077	59445	A	29252	1	1767	
29078	59446	A	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	A	29255	2	314	
29081	59449	A	29256	2977	3913	
29082	59450	A	29257	1	2091	
29083	59451	A	29258	1	751	
29084	59452	A	29259	1	927	
29085	59453	A	29260	1	1113	
29086	59454	A	29261	1	875	
29087	59455	A	29262	1	450	
29088	59456	A	29263	1	522	
29089	59457	A	29264	1	912	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29090	59458	A	29265	1	2416	MLAQLSLQALEQDGLNRIAYPV VPPHVEYSLTPLGEQVSEKVAA LADWIELNLPEVLAVRDERTRY DIAVPRKRYGHAVSRNTFALRS QERYGHSVLETVGNSGSSKQFS MDILDPCARGPGQISLITVNHKL HVRCEIAYSVQTMVVKGGSA FAAFFIAVVLWMIGYVPNVEQS TQALLGMQFIMIALPTLFFMVT LILYFRFYRLNGDTLRRQIHLL DKYRKVPPEPVHADIPVGARLS FAERVMEGLSDGGQSLQSPSAL FSKQTLKNMSIYKIPLPLNILEA ARERITWTLNTPRVCSVSGG KDSGLMLHLTAEALAROMGKKI CVLFIDWEAQFSCITINYVQSLR ELYTDVIEEFYWDALPLTTQNS LSQYQPEWQCWEPDVEWVRQP PQDAITDPDFCFYQPGMTFEQ FVREFAEWFSQKRPAAMMIGIR ADESYNRFVAIASLNKQRFADD KPWTTAAPGGHSWYIYPIYDW KVADIWTTYANHQSLCNPLYN LMYQAGVPLRHMIRICEFPGPEQ RQGLWLHYHVEIPDRWAAIGSP ADREEDAEEYLEAIMEARVTV AGMGLVMEVQDYFDGEA'DRL AKAWLP/EYTPQIKSLKDERKE AYRQIVEMSTEPQDVLVRPA NKFEMTRVREGEKEADLPVWK HLLCDESGNYPALLNHWETK VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	
29092	59460	B	29267	1	10161	
29093	59461	A	29268	1	882	
29094	59462	A	29269	1	2484	
29095	59463	A	29270	548	945	
29096	59464	A	29271	17	352	DLQDTGCFMLMNTGEKAV/KS ENGLLTIIAC/GPTGE/VNYALE GAVFMAGASI/QWLRDEMKLIN DAYDSE/YFATKVQNTNGVYV VPALPGWSLLWTRTCHRIFFRH RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIHELN TDFLCLINHVVGGHIAFTGVD DDTGA*TFEGLCLIR
29098	59466	A	29273	1	975	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29099	59467	A	29274	65	562	DFRWHGDSRKVHRKNRLIKPL MILLTRLNRTNWPLTAAVIWP GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSTSS SIHHHINSSSLQCQPCASKYLAH YFTVSSIAAYSTPVVSTQEPWA TRHHPHHQQTDRRRPATRKSPR QYHNETNRQ
29100	59468	A	29275	1409	1641	PENGRPVYAGGRDAAWRDYY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSA LGLCL* RLAGGDWCRDYSL
29101	59469	A	29276	1	3252	
29102	59470	C	29277	1	2760	
29103	59471	A	29278	1	723	
29104	59472	A	29279	14	338	
29105	59473	B	29280	1	1201	
29106	59474	B	29281	1	1866	
29107	59475	A	29282	1067	2753	
29108	59476	B	29283	1	1144	
29109	59477	A	29284	3	724	LAQLYGDPPAWPTPTRGVSEIR LALRFKSNDSLRLRHFKDSTSLY LEIVDYPGEWLLDPLMLAQDY LSWSRQMTGLLNGQRGEWSA KWRMMSEGLDPLAPADENRLA DIAAAWTDYLLHCKEQGLHFI QPGRFVLPQDMAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL Q/PLNSGHSIYDMR WPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	A	29285	1	1863	
29111	59479	B	29286	1	813	
29112	59480	A	29287	1	546	
29113	59481	B	29288	1	2691	
29114	59482	A	29289	1	1212	
29115	59483	A	29290	1	2328	
29116	59484	A	29291	1	531	
29117	59485	A	29292	188	358	
29118	59486	A	29293	2545	2713	LLVVQFFQHL*VPSGTSP*L*H LSGILWHFLQLALLYRPFVLV LCRSLGAVCLY
29119	59487	A	29294	1	2046	
29120	59488	A	29295	3	654	
29121	59489	A	29296	2	182	
29122	59490	A	29297	1	1215	
29123	59491	A	29298	141	266	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN ASGHAQRQSDGDLRSRAATGG DHSAGDWCGRRVQTSAG*LWR KARPWPNR
29125	59493	A	29300	2353	2758	SQAYHQVLPVCEAAPIPDDNHT LAALR*HGVEYEHMDQDCWA SFLPEERLFWRPIAPRSDRVEC VDSLPLTAVGKVDKKQLRQWL ASRASARAQRSSPLAEARKPQY VHQGMDNARTALQKPEQARA HTEVHWT
29126	59494	A	29301	5	793	FLQRFVADLPCGAQVVKFSTFR TQCRQTEATLKVLFHGTNNVV TSIGATTQVTNDARTDLRKQLV IDILFGIRRTLLHFLDRHNRHF CRCRSRNTFLFQLLRMIRDFND FELV/NPLSLDSVLGMQPLREEI QQADRDDDKHHQGAGLLELET ANRFPQGDADPACADHADDGR RADVGFEAIEGVGDQQWHHL WQHAVEDLFELVGTGGANAGP GSIASATESSESTPVVWNSA STPARQRTGRGRRRPTAWRRP
29127	59495	A	29302	1	2457	
29128	59496	A	29303	1	292	
29129	59497	A	29304	1	440	
29130	59498	A	29305	593	864	RTSAEPINPAPPVIRIFLISARLC* WTLSPILTLN*L*STSITSTSAVA SASSSCARVQSPVSFFGNWWM LGSTTRVSPLCHWAISSADF
29131	59499	A	29306	2	696	VPAGRYTGRDLHLHL/LPFRS LPARHRVRRYRPLEAC*TPCTD GYHRIFYRLKGESAKDGSVMT LRSFLDKDGHPIDVEDINDQAR HLVRLMPVLRRLRDARFMRRIR NGTVPNVPNVEVTARQLDFLA RELSSHQNLSDGQIRQGLSAM VQLEHYFSEQAGAGQARYRLM RRRASNEQSRWRYLDIINRMD RPGGRSYRVILLGLFATLLQAK GTLRLDKDARPLLEIE
29132	59500	A	29307	3	1405	
29133	59501	A	29308	1204	1411	LRPALYQPARLSDAAVRKTG*F AVVSGSEHAESDAG*SGELLEQ LSEVLR*PDEIFLWRCRAEREQL GL
29134	59502	A	29309	236	645	

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29135	59503	A	29310	1	776	MELAAALRSENQPQDEKPLGETL KDLFSRPVLPMTDVHLPNLN IEEFMGEQLHVTGDTDIYREHH AAEMSNIDGNTKLDALDISSQ GIVDASGTAHLSDNWVPVDITLN STLIVEPLKGDVKLKMGGAL REQLEIGVNLSPVMDMLRAHT RLAEAGLSLNVEVNSKQLYC/L AHCMSMPKESGADEKNSDNR WCRVYWLGAALYHQRNERR GGSGR*ADLRKPDVAGTGRA KRALCL*ES*YLRSGRTGTRIH
29136	59504	A	29311	955	1095	HRRHPIPLIHHRDQPFRLQLRK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	A	29312	1029	1490	RLPPAVDPTARLRPASGRYP CIPAFVGTAPVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWSQLDRQANPAQVEIIEIRQ LVRKSPQTAHSPARIWRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSQKYQSRARRRPAASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQL SLSDKCRQGTSGRLSLRKSDC TPISHASCSSSLHGH*VSVAVR LRMTDFSRVTGKDQVRFDAGL GWTLERLLSAAAFRVALKAG DMAILASRPPTVTTPNSMRLGR LYRSGVYGR

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29139	59507	A	29314	2	2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWGYDYTGADN NANFGKAVPADFNNGGSFGRGD SDEWTFGAQMEIWCYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRCGAKSPFCAIT FRVRWTIRKSTKCCANRAYKR NITVGRIRRLRRIRQPLPDATLC VLSGLQTEHNRRWPNVSVCHFSP DSTFYNDLSGRMKNVRLMFNG IHRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVEIVGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLLLSPESDLYHFERDD FWFPFGDINGREHHLHIILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFYRLEGESAEDEGSVMT LRSFLDKDGHPIECRGI*PIKAR HLVRLMPVLRLRECPVLMRR IRINGTVPNVPNVEVTARQLDF LARGGQARYRLMRRRASNEQR SWRYLDIINRMIERPETRYTREI GFTSTNIDLIYGLPKQTPESFAF TLKRVAELNPDRLSVFNVAHLP TIFAAQRKIKDADLPSPQKLDI LQETIAFLTQSGYQFIGMDHFA RPDDELAVAQREGVLHRNFQG YTTQGDITLLGMGVSAISMIGD CYAQNQKELKQYYQQVDEQG NALWRGIALTRDDCIRRDVKS LICNFRLDYAPIKKQGDHFDAD YFAEDLKLLAPLAKDGLGDVD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29140	59508	A	29315	1	2237	MLTGYRAVSRHKSQRYTADDA EEMIGKLTGMPIPLNSLRQWIL GLPGDATDYKLLDDQYRLSEITY SQNGKNWKVVYGGYDTKTQP AMPANMELTDGGQRKCLKMD NWRADGYHTLQTLFQFLDYG DTISIELRDDGDIRLLTPVEGVE HEDNLIVRAARLLMKTAADSG/ LSSDGKR/RSSSCARVQSPVSFF GNWWMLGQTTRVSPCHWAIS SAISHRRFAFAQVINIRFKRQTKA GDFQFTGAFIGSRQAISHRRFHL IDNPERFVIVHFARGTDKPRLLG VLCHDKPRINSNAVTAHARAR LKNINARVTIRQANQFPDVPNLI GTNQRHFISKSDIHIAEAVFEPSI IAADRLNPLVNELIIMPDIKRL DAFVRIAHEELLYLLGILMNPA NKDHVLPILITGPKESADYFRV LDEFVVTLGENARRHYRIIIDD AAEVARQMCKSMPLVKENRR DTGDAYSFNWSMRIAPDLQMP FEPHENMANLKYDPQPEVL AADLRRAFSGIVAGNVKEVGIR AIEEFQPYKINGDKEMRRMDD LLQGFVAQHFGSYNDLLMEL LPHLLVEGMLISA VSAESLPWL HLSCVANISKRQLICAVPLPKPP KAGLLGKNIMGTGFDFELFVHT GAGRYICGEETALINSLEGRA NPRSKPPFATSGAWGKPTCVN NVETLCNVPAILANGVEWYQNI
29141	59509	A	29316	1	2892	
29142	59510	A	29317	19	649	
29143	59511	A	29318	2471	3036	KVTWVTCISLPMTLSPSAAFSSL FRMKILSLK**KRILR/SSGKPAA RQGDMTQYGGSI VQGSAGVRI GAPTGVACSVCPGGVTS GHPV NPLLGA KVLPGETDIALPPLPF ILSRTYSSYRTKTPAPVGS LGPG WKMPADIRLQLRDNTLILSDNG GRSLYFEHLFPGEDGYSPQRVT VACAPRRGKTG
29144	59512	A	29319	1	1476	
29145	59513	A	29320	688	1578	
29146	59514	A	29321	1	1653	
29147	59515	A	29322	1	218	MLIVFSLPSDTLVL SPL*PNFRT RPF RPSSVPR**PKDKLIATSA MMEAAYSSVIANVVLVPVMDA KWLAR
29148	59516	A	29323	3	260	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR WLGHDKRATLLWLKLEAAGSP LRPLSVQVTTTPQVEAETDNHAD NSYNAGLFIVNSLYTAEGVMD KHSLWQRYVPLVRHEALRLQV RLPASVELDDLLQAGGIGLLNA VERYDALQGTAFTTYAVQRI GAMLDELA AAVTGCRACDAT RVKWHRRQ*GNWSRNLAKPR KLR*RNV
29151	59519	A	29326	1	2349	
29152	59520	B	29327	1	747	
29153	59521	A	29328	275	729	
29154	59522	B	29329	1	2469	
29155	59523	A	29330	1	969	
29156	59524	A	29331	148	1180	
29157	59525	A	29332	56	170	VHA*GSLFFPELSMHQDLSQGH EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	A	29334	482	765	
29160	59528	B	29335	1	1713	
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNT**A SAPGN/ARWNSYVG*KHH/SCQ WGDYRRQCFRGE
29162	59530	A	29337	1	3189	
29163	59531	A	29338	1	1344	
29164	59532	B	29339	1	1233	
29165	59533	A	29340	1	1572	
29166	59534	A	29341	1	3591	
29167	59535	A	29342	1	843	MNYSHDNWSAILAHIGKPEELD TSARNAGALTRRREIRDAATLL RLGLAYGPGGMSLREVTAWAQ LHDVATLSDVALLKRLRNAAD WFGILAAQTLAVRAAVTGCTS GKRLRLVDGTASAP/GGGS A WRLHMGYPDPTF/TDFELTDSR DAERLDRFAQTAD EIRADRGF GSRPECIRSLAFGEADYIVRVH WRGLRWLTAEGRMFDMMGFL RGLDCEVPDPKRRTNLSLWRITK MVIWSLQVAIRGTVSLTAYKTQ LKNARHRLNEAPRRRLQMVQ PLS
29168	59536	A	29343	2	3203	
29169	59537	A	29344	227	634	IKTLPSPDKLTRISKSIYRKQR AALFTHSFTTWVLAILEHRRFF AK*TRSISKAHVISCVAAGHTLA AAPQPHYFTRETYSPERVSTLM TSPICTNSGTLTAPVDRVAGLP PVPVAVSPFRPGSVTSSSTKFG

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29170	59538	A	29345	1	1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRLPEPPFH
29172	59540	A	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRLPEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTGSPGHRGKPGT REDEHGV/ELDRRLNFEWWK PEYGINLYQDYKQDGFVEIPD QNNPSLGDVMIMQIGQNVVPW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGVFHR FAVDSYPEAIRALSSQVDGFKE YMQSEIGSRSKFAIFVDGVNNG HHEEEKFKCAKEIRIVPIPTGSK TGGLFQVVLGAAIMVAIFYTG GASLALMGTMSSSLFMMGGA MVLGGVMQMISPPQGWNRNFEV QSSKNKPSYAFGGAVNTTGGGI PSPGPVWISRRWRNFLSRFLC RGYELKLTRLARVFFRLYNST
29175	59543	A	29350	1	8043	
29176	59544	A	29351	1	876	
29177	59545	A	29352	2020	2224	CVESRCCHATRCGSK*YSGP/PE DTDCLKTEAAGAGVACDAEAP DEAPPAKLHVLPPHPEVLKITI
29178	59546	A	29353	1	2346	
29179	59547	B	29354	50	340	
29180	59548	A	29355	284	520	
29181	59549	A	29356	2	304	
29182	59550	A	29357	79	177	
29183	59551	A	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHRHHWH/GNRE NKVNCQLICVDIIINTAQPTSES /DQRQH/TLRRQTRDRRHS HEP
29185	59553	A	29360	2	388	YTVSFLLVITQLGFCSVYFMFM ADNLQMQMVEKA/TRDLQHLPA QGDSADPHPGHSFLHADNPA LPDPVGVYPEPQGA VRLLDIGQ HHHPWEHGSDL*VYHGGDSIS QQPTLDGKLEDLLAVLYSHL
29186	59554	A	29361	467	3014	
29187	59555	A	29362	1	1174	

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29188	59556	A	29363	1	986	MKVTFEQLKAAFNRVLISRGV DSETADACAEMFARTTESGVY SHGVNRFPRFIQLENGDIIPDA QPKRITSLGAIEQWDAQRSIGN LTAKKMMMDRAIELAADHGIGL VALRNANHWMRGSGNGWQA AEKGYIGICWTNSIIVMPWPVP KECRIGTNPLIVAIRSTPITMVD MSMIKHTLPQRAAGTDRKLAM SREAQLLERHGYAFNELDLGK REPVTTEEKLFVAVCRGEREPV TEAERVWSKYMTRIKRPKRFH TLSGGKPPGKKIVIRPLPGLPV IRDLVVDMGQFYAQYEKIKP/V PVE*WTKSASSRAFTDARAARK
29189	59557	A	29364	99	375	THQPARRFPAYHYAHAAAAA PGDPLGADLQLCARHYHRQRH CVPRHAGYPRSDGLHPQPRGR WRIRCSDCLRVP/SDRGDAGDY FHL*LADR
29190	59558	A	29365	871	1206	
29191	59559	A	29366	1784	1966	RPLDVSFMSSTNSPLTDLVG YLTFSAIFLSWRLLSLLDAA*TP YPPWGSVHCRRFCSL
29192	59560	A	29367	1	1276	FHIKLVLTGATWTALPYCHSHV GLRASLKPTPPFWGRAPLGTRP SQQKTECRILNFPETPIFGNSFK YDIEVSNKSPDEEVKLRHHHLA RCMKNFKTDIYFVSTFEPSTKS VDLLTVETTFAGTVCEYADMPK EWTTTTRGLYDPHTLISASCHKV EGLFSFEDRTVA TLIRLFIHPVK SMRIGIGLTHALADVSGLAFDRI FMITEPDGADIAVKFTTGIRLKV PCPPDHPAFSITNHQTEVTALV VFECEDIAVRGSDRLRLSPGGG SNTDWVIFGLLIKENPGSLLAV GVNLLGKILLSVVAASVSESGQN FLSVLPVRSEGCFVVIDVDVEL PGLRDIADSVKGTGVIATVPAVIP ALWEAEVDVNIAAFRSQKAYIS GQVNSKSGQQAINT/DATDYSRG HQLKLCLQSECFHGIYHRIDVA

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29193	59561	A	29368	1	1815	STLEDPHYVHIAEVSVPVVIISIY GATGEKYGFITYRCSEHAALSL TKGAALRRKNPSFQLSYGGLR HFCWPRYTDYGYFELQINRLAL FSTNVTAEPTVMHLAPPVGTQL PLPHLSHDNSSKNSGGCLPGAS VSCNYREPAVRLALASTPLLR AQSPFFMHKDKDPLFWFLTVP KWRKGEVILSSRPKKTEGSW FPKTFFGFGKSHVLVKEFYNRK HHIAKQQAHAVERTRLEFCPKG LGYSKPQTQGDYAIQHF/L*T NLPTGCWAKYA VISFMRD/TV DDKHWP EEHLAKN*LGLLADS GVRV/KLPWGAPHEEERAKRLA EGFAYVEVLPKMSLEGVARVL AGAKFVVSVD TGLSHLTAALD RPNITVYGPTDPLIGGAPENG DSDSALYRLRKEMEEFHLVVG SDIFGKHQHGTE DTSTTCPSTLE EFETQWFTTGINRILLATDGD NVGIDDPKSIESMVKKQRESGV TLSTFGVGNSSNYNEAMMVRIA DVNGNYSYIDT LSEAQKVLNS EMRQMLITVAKDVKAQIEFNP AWVTEYRQIGYEKRQLRVEHF NNDNVADGIGAGKHITLLFEL TLNGQKASIDKLRYPAG
29194	59562	A	29369	3	1993	
29195	59563	A	29370	1	1782	
29196	59564	A	29371	1	3858	
29197	59565	A	29372	1	705	
29198	59566	A	29373	104	471	LWWAGA/SYLCWWMGYQMLRG ALKKEAVSAPAPQVELPKSGRS FLEAIHFGSVFSLFVGDNVGTT ARWGIFALIIVETLAWFTVVAS LFALPQMRRGYQLAKWIDGF AGALFAGFGIHLIISR
29199	59567	A	29374	50	620	
29200	59568	A	29375	194	767	LWW/AGGLYLCWWMGYQMLRG ALKKEAVSAPAPQVELAKSGRS FLKGLLTNLNAPKAIHFGSVFS LFVGDNVGTTARWGIFALIIVE TLAWFTVVASLFALPQMRRGY QLAKWIDGFAGALFAGFGIHL IISRLALIVPGLLQKNGGWRRM AHSAVIALVCHAIALAEARILPDG DSGQNLSELLNVGSLVS
29201	59569	A	29376	1	1038	
29202	59570	A	29377	1	513	
29203	59571	A	29378	485	1166	

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29204	59572	B	29379	54	275	
29205	59573	A	29380	2	215	IFLLLLPPHHLLLLLLLLLLLLLL LLLLLLLLQ/MIPLEFCRLYRKQG CICFWGSLGEILLMAEGEAGAS PSH
29206	59574	A	29381	100	393	FLLLLLLLLLLLLLLLLLPLLL LFSSSFLLLLSSFFFLSSFSFSF SFSSSPSPSPSPSFLLSSFFGV ISLDVVTLAWQSARITGVSHRT
29207	59575	A	29382	264	911	ILGFLRDGNFWRKSSQSFPPVHH LLICLLRKSSETMQLTDEHLIHD HPKRPPITELVVPGLHEHLRSN VG DYRCEPPHLLTKRNIFCILSEA TDITY*LTSSIFPGFCRLT*LLPL TEITGEAVVQPIKFCPCMCFQFS CAKIWTRGMQWHLEAWRCQK PQSPKGGVMTALAEAPKSGLL EQFMPPMPQYLAVQKKVVVF DVSVDSEKLVNRYVG
29208	59576	A	29383	1	261	
29209	59577	A	29384	3	195	
29210	59578	A	29385	1	399	LERLSAPCISLLSRSLSSLS LLFFFFFLLLLLLLLLLLLLLL LL/SPPPLLLLLLLLLLLLLLL LLLLLLLLLLLLLLDPPGDTIQGA PSRGYHPRDTIQGAPSRGHHPG DTIQGVPSRGYHPGGTIQGA
29211	59579	A	29386	15	159	SPLHLSLV*VKQLLLLLLLLLLL LLLLLLLLLLLLLLLLLLLLLLLL LLLLLLLLSSSFLPS
29212	59580	A	29387	17	429	SFFFFFFFFFFFFFFFFFFFFF/C LLLLLLPLLLLLHRRKHLCVTLG CLRWLGLQCVRLQGSCAWLQT LGWVHTYACVCTFFLDQQVAG RILLVEDPRSSLQCCLLDA/P LCCRFQKNMHFIRT*R*VHCST TSIQFNLEP
29213	59581	A	29388	3	282	RELLRGNGVYIGP*SILSFFLLLL LLLLLLLLLLLLLLLLLLLLLLLL LLLLLVN*GVCCTLLSGPEISCRS DFAQGPTPLQGAPQTALGNLAS
29214	59582	A	29389	3	264	
29215	59583	A	29390	296	421	
29216	59584	A	29391	3	210	
29217	59585	A	29392	1	252	
29218	59586	A	29393	1	1731	
29219	59587	A	29394	1102	1362	NLGTAA TLFFLFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFLFLF L/VPLLLLLLLLLSSSSCSP PPSSSLEKLYLSI
29220	59588	A	29395	3	2368	

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29221	59589	A	29396	1	318	MEKKSPAYFCCRDQMQUIHSDA ALQRLTRFNDPEGWSNLAKN QYLSTSMKQKIWQRLASHRKN NPKADSDAYETSDMILSELIS HGEVDDQMLLNATALIRSDDW DFLESALISWDNLPAVVLKELQ QNTPRNDIWAKFFLRQENSSRA QVDEALRVYYALDPDALAQLD VLAKRPYKTAAFRGEKTHRPV RRSVRQNIIDQADRLHGAQRLV INTNRTRVVDQLIEFLHHQHVN AHLAEIVRHHQPNRAGTSDRHL NAMVNSRLDVRNNEQTEYKTV RGLTRGLMLNMLNKLDSTSP CRMLVCCVPRAPPNPGGLNPR AHSLNRSPP*NPLKLLSPTGPFEG MRPLGTHFWGGIGHGQGPWEG PQFGLGMNLLVKS LGHWATW VLARAKILRFELGASMMVAST
29222	59590	A	29397	2	4002	WQE*VHYIWGVMMHGDGLISMK SRIPVWEEFVPRFQATLELGV AMIFATAVGIPGVGLAAVKRGS IFDHTAVGLALTGYSMPIFWW GMMLIMLVSVHWNLTVPVSGRV SDMVFLDDSNPVTGFMLIDTAI WGE/DHGTFMGAAPIRILPAYG LGTIPVAGFGRMTRSSMLEVLG EDYIRTARAKGLTRMRVHIVHA LRNAMLPVVTVIGLQVGTLLA GAILTETIFSWPGLGRWLIDALQ RRDYPVVQGGVLLVAT
29223	59591	A	29398	187	1710	
29224	59592	A	29399	1	791	
29225	59593	A	29400	353	646	FYWNWVPFTNWQNPRLMGQK *HARWLHLRSLLPAM*ATLL*R ENNR*LLLLTLTSIFKTRIRRLS VSKP*VKAKKKTRLIIWSTSKFL SCMMLKFT
29226	59594	A	29401	406	1023	
29227	59595	A	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLIEKMRES GDIHSHHGWHLHPDHKAGFSE EQQA1WQKAEPLFGDEPWVVR DSPGYFALMVRKFNCCVIVFR R*AQRHRYTDVVVEIACRIKR VAALA
29229	59597	A	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	A	29406	1973	2582	

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29232	59600	A	29407	1	1483	MFVLADFGHTRRTRNSRLGHNIL PARIAPDAINKWLSGFFSREVQ LRWVGPMQTRRRVKRHNTVPLS FADGYPYLLANEASLRDLQQR CPASVKMEQFRPNLVVSGASA WEEDRWKVRIGDVFVDFVVKP CSRCIFTTVSPEKGQKHAPAGEPL KTLQSFRTAQDNGGGEGEARA ANTGATHRGRHRSFSAVRYRD RLNMYVLRRMDLLYRVKTLW AALRGNYHTWPAIDITLPGNRH FHLIGSIHMGSHDMAPLPTRL KKLKNADALIVEADVSTSDTPF ANLPACEALEERISEEQNLQ HISQEMGISPSLFTQPLWQIAM VLQATQAQKLGLRAEYGIDYQ LLQAAKQQHHPVIELEGAENQI AMLLQLPDKGLALLDDTLTHW HTNARLLQMRAGGWSVKEG REKEYFQSPRGWGRSLMPSLGI IIRPP*RPKNTENRRCISAVTS EKEAPETINQYKAAVRRPFLFL ATALAQSEVRVCIATWN
29233	59601	A	29408	2	1406	
29234	59602	A	29409	1	1818	
29235	59603	A	29410	441	583	GVYRFPWFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPLGSS VSSR
29236	59604	A	29411	835	1143	RQLPVSLYVRVAFENGCFGSC SVGG*GPPAARLGEEQVRGGSS SPCIHAPRRLHSFLLLLLLLLL LLLLLLLLLLLLLHLSSSSSFSST SSSSCSRSFM
29237	59605	A	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	A	29414	1002	1145	GVYRFPWFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPLGSS VSSR
29240	59608	A	29415	2	289	
29241	59609	A	29416	1	919	
29242	59610	A	29417	329	405	
29243	59611	A	29418	48	268	
29244	59612	A	29419	2	4625	
29245	59613	A	29420	1	867	
29246	59614	A	29421	1	684	
29247	59615	A	29422	409	543	
29248	59616	A	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	A	29425	3	202	
29251	59619	A	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH S

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29252	59620	A	29427	1	1774	
29253	59621	A	29428	3	184	MSENMRCLVFCPCDTLRRMMV SSFIHVPPKDMMSIFSICLSAASI SSL*ASVCSYPSLNF
29254	59622	A	29429	667	834	
29255	59623	A	29430	1	738	
29256	59624	A	29431	39	230	QMAQHLPHLVFGSHSGSLWEL LSH*VYLLILSLPPPHTPQQAPV WDVPLPVSKCSHCSIPTYK
29257	59625	A	29432	985	1205	IPGSRGKNWVVTGTGQGCCHRG PAESDGPAGGARHWEQPPA*Y LVFLFCSQRRWPGRQQRQGSQ RSWPSVRAAP
29258	59626	A	29433	339	592	PLQAWGPSLCS*AGTPSRKPSP STAHVKKHRLCIPTRRGFSSDN WDPVSSPTCNDARQLHAQVDL EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFQLHPCPFQGS*LLCI GLAHAPLAQRSLLSLTF*CLLS IHQTHSPSSFCPLLARSCDPLEE KRHSGRFRNFQPCSGFSS
29260	59628	A	29435	517	603	
29261	59629	C	29436	1	1188	
29262	59630	A	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIIEGSLVLFHWSISLFWYQ YHAVLVTVVL*YSLKSGSVMP ALFFWLRLDSAMRALFWFHMN FKVVSNSVKKVIGSLMGMAL
29264	59632	A	29439	1	1308	
29265	59633	A	29440	162	377	YSHCSIYTRKIQFLCCPSIKTHL GTNLTS*TFFT*VNIISIYLEASLF FSFLDLGRADKGSSTLTVRSIIT
29266	59634	A	29441	1	480	
29267	59635	A	29442	731	850	
29268	59636	A	29443	531	845	
29269	59637	A	29444	11	649	
29270	59638	A	29445	1	2433	
29271	59639	A	29446	1247	2420	
29272	59640	A	29447	29	94	
29273	59641	A	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGRRSSSTSGKGTAGCPQSPCF CRCSTLRRTAASPGISPPCPKICS CSPLESIWMSNGLCRSCPPSEDS TCGC*GCCCCCCCCCCCCCR RRCPSLGS DAGTELETQRPAG TGPPTVAPATFLQSRRLMVGA GTPTLGVRTPGFLQLGFFYWL EDVERDTS
29275	59643	A	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29278	59646	A	29453	1	599	
29279	59647	A	29454	1	504	MWNCLETNKLFFQESLQKTATR LSAFSWEEAKVQLSWVVLNLA TSAMLPKFYPNEIKVTYLRCTG DEVGATSVLAPKISPLGLSS/VK ALKEPPRARKKQKTIKHS/GNIT FDEIVNVAQHMWHRLSARELS GIHKEILGTPQSVGCNVDGCHPH DIIDDINGGAVECPAN
29280	59648	A	29455	1	1269	
29281	59649	A	29456	434	655	PFSSPASSSGR*KTTSPFAKLFN ACRISLLASAEVNPNISAYLAT WISQIPSCSCLVPDFLIWSTNR YSIRF
29282	59650	A	29457	1	801	
29283	59651	A	29458	2	722	GRVGGGGQGANYLRVVPESGV YSTPSRLPPLPPKVRPPTRFKSV YLEVAPKGEVGAITSALGPQRI GPLGPVSKKKLG/DDISKA/TG\ DWKGP*GITVKLTIQNRQAQD *GGCLSASALIHKALK/EPPDRD KKQKNIKHSGNITFDEIVN/AR QMRHRLSLARETLWNHLKRSR GTAQSVGCNVDGRPHPHDIIDI NSGAVECPAVSDIFIVTVGVKG GPPSVFTEISWEVLEMVTGGVG
29284	59652	A	29459	1	330	
29285	59653	A	29460	140	214	
29286	59654	C	29461	181	381	
29287	59655	A	29462	427	957	
29288	59656	A	29463	3	241	WLRERAPEGSPETKGS/PPPPP RSVLHLSA/SSPLRPPEGL*TC RGSPSADSPRRGKHGGKTHLV SWLSQQKIPMAR
29289	59657	A	29464	122	473	
29290	59658	A	29465	1	771	
29291	59659	B	29466	1	1017	
29292	59660	B	29467	1	2568	
29293	59661	A	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I SQ*PQORYECRDNQQLDQL/V/ EQFIQTLEKAITQHRQQLNQWT QKVDIARRR
29294	59662	A	29469	1343	1714	
29295	59663	A	29470	321	2645	

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29296	59664	A	29471	611	1215	RWCVWSLFLQML/EMCPFELPS GGFVVSLSGSKVLQFTFTVNVTA HKGSVDPKRVKLTALAVSVTA LKAACLELFLPPGGFVVFAGFR SEAADLCAEGASSGLGQPREGL PRCSGGLKGSSSAARMGAEAK GAPRASQGCGRHHAVTSHRS DMGEEEGESQRYLSCPQSPSP NLLQEDASKVIVFAESGINPDSV LDLIMLH
29297	59665	A	29472	335	453	KYIWNVNLQHSVSMLL*FITS*L SGMDSLFPAAHCV
29298	59666	A	29473	1	1041	
29299	59667	A	29474	3	874	TEGQKNLIVEVTSNDVVRFP WTIDNKYYASADINLCVVPNKFL VTAIEIAESVQAFVVFSTQKS GLDSVSSWLPLAKAWLPEVMI LVCDRVSEGINRQKAQEWCI KHGFELVELSPEELPEEDDDFPE STGVKRIQALNANVWSNVVM KNDRNQGSLLNSLTGTNHSIG SADPCHPEQPHLPAADSTESLS DHRGGASNTTDAQVDSIVDPM LDLDIQLASLTTGGGDVENFE RLFSLKEMRDKAATLPHEQR KVHAEKVAKAFWMAIGGDRD EIEGLSSDEEH
29300	59668	A	29475	1	1773	
29301	59669	A	29476	1	1023	
29302	59670	A	29477	2	616	
29303	59671	A	29478	1	972	
29304	59672	A	29479	1	339	
29305	59673	A	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG EGTYGTVFKAKNRETHEIVALK RVRLDDDDGVPSSALREICLL KELKHKNIVRCAGGGCSLPVW PLGGGGG*HWTSVRRRTCLAEFF FCPLRLHDVLHSDKLLTVFEFC DQVKGGVWRTVALGR
29306	59674	A	29481	1	843	
29307	59675	A	29482	1	873	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 95/40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
29308	59676	A	29483	13	945	NRGPAGVPAAMQKYEKLE KIGEGTYGTVFKAKNRETHEIV ALKRVRLDDDEGVPSALREI CLLKLKHKINIVRLHDVLHSDK KLTLVFECDQDLKKYFDSCNG DLDPHIVKSFLLKGLGFCH SRNVLRDLLEAPATWLINREW GSWKLGVDFGPGVRAFVGFPV RCYSAEV/VSHLWYRSPDV/LF GAKLYSTIDMWSAGCIFAELA NAGRPLFPNGDVEDQLKRFRL LGTPTEEQRPSTMTKLPDYKPP MYPATTSLVNVVPKLNATGRD LLQNLKCNPVQRISAEELQH PYFDFCFPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE
29310	59678	A	29485	3	1225	
29311	59679	A	29486	1	864	
29312	59680	A	29487	1	1413	MVNPVFFDITVDGEPLGRISFEL FADKVPKTTENFRALSTGQKGF GCKSSCFHRIIPGFMY/QGGDFT RHNGTGGKSIHGEKFDDENFIL KHTGPGTSLMAIAGPNTKGSGL FIYTAKSEWLDGKHVVFGLSR GDSLKEPTSIASSRHPSYRSEP SLEPESFRSPTFGKSFHFDPLSSG SRSSSLKSAQGTGFELGQLQSIR SEGTTSTSYKSLANQTRNGSL YDSSLTPSDSPDFESVQAGPEPD PPLGYTSPFLSARLAQQREAE HPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLPG REEEPGLGDSGIQSTPGSGHAPR TSSSSDDSKRSPGLKTPLRGPV PRFGKPDGLRGRGVGSPGPGPT APYLGRSMSYSSQKAQPGVSET EEVALQPLLTTPKDEVQLKTTY KSNQGPKSLGSASPGPGQPLSS PTRGGVKKVSGVGGTTYEISV
29313	59681	A	29488	1	3126	
29314	59682	B	29489	46	114	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29315	59683	A	29490	1	704	AALLALGPRNPWTLWTPLT PNYPDRQPWTDKHPDLLTCGRCL QTFPLEAITAFMDHKKLGCQLF RGPSRGQGSEREELKALSCLRC GKQFTVAWKLLRHAQWDHGL SIYQTEQRPRRPSWAWPRWL QPCRQWWGQQLRPRAPV/HSG SGLTRRSPTCPVCKKTLSSFSNL KVHMRSHTERPYACDQCPYA CAQSSKLNRRKKTHRQVPPQSP LMADTSQEQASAAPPEAVHA
29316	59684	A	29491	3	1605	
29317	59685	A	29492	1	453	
29318	59686	A	29493	2	128	
29319	59687	A	29494	1	543	
29320	59688	A	29495	39	1092	
29321	59689	A	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/ TLRPKAL*LTFSQIFSA*RLKTD TARSPRKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
29322	59690	A	29497	1	281	VSDHAGTPALVLHP*RVQVLF* GRGKYPTSPSPPLAELATSAR NLTRPRNACSPGFLPSRVPSVR DPTGNRTVQLTWQPLPEPLEL WPKAL
29323	59691	A	29498	1	542	MRAPPKSGQLQHCPRSGALRS GDLPEWEINPLSSCSLLHEKDP MTSGPQTNPQKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAIPYFRTPSY LCAPIPVYRTPTSYLCALTPPL FWRHIRTSKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPGQGMPPAAQ
29324	59692	A	29499	1	1044	
29325	59693	A	29500	596	833	LLLDLPAED*CCLIASEAP*TITD AEL*VTLTVEGKSVPLINTEAT HSTLPSFQGPVSLASITVVGIDG QASKPLKNE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSLPFRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCPTPTPYFHDPTPFPLFW KELATCAGNLATGTRNAGSPG FLLSRVPSVWDPTENRTVQLT WQPLPEPLELWPKA/HLTDSFP DLGLAA\ED*HCTIASEAP*TI/ TDAELWVTL\TVEGKPPFLINT EATHSTLPFFQ\GPVSLASITVV GIDG\QA\SKPLKTPQ\WCQH* TIRRFKHSFLVIP\TCQVPLLG\E DTLTKLASLTIPGLQLYLIALA LPNPKPPLRPPLVSPDLNPQV*D IGVEWGKGD
29327	59695	A	29502	6958	7935	
29328	59696	A	29503	1	486	
29329	59697	A	29504	1	492	
29330	59698	A	29505	2	502	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLLPAAMVNPTMFFH IAVDGEPLGCVSEVRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFYKGCSCFH RIIPGFMCQGGDFTRHNGTGK TSKKITADCGQLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFDDIAVDGEP LGRVSEFVRGLDTKK*LLI*SIK LC*QIGLFADKVPKPAENFR/A L*SIEEKGFGL*GVPCFHRMIPGF YVSRGGDFTPP*MAPGGQVHL MGKKFER*RTSSLKHTGVGHL VPWANA WTQTMGSGQFFICTA \KT\EWLDGKHVVVLAKVKER HEILWEAMERFWVPGNKTS KKIISIADCGQLLISFDLCFYLNH QDHSLLCSPRESTPLPHLLAGS
29332	59700	A	29507	1	380	LCSCP RRRLGREGAEEPTSP VTQYLQPRSP ECKMFACAKL ACTPSLIRAGSRVAYRPISASVL SRPEASRTG/EGAA TVGVAGSG AGIGTVFGSLIIGYARNPSLKQQ LFSYAILGFALSEAMG
29333	59701	A	29508	76	385	EEPTSPVTQYLQPRSP ECKML ACAKLACTPSLIRAGSRVAYTP TSASVLSRPEASRTGEGSTAFN GAQNGALH\I\QRELHTSAIRRD IDTWCKFIGCSAATE
29334	59702	A	29509	2	230	
29335	59703	A	29510	242	427	SAPDLTCNSKTWKNGRJICFHP ASLVSLY*QPQLASWTMKKQD ENTQEGKSWDSFSDVIHI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29336	59704	A	29511	1	1497	
29337	59705	A	29512	199	766	EEPTSSCHPNISSRAVP EECKMF ACAKLAMRPPSLIRAGSRVAY RPSVASVVISTQRLSRTGEGST GI*MGPPQNGVSIQLIPKGSFQTS CNQAGGHLITGCQIYLGAGCLQ Q*GVGWFLVAGIGNSLLGKPY LG YGQKTLSPESQQLVPP* CYP GDFALALKKAMGLVFC LMVA FLILFADVTEITA
29338	59706	A	29513	427	840	
29339	59707	A	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ* DGTLLCRR CGS*GLPTFKKSTCGKCGYP AKRKRKYNWSAKAKRRNTFGTG RMRHLKIVYRRFRHGFREGTTP KPKRAVAASSSS
29341	59709	A	29516	1	668	
29342	59710	A	29517	649	992	
29343	59711	A	29518	1	2994	
29344	59712	A	29519	3	486	
29345	59713	A	29520	2	898	NSRVDDFVCPSSRRSKRD LIEFS CRIILFPLPSLPPRISFIHPSPTLAR VRIGGAVRRPHQSHSISSSFGA EPSAPGGGGSPGSLPRPWGPKS CSSSLCGARS*FFWRDVKNTGL VFGITLIMLLSLGSFSVSSVVV SIVLILGFSSSVHHQLSGI*QSSVI PSCNRKFRKKGHFPQKPNWNV DITLSSKSF SINNMNAAMVHIN RALKLIIRLFLVEDLVDSKLAV FMWLMTYVGVFNIGITLLILAE LLIFSVPVIEKYKTQIDHYVGI ARDQTSIVEIKIQAQLPGIAKK KAE
29346	59714	A	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGFFFTQVANIIS VAVNLVFCIRFLENTGVIGITIR RCPIPFSSWAF
29348	59716	A	29523	1	4368	MLFSYLEKYFYVADEL SHCVEP EPSQVPGSSRDQQQGKPPPLP ALKAKTSSRSGPYATEIKKSTD DSIFKVLDFWNRSSYSDDNK/LI PPTSPRNRVQKRN/PSQVAV DLVTDITTLRENGSKTLSPSKIE LKPVRSDSPQAEGDMLVSESC QDNNVNIKS FKMNLSSQKGT EGPGILQPFESYGTSPQSGKNM DYSQDSKSPGKNGASPSNSNY SYSVLKESDAENQVPCNTNNIG NLGEEEPKFHAAH

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29349	59717	A	29524	33	3339	TDQAKVDNQPEKLVRSAEDVS TVPTQPDNPFSPDKLKRMSKS VPAFLQDESDRETDTAESSY QLSRHKSPSSLTNLSSSGMTS LSSVSGSVMSVYSGDFGNLEVK GNIQFAIEYVESLKELVHFGAP VEGLNSSGWKKTGVIPY*KG/Y LLPNKGQMGKKKTLVVKKTIN PVYNEILRYKIEQIL*TKLNL SIWHRDTRKNSFLGEVELDLE TWDWDNKQNKQLRWYPLKRR AKALQRFQLKAMGNS
29350	59718	A	29525	946	1183	
29351	59719	A	29526	2048	3359	
29352	59720	B	29527	1	300	
29353	59721	A	29528	1	1495	
29354	59722	A	29529	1	2769	
29355	59723	A	29530	450	3061	
29356	59724	A	29531	421	1464	
29357	59725	A	29532	238	930	RLSLVSSHCGTILSSEVVCAPPT AYIDFARQKLDPKIAVAAQNCY KVTNVAFTGEISPGMIKDCG/AT WVVLGHSEKRRHVFGESEDLIGQ KVAHALAEGLRE*FACIGVEKL DERIEAGIH*GRLFFEQTCKVIAD NVKDWKSVVLAAYEPLLAIGT CKTSTPQQAQVEHEKLARGWLK SNVSDAVAQSTRIHYGGSVTGA TCKELASQPDVDGFLVGGASL KPEFV.DIINAKQ
29358	59726	A	29533	1	929	
29359	59727	A	29534	3	623	
29360	59728	A	29535	3	202	
29361	59729	A	29536	1	1046	
29362	59730	A	29537	1	1320	
29363	59731	A	29538	1	1052	
29364	59732	A	29539	922	1245	NRCLGNSFKCLCILQVGRAHA FLLCSDFMPEAVCSSIHSFIPV TKTQGAAPHTRAHSLTPDPKPS CCCCCPRPGEDPGHMCVVWP WQPSVIYAKYWTYEHQAQW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS GHYALQEAQETSQSGRESQA
29366	59734	A	29541	1364	1916	
29367	59735	A	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ PWAMIIDVFSRYSVSGSEGSTSDP *PKGELKVLMDKELPRLSLQS GKDKDAVDKLLKDPGRPMGD AQGGTFSEVHPCSVAAITSA/C HKYFEKAGLKLMPWEMFTDF LGQSIGSQGFPMFCLGIYFP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29368	59736	A	29544	175	355	FSQQLLGQAD**SFLLAGCSRLLTAVSRPKRPGEAGITPRVRCLLSNMKDILVASKFWQL
29369	59737	A	29545	482	1196	
29370	59738	A	29546	196	818	
29371	59739	A	29547	170	370	
29372	59740	B	29548	147	257	
29373	59741	A	29549	1	1278	
29374	59742	A	29550	2	152	
29375	59743	A	29551	2	187	
29376	59744	A	29553	1	915	
29377	59745	A	29554	62	430	RQQDELALIAETLKCVDH*LSDLVLPARGCA*HRELCIHDLLKGNPLRRNLAG*QTERMQLQVESQSIPEEILGLQPQLGPMGGLWNVRFLLIPTVLWGFHCSQERAFPRKLQVKSFPVAQG
29378	59746	A	29555	149	381	
29379	59747	A	29556	1	656	
29380	59748	B	29557	146	1320	
29381	59749	A	29558	629	1417	WCASHWWSGHAARHA*ASHPLHGLLCSPLPEEHHPLLHGAQSHRPPKG*GM*AHGTLAGSSTCSPAQGL*IHQSAPCV*LKVCECTNRHSVSSCSDDEDVCISLCLGQ*GP/ECI*CRIFLGPFRNLIEGAPHL/CRSAMLNPLQEGAREQASARSGWLLRLLTQEQLLRCRACIQTRDREGKTRHRKGTPEIGKGRFVWKKSLKILILFNCLRYWNAYMEIWWPALTGIPNVTVNYATSSSKDSRTDGRVDLLMAVTDGM
29382	59750	A	29559	318	608	ISQARRAAPWGPVQPEPSR*APPPASGHPVPSTTQRLRSAGARRGTGGQLHLQPRCGDPLGETSWAPESRRSAASLLKPARPRAHWEEQITPDALL
29383	59751	A	29560	88	564	SCLPVLRRALFLSPWVVDGTGRRGAAGGGRWGGSGRTGAHG VGGRLRHGGLQVPSALQEGS*GSVRNRAQPGGLALLGDPVHPLQPLARVLSPLPG/DQQGWPAAPSVGPTKPTTRNSSWPPSAAHSPGSCSLSLHTSLESCRCPSINTSLHKHA
29384	59752	A	29561	3	339	RYKDSRPHQTQEPSWLHLVDPAPRLQVELPASPALCARIPQPLG G/HGTGRRGQGAALVGEARAGLPSPSPFFSFLLSFLSFFLPSPFPLFFSLFFPFCPVNCGEQCPGKGM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29385	59753	A	29562	327	890	VMRIQVLLYYLRFADQGTGFH LVLCLRHTAGVQ*SWDS*SGLT PELV/HLDGSHV/LAASPRGSPG/ SPK*MGADQRSESSPGPGGG PRAEGPHHIQEAPRSA*AQGAG AEAAARLGAGQASGCQSTRRPA GSRREPGVSLDGGHRAVVGIQF QAPSRRAA WGHPLHDA PGRRLL MSRQLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGQWLRLKVVVWPQQCRPTG AVLDFSPGCSCLPAGQSGGPAA RHA*ASHPLHGLLCGPSI.PDEH HPLLHGAQSQRPPKG*GMRAH SAGLAGSSTCSPGAGSTR*SQL GS*VW*GRGESLCL
29387	59755	A	29564	1	2715	
29388	59756	A	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ KLLHFLYSLQKGISPNAIPPHSP HPTTAPVYSSQCERRRRQVISAF PT/GD*SLHSN*E*QGGVEGEAP AGTWAVRGA*GPAGVPGGRGL GGLRTRSSWPALLAPGRQSGSP AARH/GLSLPQPPWAPVQPEPP* GAPPPAPRRPVPSATQGLRSAS ARRRTGRQLHLQPPCGIHLVKP AGLLSLVGTWRVFM
29389	59757	A	29566	1	470	MGQPLLLVRDSSGGLQLWQKV KGEPVQQHERRIIPAREEKVK RSPAGPPSPGGLDSSRHKIPSHE QA/SGVQPACKTTHQPRGIWCS PSLPDEKCPLLHSAQSHRSPKG* GVRAHGVGLAGSSTCSPSAGSN G*SQLGS*V*NKGR*YPRTGRC
29390	59758	A	29567	777	1063	QLPPPSVFPTTPKTELVLGTFGH GQPHRGGHESSDSAGGHLPL/R ALRSGWDPSPPSVCATPTSSGL SSTPQLPLHQRRTSSSTASWSPG WGMGSC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
29391	59759	A	29568	195	1899	GSASGVVRSRRWARGLAGFRS EAADLHSECYSS*KQCGPKD*A EARFIAKSEGTKLPQCGRGPH*I QRFSTSPDSDGAQLASPSGSRTR AAGGAACQSWCRAP/STPQPLG GRWDWAPWSRGWRSSGTSGR TGAHGAGGR/PQAWRAAGPQP CPAGRQLRPETLKQNIILSLIQCI GASLVPTGTAELEPSPSQLRGRT TDAAQAIAKNEFARVQKRNLCR RGPICFEGDALS WFF EKINKIDR RLARRIKKKREKNQIEAIKNDK GDITTDPTETIQTIREYYKHLVA NKLLENLEEMDKFLDPTYLPRIS QEEVESLNRPTGSEIEAII NSLP TKKSPAPDGF TA E FY QRY KEKL IVLEVLAIRQEKKEIKGIQLGK EELKLSLFADDMIVYLENPIVSA QNLLKLISNFSK VSGYKIN VQK SQAFLYSNNRQTESQIMSELPFT IASKRKLYLGQLTRDVKDLFKE NYKPLLNEVKEDTNKWKNI PC SWIGRINIVKMAILPKIEKQTWN NSQTLQCQPFCESDVCTSTLQIQ ERFEVAPLHKAL SSEEITDKT DPSPAIEELTV
29392	59760	A	29569	77	640	
29393	59761	A	29570	384	746	APWSRGWCSSGRLGLHRSPWS GWEAQAWRAAGPEPRPAGRQL GAMSCKVETGT*DSEQRHFRFG ESWGHWPWAGAQPTGPVLSGIL NVLSFSVLALPRPTGWPRPCS AASPSRCPAQSHQH
29394	59762	A	29571	189	545	GLSCLPAGQSGGPAARHV*ASH PLHGLPCGPSLPNEHHPLLHGA QSHRPPKG*GMQAHDAGLAGS STCSPGAGSTR*SQLGS*VCCGTG RLVGTQQLRPESG*VSQPSRL WAAAEAGSC
29395	59763	A	29572	87	374	AYSSQLGESRRYSLDQCLAK*I CEGRTCIFEPCNCSSLYVRSNG GNHSHSTTTFKYNGSNWIPRW QGPSGSTQPSKARRPVAFSQGN CAMEKGN
29396	59764	A	29573	1	2453	
29397	59765	B	29574	182	1356	
29398	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS LGLSCLPVEQSGGPAARHA*AS HPLHGLLCGRSLPDEHRPLLHG AQSHRPPKG*GMRAHGAGLAG SSTCSPGAGSTRNREN

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29399	59767	A	29576	142	442	PKG VGRALAAFPQDRAPGPAA RHA*ASHPLHELLCGQSLPDKR HPLLQGAQSHRPPKG*GVQAQ GTGTGRQLHLQPWCGIHWVKP AGLLSSLGPRCFYKL
29400	59768	B	29577	1	2464	
29401	59769	A	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL SPWVVDGTGCRGAGGGAHRG GSGRTGAHGVGGR/PQAWQAA GPEPCPMGRQVRPGEKSSAVPV GQPGWGTQYTLRSHWLGC
29402	59770	B	29579	1	2598	
29403	59771	A	29580	1	2028	
29404	59772	A	29581	5917	6355	QEAQPEESANDAQGDGPPGGK PQPQPEERSSCAQGVGPPGGQQ ESQDEERSSDAPEDGPPGGQQK PQPPEERSSDAPEHDPGGQQQP QPEERSSDAPEHDPGGQQQPQ SEERSSNDAPGDGPPGGQQQP*P EERSSGAPGHSSPDV
29405	59773	A	29586	875	2090	
29406	59774	A	29587	228	505	MLGRKPNHTSASRNTRLRHCSR ARAQVKRMQRQREEREAK/R QPGTASGTSGIAERDSGKCSRK RGVQKVPG**NTRQSKLRPREQ CTTADP
29407	59775	A	29588	188	592	AAPPRSPSYRMIRKTR*MLGR/E AEPHVCQEHQVEALQHGGGP GETDATAAERR/RGRQRRQPGT ASGTSGIAERDSGKCSRKRGVQ KVPG**NTRQSKLRPREQCTTA DP*TLSTFPPEGRGTELEPGFDSG ASVLMRGCRALASASSPQGP GPQEM*ATRNWGRRQ*GRHC KLPLVLTITGLQGDVVEGVHVC ASQEPLIQNDOEVDVAWQKA EPHVQEQEIHQVEALQHGGGP ETDATAAERRAGGKDASLVQH LVPVALLSVTQGSVPEKEEFKK SLVNEILGKVNYDQGNVVPQ TLEHCPPFKGEARSWSLASTP

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29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRRQPGTASG TSGIAERDSGKWSRKKREFKKS LVNEILGKVNYDQGNVNPQQT PSHHPNLEHCPFPKGEAGAGA WLRRLRGLGSYEGLPGCALCFFF PSRVLGLRRCEQQEIAQQQGR DTQHGQQ/RSAGEGRGRPG*GPG RTGPPAAQLPQSLRTTRRSRPW GRRQ*GRGR*PPQGLMRC*RRP HHTGWSFPQNEKRQPGRSFQQH KSH*RE/RR/RARPVGQVQVAK RSQQFDDECEGDVROEHSSRRD RVAVKS
29409	59777	A	29590	2	394	
29410	59778	A	29591	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESPSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
29411	59779	A	29592	1	561	
29412	59780	A	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W TALWEMLYAEANPFSTIRILF QLEQPALGTSQYKILCSST
29413	59781	A	29594	2	704	WRGGSGSGGWESGRRGFFVAL PERSGVCQVVSIMFSNMFDP IPRVFQNRFTQYRCFSVSMIA GPNDRIMPSPALDQLSRLNITY PMLFKLTNKNSDRMTHCGVLE FVADEGICYLPHWMMQNLLLE EGGLVQVESVNLQVATYSKFQ PQSPDFLDITNPKAVYLFQISGV LLDKGECAGECVCRLENALRN FACLTGDIIVAINYNEKIYELRV METKPKDAVSIIECDMN
29414	59782	A	29595	1	1680	
29415	59783	A	29596	1	2220	

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29416	59784	A	29597	2	1114	SGRRGFFVALPERSGVCCVVSIMFSFNMFDPHPVFNQNRFTQYRCFSVSMALWPNDRSDVEKGGKIIMPSPALDQLSRLNITYPMLFKLTNKNSDRMTHCGVLEFVADGICYLPHWMMQNLLEEGGLVQVESVNLQVATYFQELSSCYLPHWLMQNLLEEGGLVQVESVQPFKWATYISNFPQSPDFLDITNPKAVLENALRNFACTLTGDDVIAINYNEKIYELRVMETKPAKPVSIHECDMNVDFAVPLGYKEPERQVQHEESTEAGEADHSGYAGELGFRFSGSGNRLDGKKGKGVSPSPKPGDIKRGIPNYEFKLKGTIRNSRPLVKKVEED EAGGRFVAFSGEGQLRKKGR
29417	59785	A	29598	15	569	
29418	59786	A	29599	30	525	YCLHHEFFQVSLVFAWCSEM HGNRQLWEIRTGEMGRRTPLG SWTAKSPIGR/SLRSARVPRTV AHSQRAKGSHSLWVLRPQKRR CAGKSPPSRLARSPRCEPLVA LARQPLCVRRAGPEERARAQR RPPRPVPLLSQPGRALLLLLRS SFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	
29420	59788	A	29601	758	1076	LPMNRPPRWITGLAPIELLLLE LQQKENMALGSRTHHGSSPNS GSAFCQMACCSSLPAL*SGRC SQP*WLWMSPLSRFISINSTSA SSSIGNAIRRRSRPGP
29421	59789	A	29602	632	835	
29422	59790	A	29603	428	1214	FIATVLPWHRSPQWYYPWVRG PVTALVRKVPVAVAGERSLWS VVGLIWKPLGLALQGVGFVIGTFVSLYFASKGWAMAGFTLTAFGGAFVVMRVFMFGWMPDRF GGVKVAIVSLLVETVGLLLLW QAPGAWVALAGAALTGAGCSL IFPALGVEVVKRVPSQVRGTAL GGYAAFDQIALGVSGPLAGML ATTFGYSSVFLAGISA VLGIV TILSFRRGQETAHQPDQQRAA Y DLQRSNRRVLPASPASACRCS D AHSR
29423	59791	A	29604	1	825	

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29424	59792	A	29605	242	945	NGCIVRGKTSGSTFICVAMSVA ASTVRR*CWLPGRKAAAWRTC WAPMT*AVMC/WSRLMYGAR LSLLVGCLVVVLSLIMGVILGLI AGYFGGLVDNIIMRVVDIMLAL PSLALLVLVAIFGPSIGNAALA LTFAGLPHYVRLTRAAVLNCL APLIVQASLGFSNAILDMAALG FLMGGAQPPTPEWGTMLSDVL QFAQSAWVVVTFPGLAILLTV LAFNLMGDGLRDALDPKLGKQ
29425	59793	A	29606	1	2433	
29426	59794	A	29607	1	1383	
29427	59795	A	29608	1	218	
29428	59796	A	29609	1055	1873	
29429	59797	A	29610	3	823	
29430	59798	A	29611	183	1163	
29431	59799	A	29612	4375	5125	
29432	59800	A	29613	1800	2031	
29433	59801	A	29614	2	848	
29434	59802	A	29615	886	949	
29435	59803	A	29616	123	315	
29436	59804	A	29617	34	343	HLCYGRVYAADPYHHALAPA PTYGVGAMNAPAPLTDKTRTS HADDVGLVLSLQASIYRGY NRFAPY*MTKP*KPSNVGRKEA FRGLSIAIHAVVHHFSNS
29437	59805	A	29618	1	305	AAAYRG AHLRGRGR TVYNTFR AAAPPPPIPAYGGVVYQDGFY ADIYGVMLHTATPSLPLPLPLP TVTVTDEFMTFSPLSPLTCSSPH LRRWCECFCTFD
29438	59806	A	29619	1	2115	
29439	59807	A	29620	1	273	FFSRVVPDSDYQAQA/MVDIVT ALGWNYVLT LASEGNYGESGV EAFQISREIGYPSLFGIQGCLHE CFAILCQVVYQFLLMLQLSDAQ TVY
29440	59808	A	29621	1	405	
29441	59809	A	29622	1	582	

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29442	59810	A	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS ICYSHGRDLAPARPAQPPQPRD QPQVRPLCSPHAAAAAAL TWSGPPAGFLTAPSAGSRVRL AARQKKAAPRKASAEPRDKKP LAPKLQNALLVGKESPRFIPL SVFFSKTFQRTARILKRSADRL PWVTSRTPCGGIRTCPAEMTRY LRFANLTGGISEVSGFRDEGIN FGSWIAIPPVKMCVCEGKRAS CPCFFLLTAKFYWLTMMQRTH SQEYAHISRVDGD
29443	59811	A	29624	1	2740	
29444	59812	A	29625	1	1614	
29445	59813	A	29626	88	540	
29446	59814	A	29627	2	577	
29447	59815	A	29628	1	2169	
29448	59816	A	29629	1	1619	
29449	59817	A	29630	674	867	LDGDGIESINSLGQYGHFDIDS SYP*AWNENLVPFVCILFYFVE QWFVALLEDVLHVPCKLDS
29450	59818	A	29631	746	1985	
29451	59819	A	29632	1	2211	
29452	59820	A	29633	139	247	KTSAHEKPKWRKERNARG* KRKRRLQMSQVNR
29453	59821	A	29634	335	556	
29454	59822	A	29635	1	586	
29455	59823	A	29636	908	1260	
29456	59824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA LSPDEFISPVCLARLVWRFC FAQKAR*SPAKYGILGELTTGS KLVLKANGLMEASTIAAILGVS AGGVLA YWHVLVA WPHAHWP TVSRQQQLMASTLPFTSPLAQ IFPWRITQRTMRMPFVIDARD ALLQGVFAAVNPSAHLNDSRH RRINKNVIEPGISQRPQHLDR AHPFGIHHQLNAFTGRQFHQR QLLYLRQTFFVVDIDHHHPRLY AAVNGVIDSANAHRTCTRQQC NIAARFDAHAMLINILRGVIIGM ISTNNAHRLCQRRRSKIRSDT GNTQPKLMQI

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29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH CWTAVACHQCEDAPCANVCP VDAISREHGHIHVEQTRCIGKKS CMLACPFGAMEVVSSRKKARA IKCDLCSWHRETGPACVEACPTK ALQCMDVEKVQRHRPRLNFLR LWYVVHAHTLMRMRPRFIQPW EEVVPRIHQHAACFQALIELLG RNGQILKP
29458	59826	A	29639	391	812	HSALCSCRMRRERLIRPTKTCK FNRLQRLCRPKRSASGNFAVV IRLERVSLAPFFYGVLKCL MPKRQCNEADHHQTHTCAGQ KKMATHPLPGENKFIIGEDREY RWALMFPNENAPVCWVGHVR *KSPLHQHIDRA
29459	59827	A	29640	589	1075	
29460	59828	A	29641	1	435	
29461	59829	A	29642	9	661	
29462	59830	A	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	A	29646	114	851	CDHRNIVIRSAENISANFSHTGS V*GWMFTVP*SPSGRVVF*FCH L*ATCGN*LN*THSLSQGQRAF CILGFLPWHSRRIRSHVGLNEC KVLLSGRSSQMGEP*GR*FSP* VGPLGGRALLQLPQPNV/YVL PVSGLLVPAGE/CPLNV*PLVCS SANVLLSTSSCFCLCLARVSGF YRHRMGA/SGGFL/M*V*RKGS SFNFLHMA/ASSWDSYSGHHFF *AGADYFFASSVSSLPLVLLHSL HSFF
29465	59833	A	29647	1	1422	
29466	59834	A	29648	1	768	
29467	59835	A	29649	1	885	

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29468	59836	A	29650	1	1253	MVSVTALKAAFLFIPPSGLV VSLASGVKLQTFVSVTAHKG SVDPKSDQHGLVSLASGVKL QTFARRAEFPASQQQREVPRHD GGNHADRFTIIDHRLMATGG RHFAIHVDRFGVPANGARRAG NIITQTVTNRFAGVESFQQCQLF GIYAVCERQGAIEIPGYARLFL ATFFIYTSSFKPPLPWLRLPRN ITPAVVRTAKGVQVTAKYVIVA GNAYLGDVPELAKRSMPCG TQVITTERLSDELARSLIPKNYC VEDCNLYLDYYRLTADNRLLY GGGVVYGARDPDDVERLVVPK LLKTFPQLKGKIDYRWGTNL QLTLSRMPQFGRQDTNIYYMQ GYSGHGVTGGSSRVGLMAGSQ ISRVS/CIN**YHRFNLHWRYV ADAISADGAFTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRDTISLYQHTAEQKHPYCW YYPADSDADSVNKHRRNATQ LHVSCSFLLSDQRFHHEAVPR RVVLFTFNTCDKYIADIRSR NGLGLYAFKQRNSHFVNAQ RHRHSACLR
29470	59838	A	29652	1164	1273	
29471	59839	A	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT EEALDQSNADLITLLADWFKDL GFNVVQVPVPGTRNKFNMLAT RRHEGRYITCMQPLPIAEQE PEMTVRYIYSSADLTAEKFATA IRNHWHVENKLHWRLDVVMN EDDCKIRRGNAELFSGIRHIAI NILTNDKVFKAGLRQGWEDIED FGETHLDFLKQYQDFENGIPVH DTIARVVSICSPAKFHECFINW MRDCHSSDDKDVAIDGKTLRH SYDKST/RRRGAIHVNNAFSTM HSLVIGQIKTDEKSNEITAPELL NMLDIKGIITTDAMGCQKDIA EKIQKQGGDYLFVAVGTQGRLL NKAFFEEKFPLKELNNPEHDSYA ISEKSHGREEIRLHIVCDVPDELI DFTFEWKGLM
29472	59840	A	29654	2	1587	
29473	59841	A	29655	236	666	
29474	59842	A	29656	1	1953	
29475	59843	A	29657	2202	2333	

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29476	59844	A	29658	1	1126	MHEVTLEDSPSSAQILITVITGHG EITLKRSSRRQNDIRMYCRRRP EAFRDHHQLRFLPGTDQAIGL MMSKVGTA RPPDKTNIREMSV HTVVLI CATRVFCFNNAGNR DFIHRIAATRQAALHGREGHRT PRGVTITGKMVRKTKTAAGWE HESGFYLDGVVKLNRFKSNVA GKMSSGGAANGSYHSNGLGGH IETGMRFTDGNWNLTPTASLTG FTADNPEYHLSNGMKS SVDT RSIYRELGATLSYNMRLGNGM EVEPWLKAAVRKEFVDDNRVK VNSDGNFVNYLSGRRGIYQAG KDLDRFKNLVLVHAARYAADL SYLPLMQELEKRYEGKLRIGTV VSRETAAGSLTGGRYH* LKVG NWKARLACR
29477	59845	A	29659	1	1989	
29478	59846	A	29660	3	159	YKELNLADSSLSEEALIQAMVD IPKLMKRPKV VANGKARIGRPP EQVL IEIVG
29479	59847	A	29661	360	744	
29480	59848	A	29662	1	996	
29481	59849	A	29663	441	446	ICRQYPSPDDRTASGAGGGDHQ QYGAGLRQTFCLCQRLSARTC* RLSASVCAT
29482	59850	B	29664	1	1608	
29483	59851	A	29665	1	2568	
29484	59852	A	29666	116	283	
29485	59853	A	29667	207	1270	
29486	59854	A	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

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29488	59856	A	29670	1	1167	MPWLSTGAAALITALAVVELN DDDDHHHRNNSPLPTPPDDES DDTPVPPTPGGDEIIPDDDDTP TPPKPVSFNNDVILDKTEKTLTI RDSVFTYTENADGTISLQDSNG RKATINLWQIDEANNTVALEG GNTSACRQALKIPKGSSDYTVT WKGGHFTFYRRWRCKVHKVV FEGSPPTICRYVLNRKNSWHV AHIFRRHAKPEEQ/CSHLFPYPF HHDLDEVLNDPDKLVVVCCT HADSHFEYAKRALEAGKNVLV EKFPPTLAQAKELFALAKSKG LTVTPYQNRFRDSCFLTAKKAI ESGKLGIVEVESHFYDYRPPVA ETKPGLPQDGAFFYGLGALFTNQ QGFFKSSLLSIFADSSSSVAGRS PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	A	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	A	29674	282	660	GPSSEPSWAYAPGKAGDPHHS AEWARNSTPSKDQA*RRPHTVIC VTAYQGVLLVGQSPNAELSA RAKQIAMGVGDGANEVYNEIRQ GQPIGLGEASNDTWITTKVRSQ LLTSDLVKSSNVKVTEN
29493	59861	A	29675	720	4525	
29494	59862	A	29676	218	990	
29495	59863	A	29677	54	723	
29496	59864	A	29678	1	2229	
29497	59865	A	29679	2	235	
29498	59866	A	29680	279	1275	
29499	59867	A	29681	692	1052	
29500	59868	A	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD CWVDDARLVLANAQMVVRKG GEVLTTRATSARRENG/GKKY SWQARGLESLSQPVERLSP
29502	59870	A	29684	1	1941	
29503	59871	B	29685	1	4107	
29504	59872	A	29686	840	1006	CHESHRTDGGAVFRVYPGGG PRRECWFSSSLDEATPGWLLQ/ LYERDRH*PASTG

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29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRLKRLLSRK TRMP/GFTNPRYGAGAAATNPDP EVFSWAATQVVTAMEATHKLG GENYVLWGGREGYETLLNTDL RQEREQLGRFMQMVVEHKHKI GFQGTLLIEPKPQEPKHKYDYD DAATVYGLKQFGLEKEIKLNI EANHATLAGHSFHIEIATAIAL GLFGSDANRGAQLGWDTD QFPNSVEENALVMEILKAGGF TTGGLNFDKVRRTSDKYDL FYGHIGAMDTMALALNIAARM IEDWQLDKRIVQR
29506	59874	C	29688	1	2130	
29507	59875	A	29689	238	1879	
29508	59876	A	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR KSVRTQVLSAADVRAKLFTLK VQDPKIDRANPTMVNMRWMM SA
29509	59877	A	29691	596	723	MCASAP*WCELPAGVVRPPAST TADYFPLFTLVHGGCAHGRF
29510	59878	B	29692	1	441	
29511	59879	A	29693	1	1422	
29512	59880	A	29694	1	2856	
29513	59881	A	29695	2	367	QKAGAVQVLLSLWSSLSAAAA GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS GSLDRPSALHSGTILSGKITSDIC CPHF*SPGRPCSKQHWAEMLV HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLEITSPAIIFSPTLHSPAHH HQYRKALHGRFPARSRDPPALA PGWRSARRER*SSPARAAARW CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE SYSFTDSV
29516	59884	A	29698	279	732	PPGATLPTVARGTPQMKGESS PAKSLAPPLCEQMGGQEDGHWG AGWGLAQVLLIALDGLLDAQQ HGGEPLGPAGRWSPRSPTRCS CPHSAPRGPLAIFSSTCIPGNQR KLGTAPHTFGQPAWR*ACRCRS GRGPP*RSSLWRCTEEGAVH
29517	59885	A	29699	353	2776	
29518	59886	A	29700	158	605	PERSGLQEAGGSGRGWGKRSL PPAETAGLSGYMCFRAWLSLRS WDESDGHWGAGWGLAQVLLI ALGWSS*CASNGWLSHWFQPG R*SRIPFTDSV*LVHILLPVGPL AIFFINLAFPIRESWEQLLILLE KPVGLEACPCCKSGKGRP

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29519	59887	A	29701	1	753	MLALDQREAMRMIFPAVAGAP APALSPYAS/ARILVDQQFCYRQ VVEQNAIAKSCAMIVAADFIP GNGIPVDSVVIDRKINPLQIKQD GGKALKLLVLWRSDEDAQQRL DMVKEFNELCHSHGLVSIIEPV VRPPRRGDKFDREQAIIIDAAKE LGDSGADLYKVEMPYKGGPQ QELLCASQRLNDHINMPWVILS SGVDEKLFPRAVRVAMTAGAS GFLAGRAVWASVVGLPDNEML LRDVCAPKSGEPIL
29520	59888	A	29702	294	479	KIHFGFFCHCAESGSLDGRHFA PGV*RSEQHSGSGAVSGTGY WCSRDYRSREIDGLYRNW
29521	59889	A	29703	1446	2103	IHTDHRPGEIAATTLANRAALS GAALRRRRRQNTIAVGVRLA GTAHACNIIISIRGYGSEDA/Q/ QRLDMVKEFNELCHSHGLVSII EPVVRPPRRGDKFDREQAIIIDA AKELGDSGADLYKVEMPYKGGP GPQQLLCASQRLNDHINMPW VILSSGVDEKLFPRAVRVAMTA GASGFLAGRAVWASVVGLPDN ELMLRDVCAPKLQQLGDIVDE MMAKR
29522	59890	A	29704	370	1080	
29523	59891	A	29705	547	928	RLTKVEMPFYKGGPQQLLCA SQLNDHINMPWVILSSGVDEK LFPRAVRVAMTAGASGFLAGR AVWASVVGLPDNEMLRDVC APKLQQLGDIVDEMMAKRFP LLRRWVDLALTRWLITVSKP

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29524	59892	A	29706	1	550	MESGVATRPADFDVYIDKLTE FVYKTNLFMKPFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILJGRPNVIEMRIQKLGLOI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVQTQEQARALIS NPTVIGAIMVQRGEADAMICGT VG DYHEHFSVVKNVFGYR DGV HTAGAMNALLPSGNTFIADTY VNDEPDAAELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTVPVLMGVAKP VHVLTPIASVRRIVNMVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRYQHGVVTLRFSG CFFAFHRHINAVFRFNIQAVFV ALRPEVIAMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIVQH VLQAEGFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTPLWAWLKLW QRIDEDNMTTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFIFANFLPATGDVIRQRYE QFVANSNKMTAVGAGSQGDQF LFALFNCQCFDADELKRIKNEL EPKMGMEMLNLVQLIAYTDWNE TQQQKPDGSWVNNYNDWMFK
29525	59893	A	29707	898	1163	
29526	59894	A	29708	81	454	NRLLAGRISSGTGDHFSGAAGI DSSLRPVW**TLRDQMSGGQS AKQPGRFQWFFYP*RLPETG*V PE*CL**CELIRAN/DHFLVSILPL RSPCVPLHLSTTPLRLAMDLTG LSGFPIPLSQSA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	1	2218	
29529	59897	A	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	C	29713	1	3126	
29532	59900	A	29714	642	825	

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29533	59901	A	29715	107	1315	KCADLPVRGLRHCWRRREDPS GADRSFSALIHSGRAAFWPCR* QGALMSIEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSQSPQSYS VLRSKFDAWLMQAEAEAGAQL ITGIRVDNLVQRDGKVVGVGEA DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVAVGVELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNT LSLGLVCGLHLLHDAKKSVPQ MLEDFKQHPAVAPLIAGGKLV EYSAHVVP EAGINMLPELVQIP CIERNAINAVKANNAARMAMR RTSAPRVSLDKVIETMYETGKD MNDKYRETSRGG LAIKV
29534	59902	A	29716	3	264	
29535	59903	B	29717	85	737	
29536	59904	A	29718	171	820	LGVCAMTNSQCG/CDEYRSKN GYEGARKALTGLSPDEIVNQVK DAGLKGRGGAGFSTGLKWSLM PKDESMNIRYLLCNADEMEPGT YKDRLLMEQLPHLLVEGMLISA FALKAYRGYIFLRGEYIEAAVN LRRAlAEATEAGLGKNIMGTG FDFELFVHTGAGRYICGEETALI NSLEGRRANPRSKPPFPATSGA WGKPTCVNNVETLCNVPAI
29537	59905	B	29719	1	486	
29538	59906	A	29720	1	605	
29539	59907	A	29721	285	449	TPAARDAQLSGGRGWY*CSAG NGLMQHRSQSGDWRAGRPFTE GW*PTPDWQIEA
29540	59908	A	29722	411	557	

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29541	59909	A	29723	1244	3261	KTINRTSLWYWLHDHWSVTG RCAFTDVTKVVDHHEPQTQTR GLVMTTS*ATT*KLTVSLTTAC VMNWV*MQVIPSPPTAKIRL*LR TSNWLTSITTLTT/NNDVNGDSI DNGTEGSAVRVGLGTQFSFTK NFSAYTDANYLGGGDVDDQDW SANDLTGITAKDAQMLSVVKP LQEFELVLAALSRGTADILK AAGATTANITQAIQMRGGESV NDQGAEDQRQALKKYITDLTE RAEQGKLDPIVGRDEEIRRTIQV LQRRTKNNPVLIGEPGVGKTAI VEGLAQRIINGEVPEGLKGRV LALDMGALVAGAKYRGFEER LKGVLNDLAKQEGNVILFIDEL HTMVGAGKADGADAGNMLK PALARGEWHCVGATLDDIAS TVKRCWTSHQHQTKNRTRRT TRNIRFPNQMEQINIALEQKGS GNFSAWVIEACRRRLTTGGPHV MYVLHHADKPNLYHGLPENPE ISETVKFWKGIWKPLAAVGF TFAASIFHYERVIFLTGQVEDH MANLJIVQMLFLEAENPEKDIY LYINSPGGVITAGMSIYDTMQFI KPDVSTICMGQAASMGAFLLT AGAKGKRFLPNSRVMIHQPL GGYQGQATDIEIHAREILKVKG RMNELMALHTGQSLEQIERDTE RDRFLSAPEAVEYGLVDSILTH
29542	59910	A	29724	1487	1821	QYRPESVLEDPRRSDHRRITDS FRETSFIVQSIVCRVLSRAILQS KRL*EPGEFPPDPSSPEQRWV CYPK*SDR*PEYPHSPGRQES QSRYLPAFRHRYVSQTTAY
29543	59911	A	29725	4063	6544	
29544	59912	A	29726	174	556	
29545	59913	A	29727	1	1926	
29546	59914	A	29728	1	1443	

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29547	59915	A	29729	1	817	MAFNEPLMLEPAYARVFFCAL AGQLGITRLTDTVSGITLDAGQI AEPLALFGEDDDMDPRPSRYQ VANGIAVLPSVGTLVSKTRALQ PYSGMTGYNGIARLQQAISDP GVDGILLMDTPGGMVSGAFD CADIHARMRDIKPIWALANDMN CSAGQLIASSASRRLVTTART GSIGVMMMAHSNYGAALKTNGV EVTLYSGDRKV\DGPNPEKLPA KDVRAFQTRIDATR\SAYTGM SVQDV/LDTEAAVFSQGQSWDN GLAE*LVHTDWL
29548	59916	A	29730	68	98	
29549	59917	A	29731	215	871	
29550	59918	A	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP EQRDAGRFCSLAKETVTPQW *GVLTSIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLGYSLVCSRVLAC FWPGSDFWPSRRKTSHTVEA FPV/VVIFVSWRNPQVAPTSAH QNRPSRNPVSRPPNTQRVARRK HYALADGY
29553	59921	A	29735	403	588	
29554	59922	A	29736	1	743	
29555	59923	A	29737	5	97	
29556	59924	A	29738	756	935	
29557	59925	A	29739	1	1056	
29558	59926	A	29740	1193	1405	
29559	59927	A	29741	1	2718	
29560	59928	A	29742	3	357	

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29561	59929	A	29743	3	1307	KYGFVHYTLHTLGGTARALVA TDYRPLTKLSLDNGFQTVVDHLQ ISQCPYIPPNFPTDTSPTGGLL QPPEGHAYDAYWRCVRAVRG QRVSALHGPPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YSGSVRSWVQPGGFARYKYDQ TGNASTVKCDYYRMAAFGHH AYRMQALTCSMTACPTTRQE TSSAWGSVSSMGDSRPPQEILG QPLLGRRIKYNCTGIGPWDGKG DESGASRPKQQAAGWLWACP RIFLVIPHSSHPAARTNGSVGG SNRNRFVIITGPGQLAPKGLW QWPIGQDPVTEIATLIGTHDLIM FDCIGVSAPTQPLEKLLSIVRY PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVFTSAF APVAVTAPRQSRQFPRLSPL DAHQRMGDVSIQAVKEARTC

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29562	59930	A	29744	1	2352	MLPDSSVRLNKYISESGICSRRE ADRYIEQGNVFLNGKRATIGDQ VKPGDVVKVNGQLIEPREAEDL VLIALNKPVGIVSTTEDGERDNI VDFVNHSKRVFPIGRDLKDSQG LIFLTNHGDLVNKILRAGNDHE KEYLVTVDKPIITEFIRGMSAG VPILGTVTCKCKVKKEAPFVFR ITLVQGLNRQIRRMCEHFGYEV KKLERTRIMNVSLSGIPLGEWR DLTDDLEIDLFLKIENSSEVKP KRRPNRKQRASNVQSLRWKKR RKKAVARRPTQSSDDAIRGQQP DGVDCRDCRAGERQRQQTDSA MMELMVVHPHFVLSLGGLLL AAEMLGGNGVLLWSGVAAVIT GLVVWLVLPGWEWQGVMAFI LTLAAWLVWKLWLSRRVREQ KHSDSHLNQRGQQLIGRRFVLE SPLVNGRGHMRVGDSSWPVSA SEDLGAGIRQCQLVAHGLQLL NVSFDLRLHFLQGRLEFGCALR LLTDSQSRLSRKPRGWRGLYG YSPPCGDIVRYHHHDLVSATLH VHINHDDCLEIAVLKQDGMGDV QHFADDVIAQRGFFAFSYEDT VIKIEKDFMTSGKPAARQGDM TQYGGSIQVGSAGVRIGAPTGV ACSVCPGGVTSGHPVNPLLGA KVLPGETDIALPGPLPFILSRYS SYRTKTPAPVGSGLGPGWKMPA DIRLQRLDNTLILSDNGGRSLYF
29563	59931	A	29745	1	3075	
29564	59932	A	29746	755	1321	
29565	59933	A	29747	397	576	
29566	59934	A	29748	1014	1266	
29567	59935	A	29749	416	724	TPGLTKTPCWEKVTFLSLQWS AYRQANTSGLRHSASSLLPLAC RY*R*WRWQKLAALVTASARQ SVKSLAYCWQRFTWRWGRFS LRRVQLPFPLKWGLRR
29568	59936	A	29750	230	1829	
29569	59937	A	29751	1	474	
29570	59938	A	29752	137	586	KTKTNIKL*AAPITRMVMVRHA VHSGSVKK*SDITMSFATISVIG LGYIGLPTAAAFASRQKQVIGV DINQHAVDTINRGEIHIVPDLA SVVKTAVEGGFLRASTTPVEAD AWLIAVPTPFKGDHEPDMTYV ESAARSAPVLKKGAL
29571	59939	A	29753	2	557	

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29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPPVYT**PTA QGLSARQGCTKGHQVRRYGRF HD
29573	59941	A	29755	66	372	
29574	59942	A	29756	1	992	
29575	59943	A	29757	1	393	
29576	59944	A	29758	1	3753	
29577	59945	A	29759	1	1098	
29578	59946	A	29760	320	703	
29579	59947	A	29761	2	673	AAFLRECKDPQTMVPAKINSVI WRIGLFYVGSVVLLVMLLPWS AYQAGQSPFVTFFSKLGVPYIG SIMNIVVLTAAALSSSLNGLYCT GRILRSMAMGGSAPSFMAKMS RQHVPYAGILATLVVYVGVF LNYLVPSRVFEIVLNFASLGIIAS WAFIIVCQMLRKAKEGKAAD AHFTPYHATPLRNVMHLIYVLN GVSFRFSVIDTNQIAQRNRFAL LCGA
29580	59948	B	29762	51	623	
29581	59949	A	29763	1184	2406	
29582	59950	A	29764	103	473	
29583	59951	A	29765	444	699	CWPGKMSWGGFPLFLGIGVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVYSGIQ LLPGLVLGGCMCRGIYA
29584	59952	A	29766	3073	3621	GVDNWRHPIHISARLQR*AGSFFS FLGETGSLSCGLSLFSKSCCEAK NCSGSRGSSP/G*IPGVQEWNI FSRF/HGVGLASLRKQAPGDQ SPITGLLGE*AHGEIPVGNRGSG KTRA/RGGPRGLEVSWSGLTH SRG*ASLTSSHNSCHIRRHGPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29585	59953	A	29767	362	1850	
29586	59954	A	29768	1	1401	
29587	59955	A	29770	1366	1515	YDQAEALDQLIHGSSSN/EQDPR/ RLPKGLTPQTLR/TLCQWIDAH QDYEFSTDG
29588	59956	A	29771	1	1827	
29589	59957	A	29772	419	1295	
29590	59958	A	29773	167	451	
29591	59959	A	29774	94	304	SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
29592	59960	A	29775	345	652	
29593	59961	A	29776	596	2297	
29594	59962	A	29777	184	283	

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29595	59963	B	29778	16	1058	
29596	59964	A	29779	715	1234	FTWIGFYANRHFCHPVTNDP HFMKWRAAAHGGENIAFKLAN LPFFGDIRESHYQVVINRADRG FNPDDFTGARQQKFVLIAGGF P*QLL*TNAVIGREFRNVQECIG LHTAGFANAVTKHF/W*M/PRL HCTIWRSGSRITIGRSRWSTAI NCRVCSFCAISTLASRTSAR
29597	59965	A	29780	938	1250	PGRVSGKADGSV/LAGNGLLP FFCPLRLRGKYQPEV/IASTIRRR YQLLFLAVASHQATAAGCGVN ALSDLRLCSVCRPKTHSVASG NGCRMRLPSSPFSVL
29598	59966	A	29781	1	1389	
29599	59967	A	29782	3059	3537	SEGKTANLFNKAITCSGAGECT RPWASDIKACQAGGISRFATGN GFKRLCDTLRYLQAIENGLKN WRLIHIATVRRCPPT/LSPATID AINVIGQWLAQDDFSGEVPYQ ADCVLAGNAVMPITDAACKIA RDQQLAEGDFGLRCEIRDWCA NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVLVHHFH AITHIRQQSQITRYIKLLRHRH TQRRFTACRLRVDAPFPNGHQC CALHCLRKIDRIQHNFNARNFIR IEKYRRRNTHTRASAA/DPSSGR H*FQFVAVVKHGRNFAAPVQVL RPSPALPLFAGQTPPRRVPLPA GYQRHMLLQYDQATVN
29601	59969	A	29784	269	753	YRPTQLQDQGRADARRGVW/ HVPFSHESV/WENIVMTRQAQ ANFT*TLFCFGIFAVIA*NCAI DPDISIRFFSKEETAT/GDRPDQI AAHLWRFPTGGRFVHHRGAY AAIIFRP*YLNGRSMAEQSMILV TGELLVELNLEPSQVQNEFAEK YYGPASQVV
29602	59970	A	29785	762	1182	
29603	59971	A	29786	3703	5889	
29604	59972	A	29787	925	1130	
29605	59973	A	29788	658	1212	
29606	59974	A	29789	904	1473	
29607	59975	A	29790	1205	2222	
29608	59976	A	29791	1	194	
29609	59977	B	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	

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29613	59981	A	29796	1	738	MQPWALPTV GELWVCGRPGA ALRAGTEPSSRALGVSETALPA EIKLRVIRVGHSSPLAQLASFQK PVLVFLRLNSRRFLFLSLARSED GILFAKSKHSSPLSLTPLRCIVL MRMYEQLMSGDLQCRVMMP RNNPGYWNQ**SEIFKGSQAQ TMATLTCSEFKKPPKIPYKAIAL ATVFLIGAFLLIIRLPSCCQGYI KQRRGRRPGPQLLIIGHSWCSY PGFYPPAHRFTMHFKGLPVVN PNE
29614	59982	A	29797	1	186	DCRLRAGDPRRSHCAVSPGTGS RALSGYRY*SVDPQRNDGVDQ *ATLRASAHLQTA VVEFSA
29615	59983	A	29798	724	1015	RSHPCQGYLQNHSTSSASFAPA RKG*NRHYAFARNDRLVAPCS HHHQ*PAPAPVHLH*PVDLST AIDAPAVNGDGKARPSKRRYQ RLSVPEVVQY
29616	59984	B	29799	1	4182	
29617	59985	B	29800	1	1191	
29618	59986	A	29801	167	504	
29619	59987	A	29802	1541	1852	FALFANRVSLAANVSGRGS PWWRRIVVCCSTNR/RSALDIA HQVDVLSLVHRLSQERGLTVIA VLHDINMAARYCDYL/APCAA VK*LLRERLRKLCAAKPSK
29620	59988	A	29803	407	3584	
29621	59989	A	29804	3	150	
29622	59990	A	29805	1	921	
29623	59991	A	29806	300	560	IRDKNRVFLRESWRRLFTTAND QPHRPARRIISIAGIKWRYSDFLI NYCAGRAVF*RETGSVVERWH HHAGWKTPFRKRAGRTAGH
29624	59992	A	29807	100	315	PIKITSALASARYVRATLSCSR NSTLRWKK*RKMALTKPSTTN GSRSNS**MNFFL*QAPPG*PSA LPFVH
29625	59993	A	29808	3	116	
29626	59994	A	29809	1	1469	
29627	59995	A	29810	1	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYQRA CSGR*VPNLRLPEVQSTDRLLS QRRRVSPDRQWWLACH
29629	59997	A	29812	438	1942	
29630	59998	A	29813	1	1464	
29631	59999	A	29814	3	602	

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29632	60000	A	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA SVVSRDGFVIAGGGGMVVVEE LEHALARGAHYAEIVGYGATS DGADMVAPSGEGAVRCMKMA MHGVDTPIDYLNHSGTSTPVG VKELAAIREVFGDKSPAISATK AMTGHSGLGAAGVQEAITYSLM LEHGFIAPSNIEELDEQAAGLNI VTETTDRELTTVMSSFGFGG TNATLVMRKLMIISASTSILR
29633	60001	A	29816	1	2472	
29634	60002	A	29817	1	469	LFNREVCCLGQGS*QMAL*LL GIESYIT*L*SGGDN*ASIGVIPDP AAIAR*RPWRSACG**PKCPLA DVFAGHSGRKRPPSMAFTATLI SPGTGRRAINSVLAQFKAGESNI WLSALPTPLTPTRITNGALPSTF SGSSTFARISPISSFSRP
29635	60003	A	29818	884	1084	
29636	60004	A	29819	1	1040	
29637	60005	A	29820	2711	3854	
29638	60006	A	29821	1	957	MKIGTQNQAFFPENILEKFRYIK EMGDFGEIDGKLLVNNIEEVK AAIKETGLPVTIACGGYDGWIG DFIEERRNLGLKQIERILEALAE VGGKIVVPAAWGMFTFRLPP MTSPRSLDGRKMVSDSLRLVL EQVAARTGTVVYLEPLNRYQD HMINTLADARRYIVENDLKHV QIIGDFYHMIJEDNLAQALHD NRDLLGHVHIADNHRYPQGS TLDFHALFEQLRADNYQQYVV YEGRIRAEADPAQAYRDSLAWL RAGQVADKVHASYYCTRDLE LVAVCD SRLSQAQALAEKYG ASVWDDPQAMLLAVKPF*FVGL VIGAGQVADKVHASYYCTRD LELVAVCD SRLSQAQALAEK YGNASVWDDPQAMLLAVKPDV
29639	60007	B	29822	96	821	
29640	60008	A	29823	3	775	
29641	60009	A	29824	961	2073	
29642	60010	A	29825	1	849	
29643	60011	A	29826	319	541	
29644	60012	A	29827	1142	1756	
29645	60013	A	29828	44	283	
29646	60014	B	29829	1	1812	
29647	60015	A	29830	685	1146	

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29648	60016	A	29831	202	918	AVDVTGLADHRDRTEHGGAFAA IVHRIVKHFITAWAICQQRNHA ALVVIRRLLEANHRRHRTGRG/S VDRVSAARSLSSGTMPPGNGVW RIGVFTQLSVA/WHQ*VDLLIVF QFVRDTTIDDDHVGIFALAAAND RAAFDNILDPTGSVDVLLPLPG RHNIANALAAAALSMVSGATL DAIKAGLANLKA VPGRLFPIQL AENQLLLDDSLVNAAQQNILS VHILNQQTGKPAADVTVTLQE
29649	60017	A	29832	1184	2409	TLKACCLVRSMCRVAVP*RC/GR QLVSSDNISNDPMNVIDWINMY ALAVSEENAAGGRVV TAPTNG ACGIIPAVLAYYDKFRRPVNER SIARYFLAAGAIGALYKMNASI SGAEVGCQGEIGVACSMAAAAG LTELGGSPAQNMEGKIDRPEE YADIATKCVTNFREKNRDRCL VILSRNDEALNSQRTSEELHHY YEIVWDEEQTHKFNISPHLQRI KAFKTLGGPHGNITVDMVISAQ ELLQEDMATFDGHIVEALMKM PEVNAMYPELKLHAIGWVKHK CIPGAKWPEIQAE MRIWKKRRE GERKETGKYTSVVDLARARAN QQYTENSTGKISPVIAAIHREYK QTWKTLLDDELAGRCFADRQN LMVCLRSMNPVFTGSCARMRC CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA MIPNFNWAFLGVTTWIFMAAG GAESVA/CTLTTSKAVRNR/SFK* SSSPGILSGYVSRSSGSPISLISP ASLCAGHMRFFCSSSKPTCSNP RTFAAALSSAWSSPSPNEGFSSN PAFLGTSLMMFHLELRRCIPIV TTDLLPLTSGDVGLVLLCVGLD GSLWSDCRMTESVSTNTTPPIIT SRNS
29652	60020	B	29835	46	893	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29653	60021	A	29836	3	2037	CTSSDPDPSGLPPGFAKLTSLHVT LVEVGVSPEPDEGWLYLAVVID LWSRAVIGWSMSPRMTAQLAC DALQMALWRRKKPRNVIVHTD RGGQFGDRWKGWLTSTRIFRWI SFQPALAPTRKAALCYLAREVN PDMADYIKKLLPGIHVREESR RYYPSGEVTAHLIGFTNVDSQG IEGVEKSFDKWLTGQPERIVR KDRYGRVIEDISSTDSQAHLN ALSIDERLQALVYRELNNAVAF NKAESGSAVLVDVNTGEVLAM ANSPSYNPNNSLTGTPKEAMRN RTITDVFEPGSTVKPMVVM TAL QRGVVRENSVLNTIPYRINGHEI KDVARITTEEDFNHASAARFVC AAAERCKTTINLVPENEVLNV LEGEDAETNALRAKRRCPKCG TAMDSYLIDPKRKLHVCNNP TCDGYEIEEGEFRIKGYDGPIVE CEKCGSEMHLKMGFRFGKYMA CTNEECKNTRKILRNGEVAPPK EDPVLPPELPECKSDAYFVLRD GAAVAARFNDDRHRRLGLAVLY ADQADLYGVADSVSAGDSL SA LYKHERRLVVPLLVSSSLFLY RHGIRLPCGSPGGIWAPWQIRR GRQAVNCLAPM/HHPGKNRAW KTYCSQ*AIVPQLPVCIGI*PRSD SYHDYQRDPRCQPLRALWRRS DSPIGGYSSAIGI*TERHCRSGNP
29654	60022	A	29837	993	1832	
29655	60023	A	29838	124	276	QEGRCQVTITRKMPLSSDLGSL HGLAGNHISPPICARTPHVATVL RQLELEDKHWNGSG*FARLG WKPSPHLCQNPPCGHCPQTAP GA
29656	60024	C	29839	64	267	
29657	60025	A	29840	3	86	
29658	60026	A	29841	1	1481	
29659	60027	A	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK*VGGSSRVNVVPQVFI SLVSQMFSENDLPLVRKRKTEP
29661	60029	A	29844	115	903	
29662	60030	A	29845	1194	2311	
29663	60031	A	29846	368	502	
29664	60032	A	29847	1156	1359	SEPVPYLCYLRQLAVQANPRR MRCIARHFNINGNRHLTTTINF *SMVSLIANRLIIDLIHTVDFY
29665	60033	A	29848	1	228	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
29666	60034	A	29849	102	296	YRNSHNLLQGWFQIHRGDLLEYH SSPHSR*KHRNRHNRARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	A	29850	1	4185	
29668	60036	A	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVVIDQCVFLIRV TNPAGSFFELRH
29670	60038	A	29853	2	834	
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNNLVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	A	29855	1591	3150	
29673	60041	A	29856	2	222	
29674	60042	A	29857	16	359	TTHKTRWQAPVPLRGSPVVAL RIPSDQSEAV/HLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLFFNRHYICFTRI RRFRWHRSSLFHGMNVKYRRS KINN
29675	60043	A	29858	207	470	ATIL*GDFYP/GSRNWLGVSSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTSGHVLGSCCV NGKTLRKSDSRWQQLLRSLIR R
29676	60044	A	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCMAIRSPIRMASSR SWEIKTMVR
29678	60046	A	29861	593	1881	
29679	60047	A	29862	3	198	
29680	60048	A	29863	1	1590	
29681	60049	C	29864	1	5421	
29682	60050	A	29865	63	185	LCQSHAPRKFPARPFRRFR*RQD CQTSVFLLRPVANRAPA
29683	60051	A	29866	1	715	
29684	60052	A	29867	1	1212	
29685	60053	A	29868	886	1185	
29686	60054	A	29869	190	433	AFAKLFIMAAALTSQVAHLSSS GTPFRPFCLPSC*LSSSRAAIST CSLYAAWFPLTLIRCGIRKSPII CGISRCRCWRQ
29687	60055	A	29870	1	439	
29688	60056	A	29871	14	106	
29689	60057	A	29872	2518	3024	
29690	60058	A	29873	448	537	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29691	60059	A	29874	463	889	FFGLVTSSPSADSPAMLDTRNV SHTGLGPIIPLTFEAGIHTRPTPN SPPRSCLAPAIKA*FFSPAARITT CCASLYRSPLKTLRSVRFWRSS ASVLMRRSSSAAPMEATI.RVL SGLRGSRSDDKAFTPHPTI*CLEA FPGSRAVFASAP*CLTLRANQR KGCW
29692	60060	A	29875	524	1006	SLLAWSGINIFASSRIAIASPLA ASVPLSMDNISLCTPSGVPEKV TSTVLTSVPQSCCKLMMKDFSGP *FP*EKRVSETSPNCTLICLLSCA STHVI.RRNDPLMLTVPWSWANS SQPHVNPKNRIQIIPFNITPSLV NQIKIETRAFTPLPLCGLITK
29693	60061	A	29876	2005	2517	
29694	60062	A	29877	1	470	MQRDGDIALIYRSKIGPRTSIT FTARRANPVQRIARILLRDHLI CRMSCTAARHANTFDLIQGGG ADNFAAIYGGANDRITRADA/V SRGCWKLAPVRDIKRQTVAAF YHQDIQPGSCHDQNAL*STGFW REQSGGQ*P*AG*TSNRTRCCIT GR
29695	60063	A	29878	734	1306	
29696	60064	A	29879	743	901	
29697	60065	A	29880	771	1013	RLGTVGTDLSWCYQYQLCYQ* ALPFSTLPAGLAGNGCQRRRCA GTHSLWHADLSVWPDADSLF QRDGRAGGGATRLLR
29698	60066	A	29881	1094	1345	
29699	60067	A	29882	2	751	
29700	60068	A	29883	239	483	PTPQHLYHALTGSTIMSQRGV DIPCHWHDITCGHAHSLPHRRG RKA*SMGNN*YSCTWCYCEGG TEKAIWPGDGCPLSV
29701	60069	B	29884	228	803	
29702	60070	A	29885	488	636	
29703	60071	A	29886	1	2117	
29704	60072	A	29887	665	795	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
29705	60073	A	29888	1743	2013	LQCTQYAVGENPAVNFAGRPK GSPCFPGGGGLN*AAADIPVAS DNPAHYADAIRYNARTPLQAG VYFVRDGPGLASVRNKERYF ANNYIYDMGRNKDGRQSTWY MGLGTDIDTGLPMSLSMNVYA KYQWQNYGAANENEWDGYRF KIKYFVPITDLWGGQLSYIGFTN FDWGSDLGDDSGNAINGIKTRT NNSIASSHILALNYDHWYSVV ARYWHGGQWNDDAELNFGN GNFNVIRSTARGWLPGTICRPDK MRQHRIRHCAPIAGCGTGCRPD KTRQASHQAQMSNAYDYSEIQ PPSEGEILLDAQPLESWSSKAFA RKVAYLPQQLPPAEGMTVREL VAIGRYPWHGALALLGAADRE KVEEAISLVGLKPLAHLRLVDSL SGGEPGVDRMLVAQDSRCLLL DEPTSALDIAHQVDVLSLVHRL SQERGLTVIAVLHDINMAARYC DYLVALRGEMIAQGTPEAIM RGETLEMIYGIPMGILPHPGA APMNTAHHAAIDPNRIVALEW LPVELLLALGIVPYGVADTINY RLWVSEPLPDSDVIDVGLRTEP NLELLTEMKPSFMVWSAGYGP SPEMLARIAPGRGFNFVRNTP LARTLQLJLREGPRGHPALVQV VDLLIEPPQLPLLVPVQTRIPRI QPQSHPAHGVNEAVRNPTVWV APFIDEIHSIHKYSI
29706	60074	A	29889	1	1584	
29707	60075	A	29890	1	1188	
29708	60076	A	29891	728	970	
29709	60077	A	29892	2447	2665	
29710	60078	A	29893	255	1360	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
29711	60079	A	29894	1	1890	MYSRFDIVVAEPICTLTTFGKET VVSDSQTRTTTTDDPLQVLQV LDRADIRPTTHNEDLPFGGALG LFGYDLGRRFESLPDIAEQDIVL PDMAVGIIYDVALIVDHQRHTV SLLSHNDVNARRAWLESQQFSP QEDFTLTSDWQSNMTREQYGE KFRQVQEYLSHGDCYQVNLAQ RFHATYSGDECQAFLLQNLHGN RAPPSAFLRLQGAAILKLSPERFI LCDNSEIQRTRPIKGLPRLPDPQ EDSKQAVKLANSKADRAENLM IVDLMRNDIGRVAVAGSVKVP ELFVVEPPFAVHLLTITATQLPE QLHASDLLRAAFPGSGITGAPK VRAMEIHDELEPQRRNAWCG/SI GYLSFCGNMDSITIRTLTAING QIFCSAGGGIVADSQEEAEYQE TFDKVNRILKQLENYRRALRDL KEEVAILRSPFELSFAFCSPSIASM ATRYPNGRHIPDDLRLPKERGIII VFTGNGKGKTTAAFGTATRAV GHGKKVGVVQFIKGTWPNGER NLLPHGVFEQVMATGFTWDT QNRESDTAACREVVQWAKRM LADSSLDMLVLLDELTVMVAYD YLPLEEVQALNERPHQQTVIIT GRGCHRDILEADTVSELRPVK HAFDAGVKAQIGIDY
29712	60080	A	29895	159	475	VKVNLPWAMLLHSGYADHPYS RFDIVVAEPICTLTDD/GRCSHIS LYAAGIINSDSKGAVIMPPIIIGA AIRLITSEPAVPHRIGSRPAIITA TVIAFGRTRRTAP
29713	60081	B	29896	158	810	
29714	60082	A	29897	1	2070	
29715	60083	A	29898	1081	1218	
29716	60084	A	29899	289	1014	
29717	60085	A	29900	145	297	
29718	60086	A	29901	452	568	
29719	60087	A	29902	21	185	VHDQPSQEIQQRTEAPGRSS RRVAQCHPQPGES*SRAQIPPAS TPKPGGGDL
29720	60088	A	29903	1	711	
29721	60089	A	29904	2	825	
29722	60090	A	29905	812	961	
29723	60091	C	29906	1	1587	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
29724	60092	A	29907	3	403	LVFDDGDVQMGFWCGCPFCLL VFLLTVRSLSCRSVGVCRSTR DLVCLGSSGGCRTVNIAEQQM LLPDCSSGIFVSEGYLAV*GVSL PLLGGASQLGLGSMAlFMIILP IHEHGMFFNLVSVSSILLSSCL
29725	60093	B	29908	168	863	
29726	60094	A	29909	340	612	
29727	60095	A	29910	1	834	
29728	60096	A	29911	92	548	
29729	60097	A	29912	1251	1682	VPVALAAARRSELSRTAAADT G*SAAAEVLNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGGQSSWAPFEWEGAPR GEEWTLVSVGALK
29730	60098	A	29913	1	1278	
29731	60099	B	29914	1	2007	
29732	60100	A	29915	406	615	
29733	60101	A	29916	52	391	SNRLKLHSSRSSCMFFSSIR SFKDFSLVDDGDVQMGFWCG CPFCLLSFPF*QSGPSAARSVGV CWRSTPDPVCLGVSSRGCTV NIAEQMMLPDRSSGSFVSEGY PAV
29734	60102	A	29917	759	1190	VPVALAAARRSELSRTAAADT G*SAAAEVLNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGRRSALGQLEWQSGQ SPAGAAIAAFDNR
29735	60103	A	29918	84	3661	

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29736	60104	A	29919	1	1230	MDAGWSDVGSWSSLWEISAHT AEGNVCHGDVINHKTENSYYV AESGLVTTVGKDLVVVQTKD AVLIADRNAVQDVKKVVEQIK ADGRHEHRVHREVPWGY DSIDAGDRYQVKRITVKPGEGL SVQMHHHRAEHVVVAGTAK VTIDGDIKLLGENESIYPLGAT HCLNPGKIPLDLIEVRSGSYLE EDDVVRFADRYGRGNDMKKL TCFKAYDIRGKLGEELNEDIAW RIGRAYGEFLPKPTIVLGGDVR LTSETLKLALAKGLQDAGVDV LDIGMSGTEIYFATFHLGVDG GIEVTASHNPMDYNGMKLVRE GARFISGDTGLRDVQRLAEAND FPPVDETKRGRYQQINLRDAYV DHLFGYINVKNLTPLKLVINS NGAAGPV/VDAIEARFKALGAP
29737	60105	A	29920	1	1398	
29738	60106	A	29921	426	1861	
29739	60107	A	29922	863	1388	EPERTSIKSGIFPGFSRQCVAPS GI*MDVVFVKQFDITINGDFCRS RDNHPVFRAVMVHLYRQALAR FHGDFAHLVAVARVDRVIFAPR TIHFAMHPMLMATIGFDLLDHF FHILYRVTVGNQHRIFGLHHYQ IFHPDGGDQARFSIHIAVFSFVIN HIAVANVALGGVADLP
29740	60108	A	29923	1	2055	
29741	60109	A	29924	1	2047	
29742	60110	A	29925	1	1294	
29743	60111	A	29926	1	1020	
29744	60112	A	29927	1	1422	
29745	60113	A	29928	1	1698	
29746	60114	A	29929	210	340	YGDVEHESWLSVVRHAHPRI FA*PTLISLQKRLGKWSGVTGA
29747	60115	A	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK GYGHHYRNLP/VPNGPPLSL P*YCKAKFKPSTSQVP
29748	60116	A	29931	63	281	
29749	60117	A	29932	345	467	LPTRCTYTNLRRRSPPAWYY* *YWHRDICRSTPARRQTE
29750	60118	A	29933	29	281	MFGKELGRRDVSQLGAAEITYI LKD*TES*EILCGGRFLPLRG RTLQGGEWPSLYFHSDCSSHAE QCLLYGFADWAPLAFFR
29751	60119	A	29934	520	714	

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29752	60120	A	29935	222	527	LPSKSLASGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAEGLHLI SFLHALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGLSPDIEG DLIQGQRHRDHIGP
29753	60121	A	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRRVLLIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSYLDALNGGD AESAGLTPPELWPRHHGHGA GVKLVEQLCQRLRPVNEIRDLA RLVAEFHDLIHTFPMNLNPKTIV KLFDSDAWRKPQORVEQLALTS EADVVRGRTGFESADYPQGRWL REAVEVAQSVPTKAVVEAGFK GVEIREELTRRIAASVSWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVFSLREQIRSHEIRRSAVS NHQHFRACGHIDRRTVQTLA HLTFRFGDKGVTRPEDFVHFV HRFRTKGDPLLTFWPSAPVTAT ILRIPLANGFFRHDHKSSCMTR VPQVPEDPVKSHAPQQFWIHH GKWFAYWDVAIGIPGPFAGRS\ CVILLGDAVREVTRVSNVPAK RYIGGSPRRGFINSNCMPGIISPG
29756	60124	A	29939	1	114	
29757	60125	B	29940	1	4191	
29758	60126	A	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSLSLRAFW ASAPVTATNPPDTLGNQFFRHD HKSSCMTRVPQVRSPTELNRSQ GASRPRGVIIQLGHRDPNGDDS HVRIGLIKHP
29761	60129	A	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	A	29946	1	936	
29764	60132	A	29947	1	966	
29765	60133	A	29948	1	675	
29766	60134	A	29949	1	792	
29767	60135	A	29950	2	929	
29768	60136	A	29951	1	969	
29769	60137	A	29952	1	420	
29770	60138	A	29953	1	549	
29771	60139	A	29954	1	450	
29772	60140	A	29955	1	606	

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29773	60141	A	29956	1	726	MARGNATLPVCGRDVVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLLTGQQTP AFGRRVSGVIECDNLKTCHTSH GSVMAETA VINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRL
29774	60142	A	29957	1	771	
29775	60143	A	29958	1	1491	
29776	60144	A	29959	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDQMAALSRLG NDYRPTSA YERGQRYASRLQN EFAGNISALADAECNLTCHT SHGSMVMAETA VINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIERYQLPQS YQRMDFRRRFLQGFCFRFNH HQTGFSPAGANQRGLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVYIAIK PTCWPLDIIIPSCALHRIETEL MGKFDEGKLPTDPHMLRLAIE TVAHDYDVIVIDSPNGLIGTIN VVCAADVLIPTPAELFDYTS LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSVMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGGNSVLRK
29777	60145	A	29960	1	1731	
29778	60146	B	29961	1	3345	
29779	60147	A	29962	1	1959	

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29780	60148	A	29963	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPV NVKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKRKNSPRIV QSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEH DGICEIHVAKYAEIFGLT SAEASKDIRQALKS FAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSP SRRLYSVHINPYLIPLLY RVPNRVVTQFRL SETK/EITHPYAMP LYESLCQYS
29781	60149	A	29964	1	1557	
29782	60150	A	29965	1	2259	
29783	60151	A	29966	1	1959	
29784	60152	A	29967	1	2277	
29785	60153	A	29968	1	2418	
29786	60154	A	29969	1	2028	
29787	60155	A	29970	1	1650	
29788	60156	A	29971	1	1170	
29789	60157	A	29972	1	1446	
29790	60158	A	29973	1	1191	
29791	60159	A	29974	22	1893	

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29792	60160	A	29975	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KIRRKNGPVSATFTSDGKIRLFY TDYSGKH YGKQSLTTAQCDNL KTCHTSHGVSMAETAVINHKK RKNSPRIVQSNDLTEAAYSLR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKS FAGKEVVYFRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITN PYAMRLYES LCQYRKPDGSGIVSL/KIDW/IIIE/ RYQLPKVPSPPEAR KITRRWRI/V KQRI*LGFLRLSEMPRKQGDY RTRIWK FEDGLSNVLVIQLNKLII ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGVSMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITN PYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRSONDF*RR GI
29794	60162	B	29977	1	1317	
29795	60163	B	29978	78	215	
29796	60164	C	29979	225	422	
29797	60165	A	29980	1	368	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVYFRPEEDAGD/EKGY ESFPWFIKRIYSR
29798	60166	A	29981	1	409	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVYFRPEKDAGDEKGY ESFPWFIKHSTNITSLWFFSS CTH
29799	60167	A	29982	1	814	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29800	60168	A	29983	3	678	GSVMAETAVINHHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR YSFPDPDYFHGLALNVCGFSRYT VQDVGGSIILGSGGQWLSSHSS SRQCP
29801	60169	A	29984	2	660	
29802	60170	A	29985	179	283	MGQGRNPQTRRTYGCQFRMV K*HGIEMKCEELIL
29803	60171	A	29986	1	643	
29804	60172	A	29987	2	1073	
29805	60173	A	29988	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAADGTVAEYNGYNV VFALAGSPEDADDTSIYMFYQK CDNLKTCHTSHGSMETA VNIHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRKIPDGGGIVSLK/ID WIIKRSQLPQSAFYQPFMGLRR ESFYFRWERRTLGPLKSFSVVKR GTEAGKFRLAALLVRL
29806	60174	A	29989	1	1692	
29807	60175	A	29990	1	1788	
29808	60176	A	29991	1	960	
29809	60177	A	29992	1	1385	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
29810	60178	A	29993	1	936	MWLVTTLESTDETHFYHHSK CYWPRALGECILSIEAACQAA GGEAGNGGSVTKATLGSRRQ AQHWKALARTIRQEKEIKGIQ GKQEVKLLPFADDMIIYLENST DSSKKLSELCNLTCTHTSHGS VMAETA VINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVYRPEEDAGDEK GYESFPWFIKRAHSPFORALYS CTICNP*ILIPFSVIGLQNRFTQF RLSETKEITNPYALRLYQSLC
29811	60179	A	29994	1	1641	
29812	60180	A	29995	1	1551	
29813	60181	B	29996	90	1515	
29814	60182	A	29997	452	1523	
29815	60183	B	29998	9	2021	
29816	60184	A	29999	1	960	
29817	60185	A	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA SSNCAPRGISPOELTVDLQTKC DNLKTCTHTSHGSVMAETA VIN HKKRKNSPRIVQSNLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVY RPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLNSLFY GVQNRFTQRLNFVQKSRLVD LALKGLRVLLVEGNDPQGTAS MYHGWWPDLHIHAEDTLLPFY LGEKDDVTYAIKPTCWPGLDIIP SCLALHRIETELMGKFDE

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29819	60187	A	30002	1	1756	MPASGNENDLNMPSGTIEIFVR CYVEVERIMDFADFGTTIKQDF RLLGQTSVDRLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRI.ES GHQAPCMKSNNALIVILGTVT DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWYPLCDN LKTCHTSHGVSMAETA VINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAM/RIPL H*LFR*TLRQTKPDNSAGKCVK I**HTQNQRSGRSQND*RRPVL LASLLGATIDYAIMATTPVLW YPLCDNLKTCHTSHGVSMAET AVINHKRRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYL PFFIGLQNRFTQFRLSETKEITNP YAMQSPYTDYSGKHVGKQSLT TAQVNVSKSDDTL KINGVEDH KTIFDGGDKGTYNQVQFIDEEN
29820	60188	A	30003	1	1653	
29821	60189	A	30004	1	1128	PWISAPVPVDVVEGAMDSVT LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHISDWCCRN YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRERHTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGVSMAETA VINHKRRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYK/SL CQYRAFVNGGEEKARGKPIL CRYGVGM

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29822	60190	A	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA QRKKKYPPWEKLQGSVRGETP VINHKERKINSPRIVQSNDFPEA AYSLSRDQKRMLYLFVAQIRKS DGTLEHGDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAAGKE VVFYRPEEDAGDEKGYESFPFW FIKRAHSPSRGLYSVINPYLIPF FIGLQNRFTQFRLSETKEITNPY AMRLYESLCQYRKPDGSGIVSL KIDWIIERYQLPQSYQRMDFR RRFLQVCVNEINSRTPMRLSYIE KKKGRQTTHIVFSFRDITSMGFF LESPTQGLASPE
29823	60191	A	30006	233	1538	
29824	60192	A	30007	1	2331	
29825	60193	A	30008	1	1857	MPLRFSSSSRIPYYVNLHKA TGERIDYNFETHSSLEIATD TISDHHPCESAANAETRPSTVL EELARAIQEKEIKIGIQGKEEV KLSLFADDMMIYLENPKDSSRK LLEWIKESNKVSGYKTHVHKS VALLYTNSDQVENQIRTPQFYN SCENKIKYLAITYLTESKDLKY RNYKTLLKEITDDTNKWKHIPC SWIVKVAGVESWIHHTQVEVW TPPEETAGSTAAGSQDQPDQPR YTCEPLEDLHLLFQKETSHTIKA STTDPEEKPLPPYKRYCDNLKT CHTSHGSMVMAETAVINHKRRK NSPRIVQSNLDEAAAYSLSRDL KRMLYLFVDHIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVINPYLIPFFIGLQ/NRF TQFRLSETKIPV/IQEA GLSQSEK QAADGIQGVAFQVQVCDGCG SSLQHFFLLMLVDFQLPPLNL RVLIMATLFTIACYVELRGYML HAFQLVSLAMSHLHLAHNQDT HPAISDLVWLVCALSHSLFHR SDVRADLSNAYSEEVKFGFLL WGLDCASLHRSDFITSSSETKYH
29826	60194	A	30009	1	944	
29827	60195	A	30010	1912	1915	
29828	60196	A	30011	1503	1961	

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29829	60197	A	30012	1	6552	MAETAVINHHKRNKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQIRLGD GSSRLSMEHGLRSIPAWTLDKFI EDYLLPDTTFGADVKSAVNVV CDFLKERC
29830	60198	A	30013	1	2679	MAETAVINHHKRNKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALK SFAGKEVVFYRPEEDAGDEKGY YESFPWFIKRAHSPSRGLYSVHI NPYLIPFFIGLQNRFTQFRLSET KEITNPYAMRLYESLCQYRKPD GSGIVSLKIDWIIERYQLPKVPS PEARKITRRWRIVKQRI*LGFL RLSEMPRKQGDYRTRIVKFE GLSNVLVIQLNKLHCVMCLVR DCDVLKTYFHR
29831	60199	A	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI NHKKRNKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSGHINPYLIPFFIG LQNRFTFRFMEQKKSPSNRFT QVRLSETKEITNPYAMRLYESL CQYRKPDGSSIVSLKIDWIIERY QLPQSYQRMPDFRRRLQVCV NEINSRTPMRLSYIEKKGRQT THIVFSFRDITSMITG

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29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK SESDIHLAEHHKQVLYDGKLAS SIAFTYNAKATDAQLCLESSPK ENASIFVHSPHALMLQILTEQV CTQVVHKPHPEPDSTVKIQNPS EQMAVLYCIVLVGGFEFDLEMN FIQDAESITCMTLEHCDVTC QAEIWSMFTAILRKSVRNLTQS TEVGLIEQCDNLKTCHTSHGVS MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPHYAMRLYESLCQYRKPDGL SIVSLKIDWIIERYQLPQSYQR MPDFRRRFLQDVQNETHGNT
29833	60201	A	30016	1514	6335	
29834	60202	A	30017	2033	4226	
29835	60203	B	30018	1	5670	
29836	60204	A	30019	1968	3130	
29837	60205	A	30020	34	431	
29838	60206	A	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	A	30023	3	1771	
29841	60209	B	30024	1	2299	
29842	60210	A	30025	2	488	
29843	60211	A	30026	1	127	
29844	60212	A	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	1	836	
29847	60215	A	30030	297	936	RTSSSLMRSSSSLLRICSGVSPRS IPRWFTSVSLPSSFIRITTFRYT PGHVAPASRRSCYKYRR*PMRL YTIMQSL/VGSRPSPGLRAFSSD CSPLPRTCSLRRRVLMITTSRS *SLTYGVDPSVRPVLAASEYF SRRYAGFQNPNNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSISCTSTGGNTTL PPSSPPDC
29848	60216	A	30031	1818	1991	SPSHIRRTAPNGLRHRYQR*IQQ* APSDQKRDFLVPHIGADSAMAK HGGSHRAVLPPQGW
29849	60217	A	30032	2	501	
29850	60218	A	30033	1419	1640	IFCASLGLGYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPPQGC DPHMESLI

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29851	60219	A	30034	1	1593	
29852	60220	A	30035	107	195	
29853	60221	A	30036	1480	1605	TILRITTFQCRSNRRRQRQ*NRFS STSQRRRCYFLLNGEDVTLTP
29854	60222	A	30037	1	373	MPSYFTSRIAAVHVSALREFEQA HHESKHHEFIAQRMFRMFYQ ARNLLHAGQENLFSGLTALTAE FTVGEEATRGTGKRGPSPDG RILRTTKTRNPRGYMQGRYLES QRDVEATDKPFEEFMNRFRLLE AAPRVEFIAYTGLCEDVIRPQL DEAIAQGYLTCEADYWQITEH GKILFLNSLLEFLADGYHMWR MIGAGAHAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPLGIEQ LPALKAFDTVFSMGVLYHRRSP LEHLWQLKDQLVNNEGELVLET LVIDGDENTVLVPGDRYAQMR NVYFIPSAALAKNWLKKGCFV DIRIADVSVTTEEQRRTWEMV TESLADFLDPHDPGKTVGEYPA PKRAVSDCAQAVKMTNMISYQ GLVRTLSTSPNNWLVFMQNG QEVVIDSGKSVS*RSVFCGCFIK HGICSMRDKKISFLV*RRLLNS LSAKKLHGAKQRAKGDLPRMG AFCVPPKRVIRVICKEGIWKA SVMSKPKQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCP PSRRQRRRSGPLPEPAPRVS*Q IFPSQYWRVQSTENQKQRLDP RGQIVNVPARRIIRQKRCKKV AGSA
29856	60224	A	30039	1	1090	
29857	60225	A	30040	1	1384	
29858	60226	A	30041	1	1377	
29859	60227	A	30042	2268	2684	RCRRCKRLLRRFRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCHCG*QRC SSDGRKITSVHRGRNADGRELT HQAVALRLAYLSDRFARHHRHL RNAHRRGPDRIKERHFPAATKL RHPTAV
29860	60228	A	30043	1130	1310	RLDKQNRGRQGRQNRNGVFHQ QPQR*RTDVIQMPHSHRHA QRDHDQQLGQHAGRNFE
29861	60229	A	30044	395	689	VAAVSSSMSCAPVLMTVVTR CTLLILSQFMRRKAIAK/LSGSL LPASEVKVLKRDGDYSE/VQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPPQGW

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29862	60230	A	30045	1	2142	
29863	60231	A	30046	1	2463	
29864	60232	A	30047	1	1066	
29865	60233	B	30048	790	820	
29866	60234	A	30049	3	126	
29867	60235	A	30050	1853	2257	
29868	60236	A	30051	90	411	
29869	60237	A	30052	1375	3174	
29870	60238	A	30053	5	206	
29871	60239	A	30054	1	1986	
29872	60240	A	30055	339	596	PPYKRKRKRRESVSDGMRNTG KTRRTTR*INLLGRS*NRNFVSV PSGQNPY*ISLDHGRENYGGYS TIQRLLRLPLSRSGCILQ
29873	60241	A	30056	634	924	
29874	60242	A	30057	42	665	KYGVNPGPYGGTTRKLYEKK LLKLREQGTESRSSTPLPTISSA ENTRQNGSSSDRYSDNEEDSK IELKLEKREPLKGRAKTPVTLK QRRVEHNQSYSQAGITETWTS GSSKGGPLQALTRETRGSRRT PRKRVETSEHRIDGPIVESTPI AETIMASSNESLVVNRVTGNFK HASPLPITEFSDIPRAPKKPLT RAEVG
29875	60243	A	30058	1822	4791	
29876	60244	A	30059	310	1275	
29877	60245	A	30060	52	390	
29878	60246	A	30061	250	1530	
29879	60247	A	30062	1	1641	
29880	60248	A	30063	1009	1140	
29881	60249	A	30064	913	1218	
29882	60250	A	30065	900	999	
29883	60251	A	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	A	30068	1	2229	
29886	60254	A	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSCFVWKTAWAQKMN LLPMARLTTTIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALLTVTT QATGLRLARQKRTATPRTIRPG ESTSSPRSSGSLAPACSPVWM

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29888	60256	A	30071	498	1155	KQPSAVSGTGAAGEANLHAVR TAEQTAVVYRHRQVRVYLLR YGILDWSPITYLKEVKHFDKDS SWAYFLYEYAGIPGTLLCGWM SDKVFRGNRGATGVFFMTLVTI ATIVYWMNPAGNPTVDMICMI VIGFLIYGPVMLIGLHALEAPK KAAGTAAGFTGLFGYLGGSVA ASAIVGYTVDFFGWDVGFMLS HELWESEFTKLKYEYNNPCASP VSGWL
29889	60257	A	30072	670	1100	NCRKTSPKRRFSDDPKSDRAK DFLAKILH*SLWRAPYPIARHLTL YRFAPRICYILALPLSQSRSTQQG ATMALPILLDCDPGHDDAIAIV LALASPELDVKAITSSAGNQTP EKLTLRNVLRLTLNRTDIPVA GGRGKTVNA
29890	60258	B	30073	861	955	
29891	60259	A	30074	1	2510	
29892	60260	A	30075	3	119	NALRKSSASSCSGRNRYPGS*PS RPDCQRCSCSHKHAGYG
29893	60261	A	30076	3	227	GGEGRASCADTGWLPDPPGC AAGALGGGGWAVAGAAAGGP CA*SAGGIGVHAPKAQHPATFS GPAEGVIPPQ
29894	60262	A	30077	1	2277	
29895	60263	A	30078	1	2187	
29896	60264	A	30079	1	3666	
29897	60265	A	30080	1	699	
29898	60266	A	30081	513	1019	TGGVCCWCARYVDALVVFAD QLFVAEVLASAHSPRLYAHAAH GDTQPQLRLNLRGQALSP*FCCN HRAALQRHQFVRPLPAROSRO MRRCNLLYQKASQRSQRDSS *RSLFFRSVDADGG*R*SHGYA FRHGRFQCHRPGLPGTGPPRH ADSAFSRRLIYPACRWRL
29899	60267	A	30082	389	462	
29900	60268	A	30083	1	278	MGVNDAVLEMHGLGNDFMVV DAGFDQLLVVEPPYDLELDFHY RMFNADGS/DSGAVRQRCALLC PFCASERTDQ*A*YPRQHRQRA DGSDRHR
29901	60269	A	30084	1240	4914	
29902	60270	A	30085	1	1308	
29903	60271	A	30086	30	164	VTWW*RAPTAGLMQC*YCRNR RARLRLTYGHAPHRNGPDV PS

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29904	60272	A	30087	3	264	TLRPNRNF*HIPDAAGVIPVGY AL*RGTSVSAVHRW/CSTVFGV NWATLAKTLMVAGIRRSGAAS RISRASPPSFVPACSVGRKKVI
29905	60273	A	30088	1	3639	
29906	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLLV FADCLAWTCRHDKLDDISDVA KITGLTSKAIRFYEEKGLVTPPM RSENGYRTYTQQHLNELTLRQ ARQVGFNLEESGELVNLFPDQ RHSADVKKRRTLEKVAEIERHIE ELQSMRDQLLALANACPGLDSD ADCPHIEHLSGCCCHHRAGKYVG LIRRVKRRIRHRCWPIKTLQRA VSEFQRLIQPNHQYQSYTRQCA PETDNHADNSYNAGLFIVNSLY TAEGVMDKHSWQRYVPLMR HEALRLQVRLPASVELDDLQA GGIGLLNAVERYDALQGTAFITT YAVQIRIGAMLD
29907	60275	A	30090	1	699	
29908	60276	A	30091	430	660	HQTHFIVEHRRIMQRTARQNI RHYQQLSAVQIRIGAMLDLRL SRDWVPRSRNRNAREVAQAIGQ MSLPLMLQVALS
29909	60277	B	30092	1	1575	
29910	60278	A	30093	1	289	MISANRPIINLDLLRTRFVAVA DLNTFAAAAAVCRQTQSAVSQ QMQRLEQPLGKNCSLVTVA TN C*LNMAFNFLVTPGKSCVLM M RSCIQPNSD
29911	60279	A	30094	1	1095	
29912	60280	A	30095	1037	1297	LILRCPSWSYRCIRILAPSS*Q TEAKPFASRASRTSDCQWANI SSVMPVKPNSTTSPILRRFSTPK CSATNCGEN*LSIMIGS
29913	60281	A	30096	905	2042	
29914	60282	A	30097	87	760	
29915	60283	A	30098	1	2793	
29916	60284	A	30099	308	485	KSLNAICYRNRTRTSMACY*PA* VRWPKHSAGLMTISPLVHVISP RHWRLCATRVGRGLG
29917	60285	A	30100	1	2784	
29918	60286	A	30101	453	1975	
29919	60287	A	30102	3	470	
29920	60288	A	30103	1447	1773	QFAFTEHHQTEHHHQRSYDC PQRDPRIHDAQVSDQRPCPDG LREPLHCAQPDGG*ADNSADH IRRNGGDGAFQKRNRRLTDPH KRQEHGGLTLRIKLSVEQAFAG
29921	60289	A	30104	1	449	

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29922	60290	A	30105	188	1508	
29923	60291	A	30106	171	410	
29924	60292	A	30107	3080	3232	
29925	60293	A	30108	1	1272	
29926	60294	A	30109	438	617	
29927	60295	A	30110	259	392	
29928	60296	A	30111	905	1545	RLTTPSLVCWRPAAKRPIPRSLKQLKKIASRKVTP*/SLGNAWNNLEKQRAYLSMMAQKRVDGDLVVCSEYPEPLLAMLEEYRHPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGLERNTGAGPPCRFYEGDGRSDDQVVDGIQFFFTNTITGRGHFRITMVDGICPCCKDGNLRFNRILEHREPFYQIPATFAYA
29929	60297	A	30112	3	466	AIVKFKRNVHQDGGYCSVQIQCRFALIFKDFCRMHRHGLIRRTISQQSVGRICVSIASGRVYYCFFALEGKKPSSSIAAPTQMAVSAARLKVAKCQSPT*KSIISTTKPCHRRSNRLPSAPPIISATRVHRQMRYSTSSGAALLSITVTPS
29930	60298	A	30113	1	1562	
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLLTSLLTSVV*IDAIDGIRFSLSWASGKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRRREREKTSERTAPV*VKITTRKLYPAERTGRIFEAF
29933	60301	A	30116	1	3095	MDKFLNTYTLPRLNREEVESLNRPVTSAGLEVIINSLPIKKSPPDGFATAFYQRYKEDAGEREGEGNQQVAVRGKRKTTERKKKLGEDVKVKESKNSGAYEVKQHRFRSLDWNLSLRQKAEFIPQLESEDDTSYFDTRSEKYHHMETEEEDDTNDEDFNVEIRQFSSCSHRFSKAAEVSTRLLSTRVTEIEGWLVQRNQKLLQSNLKQRSGEPLILDDSHVPPPELRAGYRLKKNAGCLPPELEQRREAIQ
29934	60302	A	30117	1	2583	
29935	60303	A	30118	1	3141	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
29936	60304	A	30119	1	1037	MRVVILGSGVVGVASAWYLNQ AGHEVTVIDREPGAALSTAAAN AGQISPGV AAPWAAPGVPLKAI KWMFORHAPLA VRLDGTQFQL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRA PDTLNTMPIFKA CTPDNRRAVWRHRAQTSPESR LLDMTAAWIEIANHHLQRFTTR LQQLGIKTNNLRHSGKTNAVIV YMIQSISLVDEMSCHLVLTGG TGPARRDVTDPATLAVADREM PGFGEQMRQISLHFVPTAILSRQ VGVIKQALILNLPGQPKSIKET LEGVKDA/EGVPYCIQLLEGPY VETAPEVVAAPRPSARKDVSE
29937	60305	A	30120	96	711	
29938	60306	C	30121	128	628	
29939	60307	A	30122	1024	1128	
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHFV ATTNRLALSIWYLMN
29941	60309	C	30124	202	321	
29942	60310	C	30125	150	491	
29943	60311	A	30126	1163	1257	
29944	60312	A	30127	929	1023	
29945	60313	A	30128	3	765	TARAWLLGLPVWPCVSRWSK KPSPRGGRDPSDRDPAFAAARS TVPPRISAYERPVPWGEWNDP RGPGRRASAVVSPREGNWGVL RDPRLQARKPRMVRSRQMCNT NMSVPTDGA VTTSPASEQET LVRQESSEDYSQP*LLVALFIAA KKM*KSLGKGPCTKTKRVWN LVCPLMPLNLV*FVKVLDKLV ALSMKQDILWPA/LH/DAKKL KKRNKPCPVCRQ/HNSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	A	30129	2	430	
29947	60315	A	30130	3	1088	
29948	60316	A	30131	303	529	GTGQCANTKMSVPTDGA/VTTT QIPS/SPEQETRV/PKPLL/LKLL KSVGAQKDTYYGKRFLFNLG QYIYGLNDYY
29949	60317	A	30132	3	619	
29950	60318	A	30133	123	385	

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29951	60319	A	30134	66	413	HQSEQMYQSSSECLGTTAKA RGHQLRTASACHFPSTPPFWSL TLESQREGRFKQPTLISCF/CLF MSVPVVSAPPFSSSSSSSSSSSS SRPWFDPQEAR*LTSPVERPCR GLRPA
29952	60320	A	30135	257	465	VPTSPASLESKQSCPHVLCVPW EVEGHVS*TGKPDPRPRRLLT LLLVPVWVPGQLAIKQEGQEPK KRH
29953	60321	A	30136	1564	1857	
29954	60322	A	30137	33	265	
29955	60323	A	30138	114	560	
29956	60324	B	30139	70	555	
29957	60325	A	30140	650	1045	
29958	60326	A	30141	374	575	
29959	60327	A	30142	1	1095	
29960	60328	A	30143	1	981	
29961	60329	A	30144	28	698	TACRIRHGHAGRLCCSPCLLVIP LKSSQHI/LRVLPNPNLDGRRKI A/FAHHCFFKGVGRRYA/HVVL RKAD/IDLTKEGGENSLEDEVE RVITH/LQNPRQYK/IDWFLN KTRRM*KDGTYSPPG*PIGLGQ QAPVKDLGAD*KKIRAH*/RGL RHFLGAFVRGQAHQEPLGRR GRHPSGVSKEIRSVGPCLVNKI VYIPKKKKKKKVDAAANLVV VVVVVGG
29962	60330	A	30145	107	340	
29963	60331	A	30146	428	934	
29964	60332	A	30147	1	1533	
29965	60333	B	30148	1	2652	
29966	60334	A	30149	205	450	
29967	60335	A	30150	1	879	
29968	60336	A	30151	139	1029	
29969	60337	A	30152	237	422	WFETPAQYTNRSPESGTHYRRA RSRARWHGCMCEVCRRRKSPP ANKPRLLPPVR*RCPPRA
29970	60338	A	30153	1	1134	
29971	60339	A	30154	136	411	
29972	60340	A	30155	1	3345	
29973	60341	A	30156	194	475	TPATVRRGWRPAVRVFRWVK PLTVPPRRKGPLSRGTGCRPVPL TTPSTGTVMRAGICAVKMLIVQ KSPCMPPC*HRQWTMTGLWQA PAAIRPV
29974	60342	A	30157	1	2988	
29975	60343	C	30158	1	3939	
29976	60344	A	30159	308	749	
29977	60345	A	30160	1	1338	

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29978	60346	A	30161	1	4342	MTRDNPVIFRHRREVVFQGE NGGIQNARFIAALFFQHGYNLC QRVGGLLKGGVEVFRYTSVVE RVVVDYYIRPAGFSIDTNRGS VTDDFAPDQLAKAIPGFKPRE PQRQMAVAVTQAIEKGQPLVV EAGTGTGKTYAYLAPALRAKK KVIISTGSKALQDQLYSRDLPTV SKALKYIGNVALLKGRSNLYC LERLEQQALAGGDLVPQILSDV ILLRSWSNQTVDGDISTCVSA EDSQAWPLVTSTND
29979	60347	A	30162	1	1023	
29980	60348	A	30163	1	679	MFRVTWSSGRTGLGKRLFRTP YDNDDTGYPYAFNKTHPKDNYT CTVLFIDDMASGQSLDKAQD NYRQAMKKLSSGRGNVLAQAE AFRGLGVEIKREINPDIAEQAIR LQDCVFDQTETMTTFTGTVSS ANSGYYTIFNTDTGAAFNNVS LAIGNYVVLAFSAS/VGA/DMK MVNSTITASGSKRSTTVLRQGL SQRWLLSAGARNLLQHYSFRE TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	A	30165	1	1353	

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29983	60351	A	30166	1	1661	MRGEVLLAGVPRHVAEREIATL AGSFSLEHQNIHNLPRDQGGPN TVSLEVESENITERFFVVGKRV SAEVVAAQLVKEVKRYLASTA AVGEYLADQLVLPALAGAGE FTVAHPSCHLLTNIAVVERFLP VRFSLIETDGVTRQLLGVSYRIL AMGHAEFLIQIADMRNDGGWR DFQFSGNLVMDPEPNRSQAITYIK LVKSRLGTTKRYNHKDDCPRC RWIAAMIDNPPRIKPTKSASV WHATATSASPERQMSTTVIMS ARFISCVWMTFCMPRSGPMRF VHLPCRFRDAFTGVGKLQDL GPSMSTRIRQRFTTLCPMTLSSS STEFENVSDCRPSRARSCLRFRL CRSIRCYYRLADYVQSRSLQAGF IQRPAIRHPYHHVKGAFFEYVR NNRLPETVIRVLQPALARFSPDI APLFSPPFLHDDVDTARLYAPS LMPKLRLIGLTLALSATAVSH AEETRYVSDELNTWVRSRSGPD HYRLVGTVNAGEEVTLLQTDA NTNYAQVKDSSGRTAWI/HVET T*H*AKPALPCARSGKSGQNPD R*THQYR
29984	60352	A	30167	254	496	RASRLKTCGDGCCSLSAVVSVG ASPFASRVKSSRRVW*S*VGPSS WPPGMSL*TAEIRRSRRIPVSS GSLTASFANVVR
29985	60353	A	30168	1	984	
29986	60354	A	30169	1	429	
29987	60355	A	30170	1	523	
29988	60356	A	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	671	
29992	60360	C	30175	1	2649	
29993	60361	A	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	A	30178	3	108	

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29996	60364	A	30179	404	1347	DVTILARA VLQALLKILYH/KCE FNDEMLTEGVIREKMGFNPQTL REVLQACQQQGCVANL DLDV VMIIIDGAFSGIVQNWL MNMA GYDLYKQAPALVDNRTGMER ASNGGPWQVQSLPARSYRQLD SYYGEAMAIGERALVALLDFSG PSPSGDWRYQTHHTFPPTGWR RQATLVKMRACIEAVKAVGEE LCPALGLTIPVGKDSMSMKTR WQEGNEEREMTSPLSLVISAFA RVEDVRHTITPQLSTEDNALLLI DLGKGNNALGATALAQVYRQL GDKPADVRDVAQLKGFYDAIQ ALVAQRKLLAYHDLRI
29997	60365	A	30180	494	1433	
29998	60366	A	30181	1092	1347	
29999	60367	A	30182	315	600	STPIEKTVS KAFSAGSCSILTVT NARASARSACIISITA AVSGSCA PTP*EVSSAFARSLICRSIRKPGL KLRSITIGALASKTVP LPA SPPIA
30000	60368	A	30183	535	661	
30001	60369	A	30184	1	1491	
30002	60370	A	30185	1400	1852	
30003	60371	A	30186	199	534	
30004	60372	A	30187	2	539	
30005	60373	A	30188	1	690	
30006	60374	A	30189	127	939	
30007	60375	A	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLC LTDERTRRNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERS DEIPEAAKEIMREMGINPETWE Y
30009	60377	A	30192	242	709	NYMHYHADRCITRCHGNACTV NYAGLSVPTSTVWTGLNLLT KRIKYLMAEWSGE/YISGPCVEP GKKSQSKKITVSIPLKVLKILT DERTRRQVNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERT AEIPEAAKREHA*HGGLTPET WEY
30010	60378	A	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263	514	PAHFSVAHSHLWQNNPLSSVQ CRQNHQAIPCRIFELNNVMRH/ VTRDSSSLGCSWRLTASVNR RFVDPVQILVMAMSGRRSR
30013	60381	A	30196	1	1995	
30014	60382	A	30197	141	229	

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30015	60383	A	30198	1	702	
30016	60384	A	30199	36	144	DGLLLMDERNISPLLQKRMT* QAV*VWWWKDYGV
30017	60385	A	30200	462	646	QWVPIARPMPACHVQRRTSSL ERRQPVMIMVMLRII.WYIYCSI HVLG*WICRLYYKTLK
30018	60386	A	30201	107	1200	
30019	60387	A	30202	366	500	
30020	60388	A	30203	1	1193	LADCSRYNGLEMTLSCCAGAS TDAVGGIERGGLKSPASEGEI APRLLLDGEPLALSGDKWRISP WLLVTDATITAFLOMIQEGK AITLRDGDQTISL.SGLKAALLFI DAQQKRVGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPTPL SLEERNLLDYGNGWRMNGLRCL SLDPLRREVNVTALTDKALM MISSQIFNGHMHVHIKDLVFTDH APDKGISFGSDTGMDRPARGD HRLVMHHDMTFRFLR.PHHVE NAGVHHIEIEINFHPALVGVTRH GVPLVTRSQLRQPHTRLAGFY IRDQIFVNRATVTGEEIAYAEF TNFPANGNRFYSYRHNAANNNS VNVAVNHGVLIGDKYLFNQKFI AQPLGIQRFVCRTVDALSYVHI
30021	60389	A	30204	3	1057	
30022	60390	A	30205	1	955	
30023	60391	A	30206	1281	1370	
30024	60392	B	30207	1	2199	
30025	60393	A	30208	1	589	MLKKREQTVFTHEKSVFQGLD RGNRELGPPTFGVKGAQKGN LQIFSEDKNFGPGSGEIVGHR GPKWDIPRGKRETLGKPHFFW KPSQEFGRKGLSGFSPWERVSG NKNSGKRIYPWGPVDGINCRW REPRNVDAEYRRDCGSRFRSL RHFYRSLFSLHHPASTRHQKAQ SSAVTVLQTNAQHGRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRTCAPLSSVWRCR PPRSSPPASWRSVPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCL.WTSSLAPASRP CPS*LQPPGQQRWGEPIGAIAV PL

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30027	60395	A	30210	61	641	RHKHRRRIPGRWDQIRPAPNR WQTGFQWFALPVTGVRLISGY TELLPRL/PAQKNLPYTHPAWR FVAHQGRESALECRYVPLPVRH *RNCRWREPRNVDAEYRRDC GSRFRSLRHFYRSLFSLHRPAST RHPGAQTGAVTGFADECPARK AAALAKASVNVVFHSTNATV CHRPDRSRASGSFRYYWRQE
30028	60396	A	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLSANSKNRR WRKNIKLR*SSLLK*TESPLPMA ILVLTSLTAI
30030	60398	A	30213	451	834	IWTGKKVDSARALIARGWGLH VILRRTDWMDGRRSRHTDDT DVLRLHHVIGELPTYGYRRVW ASSQTGR*FKVQNRYPFPVLS DFEHLQEPYEFGLR*PWLPA TGEFHAIEYRSVDFCKHPV
30031	60399	A	30214	1180	2547	
30032	60400	A	30215	341	505	
30033	60401	A	30216	293	4221	KPFSPCCKGRWLFNRHSSARR PTVLYYRRSTMR*NSW*PNLRR QRGNPANRS/RQSMLELSGVKD GELIPAKLFNHLVTWLQARQTL SQQNTPRPGGGEIPWCCSVLA ESERKKRGRKKQRGIDSPDVGA LLLVRATFYIWQQPPVNKIALGI EYAAASKYYGWQRQNEVRSVQ EKLEKALSQVANEPITVFCAGR TDAGVHGTGQVVHFETTALRK DAAWTLGVNANLPGDIAVRW VKTVPPDDFHARFSATAR
30034	60402	A	30217	1	1362	
30035	60403	A	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWRR*SP QYARHTRKRTSAGCSA
30037	60405	A	30220	1160	2385	
30038	60406	A	30221	290	373	
30039	60407	A	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	A	30224	1	469	
30042	60410	A	30225	241	615	
30043	60411	A	30226	1	1428	

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30044	60412	A	30227	862	1453	SFLLVSPSQACHHYAP/KIFDL/SGYTSTTEQMWGTVIVGLTNV/LATFIAIGLVDRGLGFLAMPAGM/GVLGTMHIIIGIHSPSAQYFAIA/MLLMFIVGFAMSAGPLI/WVLCS/EIQLKGRDFGITCSTATNWIAN/MIVGATFLTMTNLGNANTFW/VYAALNVLFILLTLWLVPETKH/VSLEHL/ERNLMKGRKLREIGAH/D
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCPPVS/VHFFHSRLCRDALNEAFHPSG/FQVVKCCDIARIHRNRYGDLF/AIGVVHIANVNIAHRNATFHQR/QEIGGCFTNQDFLSIGGAMNV/VDNFLQRPETYGDPFCQYHFH/QVLLYRIFGNLVGYQHQCIPR/KSDPLNADLTVNQAFINPA*NN/IWHSVFLFVLLIGLHRLCGMRQ/DVLNMVDNEFPWRWLQLAGA/NFHVLQRQILADQQRQNW
30047	60415	A	30230	2553	3845	
30048	60416	A	30231	1	656	
30049	60417	A	30232	3	228	
30050	60418	A	30233	185	206	ATVDPPFITEPGDILAGGFA*PL/SWFAGFALEHNLPLWATGDLH/SLRA
30051	60419	A	30234	12	155	
30052	60420	A	30235	698	2684	
30053	60421	A	30236	1	2004	
30054	60422	A	30237	1	811	
30055	60423	B	30238	1	7521	
30056	60424	B	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPWNRRKPVLSVIP*K/WKLKGPVALKTAYPKRLPLPI/TSFSLPGVA
30058	60426	A	30241	1	2067	
30059	60427	B	30242	1	2787	
30060	60428	A	30243	101	947	
30061	60429	A	30244	1	1917	
30062	60430	A	30245	239	469	KRVSISSRRRFSAQKASASALA/RWWRSAVNIIYVFAI*TTAQRV*QLRMTNCVRTTITACHSR*RTLL/SLSPVKPAS
30063	60431	A	30246	1	4348	
30064	60432	A	30247	1141	2244	
30065	60433	A	30248	503	649	

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30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRFLFIGAERFQHIAGSGHYR VV*NANAGSKIIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNPFNFEIFQRLVDDDP HCTIGIMFANVDHGTGTENRIRK LCFNLTNTGTQKKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	A	30250	1	526	
30068	60436	A	30251	442	684	
30069	60437	A	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPPLPTENV AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDPRLAIRDATIGISG FCSLA
30071	60439	A	30254	62	298	
30072	60440	A	30255	904	1530	
30073	60441	A	30256	701	1329	HRLSMCRGRCRWSWARTNVI SMLVFALSFASWRIVSPRTM/D ALTFAAESALPGSPTHISTDHQG QFVFGVSGYNAGNVSVTRLEDG LTMHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTPPEA CTTNKQPAQQRDKPQRGNQ RLASVIFQCQHQDHEHKEHRTY PAHQLAERHLVDRLLM
30074	60442	A	30257	8	382	
30075	60443	B	30258	1	2655	
30076	60444	A	30259	67	231	
30077	60445	A	30260	1109	1531	TFLHSIPAAKTQGPPTNTLVDT PQHL*HQQRRTQPOLALSLRT *VFLNRLRGALFAPKACLPD LVISPRGPPQGLGVTRVQVSAH TNPTRTTHNTPHYTRNTQTRPE STPRRDITTPQQRHTPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDSDSPISQSKMKIIA SITTIRMEP*AIATPYSPSSTRLM M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSDSPISQSKMKIIASITTIRMEP *AIATPYSPSSTRLM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	A	30263	3026	3217	LPQCKWDPYGVGTISPQVSIISR ANPCTSPFFV*SATKGLLYQQ TRIPALDIPSSNRRNSHG

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30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPYHGRWPQ HDFPPFKKLRPQSVTSRIQPGSD VIVCAEMDEQWGVYVGAQSRQ RWLFYAYDSLRTTVVAHVFG RSLFTGP*RRERFATQIEVGKLF AAVDMVLWLSGKAQPDVTVV KVVVL
30082	60450	A	30265	3174	4135	
30083	60451	A	30266	1	2771	
30084	60452	A	30267	1	1281	
30085	60453	A	30268	10	233	LRIQASDPEINSRRESGHIPLPYT DKAPSPPLTVDGAK*EVSRSR/R QNSQVQHPPDAAKYPSGCHK FRGFRRA
30086	60454	A	30269	300	564	SANSTLKRQTQVNRRLTVKLSA RKLPLMKVNTNRSLVVVSMV MLLSTCTRWRSRVQTRKATSSST TLKVV*SLANTSRPLIKVSRNS
30087	60455	A	30270	5259	8003	
30088	60456	A	30271	1	819	
30089	60457	A	30272	1173	1369	
30090	60458	A	30273	1	4767	
30091	60459	A	30274	905	1162	FSSVVMCSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSRCS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	A	30275	1164	1582	
30093	60461	A	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGV RLYAANQHRTCC
30095	60463	B	30278	1	954	
30096	60464	A	30279	108	530	SIRQTHVQIVRRSCLAIRHQVPS TAIRVGIVKGNFAS*AGAQP TLR*HRCCTRALTSGLVAVRLS AGCNFPELVHRRLLTWRAGR YPPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLT PFPAGQRC
30097	60465	A	30280	1	1389	
30098	60466	A	30281	1	380	
30099	60467	A	30282	1	3255	
30100	60468	A	30283	569	2547	
30101	60469	A	30284	1	585	
30102	60470	A	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGS LGPSSGPKTAGAPSSRPSPSARR RTTETRWTLRLSKDYWLITRK VGLGNLQDGGGRAGSL

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30103	60471	A	30286	737	1088	NMLMNVCLNPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRLPIIVGR RKSGGSKIRANVCSLPIFPGIG R*TTGESKRICRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPFSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAESTSPLAMVGD GINDAPAMKAAAIGIAMSGGT DVALETADAALTHNHLRGLVQ MIELARATHANIRQINITIALGLK GIFLVTTLLGMTGLWLAVLAD TGATVL
30106	60474	A	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPF IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFIIVGTSGLFNHAENIDEAW RVMTAQILAAKSEQWGQQVY AIVQNTDQAQAVMPYGPCKLY VLAQNDAALQRTENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTNASLAGIALNSMDLSP GGRVAVKESNQRCWSDGFEFC CDNGERLVRVTFALDCCDREAL HWAVTTGGFNSQTVQDVMLG AVETPLRQRSSVVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQSRHHPALRYPLQL MPHWRRSICSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIKASLS*FK*LLKPAINAG*Q AS*WRASASKPCASPDACAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	A	30294	1246	1300	
30112	60480	C	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCQVD
30114	60482	B	30297	1	3081	
30115	60483	A	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVATKLRR *RVFPAPCCG

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30116	60484	A	30299	3	421	QRRATGDLRLPTR*TARRGGRC DS*SSRRWHRAFTGACREISRQ QNRHRQRPAAGVALVGSE*Y SGILAGQRHYRVYRAGYRRSP AGYAPD*SD*RPVDGRHECGRR PVWRRENVPTAGGQIGARHET GGGLPRTVY
30117	60485	A	30300	1	3202	
30118	60486	A	30301	317	554	
30119	60487	A	30302	474	599	TTSVQRTFLPDY*APTIVLLPA RKATAARKLHRFSGRQDR
30120	60488	A	30303	212	569	TSKVVTPALRSMPSVPINNLS KVKCSKAFAASCP*NEADFLRN VPPGIRIVCSLSSSDSALTICRL VITVMLLKRESRGITICKTVLPAS RMIESPSWIKLTAASAISSFLWV LMSVL
30121	60489	A	30304	1	160	WSKMSRAVRPSDWESWTQTRE VVRQTVRCRPDPSSAAVCLTAS SPANCIGPIG**MLAEILA*RAV RPSDWESWTQREVVRQTVRC RPDPSSAAVCLTASSPANCIGPI G
30122	60490	A	30305	1	975	
30123	60491	A	30306	1	762	
30124	60492	A	30307	1	733	
30125	60493	A	30308	493	948	LGAIFLAGALFAAAWLADFRL GLGARLYRYGADWFCADGGM SAEELKFISENGAVVMDHKKP GSAAASGPKLHYIKQLLSNRM MLGVFFGQYFINTITWFFLTWF PIYIGNVVSDNR*YVAQITITW IKTYGRCPSFQRDGDGFVNRL

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30126	60494	A	30309	153	2031	RRNYQRQKKRGSEGAGRDPDR RSRISAAYSRSEFNNAAVTEH Y*NRFT/LVPRSR/HANADTVT REAVNQVIALLDGSGALRVAEKI DGLPTNQMQASRRAKEEEVHL TGQPSRVQSPRRCEEKQYMV MIVSGRSGSGKSV ALRALED GFYCV DNL PVVLLPDLARTLA DREISAAVSIDVRNMPESPEIFE QAMSNLPDAFSPQLLLDADR TLIRRYSDTRRLHPLSSKNLSLE SAIDKESDLEPLHGFDPDYDTV GFSCRRIDYVCRHKHSRRIRQV VLLNFAKSGAFSTTRGDDKTR RSLLVTLVRIFCVRVIFAYDIRD GIHVRRIQINSKSGKVGSKHNSG YSAAKFGGVGLTQSLALDLAE YGITVHSLMLGNLLKSPMFQSL LPQYATKLGIKPDQVEQYIDK VPFKRGCDYQDV LNMLLFYAS PKAVVLAPDSRSMSPAVSGRFK PRVVVAIALDDQQRIVDTLFMK GLTVFARPKIPAITGRHSGATL QKQKCSVEELAQYFDTTGTT MRKDLVILEHAGTVIRTSGGVV PDSPPHTRRDPRRFSMAFPWF NIRSAEFHHVTLLAEIPRQOND IHRPAHAAAAPKVETRSGDET NRWNRPAQHLFA
30127	60495	A	30310	720	872	EKVPVSI GPGGMQELPMQSPDR RSAGKPGPASRAGR*TGGAFA TKRDYR
30128	60496	A	30311	1967	2452	SRRCASINQRPFGHEKMMVSV RIAPASNVPTCRPITVTGSIAR SAWTHITRMVSPPLARAVRM* SPSTSSIEERVIRTMTASGIVPST MAGKIIWATASIKLPSSQMAV SISIKPVNGLESSRNTISLTRPET GVRFCQTETSMISIMPHQKIGIE
30129	60497	A	30312	1912	3960	
30130	60498	A	30313	2	250	LIRK VST*SVLMKAFLRIA*KDC ERLGLKCFWSGSEKGCPLVNT NAFGGHCEHHQWVSSVSRV SQSAGGCPFLNLLNTV
30131	60499	A	30314	1	300	SVFSH*AKKIWKGVSRALGQ NSRSGSGSCQASWTIRFPVGFH TDGTRLRRNPGMQAFLGPVAR FLALEARSLDCAFSSLLFKRKL SGRWGRASRGTKL

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30132	60500	A	30315	1	468	MTEKVKQAPVPTASDEIDIGR LVGTVEARWWVIGITTVFALC AVVYTFATPIYSADALVQIEQ NSGNSLVQDIGSALANKPPASD AEIQLIRSLVLGKTVDDLDDI AVSKNTFPIFGAGWDRMLMGRQ NETRRGFSARGTGQMLKKEGV TLMVEAIHASPGEFTVTKYST LGMINQLHNSLTVTENGK DAG VLSLTYTGEDRYTNHAGV VNT MIIIAATHNLVFENN SCEYAHF MGNAPAGLTEYQNVFYKHIDRI QGHYVWEWRDHGIAQDDHG NVWYKFGGDYGDYPNNYNFC LDGLIYSDQTPGPGKKEYKQVI APVKIHARDLTRGELKVENKL WFTTLD DYT LHA EVRAEGETL ATQQIKLRDVA PNSEAPLQITLP QLDAREAFNLITVTKDSRTRY S EAGHPATYQFPLKENTAQPV P FAPNNARPLTLEDDRLSCTVRG YNFAITFSKMSGKPTSQVNGE SLLTREPKINFFKPMIDNHKQ EY EGLWQPNHLQIMQEHLRDFAV EQSDGEVLIISRTVKPRGP ARCP DSSVGTITYCTENNPFDNGLLN AQLLQQA KPFVDERQSK*FGCH SPSYSLWLSIIGLKKLIFGSRVS SDSPFTCQDVGLPLIFEKVI AKL
30133	60501	A	30316	1	524	
30134	60502	A	30317	1669	4421	
30135	60503	A	30318	2	349	SMAKCLPKRNQGPVRS CGAWS GCLWLPSPSGTPWRSSLWILL F/SQISQLLSLLHQGFQPKPNH RGNKYLAKPGGSRSAIPD TDGP SARAGGQTDPEQEGLDPEED LSVKQLL
30136	60504	B	30319	217	368	
30137	60505	A	30320	1	951	
30138	60506	C	30321	1	3729	
30139	60507	A	30323	1	2437	

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30140	60508	A	30324	1005	1815	PDLHCQKKHPTLCSGYWPFTRT PVHYAAFS*/HALGHLAFS/EA SLHSHRGQTALTTQKKSPAKSP TAATTETRVMRKISHGTRDPPG FASLMQ*MHYGKLCAFOSELL FQSLQRSHWTQSWWLCWPHW RLCWTQNWWCWPHWTLWCW TQSWWLCWPHWRSCWTQRW WLCWPHWTLWCWTSWWLCW SHWRSCWTQSWWLCWPHWRL CWTQSWWLCWPHWRSCWTQS WWLCWPHWRLCWSQSWWLC WPHWRLYWTQSWWLCWPHW RVCWTQN
30141	60509	A	30325	2436	3678	KMPPWPPGSPGLGCSAWAEA PPAHCPCDVLHLHPACPHIQAP CGTGAPGTGLAAAADESEPLGSS APPAGRCPQAAACGLAPPLP RGWCPPPTSSWMGRRQLQSLA HPTSPAPLLAAPTAVCSCSRCSA PRSRCVARPAARTGLPTPAPAS SPAPATSPAPAESPAATASHPV AEASPAPGAPPRPAASPSPAAS PAPPAASPVLTASPLPAASPAL AASPVHTASPPVHVASPPVHTA SPPVHTASPPVHVASPPVHVAS PPVSCSGDSTSDCFPPQGAFFP HSL/VSLRWLVSSCSCSTLDGP AGGCGARGSAVWFLSNKLLP/ MLLYQMYLMLLLLLRCANQ*I DVFSELDYCGA*IQGYC*FLV LAIPR*VVTRSGCVRATAIDFL FPVSSCWNAALPLPICF
30142	60510	A	30326	929	2910	
30143	60511	A	30327	1	1488	
30144	60512	A	30328	203	701	
30145	60513	A	30329	493	924	SDPGRFHGKARITDPRGQPGRR LQGGSENGSDMKAAARKVSG NKHSTSSHQHAVWCPGVPS*SG KAWAADQRFVPRILGKGRGHV DAA*LSWKCRLHSSVSLNGE NQRFGVDARYRTRLQGSANL FKRQRCGLHQNLELL
30146	60514	A	30330	1	2193	
30147	60515	A	30331	1	2990	
30148	60516	A	30332	2512	2560	FALRYRQPVRRHW*FHLVQRH GRFSRASGATWPASAAFAWP LLVCAPLSAASAAAPLRL
30149	60517	A	30333	1	2820	
30150	60518	C	30334	194	418	
30151	60519	A	30335	25	458	

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30152	60520	A	30336	860	1209	IPGNCRDSSGVGKERETNAGS QHHM/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPEPVYEKKPK KEVKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	A	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	A	30339	1723	1845	
30156	60524	A	30340	6	983	RRWACRSLSSSGRRSLIRRMGF VKVVKNKAYFKRYQVFRRRR EGKTDYYARKRLVIQDKNKYN TPKYRMIVRVTRNDICQIAYA RIEGDMIVCATYAHLEPKYGV KVGLTNYAAAYCTGLLLARRF LNNRFGIMDKIYEGQVELTGDE YNNVESIDGQPGAFICYLDAGLA RTTTGNKVFGLKGAVDGGLS YPLTVPKRFPWF/DD5*KPRNLI AEVHRKPPHWAQNVARLHAPT LMEEDIEDAIYKQFVRQYVKN SVTPDMMEEMYYKKAHAALRE ESSSMEKKAQGGKFKKKRWR PKMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	B	30341	1	2043	
30158	60526	A	30342	390	1180	
30159	60527	A	30343	2	649	
30160	60528	A	30344	1	1929	
30161	60529	A	30345	1	773	
30162	60530	A	30346	3	484	NSSCRDPGY/CPIIVSLNSS*GSL LQDMPGPSKVISIILATRGAVNI TTVAYKSAVILSFTTASAVLSL RNVIGPLFASQPSFTIHFLFSHN GSAPLNAPDMANCFGLTALTSS LDERLFRNSAGSCCGIRNCFIS TLPPNTSTLTSVNSKGSSSVHG
30163	60531	B	30347	1	2775	
30164	60532	A	30348	1	1386	
30165	60533	A	30349	439	555	
30166	60534	A	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITRCRTK/ EQRYALSQAksiADELMTGCTN FAFGKPGTGKHNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMRVGMILNLNY EAMKTLGERIMDRMTMNGG RW
30168	60536	A	30352	1	786	
30169	60537	A	30353	1	288	
30170	60538	A	30354	711	953	

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30171	60539	C	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	A	30357	1	420	
30174	60542	A	30358	1115	1561	
30175	60543	B	30359	501	555	
30176	60544	A	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	A	30361	386	1647	
30178	60546	A	30362	1	1179	
30179	60547	A	30363	1	1215	
30180	60548	A	30364	1282	1657	
30181	60549	A	30365	388	804	
30182	60550	A	30366	1328	1978	
30183	60551	A	30367	455	1000	
30184	60552	A	30368	291	303	RVRRMMYTVTLYSFSANKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSLQTVSLL LLSFALDPSSMTLTTEESVE
30185	60553	A	30369	284	433	RVRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	A	30370	290	425	RVRRMMYTVTLSSFSANKNTY I*E*E*GLGWRHHIFLG*IQHFNR
30187	60555	A	30371	842	905	
30188	60556	A	30372	784	3453	
30189	60557	A	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSGSLGP RGGRGCCILRPSRGGGRGHGPT KAGPWPSPESRGR*DWKARGPP APSRGSPSRARARRGSGGGGPA DEPLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	A	30375	1	340	
30192	60560	A	30376	2	3336	
30193	60561	A	30377	22	419	
30194	60562	A	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECSWLF*SH MHVLLPRNRKEKLIIEFRTQTY DVNAYKASAHNRSGPG
30196	60564	C	30380	169	415	
30197	60565	A	30381	3	1324	
30198	60566	A	30382	2	3455	
30199	60567	A	30383	85	2695	
30200	60568	A	30384	69	303	
30201	60569	A	30385	1	951	
30202	60570	A	30386	1	4749	
30203	60571	A	30387	176	1553	

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30204	60572	A	30388	1	425	MDQHSFLGFRPDHVAIDIRSLRN KANPDDTFEAQLFYGDIAIVK TSHLVKIDYPKFIVHGGKGSFIK YGIDQQETSLKANIMPGEFGFA ADDSVGVLEYVNDEGVTVREE MKPEMGDYG/PR/L*CVVSNHHP RCAKL RQGI
30205	60573	A	30389	3	1890	PSQPLLWFAGRPGRDGTGCPRC KQNSTCIAAVKMEGPLSVFGDR STGETIRSQNDKESFNEQKTCRI *RKRLV*LYEVAEHEIVMAAAS IANIVKSSLGPGVGLDKMLVDDI GDVTITNDGATILKLEVEHPA AKVLCELADLQDKEVGDGTTS VVIIAAELLKNADELVKQEIHP SVISGYRLA/CKEA VR/YINENP NLLTQDELGRDCLINAAKTSMS S/QHIGINGDFFANMVVDVLA KYTDIRGQPRYPVNSVNILKAH GRSQMESMLISGYALNCVVGS QGMKPRIVNAKICLDLSLQKT KMKLG VQV/VITDPEKLDQIRQR ESDITKERIQKILATGANVILTT GGIDDMCKLYFVEAGAMAVRR VLKRDLKRIAKASGATILSTLA NLEGEETFEAAMLGQA/EEVVQ ERICDDELILIKSTKA/RTSASIIS RVPIDSMCEMERSL/HDALCV VK/RVLESK/SV/PR/GGA VEEA LSIYLENYA/TSMSGREQLAIAR VCKITLWLPNTLSS*CLPRDST DLVLQNLRAFVHNEAQV/NPER KNLKWIGLDLSNGTPRDNKQA GVFEPTIVKVRGLNFATEAAIT LRIDDLIKLHPESKDDKH/G/GS YEDAVHSGALND
30206	60574	B	30390	1	975	
30207	60575	B	30391	1	2577	
30208	60576	B	30392	1	3126	
30209	60577	B	30393	1	1134	
30210	60578	B	30394	1	2082	
30211	60579	B	30395	1	915	
30212	60580	B	30396	1	2658	
30213	60581	B	30397	1	2412	
30214	60582	B	30398	1	2454	
30215	60583	B	30399	89	2533	
30216	60584	B	30400	1	4083	
30217	60585	B	30401	1	1725	
30218	60586	C	30402	127	345	
30219	60587	A	30403	1	597	

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30220	60588	A	30404	3	3386	MPATASAGVPATVSEKQEFYQ LLKNLNPSCMVRQRQAEIYENI PGLCKTTFLDAVRNRRAGYE VRQMAAALLRRLSSGFEEVYP NLPADVQRDVKIELILAVKLET HASMRKKLCDIFAVLARNLID EDGTNHWPEGLKFLIDSIYSTN VALWEVALHVFWHFPGIFGTQ ERHDLDIKRLLDQCIQDQDHP AIKTLARAAAAFVLANNENIA LFKDFADLLPGILQAVNDSYQ DDDSVLESLEIADT
30221	60589	A	30405	1	1695	
30222	60590	A	30406	1126	1355	
30223	60591	A	30407	1	1610	MGSRLNPPPPAHSDDTTGKDSF GNIRGAETGGASACSVTSARV TCGAGSEPHSHRNPGISAVGL APSYGAARGRRRPLALQQSPQE RRHVGNSTRGLLPASLPGTAS SQSASATASAAALPLKVTGPLAR NPTPPWTAALATRGQRPEK GLFPGPAPFSLGKRKRGRGRTW ERRRRVSIETSTCFRPGCERLGA AAGANLSQLASSQRPLRERWV LYTIIMAAAGAPDGMEEPGMD TEAETVATEAPARPVNCLAEA AAGAAAEEDSGAARGSLQPAPA QPPGDPAAQASVSNGEDAGGG AGRELVDLKIIWNKTKHDVKFP LDSTGSELKQKIHISITGLPPAMQ KVMYKGLVPEDKTLREIKVTS GAKIMVVGSTINDVLAVNTPK DAAQQDAKAENKKEPLCRQK QHRKVLDKGPEDVMPSVKGA QERLPTVPLSGMYNKSQKVR LTFKLEQDQLWIGTKERTEKLP MGSIK\NVV\SDPIEGHEDYHN DGRFQLAPTEA\SYVWVWVP TQYVDAIK\DTVLGKWQYF
30224	60592	A	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP SAAGRRAMKKKLVLCLLAVV LVLVIVGLCLW/LPSASKEPDN HVYTRATVAADAKQCSEIGRK\ AEVINAREVAPSVAFASMFNSS EQSQKAL
30225	60593	A	30409	562	2376	

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30226	60594	A	30410	604	2475	RQREVTRSPSPERSGLRVQLFPP NPPVFRGQHPRLGPPSAAGR RAMKKKLVLGLLAVVLVLVI VGLCLWLPSASKEPDNHVYTR AAVAADAKQCSKIGRDALRDG GSAVDAAIAALLCVGLMNAHS MGIGGGLFLTIYNSTTRKAEVIN AREVAPRLAFATMFNSSEQSQK GGLSVAVPGEIEGYELAHQRHG RLPWARLFQPSIQLARQGFPVG KGLAAALENKRTVIEQQPVLC VFCRDRKVLREGERLTLPLQAD TYETLAIEGAQAFYNGSLTAQI VKDIAAGGIVTAEDLNNYRA ELIEHPLNISLGDVLYMPSAPL SGPVLALILNILKGYNFSRESVE SPEQKGLTYHRIVEAFRFAYAK RTLGDGPKFVDVTEASSGVSA VVRNMTSEFFAAQLRAQISDDT THPISYYKPEFYTPDDGGTAHL SVVAEDGSAVSAATSTINLYFGS KVRSPVSGILFNNEMDDFSSPSI TNEFGVPPSPANFIQPGKQLSS MCPTIMVGQDQVRMVVGAA GGTQITATALAIYINLWFGYD VKRAVEEPRLHNQLLPNVTTVE RNIDQAVTAALETRHHHTQIAS TFIAVVQAIVRTAGGWAAASDS RKGGEPAgy
30227	60595	A	30411	63	342	GRTLVPHGGLPHHYLVQCEWL PGTS*AEFPVVHLPafVARARG ADRHGHGPFPLCHLHPARPRR EDLHRKSPGEPNIEHHRSSGPG CRRl
30228	60596	A	30412	1	910	MLFRPALGSRQVVRNMTSEFF AAQLRAQISDDTHPISYYKPEF YTPVDGGTAHLSVVAEDGSAV STTSTINLYFGSKVRSPVSEILFN DEMDDFSSPNITNEFGVPPSPAN FIQPGMGWR/KQPLSSMCPTIM VGQDQVRMVVGAAAGGTQITT ATALICVTAFLPGRAPHAQPPS HADHTMPQAIYINLWFGYDV KRAVEEPRLHNQLLPNVTTVER NIDQAVTAALETRHHHTQIAST FIAVVQAIVHTAGGWAAASDS RKGGA YRILSALQEDKADKQS RDKILTRTRKGTLDGWLPm

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30229	60597	A	30413	110	868	DLCLPLTPPHLLRPAIGSRQV VRNMTSEFFSAQLRAQISDDTT HPISYYKPEFYMPDDGGTAHLS VVAEDGS AVSATSTINLYFGSK VRSPVSGILLNMEMDDFSSTIT NELGVPPSPANFIQPGKQPLSS MCPTIMVGQDGGVVRMVVGA GGTQITMATALAIYQPSWFGY DVKRAVEEPRHLNQLPNVTT VERNIDQAVTAALETRHHHTQ IASTFIADVQAVIRTAGGWA SDSRKGGEPAGY
30230	60598	A	30414	1	1626	PSGREGCLIRESLKKILWLQAS AECEGDPGYFLSYFHQILLSFV ANTPRQGLGPPSAAGRRAMKK KLVLVGLLAVVLELVIVGLCL WLPSASKEPDNHVYTRAAVAA DANLCSKIGRDALRDGGSADV AAIAALLCVGLMNAHSMGIGG GLFLTIYNSTTRKAEVINAREV APRLAFATMFNSSEQSQKGGLS VAVPGEIRGYELAHQRHGRLP WARLFQPSIQLARQGFVVGKGL AAALENKRTVIEQQPVLCVFC RDRKVLREGERLTLPLADTYE TLAIEGAQAFYNGSLTAQIVKDI QAAGGIVTAEDLNRYRAELIEH PLNLSLGDVLYMPSAPLSGPV LALAILNLKGYNFSRESVESPEQ KGLTYHRIVEVFRFAYAKRTL LGDPKFVDVTEASSGVSAIVVR NMTSEFFAAQLRAQISDDTTTHPI SYKPEFYTPDDGGTAHLSVV AEDGS AVSATSTINLYFGSKVR SPVSGILFNNEMDGLSSPSITN EFGAPPSPANFIQPGKQPLSMC LTIMVGQDGGVVRMVVGAAGG TQITDTALAIYNLCFGYDVK RAVEEPRHLNKLPNVTTVERN IDQAVTAALETRHHHTQIASTFI ADVQAVIRTAGGWAASDRK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
30232	60600	A	30416	645	2571	GRPRLFPQLFPNPVFRGQHPR QGLGPSSAAGRRAKKKLVLV GLLAVVLVLVIVGLCLWLPSAS KEPDNHVYTRAAVAADAKQC SEIGRVLVGGPAYILLLGKAEV INAREVAPRLAFASMFNSSEQS QKGGLSVAVPGEIRGYELAHQ RHGRLPWARLFQPSIQLARQGF PVGKGLAAVLENKRTVIEQQPV LWYVCGKVLREGERLTLPLRA DTYEMLAIEGAQAFYNGSLMA QIVKDIQAAGGIVTAEDLNYYR AELIEHPLNISLGDVLYMP RLSGPV/LALILNILKGYNFSRES VETPEQKGLTYHRIVEAFRFAY AKRTLLGDPKFVDVTENSIAGL LCARMDSPALGSRQVVRNMTS EFFAAQLRSQISDHTTHPISYYK PEFYTPDDGGTAHLSVVAEDGS AVSATSTINLYFGSKVCSVPVSGI LFNNEMDDFSS/PAFTNEFGAPP SPANFIQPGKQPLLMSCLTIMV GQDQQVRMVVGAAGGTQITTD TALPPSHADHTPMQAIHYNLW FGYDVKRAVEEPRLHNKLLPN VTTVERNIDQAVTAALETRHH HTQIASTFIAVVQAIVRTAGGW AAALDSRKVPTPGAGFWEGLV EVGWWEAVITAQHLDIRGTG
30233	60601	A	30417	5	439	
30234	60602	A	30418	1	423	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,410,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
30235	60603	A	30419	97	2012	WADEETWLCLPHLPVFSPTAHL PLLSSPTFSSLLPFISTPHPRGFA LPLPPSARLYLELRKLPATLPWS SVTDTGSYLSGRRERGGEGERP GRRVRVADHGFALPRTGPOGS EEELANMQGLAVERLERAVSRL ESLSAESHRPPGN/CGEVNGVI A/GVAPSRGKPLHKLMDSMVA EFLKNSRILSGDVELAEIVHS AFQAQRAFLLMASQYQQPHEN DVVAALLKP/ISEKIKETQFQRE /RTRGSNMFNHL SAVSE*1PCPL DGIAYSPKPG/PYVVKEMNDAA TFYTNRVLKD*KQSDLRHVDW VKSYLENIWSELQAYIKEHHTTG LTWE/SKTGPVASTVSAFVSLS SGAWGFP PPPPLPPG/PPSTFS EEWKGKKESSPSR/SALFAQL N/QGEKAITKGLRHVTDDQKT YKNPSLRAQGGQTQSPTKSHTP SPTSPKSYPSQKHAPVLELEGK KWRVVEYQEDRIDLVISETELKQ VAYIFKCEKSTQIKGKVNSIID NCKKLLGLVFDNVVGIVEVINSQ DIQIQVMG/RVPTISINKTEGCH IYLSSEDALDCEIVSAKSIWKWN ILYPPQGWVD/YREFPHF/EQF KTS/AWDGSKLITEP/AEIMALT SLRDRTSPSPESIKTNKKA AVK
30236	60604	B	30420	1	499	
30237	60605	B	30421	390	851	
30238	60606	B	30422	136	603	
30239	60607	B	30423	1	2190	
30240	60608	A	30424	82	242	
30241	60609	A	30425	1	330	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
30242	60610	A	30426	215	1984	LLLVTMTSNNGLDIQDKPPAPP MRNTSTMIGAGSKDAGTLNHG SKPLPPNPEKKKKDRFYRSILP GDKTNKKKEKERPEISLPSDFE HTIHVGFDVAVTGFTGMPEQW ARLLQTSNITKSEQKKNPQAVL DVLEFYNSKKTSSNQKYMSTFS GDKSAHG YIAAHPSTKTASEP PLAPPVSEEEDEEEEDENEP PPVIAAPREHTKSIYTRSVVESIA SPA VNPKEVTPPSAENANSSTL YRNTDRQRKKSKMTDEEILEKL RSIVSVGDPKKKYTRFEKIGQG PSGTVYTAMD VATGQVEVAIKQ MNLQQQPKKELIINEILVMREN KNPNIVNYLDSYLVGDELWVV MEYLAGGSLTDVVTETCMDEG QIAAVCRECLQALEFLHSNQVI HRDIKSDNILLGMDGSVKLTDF GFCAQITPEQSKLSTHG*GTPY WMAPEVVDTERAYGPK/VLDI WSLGIMAIEMIEGPPYLNENP LRALYLIATNGTPELQNPEKL/S AIFRWFNLNRCLEMDVEKRGFS/ SKELLQHQLKIGQAPSPSLTPH *LLQPKKATKEQSPKTHTHPQP HCAQAFCEINAHFRNSNS
30243	60611	A	30427	2	337	
30244	60612	A	30428	1	1644	
30245	60613	A	30429	1	330	
30246	60614	A	30430	169	440	
30247	60615	A	30431	1	1689	
30248	60616	A	30432	17	283	GHAWQLASIWLLCLLWPAVPL NCLSSYGWTLWWRIALVGA*R SLAPSRGSWSTQARPLKQRRTK WCGKSWCLSGTSEPLSHWPRL RSW
30249	60617	A	30433	16	346	RTDTYHLEDSKEQSGNRAGSG GWL*SCAE/GRRVALKSWPGRT GMSGTRRV TASSRGTSWYCGG SAGRSSTPPTGRACSPGFSFSSPE PQPPGPSAAGSSVSQGLGPCGG
30250	60618	A	30434	1	1772	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
30251	60619	A	30436	1	2607	MLTMSVTLSPRLSQDLDPMAT DASPMANMTPTVEQEGEEA MKDMDSDQYKPPPLHTGAD WKIVLHLPETWLRMTSERVR DLTYSVQQSDSKHVDVHLVQ LKDICEDISDHVEQIHALLETEF SLKILSYSVNVIVDIHAVQILW HQLRVSVLVLRERILQGLQDAN GNYTRQTDILQAFSEETKEGRL DSLTEVDDSGQLTIKCSQNYLS LDCGITAFELSDYSPSEDLISGL GDMTSSQVKTCPFDWSYSEM EKEFPPELIRSVGLLTVAADSIST NGSEAVTEESVQVSLSDVDDKG GCEEDNASAVEEQPGLTLGVSS SSGEALTNAAPSETVQQESS SSSHHDAKNQPPVCENATPKR TIRDCFNYNEDSPTQPTLPKRGL FLKEETFKNLKGNGGKRQMV DLKPEMSRSTPSLVDPDRSKL CLVLQSSYPNPSAASQSYECL HKVGNNGLENTVKFHIKEISS LGRLENDYKEKSRLLKPKHTSE EVPPCRTPKRGTSQKQAKNT KSSAVPNGELSYTSCAIEGPQT NSASTSSLEPCNQRSWNALQL QSETSSPAFTQSESSVGSNDI MSPVPLLSKHKSKKGQASSPSH VTRNGEVVEAWYGSDEYLALP SHLKQTEVLALKLENLTKLLPQ KPRGETIQNIDDWELSEMNSDS EIPTYTHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	
30253	60621	B	30438	1	702	
30254	60622	B	30439	1	936	
30255	60623	B	30440	1	1494	
30256	60624	B	30441	1	921	
30257	60625	B	30442	1	3342	
30258	60626	B	30443	1	1072	
30259	60627	B	30444	1	3711	
30260	60628	B	30445	15	674	
30261	60629	B	30446	1	2127	
30262	60630	B	30447	1	3132	
30263	60631	B	30448	103	438	
30264	60632	B	30449	1	3042	
30265	60633	B	30450	1	1425	
30266	60634	B	30451	84	1954	
30267	60635	B	30452	1	1419	
30268	60636	B	30453	130	1615	
30269	60637	B	30454	1	1794	
30270	60638	B	30455	1	3255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
30271	60639	B	30456	1	945	
30272	60640	B	30457	1	7437	
30273	60641	B	30458	1	1122	
30274	60642	B	30459	317	1630	
30275	60643	B	30460	1	1716	
30276	60644	B	30461	46	915	
30277	60645	B	30462	1	624	
30278	60646	B	30463	244	2988	
30279	60647	B	30464	1	804	
30280	60648	B	30465	1	1455	
30281	60649	B	30466	1	732	
30282	60650	B	30467	340	777	
30283	60651	B	30468	1	714	
30284	60652	B	30469	166	1337	
30285	60653	B	30470	72	617	
30286	60654	B	30471	1	1002	
30287	60655	B	30472	1	4173	
30288	60656	B	30473	1	4488	
30289	60657	B	30474	1	3822	
30290	60658	B	30475	1	1866	
30291	60659	B	30476	1	1002	
30292	60660	B	30477	1	1407	
30293	60661	B	30478	99	1046	
30294	60662	B	30479	122	1113	
30295	60663	B	30480	302	4145	
30296	60664	B	30481	1	669	
30297	60665	B	30482	1	933	
30298	60666	B	30483	1	2136	
30299	60667	B	30484	1	4017	
30300	60668	B	30485	1	1335	
30301	60669	B	30486	1	1095	
30302	60670	B	30487	1	2895	
30303	60671	B	30488	1	1215	
30304	60672	B	30489	1	2001	
30305	60673	B	30490	1	1281	
30306	60674	B	30491	1	780	
30307	60675	B	30492	1	858	
30308	60676	B	30493	1	699	
30309	60677	B	30494	1	1624	
30310	60678	B	30495	1	2958	
30311	60679	B	30496	30	658	
30312	60680	B	30497	1	1755	
30313	60681	B	30498	1	631	
30314	60682	B	30499	1	1528	
30315	60683	B	30500	1	1056	
30316	60684	B	30501	1	2305	
30317	60685	B	30502	1	723	
30318	60686	B	30503	1	2691	
30319	60687	B	30504	1	2322	
30320	60688	B	30505	401	2677	
30321	60689	B	30506	1	1218	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30322	60690	B	30507	1	906	
30323	60691	B	30508	1	2865	
30324	60692	B	30509	45	820	
30325	60693	B	30510	1	783	
30326	60694	C	30511	18	410	
30327	60695	B	30512	1	840	
30328	60696	B	30513	1	945	
30329	60697	B	30514	1	2108	
30330	60698	B	30515	1	2457	
30331	60699	B	30516	1	1156	
30332	60700	B	30517	43	4677	
30333	60701	B	30518	80	964	
30334	60702	B	30519	1	4521	
30335	60703	B	30520	1	2460	
30336	60704	B	30521	1	1854	
30337	60705	B	30522	1	1367	
30338	60706	B	30523	273	419	
30339	60707	B	30524	1	1786	
30340	60708	B	30525	1169	1443	
30341	60709	B	30526	1	486	
30342	60710	B	30527	13	1260	
30343	60711	B	30528	270	723	
30344	60712	B	30529	1	834	
30345	60713	B	30530	1	1632	
30346	60714	B	30531	1	4831	
30347	60715	B	30532	184	1593	
30348	60716	B	30533	1	615	
30349	60717	B	30534	1	3513	
30350	60718	B	30535	113	1666	
30351	60719	B	30536	101	2667	
30352	60720	B	30537	1	1692	
30353	60721	B	30538	51	142	
30354	60722	B	30539	1	3198	
30355	60723	B	30540	251	1207	
30356	60724	B	30541	1	1491	
30357	60725	B	30542	1	4024	
30358	60726	B	30543	1	3316	
30359	60727	B	30544	1	1342	
30360	60728	B	30545	91	810	
30361	60729	B	30546	17	489	
30362	60730	A	30547	1	504	MGGSNRSAAEWKLANGINIIV TSGRLLDHMQNTPGFMYNLQ CLVIDEADRLDVGFEELKQII KLLLTNRQTMLFSATQTQKVE DLARISLKKPE/LYVGDDDDNA NETVFGVTLCTDVAARGLDITE VDCIVQYDPPDPKPEYHVSGR TARGLNGRENWVFAT
30363	60731	A	30548	1	2676	
30364	60732	B	30549	1	1071	
30365	60733	A	30550	1	348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
30366	60734	A	30551	1	711	MAEIQHKTRIRPLEGRDLLAAV KTGSGKTLAVLIPAIELVVKLF MPRNGTGVILSPTRQLAMQTF GVLKELMTHHVHTYGLIIGSN RSAEAQKLANGINIIIVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPCKEPLYVGVDEDKANATVD GLEQGHFVCPSEKRYLLFTFL KKNQKKKLMVFFSACMSVKYP YGLLYIDL/PVLAIHGKQKN KHTTTF*YCNADSGTLL
30367	60735	A	30552	661	987	VTFYSEHSNPNCHKNLKARRK DTKRIILKW*HTLV*GRDI*N*NI IITRNTYSLCPWATKKLKAC FISQK*KRDVIERNSAQCLQPKS IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	KFQGSNLTSETQNGDVSEET MGRKVKKKSKQKPMNVGLSET QNGGMSQEA VGNIKVTKSPQK STVLNTEAAMQSSNESKGGK MKKKRKMVNDAEPDTKKAKT ENKGSSEESAETTKETENNVE KPDNDESEVPSLPGLGTGAF EDTSFASLCLVNENTLKAIKE MGFTNMTETQHKSIIRPLEGRD LLAAAKTGSCKTLAFLIPAVELI VVKLRFMPRNGTGVILSPVRE LAMQTFGVKELMTHHVHTY LIMGGSNRSAEAQKLGNGINIIV ATPGRLLDHMQNTPGFMYKNL QCLVIDEADRLDVGFEEELKQI IKLLPTRRQTMFSATQTRKVE DLARISLKKELPYVGVDDDKA NATVDGLEQGYVVCPEKRFL LLFTFLKKNRKKKLMVFFSSCM SVKYHYELLNYIDL/PVLAIHGK QKQNKRTTTFQFCNADSG/TL LCTDVAARGLDIPEVDWIVQY DPPDDPKETVHRVG*EQPEGLN GEEGHALASFLRPRKDLGFFFR LL*KHSGFPLSGIWTFSW/SLK ISDIQFSAWRNWIGKVITFLHKS AQEAYKSYITEPMDSFPL*NRS FNIVNNLNLASGLLCQFGFK/VP PFVDLNVNSNEGKQKRGGGG GFGLPKRTQEKLEKS/KIF*TH* ARKSSGQAGQFSH

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 25 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/00, 15/12

US CL : 536/23.1, 23.5; 435/6, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.5; 435/6, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NONEElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)
NONE**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P ---	Database Genbank, Accession No. AL135937, 15 March 2001 (15.03.2001), particularly nucleotides 29925 through 30325.	1-8 ----- 9, 19
X ---	Database Genbank, Accession No. AA004350, HILLIER et al., Generation and analysis of 280,000 Human Expressed Sequence Tags. Genome Res. 07 May 1997 (07.05.1997), Vol. 6, No. 9, pages 807-828.	1-8 ----- 9, 19

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier applications or patent published on or after the international filing date
- *L* documents which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents; such combination being obvious to a person skilled in the art
- *Z* document member of the same patent family

Date of the actual completion of the international search

23 October 2001 (23.10.2001)

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

Box PCT

Washington, D.C. 20531

Facsimile No. (703)305-3230

Date of mailing of the international search report

02 JAN 2002

Authorized officer

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest

☐
☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I-III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct inventions.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.